

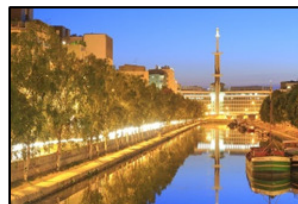


sfécologie2018

International Conference on Ecological Sciences

22-25th October 2018

Couvent des jacobins, Rennes, France





WELCOME AT SFECOLOGIE2018!

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WELCOME AT SF ECOLOGIE 2018!



Dear Colleagues,



We are delighted to welcome you at Rennes for the **Sfecologie2018**, an International Conference on Ecological Sciences (<https://sfecologie2018.sciencesconf.org/>) of the French Society of Ecology and Evolution ([Sfe²](http://sfe2.org/)). The conference is held at the historic Couvent des Jacobins (<http://centre-congres-rennes.fr/>), in the old part of the city of Rennes, ensuring convenient public transportation for the attendees.

This meeting will promote and support exchanges around the latest developments in research and the most exciting challenges raised from the different disciplines of ecology, and we hope that they will allow engaging and strengthening fruitful collaboration and intellectual exchanges.

So, we hope you will enjoy the Sfecologie2018 conference and will have a wonderful week in France!

Our warmest wishes from Rennes.

The organizing Committee

Chair of Sfecologie2018:

David RENAULT (UMR EcoBio, University Rennes 1/CNRS)



HAPPY BIRTHDAY SFE²

La SFE² a *50 ans* en 2018 !

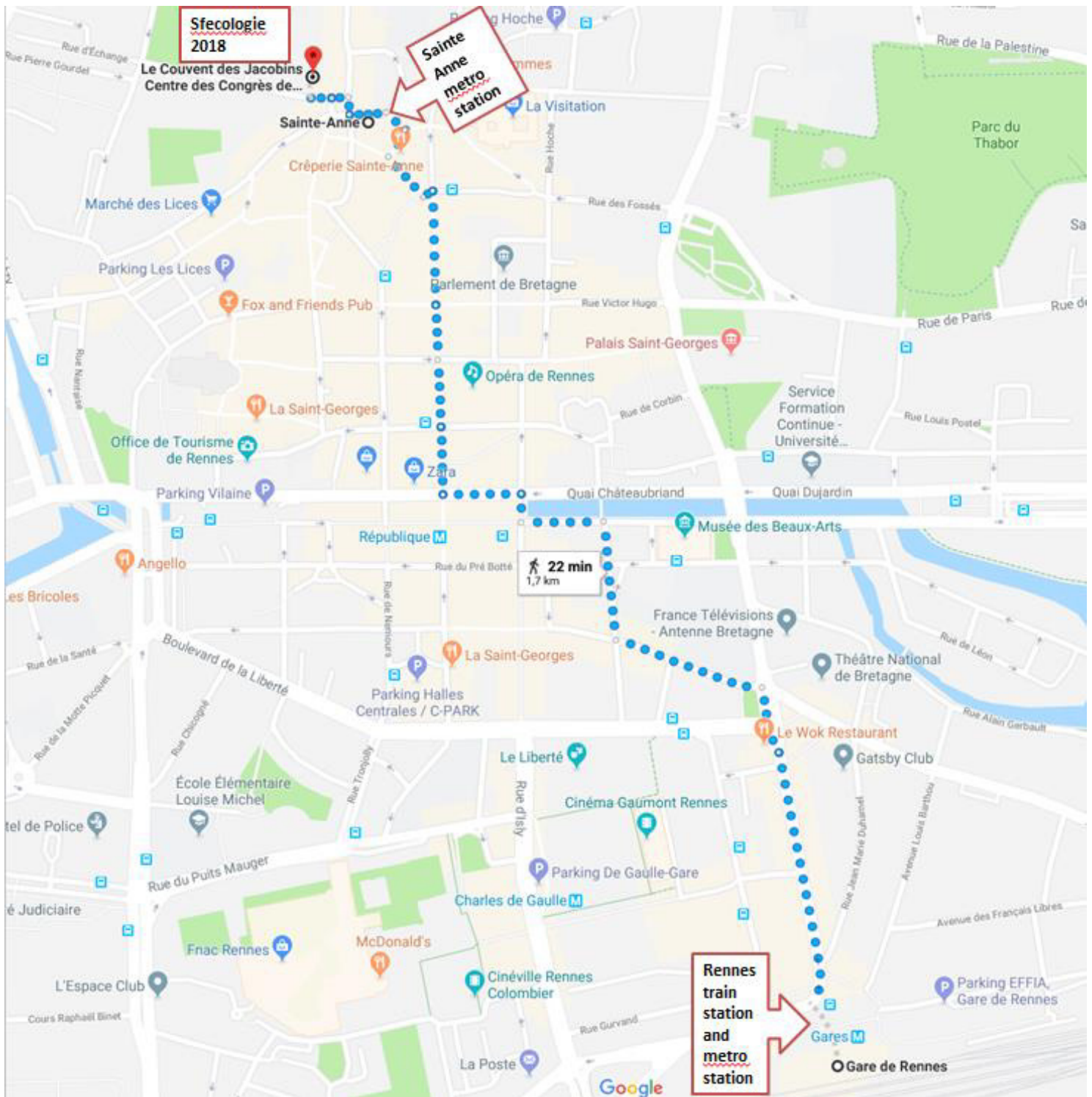
La Société Française d'Écologie et d'Évolution a été fondée en **1968**, en tant que Société d'Écologie. **En 2018 notre société a donc 50 ans** et, dans le même temps, **renait** sous la forme de Société Française d'Écologie et d'Évolution, manifestant ainsi la complémentarité entre ces deux communautés scientifiques. Cette année sera donc l'occasion de célébrer ce cinquantenaire, notamment lors du colloque [sfécologie2018](#) à Rennes!

La SFE² est une association loi 1901, reconnue d'utilité publique et membre de l'[European Ecological Federation](#) et d'[INTECOL](#). Elle a pour objectif de faire rayonner les sciences de l'écologie et de l'évolution en France en promouvant le développement, l'intégration et le partage des connaissances sous tous ses aspects. Elle représente l'ensemble de la communauté des écologues et évolutionnistes français et établit des actions communes avec les autres sociétés et associations pour que s'ouvre un vrai dialogue entre savoirs, impliquant scientifiques, gestionnaires, et usagers. [Adhérer](#) et [Soutenir la SFE²](#) c'est garantir la représentation de l'écologie et de l'évolution scientifiques dans les grands débats de notre société ainsi qu'un espace d'expression indépendant pour tous les chercheurs de ces sciences.





HOW TO COME TO THE CONFERENCE CENTER?



You can come by walking (blue dots on the map) or by metro (Leave the metro at the station St Anne).

The address of the conference Center 'Couvent des Jacobins' is:



HOW TO COME TO THE CONFERENCE CENTER?

20 Place Sainte-Anne, 35000 Rennes

Here is a picture of the conference center (you can see the people queuing at the main entry):





OVERVIEW OF THE ROOMS OF THE CONFERENCE CENTER

Niveau 3

2 salles de commission

Niveau 2

4 salles de commission

Niveau 1

5 salles de commission
Plateaux d'exposition/restauration

Niveau RDC

Auditorium de 400 places
3 salles de commission
Plateaux d'exposition/restauration
Le Déambulateur du Cloître
Le Jardin
2 espaces d'accueil

ENTRÉE PLACE SAINT-ANNE

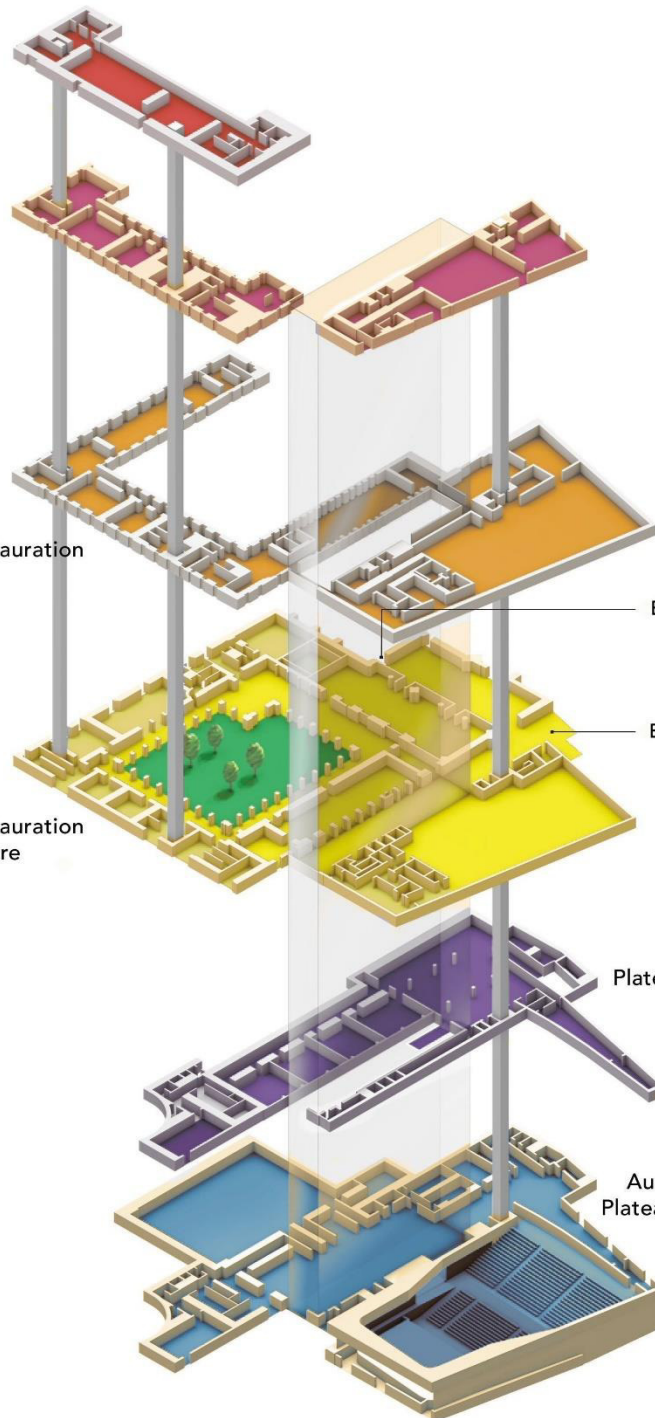
ENTRÉE RUE D'ÉCHANGE

Niveau -1

5 salles de commission
Plateau d'exposition/restauration

Niveau -2

Auditorium jusqu'à 1 200 places
Plateaux d'exposition/restauration
1 salle de commission



The sessions will take place in the auditorium (level -2), in rooms of level -1 (Salles de commission), in rooms at level 0 (RDC, salles de commission), and one room will be located at 'Le Déambulateur de Cloître'.



Audrey ALIGNIER (UMR BAGAP, INRA/Agrocampus Ouest/ESA)

Stéphanie AVIRON (UMR BAGAP, INRA/Agrocampus Ouest/ESA)

Valérie BRIAND (UMR EcoBio, CNRS/University of Rennes 1)

Anna BRIAND-BERGMANS (UMR EcoBio, CNRS/University of Rennes 1)

Anne-Marie CORTESERO (UMR IGEPP, INRA/Agrocampus Ouest/Université Rennes 1)

Marie-Agnès COUTELLEC (UMR ESE, INRA/Agrocampus Ouest)

Solène CROCI (UMR LETG, CNRS/University of Rennes 2)

Pierre-Yves LE BAIL (UR LPGP, INRA)

Alain Hervé LE GALL (OSUR)

Scott McCAIRNS (UMR ESE, INRA/Agrocampus Ouest)

Cécile MONARD UMR EcoBio, CNRS/University of Rennes 1)

Guénola PERES (UMR SAS, INRA/Agrocampus Ouest)

Isabelle PICOUAYS (UMR EcoBio, CNRS/University of Rennes 1)

David RENAULT (**Chair of Sfecologie2018**, UMR EcoBio, CNRS/University Rennes 1)

Sandra RIGAUD (UMR EcoBio, CNRS/University of Rennes 1)

Jean Marc ROUSSEL (UMR ESE, INRA/Agrocampus Ouest)

Jean-Christophe SIMON (UMR IGEPP, INRA/Agrocampus Ouest/Université Rennes 1)

Joan VAN BAAREN (UMR EcoBio, CNRS/University of Rennes 1)



The topics that were reviewed are put in brackets after the name of the experts.

1. ALIGNIER Audrey (Agroecology and ecology of agroecosystems, Ecological interactions, Soil Ecology)
2. ATLAN Anne (Interaction of ecological and social aspects in the categorization of spaces and species)
3. AUGER-ROZENBERG Marie-Anne (Biological invasions)
4. AVIRON Stéphanie (Agroecology and ecology of agroecosystems)
5. AYATA Sakina-Dorothee (Trait-based approaches in ecology)
6. BAGNERES Anne-Geneviève (Chemical ecology)
7. BERGEROT Benjamin (Landscape ecology, Urban Ecology)
8. BONIS Anne (Trait-based approaches in ecology)
9. CHABRERIE Olivier (Biological Invasions)
10. CHOLLET Simon (Conservation biology)
11. COLINET Hervé (Ecophysiology)
12. CORTESERO Anne-Marie (Chemical Ecology, Ecological interactions)
13. COUTELLE Marie-Agnès (Ecotoxicology and environmental pollution)
14. CROCI Solène (Urban ecology, Remote sensing)
15. DANIEL Hervé (Urban Ecology)
16. EDELIN Eric (Eco-evolutionary dynamics, Theoretical ecology)
17. EVANNO Guillaume (Conservation biology)
18. HAURY Jacques (The role of aquatic macrophytes in the functioning of freshwater ecosystems)
19. LAUNEY Sophie (Conservation biology)
20. LAVIALE Martin (Trait-based approaches in ecology)
21. LE GOUAR Pascaline (Spatio-temporal dynamics of ecosystems)
22. LE BAIL Pierre-Yves (Halieutic ecology, Tropical ecology)
23. LE LANN Cécile (Behavioural ecology)
24. McCAIRNS Scott (Epigenetics and environment, Evolution)
25. McDONNELL Mark (Urban Ecology)
26. MARGUERIE Dominique (Paleoecology: how today's ecosystems became what they are?)
27. MASSOL François (Eco-evolutionary dynamics, ecological interactions, theoretical ecology, tropical ecology)



28. MONARD Cécile (Population and community ecology: from micro to macroorganisms)
29. MONY Cendrine (Landscape ecology, Spatio-temporal dynamics of ecosystems)
30. MULLER Caroline (Chemical ecology)
31. NELLE Oliver (Paleoecology: how today's ecosystems became what they are?)
32. NEVOUX Marie (Conservation biology)
33. NICOLAI Annegret (Interaction of ecological and social aspects in the categorization of spaces and species, Participative science in ecology)
34. OUTREMAN Yannick (Behavioural ecology)
35. PERES Guénola (Agroecology and ecology of agroecosystems, Soil ecology)
36. PETIT Eric (Dispersal ecology)
37. PINCEBOURDE Sylvain (Ecophysiology)
38. PRINZING Andréas (Eco-evolutionary dynamics, Ecological interactions, Population and community ecology: from micro to macroorganisms)
39. RENAULT David (Behavioural ecology, Biological Invasions, Dispersal Ecology, Eco-evolutionary dynamics, Global changes and biodiversity, Polar ecology)
40. ROUSSEL Jean Marc (Conservation biology, Tropical ecology)
41. SIMON Jean-Christophe (Environmental genomics, Evolution, Holobionts and extended phenotypes)
42. THIEBAUT Gabrielle (The role of aquatic macrophytes in the functioning of freshwater ecosystems)
43. VAN BAAREN Joan (Behavioural Ecology)
44. VOITURON Yann (Ecophysiology)
45. WIEGAND Claudia (Ecotoxicology and environmental pollution)



INVITED SPEAKERS – Plenary sessions



Pr Axel Meyer

Department of Biology, University of Konstanz
Konstanz, Germany

Pr Axel Meyer studies the evolution of biodiversity, and specifically the origin of genomic, developmental and morphological diversity. In an effort to better understand adaptation and speciation, we mostly use evo-devo, molecular and bioinformatic approaches, to ask what kinds of genetic changes accompany morphological differentiation among populations and species. Specific questions include (1) patterns and processes of morphological differentiation and its developmental basis addressed within a phylogenetic framework, (2) genetic differentiation among populations and species, (3) the evolution of genes and genomes, and the evolution of novel gene functions. Most of the research on the genomics of adaptation and speciation is done on cichlid fishes from Africa and Nicaragua.



Pr David Tilman

Department of Ecology, Evolution and Behavior, University of
Minnesota, St. Paul, Minnesota, USA

Pr David Tilman, Distinguished Professor in the Bren School of UCSB and McKnight Presidential Chair in Ecology at the University of Minnesota, is an experimental and theoretical ecologist. His long-term and related theory showed that, and why, biodiversity is a major determinant of ecosystem stability, productivity, carbon storage and susceptibility to invasion. His recent work seeks solutions to major environmental problems, especially how the global impacts of agriculture on species extinction risks, greenhouse gas emissions, water pollution and human health can be reduced or eliminated while providing healthy diets for all the people of the Earth.

David Tilman is a member of the National Academy of Science and the American Academy of Arts and Sciences, and a foreign member of the UK's Royal Society. Other recognition includes the International Prize for Biology, the Heineken Prize for Environmental Sciences, the Balzan Prize in Plant Ecology and the BBVA Foundation's Frontiers of Knowledge Award.



Pr Teja Tschardtke

University of Göttingen, Germany

Teja Tschardtke is a professor of Agroecology at the University of Göttingen, Germany. His research focuses on biodiversity and community composition of plants and animals as well as multitrophic plant-insect interactions, including pollination and biological pest control in temperate and tropical regions. Particular attention is paid on the relative role of local and landscape effects on patterns and processes in land-use systems. Collaborative research on socioeconomic-ecological systems in human-dominated landscapes assesses the significance of biodiversity-related ecosystem services and landscape management. Teja Tschardtke published >350 papers and is "Highly Cited Researcher" (according to the Web of Science)



INVITED SPEAKERS

Concurrent thematic sessions: introducing our keynote speakers



Ass. Pr Mark McDonnell

Australian Research Centre for Urban Ecology, University of Melbourne, Victoria, Australia

Associated Pr Mark McDonnell has been a scientist at the New York Botanical garden where he developed urban studies from New York City up to the north of New York State. He was at the origin, among others, of the long term ecological sites in the US. He worked on a transect from relatively natural landscapes to human dominated ones. He then moved to Australia in 1998 and is the director of the Australian research center for urban ecology. He published several books on the subject among which "ecology of cities and towns, published in 2009 by Cambridge university press.

Session: Urban Ecology, Landscape ecology



Pr Nancy Moran

Department of Integrative Biology University of Texas Austin, USA

Pr. Nancy A. Moran is the Leslie Surginer Endowed Professor in the Department of Integrative Biology at the University of Texas at Austin. She completed her doctoral degree in Zoology (1982) at the University of Michigan, where she studied with Richard D. Alexander and William D. Hamilton. She previously served on the faculties of the University of Arizona and Yale University. She is a member of the US National Academy of Sciences, a fellow of the American Academy of Arts and Sciences, and a recipient of the 2010 International Prize for Biology. Moran studies genome evolution, insect biology, and endosymbiosis, with a focus on the ecology and genetics of symbiotic bacteria in insects.

Session: Holobiont, Extended phenotypes



INVITED SPEAKERS



Pr Caroline Müller

Department of Chemical Ecology, Bielefeld University
Bielefeld GERMANY

Caroline Müller is professor of Chemical Ecology at Bielefeld University, Germany. Caroline Müller investigates the role of natural products involved in the communication between plants and other organisms, such as chewing and sucking herbivorous insects, nematodes and arbuscular mycorrhiza. She combines chemical-analytical tools (untargeted and targeted metabolomics) with bioassays testing insect behavioural phenotypes and performance to elucidate the ecological and evolutionary basis of interactions between organisms, including invasive species. She is particularly interested in the tissue-specific variation in plant responses to challenges and in the role of various abiotic and biotic factors in modulating plant-antagonist interactions. Her teaching activities comprise lectures and practical courses in chemical ecology, ecology and botany. Currently, she is associate editor of *Oecologia*, editorial board member of *Phytochemistry* and advisory board member of *Chemoecology*.

Session: Chemical ecology



Dr Christina Richards

Department of Integrative Biology, University of South
Florida, Tampa, USA

Dr Christina Richards attended Swarthmore College in Swarthmore, Pennsylvania receiving a B.A. in Biology in 1995. She completed a Ph.D. degree at the University of Georgia in 2004 with a dissertation entitled "Evolution in closely adjacent salt marsh environments." She began her independent career with an appointment in the Integrative Biology department at the University of South Florida after working as a postdoctoral researcher at Stony Brook University and New York University. Her research has focused on developing and incorporating genomics tools and approaches into robust ecological experiments in a variety of model and non-model plants. These approaches are particularly insightful for understanding how organisms respond to the ecological and evolutionary challenges of natural and human altered environments.

Session: Epigenetics, phenotypic plasticity



INVITED SPEAKERS



Pr David Richardson

DST-NRF Centre of Excellence for Invasion Biology,
Stellenbosch University, Stellenbosch, SOUTH AFRICA

Dave Richardson is Director of the DST-NRF Centre of Excellence for Invasion Biology and is a Distinguished Professor of Ecology at Stellenbosch University, South Africa. His research focuses mainly on plant invasions, especially trees and shrubs. The genus *Pinus* has featured prominently in his work. He is author/co-author of about 400 peer-reviewed journal papers and chapters in edited books. He has edited/co-edited six books, including *Ecology and biogeography of Pinus* (Cambridge University Press; 1998) and *Fifty years of invasion ecology* (Wiley-Blackwell, 2011) and is co-author of *Invasion Dynamics* (Oxford University Press; 2017). He was Editor-in-Chief of the journal *Diversity and Distributions* between 1998 and 2015, and is Associate Editor or editorial board member for several journals including *Biological Invasions*. He was awarded the Hans Sigrist Prize for 2006 by the University of Bern, Switzerland. In 2012 he received the John F.W. Herschel Medal, the senior medal of the Royal Society of South Africa.

Session: Biological invasions



Pr Chris Thomas

Department of Biology, University of York
York, UK

Pr Chris Thomas works on the ecology, evolution and conservation of biodiversity in the Anthropocene. Chris is interested in understanding how humans have transformed the biological world, and how we might protect the world's remaining biodiversity. More broadly, he researches why some species decline and disappear but others are successful, aiming to quantify gains in biological diversity as well as losses; the topic of his recent book, *Inheritors of the Earth: how nature is thriving in an Age of Extinction*. His work is widely cited, and has influenced the development of national and international policies for conservation and climate change, including inputs to the Intergovernmental Panel on Climate Change, International Union for the Conservation of Nature, conservation NGOs, and UK governmental reviews and agencies. Chris is a Professor at the University of York, in England, and a Fellow of the Royal Society.

Symposium: Tracking environmental changes



INVITED SPEAKERS



Pr Nico van Straalen

Vrije Universiteit, Amsterdam, HOLLAND

Nico M. van Straalen is a professor of Animal Ecology at Vrije Universiteit Amsterdam. He studies the effects of contaminants on soil-living invertebrates and the microbial communities associated with them, including evolutionary adaptation and mechanisms of resistance. He is especially interested in genetic variation and genome organization of invertebrates and how lateral gene transfer has expanded their capacity of surviving in a microbe-dominated world. In Amsterdam Nico teaches evolutionary biology, ecology, ecotoxicology, ecogenomics and human evolution.

Session: Ecotoxicology



TALKS - Tuesday (October 23rd)

Tuesday, October 23, 2018

08:00	Welcome Coffee								
09:00	Opening Ceremony - S. Thiébaud (InEE-CNRS), M. Tixier-boichard (INRA), JF. Carpentier (University of Rennes 1), J. van Baaren (UMR EcoBio), S Barot (SFE ²) > Auditorium								
10:00	Plenary session > Auditorium								
10:15	Coffee break								
11:00	Biological invasions <i>Moderator: David Richardson</i> > Room 1	Participative sciences in ecology <i>Moderator: Annegret Nicolai</i> > Room 5	Behavioural and dispersal ecology <i>Moderator: Bregje Wertheim</i> > Room 2	Trait-based approaches in ecology <i>Moderators: Sakina Ayata & Martin Laviale</i> > Room 3	Population and community ecology, from micro to macroorganisms <i>Moderator: Andreas Prinzing</i> > Room 4	Conservation biology <i>Moderator: Emma Jeavons</i> > Room 9	Holobiont and extended phenotype <i>Moderator: Nancy Moran</i> > Room 7	Agroecology and ecology of agroecosystems <i>Moderator: Alison Specht</i> > Auditorium	All you can eat: perspectives in nutritional ecology (Symposium) <i>Moderator: Apostolos-Manuel Koussoroplis</i> > Room 8
13:00	Lunch								
14:00	Session Jeunes Ecologues <i>Julia Clause, Pierre Quévieux</i> > Room 1								
15:00	Biological invasions <i>Moderator: David Richardson</i> > Room 1	Behavioural and dispersal ecology <i>Moderator: Bregje Wertheim</i> > Room 2	Trait-based approaches in ecology <i>Moderators: Sakina Ayata & Martin Laviale</i> > Room 3	Population and community ecology, from micro to macroorganisms <i>Moderator: Javier Fernandez-de-Simon</i> > Room 4	Conservation biology <i>Moderator: Sébastien Gallet</i> > Room 9	Ecosystem services in agricultural landscape <i>Moderators: Francisca C. Aguiar & Manuel Plantagenest</i> > Room 8	Holobiont and extended phenotype <i>Moderator: Nancy Moran</i> > Room 7	Eco-evolutionary feedback loops in theory and practice: an assessment of how synthetic the newest synthesis has come to be (Symposium) <i>Moderator: Eric Edeline</i> > Auditorium	Monitoring biodiversity: the essential biodiversity variables framework (Symposium) <i>Moderator: Denis Couvet</i> > Room 5
17:00	Poster session > Room 1	Inside event - Networking INRA EFPA (EGP) > Room 2	Inside event - Networking INRA EFPA (Prairies) > Room 7	Inside event - Networking INRA EFPA (RSYST) > Room 5	Inside event - Networking CESAB <i>Moderators: Alison Specht, Sébastien Barot</i> > Room 1	Inside event - Networking SFE² Heredity > Room 3	Inside event - Networking SFE² Ecology and Agriculture > Room 4	Inside event - Networking 'How do animal use space?' > Room 8	
18:00									
19:00									



TALKS - Wednesday (October 24th)

Wednesday, October 24, 2018

08:00	<p>>8:00 (30mn)</p> <p style="text-align: center;">Welcome Coffee</p>									
	<p>>8:30 (1h)</p> <p style="text-align: center;">Plenary session</p>									
09:00	> Auditorium									
	<p>>9:30 (45mn)</p> <p style="text-align: center;">Coffee break</p>									
10:00	<p>>10:15 (2h)</p> <p>Biological invasions Moderator: Maud Bernard-Verdier</p>	<p>>10:15 (2h)</p> <p>Behavioural and dispersal ecology Moderator: Cécile Le Lann</p>	<p>>10:15 (2h)</p> <p>Trait-based approaches in ecology Moderators: Sakina Ayata & Martin Laviale</p>	<p>>10:15 (2h)</p> <p>Urban ecology Moderator: Mark McDonnell</p>	<p>>10:15 (2h)</p> <p>Global changes and biodiversity Moderator: Virginia Iglesias</p>	<p>>10:15 (2h)</p> <p>Epigenetics, phenotypic plasticity and physiological ecology Moderator: Christina Richards</p>	<p>>10:15 (2h)</p> <p>Agroecology and ecology of agroecosystems Moderators: Audrey Alignier & Stéphanie Aviron</p>	<p>>10:15 (2h)</p> <p>The role of aquatic macrophytes in the functioning of freshwater ecosystems Moderators: Anniët Laverman & Gabrielle Thiébaud</p>	<p>>10:15 (2h)</p> <p>Spatio-temporal dynamics of ecosystems, restoration ecology Moderator: Armin Bischoff</p>	
11:00										
12:00	> Room 1	> Room 2	> Room 3	> Room 9	> Room 4	> Room 8	> Auditorium	> Room 7	> Room 5	
	<p>>12:15 (1h30)</p> <p style="text-align: center;">Lunch</p>		<p>>12:30 (1h15)</p> <p>Peer Community In (PCI) Ecology et PCI Evolutionary Biology Thomas Guillemaud</p>			<p>>12:30 (1h15)</p> <p>Atelier RAP (Analyse citoyenne des données) Sylvie Blangy, Isabelle Chuine</p>		<p>>12:45 (55mn)</p> <p style="text-align: center;">Meet SFE²</p>		
13:00			> Auditorium			> Room 8		> Room 2		
14:00	<p>>14:00 (2h15)</p> <p>Current challenges in landscape ecology: habitat amount, landscape connectivity, landscape history (Symposium) Moderator: Laurent Bergès</p>	<p>>14:00 (2h15)</p> <p>Does evolution matter for ecosystem ecology? (Symposium) Moderator: Isabelle Gounand</p>	<p>>14:00 (2h15)</p> <p>Tracking environmental variability and global changes (Symposium) Moderator: David Renault</p>	<p>>14:00 (2h15)</p> <p>Fisheries ecology: Using models to understand and predict human impacts on aquatic ecosystems (Symposium) Moderator: Didier Gascuel</p>	<p>>14:00 (2h15)</p> <p>Conservation biology Moderator: Irène Till-Bottraud</p>	<p>>14:00 (2h15)</p> <p>Ecological interactions Moderator: Andreas Prinzing</p>	<p>>14:00 (2h15)</p> <p>Agroecology and ecology of agroecosystems Moderator: Armin Bischoff</p>	<p>>14:00 (2h15)</p> <p>Theoretical ecology Moderators: Jean-Sébastien Pierre & Fabien Laroche</p>	<p>>14:00 (2h)</p> <p>Environmental genomics Moderators: Samuel Chaffron & Eric Pelletier</p>	
15:00										
16:00	> Room 3	> Room 8	> Room 1	> Room 7	> Room 9	> Room 4	> Auditorium	> Room 2	> Room 5	
	<p>>16:15 (2h)</p> <p>Poster session</p>	<p>>16:15 (2h)</p> <p>Inside event - Networking SFE² Interactions durables</p>	<p>>16:15 (2h)</p> <p>Interaction of ecological and social aspects in the categorization of spaces and species Moderator: Anne Atlan</p>	<p>>16:15 (2h)</p> <p>Halieutic and marine ecology Moderators: Hilaire Drouineau & Pierre-Yves Hervann</p>	<p>>16:30 (2h)</p> <p>Inside event - Networking SFE² Landscape Ecology</p>		<p>>16:30 (2h)</p> <p>Epigenetics, phenotypic plasticity and physiological ecology Moderator: Patricia Gibert</p>	<p>>16:30 (2h)</p> <p>Inside Event - Workshop 'Réseau des Zones Atelier' Sabrina Gaba</p>	<p>>16:30 (2h)</p> <p>Theoretical ecology Moderators: Jean-Sébastien Pierre & Fabien Laroche</p>	<p>>16:30 (2h)</p> <p>Environmental genomics Moderators: Denis Faure & Jean-Christophe Simon</p>
17:00		> Room 1	> Room 9	> Room 7	> Room 3	> Room 8	> Room 4	> Room 2	> Room 5	
18:00	<p>>19:00 (4h)</p> <p style="text-align: center;">Closing Gala</p>									
19:00										
20:00										



TALKS - Thursday (October 25th)

Thursday, October 25, 2018

08:00	Welcome Coffee									
09:00	Plenary session									
10:00	Coffee break									
11:00	Paleoecology: How todays ecosystems became what they are? Moderators: Oliver Nelle, Stéphanie Thiébaud > Room 3	Urban ecology Moderator: Mark McDonnell > Auditorium	Global changes and biodiversity Moderator: Julie Bjorge > Room 1	Ecological interactions Moderator: Andreas Prinzing > Room 4	Pollination in the Anthropocene (Symposium) Moderator: Bertrand Schatz > Room 7	Biotic interactions under abiotic constraints: from molecular to ecosystem level (Symposium) Moderators: Cécile Le Lann & Cécile Sulmon Room 2	Resilience in long-term social-ecological systems research sites (Symposium) Moderators: Sabrina Gaba & Camille M... Room 9	Agroecology and ecology of agroecosystems Moderator: Julien Pétilion > Room 8	Evolution Moderator: Malika Ainouche > Room 5	
12:00										Landscape ecology > Auditorium
13:00	Lunch									
14:00	Paleoecology: How todays ecosystems became what they are? Moderators: Dominique Marguerie & Stéphanie Thiébaud > Room 3	Landscape ecology Moderator: Fabien Laroche > Room 9	Global changes and biodiversity Moderator: Stéphane Boyer > Room 1	Ecological interactions Moderator: Olivier Chabrerie > Room 4	Chemical ecology Moderator: Caroline Muller & Anne-Marie Cortesero > Room 2	Tropical ecology Moderator: Julien Pétilion > Room 7	Soil ecology Moderator: Guénola Pérès > Room 8	Eco-evolutionary dynamics Moderator: Andreas Prinzing > Room 5	Ecotoxicology and environmental pollution Moderators: Nico Van Straalen & Marie-Agnès Coztales Auditorium	
15:00										
16:00	Paleoecology: How todays ecosystems became what they are? Moderators: Oliver Nelle, Stéphanie Thiébaud > Room 3	Landscape ecology Moderator: Fabien Laroche > Room 9	Global changes and biodiversity Moderator: Georges Kunstler > Room 1	Ecological interactions Moderator: Olivier Chabrerie > Room 4	Chemical ecology Moderator: Caroline Muller & Anne-Geneviève Bagnères > Room 2	Tropical ecology Moderator: Kévin Cilleros > Room 7	Soil ecology Moderator: Guénola Pérès > Room 8	Eco-evolutionary dynamics Moderator: Eric Petit > Room 5	Ecotoxicology and environmental pollution Moderators: Nico Van Straalen & Scott McCaig Auditorium	
17:00										



SYMPOsia

Symposia will put a spotlight on a specific topic, and will include a timely review of the literature, as well as perspectives presented by leaders in the particular field.

- Monitoring Biodiversity: the Essential Biodiversity Variables Framework (Main organiser: Aurélie DELAUAUD)

[Read more here](#)

- Current Challenges in Landscape Ecology: Habitat Amount, Landscape Connectivity, Landscape History (Main organiser: Laurent BERGES)

[Read more here](#)

- Ecological Models in Fisheries Sciences: From Knowledge to Management (Main organiser: Didier GASCUEL)

[Read more here](#)

- Eco-evolutionary Feedback Loops in Theory and Practice: an Assessment of How Synthetic the Newest Synthesis Has Come to Be (Main organiser: Eric EDELINE)

[Read more here](#)

- Does Evolution Matter for Ecosystem Ecology? (Main Organiser: Isabelle GOUNAND)

[Read more here](#)

- Resilience in Long-Term Social-Ecological Systems Research Sites (Main organisers: Sabrina GABA and Camille MAZE)

[Read more here](#)

- Biotic Interactions Under Abiotic Constraints: from Molecular to Ecosystem Level (Main organiser: Cécile SULMON)

[Read more here](#)

- Pollination in the Anthropocene (Main organiser: Bertrand SCHATZ)

[Read more here](#)

- All You Can Eat: Perspectives in Nutritional Ecology (Main Organiser: Apostolos-Manuel KOUSSOROPLIS)

[Read more here](#)

- Tracking Environmental Variability and Global Changes (Main organiser: David RENAULT)

[Read more here](#)



POSTER SESSION - Tuesday (October 23rd)

Behavioural and dispersal ecology

Presenters

- 1 Hatching event influences long-term decisions of pied avocets (*Recurvirostra avosetta*) Chambon Rémi
- 2 The genomic response to male courtship and kin avoidance during mate choice in the parasitoid wasp *Venturia canescens*. Gallot Aurore
- 3 Impacts of light pollution on energy reserves and state-dependent decision-making in a parasitic wasp Gomes Elisa
- 4 Common drivers of seasonal movements on the migration? residency behavior continuum in a red deer Saïd Sonia

Biological invasions

- 5 Restricted gene flow and strong genetic drift in an invasive species Bélouard Nadège
- 6 Life at the expanding front: Freshwater invasive clams reproduce earlier in populations with reduced per capita rate of increase Bonel Nicolás
- 7 Contribution to the study of Phlebotomine (Diptera: Psychodidae) in the region of Tizi Ouzou Brahmi Karima
- 8 Empirical evidence that *P. antipodarum* is a low quality food for fishes Butkus Rokas
- 9 To control or not to control: when the ecological costs of management-driven phenotypic changes counterbalance the benefits of invasive species removal Cucherousset Julien
- 10 Global economic costs of invasive species Diagne Christophe
- 11 Behavioural responses to control practices: lessons from common mynas Diquelou Marie
- 12 Cold acclimation triggers major transcriptional changes in *Drosophila suzukii* Enriquez Thomas
- 13 Bee hotels as a tool to monitor the expansion of the exotic bee *Megachile sculpturalis* Geslin Benoit
- 14 Challenges and Difficulties of sharing data on biological invasions management Hudin Stéphanie
- 15 Do native birds drive away invasive birds from urbanised Australia? Lermite Françoise
- 16 Water primrose, an evolutionary success? Portillo Luis
- 17 Native versus invasive strains of *Drosophila suzukii* : changes in life history traits Prevost Genevieve
- 18 Invasion success of Black cherry (*Prunus serotina*) in Europe: importance of root traits and associated mycorrhizae Tardif Antoine
- 19 Morphological variations of *Myriophyllum heterophyllum*, a new invader in French freshwaters Thiebaut Gabrielle



Conservation biology

- | | | |
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| 20 | Increasing disturbance: the challenge of conserving the last subpopulations of endangered megafauna in the southeast of Nicaragua. | Dans Chavarria Armando |
| 21 | Phytoecological study of <i>Rhus pentaphylla</i> (Anacardiaceae) groups in north-western Algeria. | Hassani Faïçal |
| 22 | Density-dependent detectability of a vulnerable beetle species in hollow trees | Laroche Fabien |
| 23 | An individual based model to optimize population introductions. Applications to conservation biology and biological control. | Mailleret Ludovic |
| 24 | Climate sentinels research program : the effects of climate change on biodiversity in the region of New Aquitaine (South-West, France) | Mallard Fanny |
| 25 | Macroinfauna diversity associated to seagrass meadows on the northeast of Cancún, Quintana Roo, México | Martinez Ochoa Francisco |
| 26 | Integrating niche models into demographic studies: a step forward to reconcile conservation and niche models | Monnet Anne-Christine |
| 27 | Semantic management and valorisation of data from biodiversity and ecosystem studies within the AnaEE-France research infrastructure | Pichot Christian |
| 28 | Population dynamics of the highly endangered <i>Eryngium viviparum</i> within its last French locality. | Rasclé Pauline |

Environmental genomics

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| 29 | Evolutionary dynamics of repeated sequences in polyploid <i>Spartina</i> species | Giraud Delphine |
| 30 | Differential gene expression revealed with RNA-Seq and parallel genotype selection of the Ornithine Decarboxylase gene in fish inhabiting polluted areas | Vega-Retter Caren |

Epigenetics, phenotypic plasticity and physiological ecology

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| 31 | Cardiac activity, filtration and respiration rates as non-invasive physiological indicators of the oyster (<i>Crassostrea gigas</i>) susceptibility during a disease event | Alunno-Bruscia Marianne |
| 32 | Comparative study of the resilience capacity of different populations of <i>Alphitobius diaperinus</i> exposed to different durations of thermal stress | Bjorge Julie |
| 33 | How migration ecology may influence hormonal status in birds ? | Dillenseger Guillaume |
| 34 | What determines the interannual variability of fecundity in holm oak (<i>Quercus ilex</i> L.)? | Le Roncé Iris |



POSTER SESSION - Tuesday (October 23rd)

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| 35 | Respirometry of ground beetles according to increasing weights | Le Roux Vincent |
| 36 | The tolerance to low temperature of tropical cockroach <i>Gromphadorhina coquereliana</i> | Lubawy Jan |
| 37 | Changes in accumulation of essential macronutrients during vegetative growth of rapeseed exposed to NaCl | Putnik Delic Marina |
| 38 | Microcalorimetry : a powerful tool to investigate stoichiometric constraints on small ectotherms | Ruiz Thomas |
| 39 | Morphological responses of the invasive species <i>Elodea canadensis</i> and <i>Elodea nuttallii</i> under salt pulses. | Thiebaut Gabrielle |
| 40 | Metatranscriptomic profiling of microbial consortia during root colonization in a gnotobiotic system. | Vannier Nathan |

Halieutic and marine ecology

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| 41 | Genetic connectivity and local adaptation of a Mediterranean Brown seaweed. | Reynes Lauric |
| 42 | Mapping the kelp distribution area of the Sept-Iles marine reserve (Brittany, France) using hydroacoustics | Martignac François |
| 43 | Sources partitioning in the diet of the shipworm <i>Bankia carinata</i> (Gray, 1827): an experimental study based on stable isotopes | Charles François |
| 44 | Towards faster and less efficient biomass transfers in marine food webs? | Du Pontavice Hubert |
| 45 | Feeding marine ecosystem models from the space: improving realism of trophic models using satellite-derived zooplankton favourable habitats | Hervann Pierre-Yves |
| 46 | Trophic links between macrobenthic invertebrates and demersal fish communities in the Mont Saint-Michel macrotidal estuary prior to dams removal on the Sélune river | Roussel Jean Marc |
| 47 | Determining long-term ray community changes in the Bay of Biscay using grouped landings and limited species data | Trenkel Verena |

Holobiont and extended phenotype

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| 48 | New Insights into the Nature of Symbiotic Associations in Aphids: the Case of Gut-Associated <i>Serratia symbiotica</i> | Pons Guillouard Inès |
| 49 | Microbial interactions in mosquito microbiomes: Patterns in presence and absence of WNV infection | Rodriguez-Ruano Sonia M |



POSTER SESSION - Tuesday (October 23rd)

- 50 Impact of various land uses and the associated practices of management, on earthworm communities in the urban soils of Ile-de-France via an approach of participative science Guillocheau Sarah
- 51 French national long-term monitoring program to assess earthworms' response to the agricultural practices in farmlands Guillocheau Sarah
- 52 The Herbonauts website: a citizen science project to acquire plant metadata over the four past centuries, from herbarium collections Invernon Vanessa
- 53 First Bioblitz on a French campus: Rapid biotic and abiotic inventory at Campus Beaulieu of the University Rennes Nicolai Annegret
- 54 Influence of taxonomical resolution on mutualistic network properties Renaud Estelle
- 55 Expeditionary Learning: High school students investigate aspects of landscape and marine ecology Schöps Katrin

Population and community ecology, from micro to macroorganisms

- 56 Top-down control of prokaryotic population in temperate freshwater systems (French Massif Central) Angia Sriram Pradeep Ram
- 57 Population genetics structure of a desert-adapted Hindu sacred tree: *Prosopis cineraria* Baibout Myriam
- 58 The Ascochyta blight Complex on pea: Competition between different strains of two pathogenic fungi exhibiting different life history strategies Dutt Agathe
- 59 Transgenerational plasticity in response to competition in clonal plants Hervé Alix
- 60 Local foraging habitat selection as a tool for measuring spatial partitioning of two sympatric seal species *Halichoerus grypus* and *Phoca vitulina* in the Northeast Atlantic Huon Mathilde
- 61 Response of carabid communities to tree species mixtures in the context of climate change Jouveau Séverin
- 62 Use of sterols as biomarkers of trophic relationships in a mountain headwater stream. Labeled-Veydert Tiphaine
- 63 Comparison of species and individual fish habitat selection models in rivers Plichard Laura
- 64 Vegetative sprouting responses of cork oak (*Quercus suber* L.) in relation to fire damage in the Beni Ghobri forest (North center, Algeria) Sahar Ouahiba



Remote sensing in ecology

- 65 Assessment of Worldview 2 imagery for long term monitoring of fast evolving Natura 2000 coastal habitats Campagna Julie
- 66 Large scale monitoring of grassland biomass dynamics with Sentinel-2 satellite images Jabot Franck

Restoration ecology

- 67 REaménagement de Carrière ALLuvionnaire (RECALL): ecological diagnostic of alluvial quarries as part of their rehabilitation De Wilde Mélissa
- 68 Ecological restoration and plant succession of dry grasslands in the Haute-Durance valley following soil disturbance Durbecq Aure
- 69 Indicators development to evaluate wetlands restoration actions for managers Hudin Stéphanie
- 70 Annual seed rain dynamics in degraded and preserved areas of a tropical grassland Jardim Arruda Andre
- 71 Restoration of Mediterranean dry grasslands in photovoltaic power stations? the effect of solar panels Lambert Quentin
- 72 Use of ecological and geomorphological processes to assess the resilience of stream ecosystem functions after hydromorphological restoration Piscart Christophe

Soil ecology

- 73 Spatial dependence of soil organic carbon, abundance, biomass and diversity of earthworms in 15 temperate agroforestry systems Hoeffner Kevin
- 74 Feeding behavior of epi-anecic earthworm species and their impact on soil microbial communities Hoeffner Kevin
- 75 Influence of organic matter and land use on the evolution of Technosols properties constructed with urban wastes Lerch Thomas
- 76 The presence or absence of copper in the interactive arbuscular mycorrhizal fungi-microbial diversity-plant community relationships Mortazavi Ardestani Masoud
- 77 Relationships between above ground and below ground soil biodiversity in agroecosystems - from functions to ecosystem services Pérès Guénola



Spatio-temporal dynamics of ecosystems

- 78 Faune des Hydrachnidia (Acari: Hydrachnellae) de la région de Collo (Nord-est Algérie): Répartition spatio-temporelle et corrélation avec les facteurs du milieu. Boudemagh Nour El Houda
- 79 Spatio-temporal structural equation modeling in a hierarchical Bayesian framework: ecology of wet heathlands Damgaard Christian
- 80 Hedgerow networks monitoring in France : from the map to the field Morin Pinaud Sophie

The role of aquatic macrophytes in the functioning of freshwater ecosystems

- 81 Aquatic Plants Research, Teaching and Pedagogic Innovation: How several lanes could merge into a single one for mutual benefits. Combroux Isabelle
- 82 Reduction of wet grassland biodiversity due to Water Primrose proliferation in the « Marais Poitevin » (France) Douchin Gaëtan
- 83 How physical heterogeneity of water masses in large shallow lakes shapes plankton community? Roose-Amsaleg Céline

Theoretical ecology

- 84 Modelling the dynamic of forest plant metacommunities Delvoye Gauthier
- 85 Concepts and measures of diversity, rarity and originality in ecology and evolution Kondratyeva Anna
- 86 Stabilizing niche differences are still required to maintain species-rich communities in temporally variable environments Picoche Coralie

Urban ecology

- 87 Trait-based approaches in aquatic ecology: a common language for freshwater and marine ecologists? Martini Séverine
- 88 Diversity-function relationships in contaminated soils ? A functional trait approach Maunoury-Danger Florence
- 89 Using ecomorphology and functional traits to understand the efficiency of a selective device in a multi-species fishery Mouchet Maud
- 90 Growth success of seedlings of different populations of *Ludwigia hexapetala* and *Ludwigia peploides* subsp. *montevidensis*. Thiebaut Gabrielle



Urban ecology

- | | | |
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| 91 | Severity of human-rhesus macaque conflict in urban landscape and possible mitigation strategies in Delhi NCR, India | Chauhan Netrapal |
| 92 | Characterization of earthworm communities in reconstituted anthropic soils of urban areas | Guillocheau Sarah |
| 93 | Impact of urbanisation on entomophile plants and pollinators | Lesturgie Pierre
Leve Marine |
| 94 | From weeds to cultivated flora : turnover of floral resources in domestic gardens is linked to environmental rather than human characteristics | |



Agroecology and ecology of agroecosystems

Presenters

- | | | |
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| 1 | Diversification of crop and non-crop vegetation in agricultural landscapes: a benefit for the diversity of pollinator communities ? | Airon Stéphanie |
| 2 | Disentangling the relative effects of semi-natural elements and organic farming practices to enhance biodiversity in agricultural landscapes | Bonthoux Sébastien |
| 3 | Effects of the energy crop <i>Miscanthus x giganteus</i> on soil quality across a pollution gradient | Brami Claire |
| 4 | Biodiversity conservation in agricultural land: statistical analysis method to understand media representation of policies and species | Delclaux Julie |
| 5 | Agroecology, Research, and the place of ecology and biodiversity: A review | Detrey Jeremy |
| 6 | Certified and peasant seeds: which network for millet seed supply? | Doncieux Antoine |
| 7 | Is the perception of urban biodiversity related to ecosystem services? | Duffaut Chloé |
| 8 | Multiple ecosystem services valuation with theoretical bio-economic modeling in intensive agricultural-landscape | Faure Jérôme |
| 9 | Impact of intercropping cultures on truffle production and soil microbial communities in Mediterranean oak orchards | Geoffroy Alexandre |
| 10 | Flower strips increase natural enemies abundances: experimental evidence across French agricultural fields. | Giffard Brice |
| 11 | Insecticidal activities of essential oil from <i>Piper borbonense</i> (Miq.) C. DC., an endemic Piperaceae from Reunion island | Grondin Isabelle |
| 12 | Documenting crop diversity management practices in West-Africa: raising perspectives for improving governance frameworks | Labeyrie Vanesse |
| 13 | Soil legacy effects of climatic stress, management and plant functional composition on microbial communities influence the response of <i>Lolium perenne</i> to a new drought event | Legay Nicolas |
| 14 | Rubber tree plantations in Northern Thailand: challenging the positive impact of "afforestation" on soil degradation | Neyret Margot |
| 15 | SEGAE : A Serious Game for Agroecology learning | Olivier Godinot |
| 16 | Impact and bioecology of <i>Tuta absoluta</i> (Meyrick, 1917) on three greenhouse tomato varieties (Tavira, Kawa and Barbarina). | Omar Kisserli |
| 17 | The effect of agroecological practices (reduced tillage, pasture-crop rotation, organic farming) on soil biodiversity and ecosystem services: SoilMan project | Pères Guénola |



POSTER SESSION – Wednesday (October 24th)

- 18** Eukaryotic communities characterized using airborne DNA from poultry buildings: first insights towards pest control improvement in layer henhouses Taudiere Adrien
- 19** Effect of polycultural systems on the abundance of arthropods and crop yield Thomine Eva
- 20** Securisation of the production of Gwell, a fermented milk specialty from Bretagne Von Gastrow Lucas
- 21** Multi-scale analysis of the trade-off between ecosystem services provided by arable weeds community Yvoz Séverin

Chemical ecology

- 22** *Cleome Arabica* L. (capparidaceae) a spontaneous plant of South-Algerian proposed as a remedy for Alzheimer's disease Abdelli Imane
- 23** Overcoming specialized metabolites by gaining essential nutrients: a lichen/snail case study Charrier Maryvonne
- 24** The quality of saffron: *Crocus Stavum* in western Algeria Kerzabi Rachida

Eco-evolutionary dynamics

- 25** Rapid evolution of an annual plant species uncovers coexistence mechanisms Nottebrock Henning
- 26** Erosion of phylogenetic signal of niches through eco-macroevolutionary feedback Prinzing Andreas

Ecological interactions

- 27** The breeding system of *Watsonia knysnana* (Iridaceae): an assessment of pollinator effectiveness Bestea Louise
- 28** Study of the trophic ecology of Fennec in the area of Ouargla Brahmi Karima
- 29** Inventaire comparatif des tiques de la région de Bouzeguène et la détection moléculaire des *Rickettsia*. Brahmi Karima
- 30** Intraspecific interference does not reduce weed seed consumption in two carabid species. Carbonne Benjamin
- 31** An empirical Niche model-based approach to identify the structure of complex foodwebs and assess species invasiveness Frossard Victor
- 32** Fluxweb: a package to easily estimate energy fluxes in food webs Gauzens Benoit
- 33** From coexistence to water competition between two native species in an environment of high rainfall: a study case on Trindade Island. Gomes Anabele
- 34** Pine seedling survival results from direct and indirect biotic interactions mediated by shrubs. Guignabert Arthur



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- 35 Arbuscular mycorrhizal fungi cooperates behavior generates plastic responses on *G. hederacea* functional traits Ricono Claire
- 36 Differential phenotypic selection on floral odours in three orchid taxa growing in distinct environments Schatz Bertrand
- 37 Importance of mating system and pollinator activity in the conservation of an endangered plant species (*Astragalus tragacantha*, Fabaceae) Schurr Lucie
- 38 Parasitic study of the cattle egret *Bubulcus ibis* (Linnaeus, 1758), (Ciconiiformes: Ardeidae) in northeastern Algeria Temimi Ines
- 39 Is the mycorrhizal fungi distribution limiting the orchid establishment in restored meadows? Vogt-Schilb H el ene
- 40 Modelling and predicting the dynamics of trophic networks; peri-urban agroecosystems as a case study Zarzoso-Lacoste Diane

Ecotoxicology and environmental pollution

- 41 Can SSD models help assessing interspecific competition impact on organisms' tolerance against chemical stress? Baillard Vincent
- 42 Use of macrophytes in the assessment of littoral water pollution by heavy metals and hydrocarbons - Case of the great beach Bouras Nour El Houda Yasmina
- 43 Embryotoxic effects of an anxiolytic drug to a freshwater gastropod: coupling of macroscopic, transcriptomic and proteogenomic approaches Lebreton Morgane
- 44 The effect of various doses of Cd on productive features and quality of wheat Maksimovic Ivana
- 45 Effects of Titanium Dioxide Nanoparticles on the Antioxidant System of *Galleria mellonella* Nurullaholu Ulya
- 46 Responses of wild fish populations to multiple stressors, a multilevel approach to assess the combined effects of temperature and immune challenge Petitjean Quentin
- 47 Modeling the direct and indirect effects of copper on phytoplankton-zooplankton interactions Prosnier Lo c
- 48 Developmental and reproductive responses of two bio-indicator freshwater species to pharmaceutical drug exposure: setting the stage for evaluating aquatic micro-pollutant environmental impact Saunier Alice
- 49 Seasonal Morphometric Variation in Field Collected Populations of *Culex pipiens* complex Taskin Vatan

Environmental health

- 50 The Anacardiaceae family medicinal interest theoretical study Abdelli Imane



POSTER SESSION – Wednesday (October 24th)

- 51 Study of *Vibrio tapetis*' type IV secretion system by mutagenesis approach: the case of Brown Ring Disease (BRD) affecting the Manila Clam *Ruditapes philippinarum* Rahmani Alexandra

Evolution

- 52 Chronology of selection events during sheep domestication. Her Charlotte
- 53 Ecological distribution and local adaptations of egg parasitoids *Trichogramma* in a heterogeneous environment: Implications in evolutionary ecology and biological control Ion Scotta Michela
- 54 Local adaptation of *Euchiloglanis* fish complex Peng Zuogang
- 55 Patterns of genomic divergence between parasitic and non-parasitic lamprey ecotype Souissi Ahmed
- 56 Maternal or paternal contributions to transgenerational plasticity of the freshwater snail *Physa acuta* in response to predation Tariel Juliette

Global changes and biodiversity

- 57 Public knowledge and awareness of climate changes among people in China Almutairi Khalid
- 58 Plant-herbivore interactions in the context of climate change: Effects of elevated atmospheric CO₂ on grapevine and European grapevine moth Becker Christine
- 59 Phytobiogeographic study of *Withania frutescens* in the Sebaa Chioukh and Middle Tafna stations in the Tlemcen region Bouayed Ibtissam Sarra
- 60 The ecology of tropical temporary ponds at UWI Mona, Kingston, Jamaica Campbell Gavin
- 61 Belowground interaction between plants does include exchange of nutrients Fernandez Marine
- 62 Phytobiogeographic study of *Lavatera maritima* (malvaceae) in the coastal region of Rachgoune Ain-Temouchent Algeria Ghalem Sarah
- 63 Taking into account a diversity of environmental drivers for the analysis of biodiversity patterns: a methodological challenge Grange Marie
- 64 European tree species extinction and colonization across their ranges Guyennon Arnaud
- 65 The anthropogenic and climatic impact on the halophytic vegetation in Arid and semi-arid zones of western Algeria Kerzabi Rachida
- 66 Phenotypic plasticity in maize Marchadier Elodie
- 67 Effects of tree species interactions and climate on water use efficiency of trees. Martin-Blangy Soline
- 68 Rainwater deficit affects litter mass loss and microbial decomposer communities in a Mediterranean forest Mirleau Pascal



POSTER SESSION – Wednesday (October 24th)

- 69 Conservation of freshwater biodiversity in Tunisia in a global warming context: combining amphipod distribution data and molecular analyses to improve priorities Piscart Christophe
- 70 Estimation of partial population replacement using spatiotemporally explicit simulations and ancient DNA Rio Jeremy

Interaction of ecological and social aspects in the categorization of spaces and species

- 71 A practical framework to analyse the resilience of socio-ecological systems Boulangeat Isabelle
- 72 National specific production system induce different perceptions of management impacts on soil biodiversity functions: comparison of five European countries Hervé Morgane
- 73 Effects of inter row soil cultivation in French vineyards - Benefits for earthworms and economic implications Morgane Hervé
- 74 Consumers' Awareness of Eco-designed Packaging: A Big Step towards Solving Ecological Issues Renko Sanda
- 75 Eco-anthropology in Lower Loire: waterfowl hunting and related knowledges Suard Louison
- 76 Historical overview patterns of natural vegetation cover as support for the regularization of the compensation mechanisms from Legal Reserve established by the New Forest Act Tavares Paulo A

Landscape ecology

- 77 Impact of urbanisation on plant compositional and functional diversity Basquin Hugo
- 78 Factors influencing the distribution of common herbaceous plants within vineyard landscapes Daniel Hervé
- 79 Role of host plant distribution at the landscape level on *Drosophila suzukii* (Matsumura) (Diptera: Drosophilidae) colonization in vineyards Delbac Lionel
- 80 Landscape effects on pollinator communities in grasslands and wet meadows along the Sélune river, France Leroy David
- 81 A methodological approach to consider ecological equivalence for native vegetation compensation in Brazil Mello Kaline
- 82 Key drivers of earthworm community and soil microbial biomass distribution at landscape scale and ecosystem service associated: SoilServ project. Rubio-Dorantes Monica



Paleoecology: How today's ecosystems became what they are?

- 83** Micro-biodiversity patterns assessment of peat bog in Pays de Bitches (Moselle): consequences of environmental and biochemical changes? Florent Perrine
- 84** Investigating the long-term recurrence of nostocalean cyanobacteria through a 6 700 years core in a eutrophic Lake. Miras Yannick

Tropical ecology

- 85** Patterns of within and between-population genetic diversity across a high species richness riverine network: describing the multi-species fishery of the Upper-Maroni in East Guianas. Delord Chrystelle
- 86** Predictive models for freshwater fish communities reveal spatial factors more important than seasonal factors in determining species distributions in two contrasting tropical ecoregions in India Mondal Rubina
- 87** Seasonal and Spatial Variations in Physico Chemical Water Quality of a Tropical River at some of its Natural Points Omoniyi Gbenga
- 88** Ecology of the genus *Millettia* (Fabaceae) for land restoration and its valorization on oil production in Madagascar Rakoto Joseph Felana Niaina
- 89** Habitat loss and frugivores defaunation in Réunion island (Indian Ocean) Strasberg Dominique
- 90** Lack of evidence of fragmentation effects on necromass stocks and heterotrophic respiration in Brazilian Atlantic forest Villela Dora
- 91** Vegetation carbon stocks of mangroves in Futian Mangrove National Nature Reserve, China, based on UAV images Zhen Li

Dealing with heterogeneous data (CESAB/FRB)

- 92** Synthesis and collaborative science in ecology Monnet Anne-Christine

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The French Ecological Society is a learned society which aims to promote and associate the ecological disciplines and to strengthen their visibility in France.

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At the interface of social, earth and life sciences, the CNRS Institute of Ecology and Environment (INEE) has developed an integrative approach to environmental sciences that aims to promote global ecology at every scale of time and space. INEE is a fundamental research institute that combines research with action, and contributes to the advancement of knowledge for sustainable development.

The website of CNRS-InEE is accessible [here](#).

INRA



The main goal of the research units from INRA are to develop agricultural systems that (i) Better meet people's nutritional needs and can be used in novel ways (e.g., in the realm of chemistry, materials science, and energy production), (ii) Are efficient and competitive and (iii) Respect the environment and natural resources and use land responsibly.

The website of INRA is accessible [here](#).



University of Rennes 1

The website of University of Rennes 1 is accessible [here](#).



UMR CNRS EcoBio, University of Rennes 1

ECOBIO "*Ecosystems, Biodiversity and Evolution*" is a multidisciplinary research unit aiming at running investigations on the biodiversity of continental and island ecosystems, from the molecule to the ecosystems.

The website of this department is accessible [here](#).



UMR INRA IGEPP, Univ. Rennes 1, Agrocampus Ouest

IGEPP, the Institute for Genetics, Environment and Plant Protection, is a joint research unit involving staff from INRA, Agrocampus Ouest and Université Rennes 1 and working on plant health improvement through ecological, evolutionary and genetic approaches. Research at IGEPP tackles important societal challenges in Agronomy by contributing to agriculture practices reducing pesticides and fertilizers uses, and by protecting and using biodiversity.

The website of this department is accessible [here](#).

INRA ESE



ESE, the Ecology and Ecosystem Health research unit, brings together scientists from INRA and Agrocampus Ouest to study aquatic ecosystems and their transformations in the context of anthropogenic and global change. Research at ESE focuses on processes spanning the freshwater-marine continuum – from headwaters to estuaries, oceans and islands – and at various levels of biological organisation – from genes to organisms, populations and communities. Its main research areas aim to: 1) analyse the ecological impacts and responses to stresses induced by human activities; 2) understand and stimulate mechanisms of ecological restoration; 3) assist in developing guidelines for the sustainable management of aquatic ecosystems.

The website of this department is accessible [here](#).

UMR INRA BAGAP, ESA, AgroCampus Ouest



L'UMR BAGAP développe des recherches interdisciplinaires qui visent à contribuer au développement d'une agroécologie pour l'action, promouvant la multifonctionnalité des paysages (fonctions écologiques sous-jacentes aux services écosystémiques d'approvisionnement, de régulation biologique et de support de la biodiversité). Dans ces recherches, les acteurs de l'agriculture et de l'aménagement du territoire (agricole, périurbain à urbain), ainsi que leurs organisations, sont considérés comme parties prenantes des écosystèmes dans les paysages agricoles.

UMR CNRS LETG, University of Rennes 2



LETG studies geography of the environment. With its expertise in human geography, physical geography and geomatics, its scientific program aims to contribute to knowledge on nature-society interactions through a modelling and integrative approach lying at the geographical interfaces between land, sea and atmosphere..

The website of this department is accessible [here](#).



IRBI Tours, University of Tours

The website of this department is accessible [here](#).

UR Zoologie Forestière, INRA, Orléans



The website of this department is accessible [here](#).

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The website of CNRS-InEE is accessible [here](#).



Earth Sciences and Astronomy Observatory: OSUR Rennes (OSUR)

The website of OSUR is accessible [here](#).

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The website of Agence Française pour la Biodiversité is accessible [here](#).

Réseau R-Syst

R-Syst est un réseau national regroupant une douzaine d'équipes de recherche de deux départements INRA (SPE et EFPA) impliquées dans la caractérisation moléculaire et morphologique d'organismes. Le réseau R-Syst s'intéresse à la systématique et au (méta) barcoding avec comme entrée la constitution de bases de données moléculaires fiables pour l'identification et la mise à disposition d'outils précis de diagnostic et d'inventaires. Les enjeux sont à la fois un diagnostic précis d'organismes d'intérêt (par exemple reconnus comme pathogènes), et la production d'inventaires aussi complets que possible de différentes communautés. Le réseau fonctionne comme un lieu de partage d'expériences entre des groupes thématiques, liés à un groupe taxonomique particulier. Les groupes thématiques actuellement concernés par le réseau sont : les arbres de Guyane, les insectes, les micro-algues, les nématodes, les bactéries, les champignons et les virus mais le réseau est ouvert et d'autres groupes thématiques peuvent l'intégrer.



Depuis sa création en 2008, le réseau R-syst organise tous les ans à l'automne une réunion ouverte à tous. De plus le réseau, en collaboration avec le Muséum d'Histoire Naturelle (MNHN) et l'Institut Pasteur, a organisé en 2015 à Versailles le colloque 'Taxonomie intégrative : de la génomique aux collections'. Le site internet de ce réseau se trouve ici [here](#).

Animation : Alain Franc (INRA, UMR BIOGECO Biodiversité, Gènes et Communauté) & Valérie Laval (INRA, UMR BIOGER Biologie et Gestion des Risques en Agriculture).



Réseau MiDi - Milieux & Diversité

Réseau thématique de recherche en Région Val de Loire

Réseau Ecologie et Génétique du Parasitisme



Ce réseau vise à favoriser les échanges entre chercheurs du département EFPA travaillant sur le parasitisme (par différents types d'agents comme invertébrés, champignons, virus) de populations animales ou végétales, sauvages ou partiellement domestiquées. Le réseau a vocation à favoriser les synergies entre équipes/disciplines sur des pathosystèmes communs et le partage de concepts et méthodes sur des objets d'étude différents. Les activités du réseau s'articulent avec celles de différents réseaux nationaux, en particulier le Réseau Écologie des Interactions Durables, le GDR Invasions Biologiques, et Groupe Francophone de Pathologie Forestière.

Animation : Marie-Laure Loustau (INRA, UMR BIOGECO Biodiversité, Gènes et Communautés) & Nathalie Charbonnel (INRA, UMR CBGP Centre de Biologie pour la Gestion des Populations).

Réseau Prairies



Prairies - Ce réseau vise à améliorer la coordination et les échanges au sein d'une communauté scientifique mobilisée autour de « la prairie », comme objet de recherche principal ou comme élément de contexte. Le champ d'analyse du réseau couvre une large gamme de couverts allant des prairies temporaires aux prairies permanentes et à des végétations de parcours. Sa mission première est de créer des conditions favorables pour que les chercheurs des différents champs disciplinaires échangent et se forment. L'enjeu est de débloquent 'les verrous' méthodologiques, conceptuels, d'aborder des concepts originaux, voire de s'approprier de nouveaux paradigmes. Le travail du réseau a été ainsi focalisé sur des questions de recherches transversales à plusieurs disciplines et départements (8 départements INRA). Que ce soit à l'échelle de la zone homogène intra parcelle ou de l'exploitation, la dimension systémique est privilégiée (analyse des interactions) afin de pouvoir opérer une intégration des connaissances et d'aborder les questions de changement d'échelle. En huit ans d'existence, le réseau a animé sept séminaires annuels (thèmes : Intérêt de l'écologie fonctionnelle pour l'étude des prairies semées et naturelles ; Changements d'échelles et niveaux de gestion ou d'organisation ; Services écosystémiques ; Dépasser le paradoxe entre connaissances scientifiques sur l'intérêt des prairies et limites rencontrées à leur utilisation dans les élevages ; Les prairies et l'agroécologie ; Diversité des ressources végétales, ce dernier co-organisé avec le CIRAD), et contribué à l'émergence de projets

pluridisciplinaires.

Animation : Pascal Carrère (INRA, UMR UREP Ecosystème Prairial) & Michel Duru (INRA, UMR AGIR, Agroécologie, Innovations, Territoires)



University of Rennes 2

The website of University of Rennes 2 is accessible [here](#).



Biogenouest

The website of Biogenouest is accessible [here](#).



Rennes Métropole

The website of Rennes Métropole is accessible [here](#).



Université Bretagne - Loire

The website of Université Bretagne-Loire is accessible [here](#).



Thermo Fisher Scientific

The website of Thermo Fisher Scientific is accessible [here](#).

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Plenary Sessions

Genomics of parallel evolution and speciation during repeated adaptive radiations in cichlid fishes

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Sympatric speciation and speciation with gene flow more generally remain hotly debated in evolutionary biology. Still only a handful of empirical examples are widely accepted. Moreover, the respective roles of natural and sexual selection during sympatric speciation in cichlid fishes remains unclear. Rarely, traits - termed ‘magic traits’ - might be both under disruptive selection and also involved in assortative mating and drive ecological differentiation and speciation. Hypertrophied lips in the repeated adaptive radiations of African (here we included a QTL-cross from Lake Victoria) and Nicaraguan crater lake cichlids play a role in natural as well as sexual selection. Through QTL-crosses and the analysis of whole re-sequenced genomes of hundreds of individuals we find that the genomic basis of hypertrophied lips in African cichlids is polygenic (about 12 QTLs contribute), but only a single major effect locus underlies this trait in New World cichlids. We found a functional trade-off in feeding behaviour between thick- and thin-lipped ecotypes suggesting that this trait is under disruptive selection. Using enclosures in lakes, we validated the laboratory results of ecological segregation. Almost no mixed pairs were found indicating very strong assortative mating. The degree of genetic differentiation between ecotypes is related to the time since colonization of several crater lake species flocks in this natural experiment - reflecting the speciation-continuum - being subtle in *L. Masaya* (1,700 generations ago) and still absent in the even younger *L. Apoyeque* (< 600 generations ago). Genome-wide differentiation between ecotypes was highest in the older source lakes (great Lakes Nicaragua and Managua) than in the young crater lakes. A “de-speciation” hypothesis might best explain these findings, i.e. the simple genetic basis of species differences in the great old lakes is insufficient to keep the gene pools apart in the crater lakes when conditions (e.g. cost for choosiness) change. Hypertrophied lips are acting as a ‘magic trait’ in that trait, cue, and preference are genetically linked.

Biodiversity: From evolutionary origins to ecosystem functioning and extinction

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The amazing diversity of life on Earth is the direct result of evolutionarily unavoidable tradeoffs that all life has faced since, at the least, the Cambrian explosion. Because of such tradeoffs, newly emerging species coexisted with, and did not displace, established species. These same tradeoffs explain why greater diversity is associated with greater and more stable ecosystem productivity, and with increased resistance to invasion by novel species. Humans, the only species to escape these tradeoffs, caused waves of extinction of large land animals around the globe during the past 50K years. In this, the final period of rapid increases in human environmental impacts, another massive wave of species extinctions seems likely. Preventing this imminent extinction event will require greatly increased efforts at conservation and major changes to fossil fuel use, diets, and agriculture.

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Integrating biodiversity services in agriculture

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Under the current scenario of rapid human population increase, combining efficient and productive agricultural land use with conserving biodiversity is a global challenge. A major argument for wildlife friendly farming and agroecological intensification is that crucial ecosystem services are provided by the “planned” and “associated” biodiversity. Loss of biological control can result in dramatic increases of pest densities, pollinator services affect a third of global human food supply, and inappropriate agricultural management can lead to environmental degradation. Hence, the true value of functional biodiversity on the farm is often inadequately acknowledged or understood, while conventional intensification tends to disrupt beneficial functions of biodiversity. Even during the last decades, high percentages of populations and species have gone extinct in human-dominated landscapes.

This presentation is subdivided in three parts: Local management of biodiversity services, landscape design, combining land sharing with land sparing, and at a global scale, adapted solutions for smallholders. Negative externalities of pesticide use, nitrogen losses as well as disappearing pollination, biocontrol and cultural services are discussed. Landscape structure is a key factor of local ecosystem processes, so we need to better understand how to design the configurational and compositional landscape heterogeneity. At a global scale, agriculture practiced under smallholder dominated landscapes, and not large-scale farming, is the backbone of global food security. In conclusion, linking agricultural intensification with biodiversity conservation and hunger reduction requires well-informed regional solutions at different spatial scales.

*Speaker

TALKS

Agroecology and Ecology of Agroecosystems

Are there easy changes for farmers to mitigate the impacts of conventional farming on biodiversity?

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In a European context of farmland biodiversity collapse, solutions should be found to stop these losses. Due to the intensification of the most part of agriculture, improvements are easily accessible such as input and soil tillage reduction. Such changes are known to positively affect biodiversity. However, because these changes are very complex and inter-correlated, studies are often focused at low accurate levels of management changes (e.g. organic versus conventional farming, tillage versus conservation tillage...), leading sometimes to no consensus about effects on biodiversity. Moreover, impacts of farming on some taxa at the top of trophic network such as insectivorous bats remains poorly known.

With the aim to find efficient solutions for biodiversity conservation, we published 2 studies linking farming practices to passerine bird and bat communities. We focused our sampling design on tillage types and underlying weed-control possibilities such as the intensification of cover-crop or herbicide use, in the Ile-de-France region. Studied farming systems are commonly performed, which potentially allows to make results more easily transferable to farmers and needing low changes and risk taking about yield losses.

Our results demonstrated that the benefit of the tillage reduction for birds and bats strongly depends of the underlying practices (i.e. weed-control methods to offset the tillage reduction). Results highlighted an even more negative impact of herbicides than tillage, showing that stopping tillage to intensify herbicide use is not a promising way compared to a conventional tillage. In contrast, direct-seeding, consisting in a no-tillage with a cover-crop in the intercrop period to control weeds, appears to be very efficient. These studies also showed that even if organic farming is presently difficult to implement and requires a change of economic context for farmers, considerable and easy improvements in conventional farming are attainable with herbicide and tillage reduction, while maintaining yields.

*Speaker

Estimating pollination potential in orchards: looking for a simple field method

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Pollination is a critical ecosystem service due to its essential role in sustaining food production, and the recent observed decline of pollinating insects worldwide. However estimating the pollination service is complicated by the existence of multiple definitions and associated estimation methods. Here, based on a systematic bibliographic review we focused on methods for estimating the potential pollination allowed by the presence of pollinators. We tested a protocol including direct estimation of pollinator abundance and richness, and indirect proxies based on landscape context and orchard feeding and nesting resources. We aimed to identify the subset of variables accounting for potential pollination from insect presence, from which a simplified and standardized method could be designed for environmental impact studies. The method comprised 3 steps: a land cover analysis, field observations of plot-scale resources and insect focal observations. We worked in orchards of the Grenoble region during two consecutive years, sampling 8 orchards in 2017 and 31 in 2018. Mixed linear models with orchard identity as random effect showed that pollinator abundance was significantly impacted by landscape composition within a 2-km radius. For 2017, it decreased with increasing built-up land. For 2018, it increased with increasing grassland area. For both years, floral resources of orchard ground layer, and specifically richness in flower shapes, favoured pollinator abundance. Conversely orchard edge features had only weak marginal impacts on pollinator abundance or richness. For 2017, a combined model with built-up area and an indicator of orchard management intensity explained 42% of variation in pollinator abundance and 50% of variation in pollinator richness. For 2018, a combined model with grassland area and flower shape richness explained only 23% of variation in pollinator abundance. Consequently, a protocol simplification excluding direct observations of pollinators does not seem yet possible. Further work could explore potential influences of orchard management practices.

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Using molecular tools to shed light on trophic interactions in agricultural systems

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Modern monocultural agro-ecosystems can be perceived as a simplification of natural ecosystems, where a single plant species is usually grown over vast areas. Because of this apparent simplicity, species interactions have often been treated as linear in agricultural landscapes. For example, in these systems, it has historically been assumed that the concept of a food chain can describe the relationships between an insect pest and a single biocontrol agent. In reality, multiple ecological interactions are involved, comprising potentially complex food webs. The disentangling of these interaction networks and quantification of the relative strengths of the multi-trophic interactions are very difficult using orthodox methods such as dissection and subsequent visual gut-content identification. An emerging field of study using molecular tools to analyse these interactions in agricultural systems can now begin to address these impediments and help to better understand multi-trophic dynamics. In this presentation, we will present cases studies focusing on host parasitoid, plant-pollinator and plant-phytophagous insect networks for which we used molecular tools to reveal trophic interactions. For each of these studies we used a DNA metabarcoding approach to describe the breadth of biotic interactions among our species of interest. Our results show that high-throughput DNA sequencing can reveal a world of otherwise unseen trophic relationships within agricultural ecosystems. Based on our results and our review of the literature, we propose recommendations and future directions for the use of molecular methods (including high-throughput DNA sequencing) for a better understanding of trophic interactions in agricultural landscapes and potential applications for improved biological control.

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Effect of Mulch Physical properties on soil invertebrate communities

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Mulching is a practice providing numerous agroecological benefits such as weed control, improvement of soil organic matter, and the creation of favorable habitat for soil invertebrates. Although the effect of mulch on weed control has already been studied, very little is known about how the mulch affects soil fauna and the underlying mechanisms. The chemical composition of mulch or litter is often studied as the main factor affecting soil fauna community but recent works also highlight the role of habitat physical structure on invertebrate communities. In the present work, we investigated the role of mulch physical properties on invertebrate community composition through a field experiment testing the effect of seven kind of mulch having contrasted physical structures. The experiment was carried out during two month in a tropical agroecosystem (Martinique, Lesser Antilles). Weeds were monitored and soil invertebrates were sampled in each kind of mulch as well as in the bare-soil control treatments. Mulch physical properties has been characterized through trait measurements such as 3D index, solid volume fraction and mulch area index (MAI) which is the equivalent of leaf area index (LAI) for mulch. These variables were measured in order to be linked with data on soil fauna communities. Furthermore, according to the grain size hypothesis, it is predicted that organisms having long leg relative to their body size tend to live in a more complex (rugose) habitat. Trait measurements on soil invertebrate (body size and leg size) were also realized in order to test such hypothesis.

*Speaker

Weed flora evolution in direct seeding under cover

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Direct seeding under cover, by its emergent properties, raises new questions of research on weed communities. The absence of soil disturbance and the implementation of cover crops, modify all factors of conventional agriculture and lead to a complete change of habitat for and management of the weed flora. In addition, these systems allow the development of a certain number of animal communities that interact with one another and with plant communities and thus potentially promote the regulations expected in Agroecology. Finally, there is the issue of annual weed species diversity in systems where tillage is strongly reduced.

This thesis, started in November 2017, has as main objective to provide an understanding of direct seeding under cover cropping systems effects over time on weed communities. In different pedoclimatic conditions of the region Bourgogne Franche-Comte, 73 winter-wheat fields, belonging to different age classes (1 to 3 years, 4 to 6 years, > 6 years since the adoption of direct seeding under cover), have been studied. In each field, weed communities were surveyed 2 or 3 times in 2018: resumption of growth (March), before harvest (mid-June) and during the cover cropping period.

First results (March 2018) show that species richness, ranging from 1 to 25 species per field is higher than in conventional agricultural fields. Difference in weed flora diversity occurs between the different categories and species richness appears higher in the oldest, more stable systems (3 to 4 more species per field in average in the > 6 years category). In the same time, differences in composition are also expected between the different age classes but no trend of perennial weed selection (hemicryptophytes, geophytes) in weed communities with increasing time to conversion to direct seeding under cover appears.

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Multiple ecosystem services valuation with theoretical bio-economic modeling in intensive agricultural-landscape

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Global change is a significant contributor to biodiversity loss and hence affects ecosystem services delivery. Ecosystem services are sustained by complex ecological processes or functions that are emergent properties of the natural system. The social or monetary value of ecosystem services depend on the ways that particular services are used by different stakeholders. Therefore, to assess ecosystem services delivery and the inherent trade-offs among them, it is essential to separate the valuation (monetary or not) of individual services from the ecological patterns and processes that deliver the former. Understanding how changes in biodiversity affects trade-offs among ecosystem services requires to include querying stakeholders and components of well-being from their perspective.

Here, we explored scenarios of public policies to determine the landscape composition that best supports sustainable and multifunctional agricultural landscapes. We develop a bio-economic model to analyse the dynamics of ecosystem services in an intensive-agricultural landscape. We consider four ecosystem services among which crop pollination service, which is key by linking the ecological and the economic models. We also consider two stakeholders: farmers and beekeepers with different demand in ecosystem services delivery. The analysis of scenarios of public policies focused on beekeeping support reveals a perverse effect of this policy on biodiversity conservation, because of an existing substitution between wild and domestic pollinators. Furthermore, a structural antagonism between ecological and economic good state exists but can be reduced by supporting both farmers and beekeepers. In this way, our model highlights the importance to have a wide overview in public policy planning and show that various levers to promote multifunctional and resilient agricultural landscapes.

*Speaker

Microbiome of Canola Root: Structure and Variations

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The fungi in the rhizosphere have a large influence on plant development and growth. Some of these **micro-organisms** protect plants against pathogens, mitigate the impact of abiotic stress, or facilitate plant nutrition. These organisms influence each other and form complex webs of interactions. Deciphering the structure and function of the fungal **microbiome** of crop plant rhizosphere is a necessary step toward optimizing the efficiency of plant production. We tested the hypotheses that (1) the diversification of cropping systems influences the fungal microbiome of canola **rhizosphere**, (2) canola has a fungal **core-microbiome**, i.e. a set of fungi that are always associated with canola, and (3) that some taxa have a determining influence on the structure of the communities (hub-taxa) within the core-microbiome. In 2013 and 2016 we used the canola phase of five cropping system, from the less to the most diversified, that included one of two types of canola (Roundup Ready[®] and Liberty Link[®] in an existing long-term (6 years) field experiment. The experiment has a randomized complete block design with four blocks, and is replicated at three locations: Lacombe (Alberta), Lethbridge (Alberta) and Scott (Saskatchewan). Our results show that **crop diversification** has significant impact on the structure of rhizosphere fungal communities ($p = 0.0337$) for all sites. We also discover and described a canola core-microbiome made of **47 OTUs** in 2013 and identified *Exophiala sp.*, *Mortierella sp.*, *Fusarium solani*, *Ulocladium daucii* and *Humicola grisea* as the **hub-taxa** among this core. However this core microbiome was variable and could identify only one member in 2016: *Olpidium brassicae*. Our results are presented as a basis for the development of ecological engineering strategies for the improvement of canola production.

*Speaker

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Do stable isotopes can help to better understand the effect of agroecosystems on their inter-connected ecosystems: a case study of fishpond dams effect on temporary streams?

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Fishpond dams as extensively manage agroecosystems can strongly affect temporary low-order stream functioning, especially through changes in water quality and loss of ecological continuity. In addition, the presence of these lentic agroecosystems promotes the production of autochthonous organic matter, changing the trophic resources in the receiving streams. Yet, the consequences of these changes on communities and stream functioning remain largely understudied. We investigated the effects of these agroecosystems on the trophic ecology of macroinvertebrate assemblages in temporary low-order streams using C and N stable isotopes. Available food resources and macroinvertebrates were sampled in one upstream- and one downstream site of two temporary low-order streams, one with a fishpond (impacted stream) and another with- out fishpond (reference stream). Macroinvertebrate assemblages and densities, as well as stable isotope composition of food resources and dominant macroinvertebrate taxa were measured. Functional diversity indexes were calculated to detect and quantify differences in invertebrate trophic niches. Bayesian stable-isotope mixing models were used to investigate the differences in food sources assimilated by macroinvertebrate communities. Upstream site of the impacted stream and both reference sites showed similar invertebrate assemblages and isotopic compositions suggesting moderate effects of fishponds on the upstream tributaries. In contrast, at the downstream site of the impacted stream, we recorded ten times higher invertebrate biomasses. Modifications in the invertebrate trophic niches and food sources assimilation were also evidenced. Isotope

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analyses and invertebrates assemblages allow us to identify that by modifying the food sources fishpond dams tend to alter invertebrate assemblages but also shift the trophic dynamics downstream the fishpond. This assessment underlines the usefulness of these tools to explore interactions between adjacent and/or interconnected (agro) ecosystems.

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Assessing non-intended effects of farming practices on field margin vegetation with a functional approach

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To assess the unwanted side effects of farming practices, we used a nationwide survey of the vegetation of arable field margin strips. The vegetation was surveyed during two years in 430 field margins distributed over all regions of France. We used two complementary trait-based approaches to examine how ten plant traits were related to ten environmental variables describing abiotic conditions, landscape factors, field margin management and in-field practices. Generalized additive mixed models were developed to assess how the same environmental variables correlated with species richness and functional diversity. Our study highlighted that the composition and the diversity of vegetation in arable field margins were primarily driven by the direct field margin management and by landscape factors. However, among farming practices, distinct non-intended effects of fertilization and herbicides were highlighted. The level of nitrogen fertilizers had the strongest effects on the functional composition of field margin vegetation with a change toward more nutrient-demanding species, while the intensity of herbicides use was related to a slight decrease in species richness with no effects on functional composition or diversity. Species depending on animals for their reproduction (obligate entomogamous species) or for their dispersal (zoochorous species) were associated with smaller less intensively managed fields in landscapes with a high proportion of non-arable habitats. Some of the observed patterns seemed to be driven by differential responses of agrotolerant versus hemerophobic species, with the latter being more species-rich under organic than under conventional farming. Despite efforts to reduce nitrogen inputs since the 2000s, our results shows that N-fertilization still has significant non-intended effects on field margin vegetation. These first results show the usefulness of this new network of fields ("500 ENI") set up by the Ministry of Agriculture in order to monitor biodiversity in relation to farming practices, especially use of agrochemicals.

*Speaker

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The effect of contrasted perennial flower strips on the parasitism of oilseed rape and faba bean herbivores

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The implementation of habitats to improve functional biodiversity generally benefits to natural enemies, but it does not always improve biological control. To understand why some plant mixtures perform better than others, we compared the effect of eight contrasting floral mixtures comprising native and perennial plants during a four-year field experiment. We have varied the proportion, the species and functional diversity of plants providing resources towards natural enemies. These mixtures were compared with control strips sown with the crop species. In the adjacent crop, we evaluated parasitism levels of (1) larvae of *Meligethes aeneus* collected from rapeseed flowers, (2) *Dasineura brassicae* collected in the soil after the rapeseed harvest and (3) *Bruchus rufimanus* within faba bean seeds. These parasitism rates were also compared to those found in control fields at 250m away from our experiment.

Parasitism of *M. aeneus* larvae was 8% on the control plots. It varied between 8 and 19% at 5m from each flower strip and was positively related to the proportion of flowering species in April providing easily accessible nectar. For *D. brassicae*, 55% of pupae were parasitized without any effect of flower mixtures or distance to the strip. In faba bean seeds, parasitism of *B. rufimanus* was 25% in the control field, 33% in the control plots and 47% in front of the flower strips, without any distance effect. The parasitism rate increased with the amount of flowering species providing easily accessible nectar in May. The proportion of seed damaged by *B. rufimanus* was lower at 5 than 20m from the flower strips (54 vs 70%).

For two of the three herbivores studied, we demonstrate that the composition of plant communities near crops influences their parasitism rate and that this biological control can be strengthened by flower strips providing food resources during the parasitoid activity period.

*Speaker

Intra-field floral resources to enhance biological control: do interactions with other flower-visiting insects affect parasitism rate?

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Developing more sustainable cropping systems has become a major challenge in the current context of pesticide reduction. Supporting natural regulation processes, such as pest control by arthropods (called natural enemies), could help achieve this goal. It is known that increasing plant diversity should enhance abundance and diversity of natural enemies through an increased provision of resources (prey resources and plant resources such as nectar and pollen). Adding floral resources nearby crops should thus enhance pest control. Nevertheless, interactions between flower-visiting arthropods, and their effect on pest control, is very scarcely considered. In particular, floral resources also attract pollinators, such as honeybees that harvest in large quantities on many plant species and are often in strong numeric imbalance. Therefore, a competition for floral resources between floral-visitors can be hypothesized. In this study, we focus on the effect of intra-field floral resources on aphid control by parasitoid wasps along a gradient of pollinator abundance. The model used was cereal crops mixed with two flowering crops: faba bean (*Vicia faba*) and pea (*Pisum sativum*). We expect that (a) the presence of faba bean and pea in cereal crops (mixed cultures) will increase aphid parasitism rate compared to cereal mono-cultures, as they provide food (faba bean extra-floral nectar) and alternative aphid hosts; (b) a high abundance of bees could lead to a reduction of the aphid parasitism rate. On 18 fields (10 crop mixtures and 8 cereal mono-cultures), aphid parasitism rate was estimated every two weeks (by direct counting in the field and by barcoding), along with pollinator abundance (with colored pan-traps) and flower-visitors foraging behaviors. This study could provide knowledge on possible interactions between beneficial insects, that appears important to evaluate current plant diversification strategies used in agriculture, and optimize them to enhance both crop pollination and conservation biological control.

*Speaker

Supporting the development of biodiversity-based agricultures: understanding and strengthening local networks for agroecological knowledge circulation, insights from the global South

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Most countries in the global South are engaged in an agricultural transition driven by integration into the market economy and strongly supported by development programs. This transition leads to the homogenization of cropping systems and the specialization of production and agrarian systems, which leads to the reduction of plant diversity from the scale of the plot to that of the landscape, from the farm to the region. This loss of diversity at different scales alters ecosystems functioning and affects the different services they provide to humans. Rural population in these areas, however, mostly continues to practice biodiversity-based agriculture (BBA) based on the management of plant diversity not only within plots but also more widely in the landscapes in which they are integrated. This type of agriculture is a promising alternative for the sustainable development of rural areas, but requires appropriate forms of support. Agroecological knowledge is especially a pivotal input of BBA. Promoting farmers' access to operational knowledge on how to manage plant diversity is thus a key lever to foster an agricultural transition based on BBA. Local networks for the circulation of agroecological knowledge play a major role in learning, involving both individuals and organizations and being largely conditioned by pre-existing social relations. Although some studies have highlighted the importance of these networks for BBA, their role remains largely unknown and is not taken into account in agricultural development initiatives. We propose an approach to characterize these local networks of knowledge circulation and their effect on farmers' plant diversity management practices, from plot to landscape. We also propose ways to strengthen and expand these networks by promoting knowledge sharing not only at the local level between farmers, but also with other types of actors carrying scientific and technical knowledge, using participatory modeling.

*Speaker

The effect of landscape configuration on pest-predator dynamics and the implications for biological control - a spatiotemporal model

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Intensive agriculture has induced agricultural landscape simplification. It negatively impacts biodiversity, such as natural enemies, leading to a potential decrease in the ecosystem service of pest regulation. Biological pest regulation in agroecosystems is an important and complex process, affected by landscape configuration and farming practices. These factors influence the dynamics of both pests and natural enemies, but also the way the latter deliver regulation. The dynamics depend on how life cycles are completed which requires a diversity of resources in the landscape, such as food, or hibernation sites. The success of pest regulation also depends on aspects of the spatiotemporal dynamics, e.g. how the natural enemies are able to find and control pests on crops. However, the relations between landscape features, biodiversity dynamics and service provision are still poorly understood.

In this work we develop a mechanistic model that simulates the spatiotemporal dynamic of a pest-predator interaction, through various scenarios for landscape configuration. In particular, we study the effect of the proportion of semi-natural habitats, and their spatial arrangement on biological control for different pest pressures.

Our model predicts potential relations between landscape structure, biodiversity dynamics and effective regulation. We find that both landscape structure and pest dynamics influence predator dynamics and the effectiveness of pest control. We show that the optimal proportion of semi-natural habitat in the landscape for pest regulation depends on pest abundance. These findings imply that landscape structure will influence the efficiency of biological control, which requires spatial and temporal co-occurrence of pests and natural enemies. Furthermore, one of the originalities of our work is to simulate gain in crop loss due to biological control, which allows quantifying directly the ecosystem service.

Our model could be a tool to design pest management strategies that consider landscape configuration as a lever for a more sustainable agriculture.

Effects of cereal-legume intercropping on sugar consumption and parasitism by *Aphidius* parasitoids

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Most parasitoid wasps rely on plant-derived food sources such as nectar, to ensure their survival and dispersal. However, in conventional single crop farming, flower resources are scarce and often restricted to the border of fields. Lack of such resources leads to a lower abundance and performance of parasitoids, especially in the centre of the fields. There has recently been a growing interest in field diversification, for various purposes, and notably as a way to provide food sources for parasitoids. For instance, intercropping allows mixing crops that do not produce such resources (e.g. wheat) with crops such as faba bean, which produces extrafloral nectar on which parasitoids can feed as demonstrated in laboratory bioassays. Nectar provision in intercropped fields may then allow increased food consumption by parasitoids, leading to better parasitoid performances and parasitism, thus increasing pest population control. Here, we studied sugar uptake and parasitism patterns of *Aphidius* aphid parasitoids in wheat single crops and wheat-faba bean intercrops. We tested the hypotheses that a) *Aphidius* parasitoids feed more in intercrops than in single crops and b) increased nectar consumption in intercropped fields leads to higher aphid parasitism. Parasitoid captures and parasitism surveys were carried out in an organic field network around Angers, France. Several sampling points were made at different positions in the field (center, border) to consider nectar uptake outside the field. Feeding history of field-caught parasitoids was inferred from their sugar profile, using HPLC. *Aphidius* feeding patterns were then linked to estimated parasitism rates.

*Speaker

A trait-based approach to understand and predict the performance of arable annual mixed crops

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One of the challenges in low-input annual arable mixed crops (i.e. species and variety mixtures) is to determine which species / varieties go well together to improve overall system performance.

Theories coming from community ecology suggest that two ecological processes are particularly involved in mixed crops performance by improving resource use efficiency [1]. Niche complementarity can be quantified by the distance between target functional traits between two plants. Phenotypic plasticity can be quantified by the variance of target functional traits between crop- ping environments (including crop management). We aim to apply this ecological theory in an agronomical context by calculating these complementarity and plasticity metrics to predict crop yield of various mixed crops in different environments.

A plant trait database on wheat and pea mixtures was built, gathering ten experiments with various management practices over six years, localized in two French sites (Angers, Toulouse).

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Plant traits were measured dynamically (crop height, aerial biomass, nitrogen content) to quantify crop growth and development over key phenological stages and at harvest (yield, grain quality) to quantify crop performance.

Together with environmental (climate and soil) indicators we considered both trait by trait and multi-traits methods to analyze performance variability.

Litrico and Violle (2015). *Trends Plant Sci.* 20, 604-613.

*Speaker

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Using plant-soil feedback knowledge to improve agricultural sustainability and productivity

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A new vision for the sustainable management of agricultural systems is needed to address population demands for food production and declining ecosystem health. Wild and cultivated plant species both influence root-associated organisms, such as soil-borne pathogens, beneficial symbionts, and saprotrophs that break down plant litter. These organisms can, in turn, affect plant performance either negatively or positively. The sum of these negative and positive interactions determines the sign and strength of plant-soil feedback (PSF).

Insights from natural systems, which contain the full complexity of diverse plant and soil communities, can help to tackle the grand challenges facing sustainable agriculture, such as disease control, nutrient retention, and resistance to extreme climatic events. Ecologists are accustomed to look across a range of communities, trophic levels and species, in interaction with their environment, over a range of different temporal and spatial scales. Coverage of this depth and breadth offers an opportunity to test the generality and context-dependent nature of PSF, which can in turn be applied to managing agricultural systems.

In this talk, I will demonstrate how the recent developments in PSF research in natural systems can assist in developing more targeted approaches in managing plant-soil organism interactions in agricultural systems and present avenues for future research. For example, targeting positive PSF effects might be the key to improve the sustainability of food production whilst maintaining productivity. This can be achieved by adding organic inputs to close the nutrient cycle, and to steer the decomposer community with the aim of increasing soil nutrient availability. Developing trait-based ecology for soil organisms are also promising to better understand the functional role of species and groups of soil organisms and will also be discussed together with few other examples of how plant-soil feedback can be manipulated to increase the sustainability of agroecosystems.

*Speaker

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Effect of plant genetic diversity on biomass production, structuration of species in sown grassland communities and microbial diversity in soil

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Many studies highlighted the importance of species diversity in ecosystems functioning and supplying of the ecosystems services. The diversity effect on ecosystem functioning has been largely described at species level, but remains little invested at within-species level (i.e. genetic diversity). In our experimental approach, at INRA in Lusignan, we highlighted a genetic diversity benefit on biomass production and its stability over years, and on species composition of sown grasslands. We also observed an increase in species equitability with genetic diversity. Currently, we are studying plant genetic diversity effect on soil microbial diversity.

*Speaker

Bringing macroecology into agricultural Science: promises and challenges

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Given the multiple challenges imposed by global changes, including climate change, land use conversion, biological invasions, and habitat loss, ecology has received more societal attention in the last decades than ever before. Indeed, global change imposes a number of new challenges for global food security, including the need to adapt agricultural systems to new environmental conditions and potentially new pests and diseases. Planning for these changes requires a better understanding of the factors influencing agricultural productivity and stability, as well as the design and use of predictive tools to allow forecasting and comparisons between potential management strategies. More importantly, the goals of sustainability, along with the need to adapt and forecast, impose a need to abandon the case-by-case approaches and to come up with broader, more generalizable strategies that will allow maintaining and increasing productivity in a more biodiversity-friendly manner. Macroecology focuses on finding general patterns across ecological communities at large scales, in particular with respect to abundance, distributions and biodiversity. It is therefore particularly well suited to study and answer questions of global change as applied to agricultural landscapes. However, as in many other fields in ecology, macroecologists have focused largely on the study of natural or semi-natural systems. Here I review major macroecological fields of study that can contribute to a more predictive agricultural management strategy. The main goals of this review will be to (1) synthesize what we know about macroecological patterns that need to be tested and applied to agricultural systems; (2) identify areas where macroecological research has already been contributing to agricultural planning as well as (3) identifying gaps where we can bring more macroecology into agricultural sciences. The emphasis will be on the particular challenges and opportunities that agricultural settings can provide for such a macroecological perspective.

*Speaker

Crop diversification positively alter the intensity of soil-plant interactions in intensive agrosystems giving clues for agroecological transition

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Crop diversification (Eisenhauer, 2016) and crop rotation (King & Blesh, 2018) could modify rhizosphere functioning by altering the potential reservoir recruitable by plants (Benitez et al., 2017). Consequences are modifications of the plant performances through modifications of ecological functions fulfilled by rhizosphere microorganisms as disease suppressiveness (Peralta et al., 2018) or SOM turnover (Coskun et al., 2017 ; Hinsinger, 2001). Our aim is to estimate at the field scale and along a crop cycle if "rhizosphere effect" can be estimated in order to qualify the potential of plant-soil interactions in order to replace synthetic inputs by ecological regulations. We hypothesized that (i) a Rhizosphere Effect Index (REI) can be estimated (ii) and, the value of the REI will describe a gradient of crop diversification. Accordingly, we monitored a wheat field (*Triticum aestivum*) in 3 farms located in North differing by their crop diversity index (*sensu* Tiemann et al., 2015). Plant variables (diseases damages, development stages and aerial biomass) and soil variables (enzymatic activities, nitrate and phosphate fluxes, microbial diversity) in both rhizosphere and bulk soil were determined to calculate the REI. The suggested REI discriminate the rhizosphere soil compared to bulk soils with systematically lower REI value for the less diversified farm. Our results showed significant differences ($p < 0,05$) between rhizosphere and bulk soils, but some variables as enzymatic activities better defined the rhizosphere effect. Interestingly, temporal patterns can be analysed with the REI. Based on these results, we can consider that the crop diversification, even in intensive farms influence the rhizosphere effect, which is exacerbated in high diversification farms, suggesting limitations for agroecological transitions in the lower diversification farm. However, further developments of the REI are needed to determine correlations with plant performances and quantify causal links with inherent soil properties and practices.

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Mechanistic-statistical modelling of Coffee Berry Disease dynamics and elucidation of the epidemiological mechanisms affected by shade

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Coffee berry disease (CBD), which is widespread in Africa, has been responsible for massive yield losses of *Coffea arabica*. In Cameroon, *C. arabica* is mainly cropped in agroforestry systems on smallholder farms where low incomes hinder the use of chemicals to manage the disease. Investigations on novel agroecological strategies to control CBD are expected to be implemented and even increase in the current context of global changes. Shade trees are supposed to reduce the dispersion of CBD by forming a barrier against rain. Nevertheless, data collected over two consecutive years in West Cameroon showed that shading did not necessarily reduce the disease and could even increase it. The objective of our study was to determine the epidemiological mechanisms and environmental covariates involved in the differences of epidemics observed under shade and full sun. For this purpose, we have developed a Susceptible – Exposed - Infectious - Removed model (SEIR), some parameters of which being functions of environmental covariates. This dynamic model has been coupled to a probabilistic model of observation via a mechanistic-statistical approach. The estimation of model parameters was performed in a Bayesian framework with the JAGS software. Our results showed that (i) CBD was governed by subtle balances between microclimate variables and (ii) shade had antagonistic effects on several epidemiological parameters. These findings suggest that depending on the local conditions, a particular effect could take the advantage resulting in a high variability between experiments described in the literature. Hence contrasting effects of shade trees on disease dynamics need more in depth evaluation to precise the possible trade-offs between the epidemiological and environmental variables at stake. We recommend the mechanistic-statistical modelling approach to help design novel, cost-effective and environmentally friendly management strategies both at the plot and landscape scales.

*Speaker

Bundling the ecosystem services supplied by agro-ecosystems as part of the French Evaluation of Ecosystems and Ecosystem Services (EFESE).

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In line with the European program "Mapping and Assessment of Ecosystem and their Services", the French Ministry for the Environment implemented its National Ecosystem assessment (i.e. French Evaluation of Ecosystems and Ecosystem Services, EFESE) in 2012. Here, we present the analysis of the associations among ecosystem services (ES) supplied by agro-ecosystems and quantitatively estimated by a group of experts coordinated by the French National Institute for Agricultural Research.

Ten ES were represented by fourteen indicators, which were quantified at the Small Agricultural Region (SAR) level. We first identified associations among ES using a correlation network. Our results highlighted three broad nodes of ES: a first node combines ES related to water and nitrogen cycles, a second node combines ES sensitive to semi-natural habitats or intensity of agricultural practices and, a third node combines ES related to carbon fluxes and stocks.

In a second step, we differentiated ES bundles corresponding to two beneficiary groups: society and farmers. For each beneficiary-oriented bundle, we identified spatial clusters of SARs based on their similarity in ES supply using self-organizing maps and the Silhouette index. We then explored the spatial congruence of the clusters of SARs between the two beneficiary-oriented bundles. The analysis of congruence between the different types of ES bundles to society and farmers allowed characterising SARs according to their multifunctional character.

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Finally, we investigated the relationships between bundles of ES and several management parameters related to measures for the degree of intensification (the relative area of croplands, expenses in phytosanitary products and agricultural inputs).

Although a higher diversity and supply of multiple ES were expected for SARs with low phytosanitary inputs and a lower proportion of croplands, we did not find such a clear relationship between agricultural inputs and multi-ES supply.

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Evidence that organic farming promotes pest control

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Agroecology, based on optimizing ecological functions, such as biological pest control, to replace the use of synthetic agrochemicals is a promising way to reduce the ecological footprint of agriculture while maintaining commodity production. Organic farming is often considered an ideal prototype of agroecology, but the performance of organic farming in terms of the ecological functions it provides remains poorly explored. Using two distinct meta-analyses, we assessed the effect of organic farming on the potential for biological control (parasitism or predation rates and soil-suppressiveness) and pest infestation (weeds, animal pests and pathogens). The two meta-analyses used data extracted respectively from 43 and 134 studies comparing organic and conventional farming systems. Our results show that organic farming enhances overall biological pest control potential compared to conventional cropping systems. Moreover, we found that organic farming had lower levels of pathogen infestation, similar levels of animal pest infestation and much higher levels of weed infestation. Our study provides evidence that organic farming can enhance pest control and suggests that organic farming offers a way to reduce the use of synthetic pesticide for the management of animal pests and pathogens without increasing their levels of infestation.

*Speaker

Farming systems at local and landscape scales are stronger drivers of predator communities and biological pest control services than semi-natural habitats

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Identifying landscape variables and farming practices that foster service-providing communities is an important topic for biodiversity conservation and the development of agroecological farming systems optimizing ecological processes. While organic farming practices at the local scale are known to enhance biodiversity, their effects on the delivery of ecosystem services, such as biological pest control, remain poorly explored. Moreover, how the spatial expansion of organic farming at the landscape scale modulates the relative effect of organic farming at the local scale on biodiversity and ecosystem functioning is still unknown. Here, using a multi-scale hierarchical design in southwestern France, we examined the effects of organic farming and semi-natural habitats at the local and landscape scales on natural enemy communities and the level of pest control services in 42 vineyards. We found that the proportion of organic farming in the landscape was a stronger driver of natural enemy abundance and richness than the proportion of semi-natural habitats. In addition, the responses of the different natural enemy communities were highly idiosyncratic and suggest spillover between organic and conventional vineyards. Organic farming at the local and landscape scales were found to be beneficial to the mean and the temporal stability of biological control services, while the proportion of semi-natural habitats in the landscape reduced the level of biological pest control. Finally, we show that specific farming practices, such as pesticide use or crop productivity, were important variables affecting natural enemy communities and levels of biological control services independently of farming system type. Our study highlights the major importance of considering the diversity of farming practices within the landscape to design functional landscapes that optimize biological pest control services.

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Land-use change impacts weed communities' assembly and soil protection in mountainous Northern Thailand

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Soil protection is one of today's major challenges in insuring agriculture sustainability, and could be favored by enhanced management of non-cultivated plants. In Mountainous South-East Asia, rapid agricultural intensification in the past decades led to drastic biodiversity losses and intense soil degradation. Weeds provide diverse ecosystem services, including soil protection and support of biodiversity at higher levels. However, the determinants of weed communities in mountainous areas of SE Asia, and the precise interactions of these communities with soil characteristics, are still largely unknown. Here we show that land use and to a lesser extent landscape and past land uses are the main drivers of plant communities. We conducted soil characterization and botanical inventories in Huai Lang, Northern Thailand, in 20 fields from different land uses along the transition from annual crops to mature rubber tree plantations twice a year from 2016 to 2018. We found that species richness was mostly affected by landscape (e.g. increased with forested area) while plant biomass was affected primarily by land use. Mature rubber tree plantations had very specific weed communities, usually associated with low plant biomass. This low abundance and richness of weeds might explain the high rates of soil erosion under rubber trees described elsewhere. Altogether, our results suggest that less intense weeding practices could provide cost-effective and sustainable support for soil protection in threatened forested areas.

*Speaker

A mechanistic understanding of plant-pollinator interactions in agricultural landscapes

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Pollinator health is globally declining in agricultural landscapes and important factors include the use of insecticides, reduced habitat and lack of nutritional resources. Pollinators play a key role in ecosystem functioning because they mediate interactions between species and facilitate ecological and economic impacts. However, pollinator-mediated interactions in agricultural landscapes are insufficiently understood. One of the greatest challenges is to understand how pollination services contribute to maximize ecosystem functioning, thus enhancing ecosystem services.

We are using *Brassica carinata*, to study plant-pollinator interactions in agricultural ecosystem. We developed a mechanistic trait-based understanding of plant-pollinator interactions, to quantify the ecosystem services contributed by *carinata*. We observed pollinator visits to focal individuals of *carinata* and measured seed set, sampled floral resources (nectar and pollen), different plant traits, such as plant density, height and number of flowers. Thus, we established floral resource landscapes from individual-based maps at different spatiotemporal scales and related them to pollinator visits and crop seed set.

We found that pollinators are attracted to floral resources (nectar and pollen) at different spatial scales and in turn, pollinators provide pollination services to *carinata* by doubling seed set at high visitation rates. Moreover, *carinata* individuals can facilitate each other by attracting pollinators at a smaller scale but compete for pollination services at a larger scale with increasing resource availability. Focusing on *carinata* reveals that the addition of floral resources to the agricultural ecosystem can increase ecosystem functioning by stabilizing pollinator communities. However, species interactions are influenced by the use of insecticides and habitat size (area of planted crop fields) that might influence plant-pollinator interactions.

These results are important to mechanistically understanding the role of plant-pollinator interactions in agricultural ecosystems. Our results contribute to the understanding of ecosystem services such as wider ecosystem stability, crop production, food security, human welfare and crop associated biodiversity benefits.

*Speaker

Soil biodiversity, ecosystem services and agricultural practices: an integrated approach to assess the effect of reduced tillage systems

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Many studies worldwide have analysed the impact of reduced tillage systems on different soil functions, but without an overview of the impact of these systems. The SUSTAIN project (European SNOWMAN programme), performed in France and the Netherlands, proposes an interdisciplinary collaboration. One of the goal of SUSTAIN is: how reduced-tillage systems impact on ecosystem services such as soil biodiversity regulation (earthworms, nematodes, microorganisms), soil structure maintenance (aggregate stability, soil erosion), water regulation and quality (run-off, transfer of pesticides) and food production. Data have been collected from long term experimental fields within conventional and organic farming managements (from 5 up to 13 years), and have been complemented with data from farm networks. The impact of different reduced tillage systems (direct seeding, minimum tillage, non-inverse tillage, superficial ploughing) have been analysed and compared to conventional ploughing. Measurements (biological, chemical, physical, agronomical) have been done at several dates which allow an overview of the evolution of soil properties according to climate variation and crop rotation. The study will present some results and conclusions of this collaborative work, thereby shedding light on the benefits and trade-offs related to reduced tillage systems in NW Europe.

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Influence of grazing intensity on dung beetle species assemblages in two distinct bioclimatic contexts

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In European grasslands, livestock is the main source of grazing and one of the largest land use sector in rural economies. Livestock management and the intensity of grazing are likely to deeply modify the ecosystems. While intensive farming is increasing within some regions, more traditional practices are declining within others. Both may give rise to negative effects on biodiversity. A common approach to study the effects of grazing intensity is to compare pastures along gradients characterized by different stocking rates, such as intensive versus extensive grazing, or abandoned, lowly and moderately grazed pastures. But in a given rangeland, the behavior of domestic mammals and the spatio-temporal variability of their activities may result in a non-homogeneous distribution of defoliation, trampling and organic inputs. This heterogeneity of intra-pasture grazing is rarely considered and entirely depends on the type of livestock management. Our aim is to investigate the spatial heterogeneity of grazing on the structure of dung beetle species assemblages. Despite their dependency to herbivorous mammals, which provide suitable dung pats for feed and reproduce, there is little information about the effects of grazing on dung beetles. We sampled rangelands within two contrasted areas in terms of bioclimatic conditions, supporting distinct dung beetle species pools: the Crau steppe near the Mediterranean Sea, and the Vanoise mountains in northern French Alps. We hypothesized that grazing pressure may shape the structure of local species assemblages through several processes: dung quantity (abundance of resource), herbaceous cover and soil trampling (habitat). Grazing pressure may act as a filter would select dung beetles depending on their functional traits. First, we compared the observed patterns between the two study areas. We then disentangle the relative effects of grazing, the environmental conditions and the spatial structure, in order to highlight the relative importance of these processes structuring species assemblages.

*Speaker

Pollinators contributions to crop production in two important mass flowering crops: empirical and experimental assessments under realistic field conditions over four years

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Global food production strongly relies on insect pollination. More than two thirds of crop plants depend on pollinators for their pollination. Oilseed rape (*Brassica Napus* L.) and sunflower (*Heliantus Annuus* L.) are two important mass-flowering crops often found in European landscapes. Their yield was previously shown to rely on insect pollination but the contributions of pollinators varied strongly between studies from null to doubling the yield. Moreover, assessments of pollinator contributions have mostly been conducted on a small scale or under simplified conditions, which do not represent the real contributions at the field scale and do therefore not reflect the importance of pollinators for farmers. In our study, we quantified the contributions of pollinators for these two crops under real field conditions, i.e. directly in the fields of farmers. These estimations were realized at the field scale in order to correctly estimate the contribution of pollinators to yield as well as at the plant scale to understand mechanisms that permit the increase of crop yield. This study also allows identifying pollinators implicated in crop pollination. We show that oilseed rape and sunflower share honeybees as effective pollinators. In addition, wild bees and particularly the genus *Lasioglossum* also increased oilseed rape yield but this was not found for sunflower. We estimated that pollinators increase yield for oilseed rape and sunflower by up to 35% and 40% respectively by comparing yields between fields with low and high pollinator abundances. For both two crops at the field scale, pollinators increased seed fructification success of flowers which increased seed production at plant scale. This study confirms the crucial role of pollinators in crop production and thus the importance to promote

*Speaker

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them in agricultural landscapes for a sustainable production.

*Speaker

Does eco-intensive agriculture improve the resilience of N-cycling related ecosystem services to climatic stresses through modifications of soil microbial community traits and diversity ?

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Conventional agriculture (CA) relies heavily on human inputs and often disregards soil biodiversity and its associated functions. Ecological intensification (EI) has been proposed as an approach to integrate ecological processes into management strategies to enhance ecosystem services (ES). With extreme events becoming more intense and frequent with climate change, the ability to maintain ES under extreme weather is crucial for agroecosystems. Plant and microbial responses to climate events vary between species depending on their functional traits, with fungal dominated microbial communities and conservative plants being expected to be more resistant. The insurance hypothesis claims that higher species diversity insures ecosystems against declines in functioning when facing perturbations. By promoting diversity and selecting for conservative plants and soil fungal communities, we make the hypothesis that EI has a better ability to maintain ES under climatic stresses. Our study aimed to test this hypothesis, comparing responses to climatic stresses (9 months under Drought, Flood or Intermittent rain regimes and 3 months of recovery) of EI versus CA in three land use systems across Europe (arable cropping, grasslands, agroforestry) using common incubations of terrestrial model ecosystems. We focused our investigation on N-cycle related ES (plant N provisioning, soil N retention) and indicators:

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microbial properties (PLFA, enzymatic activities and functional gene abundances and diversity) and soil N pools. Our preliminary results partially support our hypothesis with few beneficial effects of country specific EI management. Furthermore, we observed negative correlation between metalloproteinase gene diversity and leucine aminopeptidase resistance undermining the insurance (biodiversity-stability) hypothesis. Plant and microbial community traits were found to have strong links with N cycling ES level and stability, supporting the interest of trait based approach to understand general drivers of ES in a global change context.

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Bacterial endosymbionts compromise the efficiency of biological control of aphids in strawberry crops

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Insect parasitoids are widely used as biological control agents against insect pests in numerous crops, especially in greenhouses where inundative releases can be implemented. Despite the high density of biocontrol agents, some ecological and biological factors may limit their efficiency. In some insect pests, resistance against parasitoids may exist and lead to the reduction of the biocontrol program effectiveness. In aphids, such a resistance mainly relies on the association with facultative bacterial endosymbionts: some symbionts like *Hamiltonella defensa* can indeed confer a strong protection against parasitoids, limiting their parasitism and by extent, compromising aphid pests control in greenhouses. In France, aphid biological control by using insect parasitoids is often inefficient in strawberry crops. First, we investigated prevalence of bacterial endosymbionts in aphids collected in various strawberry crops. During two successive years, we sampled individuals from seven aphid species in French strawberry greenhouses at the national scale and detected presence of bacterial symbionts using molecular tools. In the three dominant strawberry aphid pests (*Acyrtosiphon malvae*, *Macrosiphum euphorbiae* and *Rhodobium porosum*), we found high prevalence of *H. defensa*, sometimes co-occurring with *Regiella insecticola*, another potentially protective endosymbiont in aphids. In order to correlate symbiont prevalences with parasitism efficiency, the level of protection conferred by these symbionts against parasitoids were secondly measured on aphids sampled in various strawberry crops by considering the two major parasitoid species released in strawberry crops: *Aphidius ervi* and *Praon volucre*. Both field and empirical approaches show that bacterial symbionts may partly explain the inefficiency of the aphid biocontrol program in French strawberry crops.

*Speaker

Ecosystem services and ecological compensation, an approach to favour agroecological transition

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We aimed at defining possible means to combine the ecological compensation obligation and the related environmental added-value with the agroecological transition. Our approach meets two current objectives of environmental and agricultural public policies: the agroecological transition that implies a material change in agricultural practices, and the effective implementation of ecological compensation, that aims at achieving at least no net loss of biodiversity and even net positive impacts. We describe and assess the various relations among agricultural lands, ordinary nature, ecosystem functions and services, and to come up with concrete methodological proposals to construct operational bioindicators based, in particular, on the ecosystems services.

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The synergy of seed-eating carabids and crop rotation in weed regulation

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Global population growth and increasing demand for food has resulted in unsustainable expansion and intensification of agriculture, and is one of the most pressing environmental challenge we face. It is widely recognized that agricultural production, and food security, depends strongly on ecosystem services such as pollination and pest management, but limited understanding of the drivers and processes involved in the provision of these services restricts our capability to manage and fully integrate their benefits into agricultural systems. Here we use advanced modelling approaches to analyse the effect of crop rotation and carabids on in-field weed regulation, revisiting data from the largest agricultural field experiment ever conducted in Great-Britain. The Farm Scale Evaluation (FSE) collected data on crop history, seed bank composition and amount, standing weed communities, seed rain and ground beetle communities in 257 conventionally managed fields over a 4-year period. Using structural equation modelling (SEM) approaches and food network analysis, we quantify the combined roles of crop rotation, management practices and biological control (via ground beetles: Carabidae) on in-field weed control and seed bank dynamics. In contrast to previous "piecemeal" analyses of the FSE data, our integrated approach based on causal inferences provides a mechanistic understanding that quantifies the impact of infield biodiversity on weed regulation. Our results show clearly a regulating effect of ground beetles on the composition and the density of weed seed in the seed bank. This study highlights the benefit of measures aimed at maintaining populations of ground-beetles and resilient food webs for integrated weed regulation in arable fields, contributing to both the maintenance of productivity and mitigating environmental impact of agriculture by reducing farmer-dependence on chemical pest management.

*Speaker

Effects of a nitrogen fixing shrub introduced as a fertilizer for maritime pine forestry in the south-west of France

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Nitrogen fixing species are a well-known leverage for increasing the soil fertility in agriculture. Nevertheless they are uncommonly used in forest ecosystems. The ”Landes de Gascogne” forest (SW France) has soil fertility issues and *Ulex europaeus* – a very vigorous species also known as *common gorse* – is native from this region. For these reasons, this forest is a suitable ecosystem for trials associating trees dedicated to wood production and N-fixing understory species.

The forestry itinerary developed here distinguishes two main periods separated by the whole gorse population crushing. This trial is in a relatively rich site of the forest. Firstly, when gorse individuals grew and became a dense stand, pine mortality increased during dry season, underlying competition for water. Meanwhile, growth was affected too, but only in diameter, indicating a pine stem elongation to avoid light competition induced by gorses. Pine morphological traits were rather badly affected regarding to straightness and verticality. However, a natural pine pruning effect was enhanced in the presence of a dense gorse stand.

Gorse stand was crushed after five years. Quickly afterward, we measured a nitrogen needle enrichment reflecting a fertilizing effect of gorse remnants. Crushing also made pine free from shrub competition and a ”catch-up growth” was identified regarding diameter. Two years after the gorse crushing, tree size and biomass were similar among experimental treatments that included – or not– gorse.

In conclusion, during the eight first years of this study, gorse introduction in pine tree forestry appeared to have mixed effects: gorse induced competition. On the other hand, gorse led to high input in nitrogen into the ecosystem with positive effects on tree nutritional status. Therefore, it is necessary to continue the assessment of the pine-gorse association in the ”Landes de Gascogne”, for higher time scales and on poorer sites.

*Speaker

Behavioural and Dispersal Ecology

Movement patterns of yellow eels (*Anguilla anguilla*): a 3-year RFID study

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Animal capture-recapture and individual identification within a population provide estimations about population structure and dynamics. In the case of migratory fish population monitoring, radio frequency identification methods (RFID) are used to collect information on life-history traits (growth, age of sexual maturity, reproduction, etc.) or dispersal into the river (for food research or reproduction). In this context, from 2015 to 2017, our study aims to analyse yellow eel behaviour into rivers. Identified as a Critically Endangered species on the IUCN red list, understanding eel behaviour during its freshwater phase is essential to manage their populations. Unlike conventional fishing methods, RFID studies are efficient to track eels even in water depth higher than 70 cm while these areas may represent a significant part of the stock. In Oir River, tributary of Selune River (Low-Normandy), every caught eel larger than 20 cm have been tagged with 12mm PIT-tags in low frequency (134.2 kHz), with Half-Duplex technology. On this river, a network of 9 pass-through antennas was set up along a 500 m long section to detect eels' movements. The whole site was frequently scanned with a transportable antenna (i.e. backpack-mounted) to search for less mobile individuals. Among tagged individuals, 559 eels are identified with their PIT-tag number whose 93% are detected during various monitoring occasions. The first results highlight behavioural differences between sedentary and transient yellow eels, a typical nocturnal activity, and day-to-day movements around their capture area. Additional analysis of recaptures data will estimate individual growth in this river.

*Speaker

Host suitability for *Aphidius colemani* (Hymenoptera: Braconidae): Can host origin influence parasitoid's choice and progeny fitness?

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Plant diversity in agroecosystems is known to increase the stability of communities and the ecosystem service of biocontrol, through providing refuges and different food resources for alternative hosts and for pest natural enemies. Alternative hosts could allow parasitoids to overwinter, favoring an early colonization of target crops, then increasing the attack of pest hosts. However, it is necessary to check whether this transition between two host species by parasitoids affect the host-searching behavior of the female parasitoid and the fitness of the first generation in the target host species. The aphid species *Myzus persicae* on peach orchards and *Rhopalosiphum padi* in cereals share natural enemies, such as the parasitoid *Aphidius colemani*. During winter months in Chile, *R. padi* is parasitized by *A. colemani* on the first stages of winter grasses, being able to act as a refuge for parasitoids to ensure the early arrival of *A. colemani* to peach orchards for the control of *M. persicae*. It is hypothesized that there is no host preference by *A. colemani*, regardless the host of origin, and that both aphid species represent equal quality hosts for *A. colemani*. To test these hypotheses, we evaluated the host preference and performance of *A. colemani* collected from *R. padi* in cereals and *M. persicae* in peaches, through different behaviors and fitness traits as parasitism rate, progeny survival and developmental time. Our results showed preference of females *A. colemani* to one aphid host (*R. padi*) regardless of the host of origin. Higher defensive behavior of *M. persicae* could be an explanation for its less profitability. Despite differences, both aphid species are suitable for development. Further investigation of the interactions among *A. colemani* and both *M. persicae* and *R. padi*, are therefore important for the implementation of this biocontrol method.

*Speaker

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Home range size and environmental heterogeneity: a review of metrics and an inter- and intra-specific comparative study

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Understanding how animals move in heterogeneous landscapes is key to forecast their response to environmental changes, at the scales of individual decision-making, individual home ranges, population density, and species distributions. After decades of research (Kie et al. 2002), we still have issues addressing this fundamental question of the link between the heterogeneity of the environment and the spatial ecology of animals. This is largely because of inconsistent definitions of heterogeneity, but also because we lack a clear understanding of species- and individual-variation in spatial behavior. For my PhD work (2017-2020), I focus on the intra- and inter-specific differences in movement behavior in four species of ungulates (roe deer, red deer, chamois and mouflon) at seven heterogeneous study sites in France. These species and populations have broadly similar ecologies, but they exhibit key differences, e.g., in post-natal behavior, predator avoidance, feeding strategy and in the amount of thermal stress. I study the causes and consequences of these differences as they pertain to spatial ecology, with the broader objective to upscale the insights into population and community-level inference. I jointly document the variation in home range size and the variation in environmental heterogeneity. I compare different metrics of heterogeneity focusing on different scales and on spatial vs. temporal heterogeneity. Among metrics of heterogeneity, I particularly focus on those derived from spectral analyses (e.g., Fourier transform). This presentation would be suitable for a thematic session on "Movement Ecology" with its main organizer Simon Chamaillé-James.

*Speaker

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Modelling the response of the distribution of benthic marine species to climate change

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In a context of climate change, understanding the response of species to changes in the environment and the implications for their geographic distribution is of paramount importance. Through the formulation of relationships between the organism and its environment, species distribution models (SDM) provide a tool to assess how species distribution would respond to environmental stressors. Our study presents the development and a first application of a mechanistic and generic SDM, using a multi-agent modelling platform: NetLogo. The model simulates the spatial and temporal population dynamics of a marine benthic-pelagic species with an individual-based mechanistic approach of the life cycle. It couples a Dynamic Energy Budget model of the individual life history traits in relation to temperature and food concentration (e.g. phytoplankton), larval dispersal due to currents (oceanographic connectivity) and competition for space at the recruitment phase. The model is applied to the blue mussel *Mytilus edulis* along the coast of Brittany and scenarios of environmental changes target the effect of seawater warming based on the results of a climate model (Representative Concentration Pathway RCP8.5, model CNRM-CM5). We show that oceanographic connectivity drives the population dynamics and local changes are likely to affect distant population structure. Simulations show that seawater warming modifies the demographic structure of *M. edulis* and the phenology of the reproduction but temporal changes are smaller than the differences due to local environmental conditions.

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Disease avoidance conditions the dispersal patterns of western lowland gorilla females

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Social dispersal is an important feature of species dynamics. When mammal females are structured in polygynous groups, their dispersal decisions are conditioned by various female-, male-, and group-related factors. Among them, the influence of disease often remains difficult to assess. The major drivers of female social dispersal are inbreeding avoidance, reduction of predation risk, reduction of competition, selection of a higher-quality male, and reduction of pathogen transmission. However, among them, the influence of disease often remains difficult to assess and has been little investigated in social species. To address this challenge, we investigated the extent to which disease avoidance drives the dispersal decisions of gorilla (*Gorilla gorilla gorilla*) adult females, after controlling for other potentially influential factors. Studies on wildlife and humans show that individuals attempt to avoid disease transmission using external signs of disease on conspecifics. Therefore, we studied disease avoidance in gorillas using yaw-like skin lesions as visible signs of disease in two long-term monitored populations. Yaw prevalence, which was mostly expressed through facial lesions, was 16-22% individuals depending on the year and population. We monitored 212 different females and observed 112 dispersal events. Whatever the population, we showed that adult females avoided breeding groups with a high prevalence of skin disease by emigrating from them and immigrating into healthier ones. By contrast, females did not choose silverbacks according to their disease status. Instead, the critical silverback's feature seemed to be his age. Indeed, females preferentially joined young groups led by young fully-grown silverbacks, rather than older ones. Those silverbacks could be of higher reproductive and protective value. Our study highlights that disease avoidance and selection of high-quality males are critical drivers of gorilla female dispersal decision.

*Speaker

Intra-specific morphological variation of the spermatheca in the simultaneously hermaphroditic land snail *Helix aperta*

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In the majority of internally fertilizing animals, females are equipped with sperm storage organs where they store the sperm received during copulation. In many simultaneously hermaphroditic pulmonates, these organs consist of complex spermathecae that show inter- and intraspecific variation in their structure. This variability is theoretically predicted by postcopulatory sexual selection in the context of sperm competition and cryptic female choice. In this study, the variation in the structure of the spermatheca was investigated in the land snail *Helix aperta* from four natural populations near Bejaia in northern Algeria. The populations were different in local snail density, probably also reflecting the intensity of sperm competition. We tested whether the spermatheca showed differences that are predicted by sperm competition theory. In addition, we tested whether the spermathecal structure depends on the shell size and/or is correlated with other reproductive organs that are thought to be affected by sexual selection. We found that the fertilization pouch of *H. aperta* consists of a simple fertilization chamber and 3–9 spermathecal tubules. The four populations did not differ significantly in the mean number of these tubules. However, significant differences were found in the length of the main tubule, the length of the fertilization chamber, and the average length of lateral tubules. In addition, strong associations were detected between the lengths of these structures and the local snail density, while no effect of shell size or reproductive organs was found. Our results indicate that the intensity of sperm competition may not affect the total number of spermathecal tubules, but may increase their lengths. This increase in spermathecal length may reflect an improved sperm storage capacity that is probably beneficial in situations of high sperm competitions intensity.

*Speaker

Spatial behavior of female red deer in response to hunting

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Spatial behavior in response to predation is the result of a trade-off between the perception of the risk and the benefits to be gained from engaging in another activity. Hunting, including drive hunts, can be considered as a predation process. Although drive hunts are spatially well defined, the scale at which the hunting risk is perceived by preys remains poorly documented. It is unclear whether hunting disturbance occurs beyond the hunted areas and how it may trigger anti-predator behaviors. The present study aims at (1) investigating the effects of drive hunt on the spatial behaviour of red deer and (2) understanding the main determinants affecting the intensity of the spatial response at the individual level. We hypothesize that (H1) the distance to hunters affects the intensity of spatial anti-predator responses and (H2) topographic obstacles and vegetation cover modify the risk perception by animals.

We used GPS and activity data from 91 female red deer collected in the National Hunting and Wildlife Reserve of La Petite Pierre (Bas-Rhin, France), between 2004 and 2017. Each year, drive hunts were conducted by about 40 hunters and 5 dogs, once a week from October to February.

Female red deer increased their activities and their speed, and enlarged their home-range size in response to hunting. The intensity of the spatial response appeared linked to the distance to hunters, while topographic obstacles and vegetation cover had no significant effect. Animals almost doubled their home-range size for short distances to hunters while no change in home-range size was found in low-risk situations (distance > 500 m).

This study brings new insights into our understanding of non-lethal effects of human predation on animal spatial behaviour. It allows to rethink hunting practices at the right spatial scale, in the new ‘hunting for fear’ context for ungulates management.

*Speaker

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Future flights across the Arctic basin: Will climate change overturn bird migration?

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Climate models predict that from 2050, the Arctic Ocean will be sea-ice free each summer. This will modify a wide range of ecological processes, including bird migration. We assessed the potential for new transarctic bird migration (overturning migration from the Atlantic into the Pacific) and/or arctic year-round residency as a result of a disappearing arctic sea-ice cover following global warming.

Among the 449 bird species which breed in the Arctic, we identified 24 which may stop migrating, and 29 which may engage in trans-arctic migration, on the basis of their biological characteristics. Potential future resident species were mainly pelagic seabirds and coastal migrants, whereas only arctic pelagic migratory birds may potentially engage in future transarctic migrations regarding sea-ice melt.

To illustrate the opportunities and constraints acting upon the birds engaged in those strategies, we performed an in-depth modelling study of the biogeography of the Little auk (*Alle alle*), a pelagic, migratory bird endemic to the Arctic, and one of the most numerous seabirds in the area. By coupling species distribution models (SDM) and climatic models, we estimated the range of future wintering and breeding areas, for resident or transarctic migratory individuals. Further, we used a mechanistic bioenergetics model (NicheMapper), to compare the energetic costs of current little auk migration from the high-Arctic into the temperate Atlantic, with potential future strategies of high-Arctic residency or transarctic migration from the North Atlantic into the North Pacific. Overall, we demonstrate that all three migratory strategies may occur in little auks; but that even if bird thermoregulatory costs may be reduced in a warming Arctic, transport costs across the arctic basin will remain substantial.

This study illustrates how global warming may impact the biogeography of migratory species, and how seascape conservation and marine management should integrate these upcoming major changes.

*Speaker

Is dispersal ability context- or phenotype-dependent in the long-lived land snail *Notodiscus hookeri*

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Dispersal is a fundamental life-history trait of organisms, with its costs/benefits balance shaping how eco-evolutionary processes unfurl in space. In land gastropods (> 20,000 species), variation in dispersal ability has been so far virtually unstudied outside of a few invasive or model species. This is despite the molluscs having one, if not the most costly movement type among animals.

On the Sub-Antarctic Possession Island, the endemic land snail *Notodiscus hookeri* is a lichen-feeding species that presents two contrasted shell ecophenotypes (soft organic shell or hard mineralised shell) depending on calcium availability.

We used mark-recapture to study the dispersal movements of three populations, differing in shell ecophenotype. Based on previous work on dispersal and this species ecology, we hypothesized that (i) dispersal in *N. hookeri* would be context-dependent, with unfavourable habitats left more readily, despite high movement costs making dispersal beyond short distances nearly impossible, (ii) lichen availability, and snails' trophic preferences, would drive this context-dependency, and that (iii) dispersal would be phenotype-dependent, with the morph investing less energy in shell production (i.e. the hard one) being potentially the most dispersive.

Patch choice after 28 days was strongly constrained by distance, with most recaptured snails settling within 0.5 m from their release point. Snails nonetheless made informed dispersal decisions, with low lichen availability and small patch size strongly increasing emigration probability (with a ~4-fold increase between the best and worst-quality patches). Dispersal was also seasonal, with limited movements during winter. Dispersal tendency varied among populations, but this could not be linked to shell phenotype.

These results confirm the ubiquitousness of context-dependent dispersal and add to our knowledge of an ecologically important but overlooked process in land gastropods; they simultaneously raise questions about how such a poor active disperser was able to colonize the near totality of Possession Island.

*Speaker

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Surrounding pathogens shape maternal egg care but not egg production in the European earwig

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Pathogens are ubiquitous in nature and typically entail major fitness costs in their hosts. These costs can be particularly important when individuals exhibit poor immune defenses, as it is often the case during early developmental stages. Hence, selection should favor parental strategies limiting the risks of pathogen exposure and infection in their offspring. In this study, we investigated 1) whether females of the European earwig *Forficula auricularia* avoid areas contaminated with spores of the entomopathogenic fungus *Metarhizium brunneum* prior to and at egg laying, as well as 2) whether spore presence entails an increase in females’ investment into both pre-hatching forms of care and clutch quantity and quality. Our results first show that females did not avoid contaminated areas prior to and at egg laying. However, females returned to their eggs faster in presence of living spores compared to UV-killed or no spores. They were also more likely to construct a nest when in presence of both living and UV-killed spores (but only in one studied population). Finally, we found that spore presence did not influence maternal investment into egg grooming, egg gathering and egg defense, as well as into clutch quantity and quality. Overall, our results demonstrate that earwig females do not avoid contaminated environments, but could mitigate the associated costs of pathogen exposure by adjusting their level of egg care. These findings emphasize the importance of pathogens in the evolution of pre-hatching parental care and, more generally, in the emergence and maintenance of family life in nature.

*Speaker

Habitat characteristics and species interference influence space use and nest-site occupancy: implications for social variation in two rodent sister species

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Nest-site selection is an important component of species socio-ecology, being a crucial factor in establishment of group living.

Consequently, nest-site characteristics together with space-use proxies may reveal species social characteristics, a fact particularly interesting when direct observation of social interactions is hindered in nature. We used this approach to assess social variation between two sister species of a southern African rodent (*Rhabdomys bechuanae* and *R. dilectus dilectus*) comparing patterns in allopatry and sympatry. Our results indicate that habitat preference and its impact on space-use and nest-site characteristics could act as an important driver of social divergence in our study models, and that interference between sister species could induce new ecological pressures that may influence their social evolution.

*Speaker

Bodyguard or unfair competitor: Is the African elephant a modifier of predator-prey relationships at waterholes?

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In natural communities, modifications of interspecific interactions (e.g. competition or predation) are difficult to investigate. Large mammalian communities of African savannas are ideal to assess such interaction modifications, particularly near waterholes where numerous species aggregate. Here, we assessed the role of the African elephant as a modifier of predator-prey interactions, in Hwange National Park, Zimbabwe, characterized by one of the highest elephant population density. Previous studies investigating competition for access to water between elephants and other herbivores revealed an aggregation of some herbivore species to elephants when water becomes scarce, contrarily to expectations under a competition hypothesis. Here, we considered two alternative hypotheses to explain this pattern. (i) The "bodyguard hypothesis" suggests that elephants reduce the perceived predation risk of other herbivores because of the mobbing behaviour of elephants toward predators, making closeness to elephants beneficial for other herbivores. Using behavioural experiments with lion roaring playbacks as stimuli of predator presence and video recording of herbivore behavioural responses (n = 32), we assessed the effect of elephant presence on herbivore aggregation and vigilance behaviour. Whereas vigilance levels increased after lion roaring, no effect of elephant presence on aggregation and vigilance of herbivores was detected. (ii) The "water quality hypothesis" suggests that heterogeneity in water quality inside waterholes drives the aggregation of elephants and herbivores in places where water quality is the highest. Based on physicochemical variables to assess water quality combined with measures of distances between herbivores and areas of good-quality water (n = 315), we investigated the effect of elephant presence on access to good-quality water. Our results support the heterogeneity of water quality inside waterholes but did not suggest any effect of elephant presence on the drinking behaviour or water quality selection by herbivores. We discussed these results and the potential role of African elephants as interaction modifiers.

*Speaker

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Blue tits and caterpillars in a boreal forest: impacts of early life food conditions on nestling growth, fitness and personality

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Among all environmental variables causing variation in phenotypes, food supply is thought to be the most important, for it is the fuel for growth and development. Especially in early life, food conditions can shape growth, which in turn is determinant for survival, reproductive success, and therefore fitness. During 10 years, we collected data on caterpillars and on 752 broods of blue tits (*Cyanistes caeruleus*), in a boreal forest of Southern Finland. The aim was to investigate the importance of food availability, especially during the first days of life, in the development of nestlings. Caterpillars are supposedly the main food resource for blue tits nestlings (40-80% of their diet, depending on the habitat). We found seasonal variation in caterpillar biomass in birches (*Betula sp.*), typically raising in May, reaching a maximum in early June and declining in the course of June. Caterpillar biomass also showed strong annual fluctuations, with no distinct seasonal peak in years with low biomass. This absence of clear peak is uncommon, and prevented us from determining the synchrony of broods with food supply. Therefore, we opted for a "time- window" approach, measuring the total amount caterpillar available for broods, during 3 time- windows of the nestling period. We found a positive relationship between nestling growth and caterpillar biomass, during the different time-windows, proving that blue tits in this population actually rely on caterpillars. We measured the influence of early food conditions (caterpillar biomass before day 9) on 16 day-old nestlings, and found a positive effect on body development (tarsus, wing and tail length) and on personality (aggression), but not on fitness (nestling survival and mass). The population's breeding success also increased with daily caterpillar biomass. These results, obtained with a new approach, highlight the impacts of food availability on nestling development and are consistent with previous studies.

*Speaker

Why produce males when your daughters are parthenogenetic ? The case of *Mesorhabditis*

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Sperm-dependent parthenogenesis, also called pseudogamy, is a reproductive strategy in which females use the sperm of males from another species to activate their oocytes. Later, the sperm DNA does not participate to the development of the zygote, which produces only females. Here we report a new and unique reproductive strategy found in the pseudogamous nematode species *Mesorhabditis belari*, which produces its own males. While fertilization is needed to activate all female oocytes, 92% of oocytes undergo a single meiotic division, do not decondense the male DNA and produce diploid females by gynogenesis. In 8% of the cases, oocytes undergo two rounds of meiotic divisions, the paternal DNA decondenses and mixes with the female DNA, producing exclusively diploid male individuals. The question is then: 'Why do females produce these males instead of relying on the other's sons?' since their genetic material does not participate to the female fitness. A game theory model completed by computer simulations, explains why males are maintained in these populations provided they behave in a particular and efficient way. The behaviour of the males was then studied experimentally and was shown to fit the model's requirements.

*Speaker

Relationship between abundance and habitat suitability: spatial and temporal variation in a Houbara bustard population

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Information on the species distribution, both in terms of presence or abundance, is critical in conservation to predict the consequences of climate or other human-induced changes on species dynamics and ecosystem functioning and to take informed decisions concerning biodiversity management.

In recent decades, Species Distribution Models (SDMs) have been increasingly used and considered as useful tools to understand and predict the relationship between species presences and environmental variables. These models statistically link species occurrences statistically to environmental variables, providing an index of habitat suitability, called here "HS index". However, the relationship between environmental quality and local abundance of a species is not straightforward, and might vary over time. A triangular relationship between abundance and environmental suitability is expected, with low abundances for low habitat quality, and both low and high abundances in places with high HS.

Using long-term monitoring of a North African Houbara bustard (*Chlamydotis undulata undulata*) population, we studied how temporal variation in population abundances influences the relationship between abundance and environmental quality. We estimated the abundances of the bustard population and studied the abundance-HS index relationship. We then evaluated the deviations to this relationship with the observed growth rates of the population, demonstrating the effects of the spatial and temporal variation of population abundances on SDM prediction. Our results confirmed our predictions: a triangular relationship is observed between abundance and habitat suitability predicted by niche models, as well as a local deficit of abundances compared to the predicted potentialities of the environment. Our results provide one step forward toward a better understanding of the relationship between habitat suitability and demographic processes. We will also discuss the implications of these results for the use of SDMs in the context of population reinforcement.

*Speaker

The effects of the identity of the experimenters on the behavioural response of Montagu's harrier chicks during field monitoring

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Human activities are stress factors for animals which perceive them as a predation risk. Animals facing anthropogenic disturbances may exhibit different behavioural responses depending on their perception of the risk. Experimental measures of behavioural, physiological and life history traits may be biased by the disturbance due to experimenter handlings and activities. In this study, we assessed the effects of repeated visits on 16 nests of Montagu's harrier (*Circus pygargus*) on the behavioural responses of chicks, by changing or not the identity of experimenters at each visit. These nests were divided into two groups: Group A = nests were visited by the same three experimenters at each visit and Group B = nests were visited by three different experimenters at each visit. Nests were visited four times. We noted that the two groups of experimenters had different effects on chick behaviours depending on the order of nest visits. Contrary to our hypothesis, handling by the same persons at each visit did not reduce aggressive behaviours (scores of movements and attacks with beak and claws) of the chicks towards experimenters. These results suggest that the identity of the experimenters may affect the development of the behaviour of the chicks and are discussed for their implication in studies of conservation biology.

*Speaker

Moonlight selection on the plumage coloration of barn owls

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Evolution of colour polymorphism is linked to environmental light conditions. If the role of variation in diurnal light has been largely studied, the evolutionary implications of its nocturnal counterpart, moonlight variation, are barely known. The lunar cycle results in repeatedly changing light conditions, setting the ground for the coexistence of alternative colour forms. Using a long-term monitored population of barn owls, we investigated the consequences of moonlight variation on food provisioning and fitness of owls with white-to-rufous plumage coloration. Rufous owls provided less prey to their nestlings during full-moon nights than during new-moon nights, which associated with lower body mass and survival of their offspring. Moonlight did not affect food provisioning in white owls. However, contrary to rufous owls, the survival of the white owls' youngest nestlings was favoured by full-moon days. In the laboratory, we investigated the antipredator behaviour of the barn owl's common prey, the common vole, under full- and new-moon light conditions and when exposed to simulated attacks of white and rufous owls. Both white and rufous owls were more easily detected by voles under full-moon light conditions but white owls induced longer freezing times on rodents under full-moon light conditions. By inducing longer freezing times in voles, white owls may see their hunting success enhanced during full-moon nights. This could palliate the negative effect of increasing moonlight levels on hunting success and fitness as observed in rufous but not in white owls. It also suggests that the rare white coloration of barn owls might have evolved to exploit moonlight variation and prey sensory biases. Although our results show that the lunar cycle alone cannot explain maintenance of colour variation in barn owls, they highlight that moonlight can select for the coloration of nocturnal species, altering the fitness benefits derived by alternative colour phenotypes.

*Speaker

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Impact of landscape linear features on movements and home range distribution in 5 species of large herbivores

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Identifying the environmental or behavioral factors that promote or constrain animal movement and the establishment of their home range is an essential step in understanding the ecological consequences of habitat fragmentation. Among these factors, the configuration of the landscape, in particular the distribution of anthropogenic and natural linear features has been found to favor or to impede the movements of animals. In territorial species, these elements of the landscape are also often very important in the division of space between neighboring individuals/groups. However, we can expect a strong variability of the role of linear features on the movements and spatial distribution of home ranges, related to the environmental context, the nature of anthropogenic disturbances, both the evolutionary and ecological traits of species and finally, individual characteristics. A better understanding of how these different factors influence the behavioural response of individuals to linear features requires to rely on comparative approaches contrasting species and populations. We present here a comprehensive spatial analysis of GPS data collected in 7 populations of 5 species of ungulates (ibex, roe deer, chamois, red deer, and mouflon). Populations differ in their level of heterogeneity and anthropic disturbance, whereas species are contrasted in terms of territoriality, gregariousness, and diet. Our work should help to better understand the link between the rules governing the movement of individuals, according to the species-specific evolutionary constraints and the environmental characteristics they encounter, and the design of their home ranges in fragmented landscapes. This presentation would be suitable for a thematic session on "Movement Ecology" (main organiser: Simon Chamaillé-James).

*Speaker

Niche conservatism in stream diatoms

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Niche conservatism, whereby species niche characteristics are conserved over space and time, is an important cause for large-scale species distributions and diversity gradients on Earth. Dispersal mechanisms are expected to have a strong effect on niche conservatism, considering that high dispersal rate may prevent local adaptation and favor niche conservatism. In freshwater ecosystems, diatoms are usually recognized as cosmopolitan species, due to low dispersal limitation and high reproductive rates. However, the extent to which niche characteristics of diatoms are conserved across space has rarely been tested and should give interesting insights for the understanding of their biogeographic distribution. To address this question, we implemented species distribution modeling and analyses of species niche breadths and optima. Species distribution models (SDMs) along environmental and climatic gradients were developed with data from the US and then tested with datasets from France, Finland, New Zealand, Antilles and La Réunion islands. Given that the US SDMs poorly predicted the species distributions in other regions, we concluded that diatoms do not appear to exhibit niche conservatism. Weak correspondence of niche optima and niche breadths in one region with the respective species properties in another region further indicated a general lack of niche conservatism. Analyses of species differing in occupancy (i.e., core vs. satellite species) and traits (i.e., diatom ecological guilds) further confirmed that niche conservatism was also weak across functional groups. Although diatoms species are considered to be generally dispersal-unlimited, our results indicate that their dispersal rate may be more moderate than previously thought. Finally, the capacity to adapt locally to environmental and climatic conditions may allow diatoms to better cope with global environmental changes.

*Speaker

Intra- and transgenerational carry-over effects on behavioural reaction norms of the freshwater snail *Physa acuta* in response to predation

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Behaviour is a labile and reversible trait allowing a rapid response to environmental changes. Evidence is accumulating that individuals differ in the degree and extent of behavioural plasticity, even within a same population. What is the role of past environmental conditions on between-individual differences in this form of phenotypic plasticity is still not well understood. Although previous environments experienced by animals themselves can be a source of between individual difference in behavioural responses, less is known about the effect of ancestral environment. Ancestral environment can indeed have long-lasting effects on offspring phenotype (e.g. morphology) and some studies showed such effects on average behavioural responses. These transgenerational carry-over effects (called transgenerational plasticity) could also influence the between-individual variation in behavioural plasticity. In this context, we used the concept of behavioural reaction norms to study how intra- and transgenerational carry-over effects influence between-individual variation in both personality and level of behavioural plasticity (respectively intercept and slope of the behavioural reaction norm). We investigated the behavioural reaction norms of the freshwater snail *Physa acuta* in response to predator cues according to past (intra- and transgenerational) experience of predation risk. This species is known to increase its survival by expressing anti-predator behaviours (especially crawling-out the water) when the predator is detected. Moreover, as this species has a short generation time, parental environment should be a good proxy of offspring environment in the wild, and transgenerational carry-over effects should have been selected. Two generations (parental and offspring generations) were raised in control or predator-cue environments. We then measured in all mature offspring two behavioural traits in control and in predator-cue environments: exploration (total distance crawled in the water) and escape behaviour (time to crawl out the water).

*Speaker

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Who are you? No kin discrimination during egg care in the European earwig

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Kin discrimination is the ability of an individual to distinguish between close genetic kin and non-kin and to adapt its behaviours accordingly. Kin discrimination is often considered as a keystone in the evolution of parental care, as it allows parents to address cooperative behaviours towards their own offspring, while limiting the risk of social parasitism and the resulting costs of providing care to unrelated individuals. In this study, we investigated whether females discriminate between related and unrelated eggs in the European earwig *Forficula auricularia*. In this insect species, females provide extensive forms of care towards their eggs over winter, without any food intake. We set up four types of experimental clutches, in which females tended either their own clutch of eggs, an unrelated clutch with a similar number of eggs or no egg at all, or in which eggs were maternally deprived. Our results first confirm that maternal deprivation leads to a total failure in term of eggs development and hatching success. However, we found that the level of maternal investment into egg grooming, egg defence and egg abandonment was independent of eggs origin. Similarly, egg hatching success and juveniles quality were not associated with their genetic relatedness to the tending mother. Overall, these results reveal that earwig mothers do not discriminate against foreign eggs. More generally, they show that the evolution of parental care does not necessarily rely on and/or lead to the emergence of kin discrimination in insects.

*Speaker

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Antagonistic co-evolution as driver of behavioural traits

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The interactions of individuals with members of their own species and with members of other species are a strong driver for the rich diversity in forms, functions, strategies and behaviors. We study the evolution of traits and behaviours in various ecological interactions of *Drosophila*, including sexual conflicts, interference competition for food, host-parasitoid co-evolution, and the invasive biology of a pest species. In particular, we focus on the genomic basis of adaptive evolution of complex traits and behaviours, especially in antagonistic interactions. Antagonistic interactions can result in continual adaptations and counter-adaptations among the involved parties, and can lead to dynamic and rapid evolution. This is also exemplified in that the fastest evolving genes are those that are involved in defense and sexual conflict. In this presentation, I will present our current studies of antagonistic co-evolution as driver of phenotypic and genetic variation in behavioural traits.

*Speaker

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Consistent fission-fusion dynamics across populations of Cape buffalo (*Syncerus caffer caffer*)

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Fission-fusion dynamics allow animals to flexibly balance costs and benefits of group living, and respond to changing environmental conditions by adjusting group size. Most studies on fission-fusion dynamics published to date focus on one population only, but little is known about the degree of variation in fission-fusion dynamics within the same species. In this study, we investigated the consistency of patterns and drivers of fission-fusion dynamics across three populations of Cape buffalo, in different protected areas in southern Africa (Hwange National Park and Gonarezhou National Park, Zimbabwe, Kruger National Park, South Africa). During 2008-2013, we tracked 54 adult female buffalos in different groups using GPS collars. We used GPS-tracking data to assess home-range overlap (HRO) and association patterns between individuals. We also investigated the temporal dynamics of fission-fusion events at daily and seasonal scales and examined the main ecological factors influencing those events. We found that in all populations association patterns increased non-linearly with HRO, similarly across seasons, but remain highly variable for specific HRO. Fission-fusion dynamics varied seasonally and similarly in all populations: fission and fusion frequency, as well as the duration of fusion periods, was greater in the wet season than in the dry season. Duration of fission periods were shorter in the wet season. At the daily scale, fission and fusion events were more likely to occur in the early morning and from mid-afternoon to early evening. Finally, whilst habitat structure did not influence both fusion and fission locations, we showed a strong effect of water availability on fission-fusion dynamics in one population. Our study sheds light on the consistency of fission-fusion dynamics within species.

*Speaker

Biological invasions

Black locust (*Robinia pseudoacacia*) effects on above- and belowground ecosystem compartments in Northern France

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Invasive alien species, such as Black Locust (*Robinia pseudoacacia* L., Fabaceae), are a source of increasing concern among anthropogenic global changes. *R. pseudoacacia* is a tree of North American origin frequently encountered in European forests. While favored by economic actor, notably for its high wood quality, negative environmental effects have been documented such as on native plant communities (Vilà et al., 2011), nutrient cycling (Pereira et al., 2011) and arthropod abundance (Buchholz et al., 2015). Here we attempted to assess results in a different context and provide new data on other compartments of soil ecosystems. We sampled and measured native vegetation, soil, soil fauna and habitat structure in pure *R. pseudoacacia* plots, pure native plots (*Quercus petraea* and *Castanea sativa*) and mixed plots within 6 forests in north-western France. We observed differences in habitat structure (higher canopy openness and stem density) and environmental physico-chemical properties (higher nitrogen content, especially of nitrates). We found no congruent differences in leaf litter decomposition rates or soil microbial respiration. Microbial and fungal biomass showed important differences in some forests, but not all. We also showed important differences in plant community structure, both taxonomically and functionally, between invaded and uninvaded plots. Mesofauna communities (Collembola and Acari) were also affected, generally but not always positively, by *R. pseudoacacia*. *R. pseudoacacia* presence, especially in monospecific plots. Macrofauna species richness also tended increased in *R. pseudoacacia* plots while abundance tended to decrease although this was strongly dependent on which native species was considered as a control. Overall, we showed some overarching effects of *R. pseudoacacia* on some taxa or particular variables (Nitrogen, for instance). Invasive species clearly modified above and belowground compartments although several additional effects were more contextual and dependent on site and control (tree species) type.

*Speaker

Genome merger and duplication as springboards for plant invasion: lessons from *Spartina*

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During the last centuries, species introductions outside their native range have dramatically increased and have accelerated ecological changes, native species threat, but also biological diversification through rapid expansion of introduced plants, interspecific hybridization with natives and allopolyploid speciation. In evolutionary ecology, the polyploid grass genus *Spartina* provides one of the most fascinating examples with this respect, and it well-illustrates the multifaceted challenges of invasive population management. *Spartina* contains several species that have become highly successful invaders of intertidal mudflats and saltmarshes where they play an important ecological role as "ecosystem engineers". In Europe, such examples include (i) the cryptic introduction of the East-American tetraploid *S. patens* (which has until recently been considered as a Mediterranean endemic under the name of *S. versicolor*), (ii) introduction of the South-American heptaploid *S. densiflora* to the south-west coasts of the Iberian Peninsula and its subsequent hybridization with the native hexaploid *S. maritima* and (iii) introduction of the East-American hexaploid *S. alterniflora* to western Europe (UK, France, Spain) and its hybridization with *S. maritima* in England and in southwest France. In England, hybrid genome duplication resulted in a highly successful allododecaploid species, *S. anglica* that has now colonized European saltmarshes and is introduced in several continents. *Spartina* represents then an excellent model system to explore at various evolutionary time scales the genomic determinants of species expansion. Hybrid and polyploid genome dynamics, gene expression evolution in stressful conditions will be discussed in the light of their ecological implications

*Speaker

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Understanding the past for the future management: Effects of current and historic land Use on invasive plant diversity in Southeastern Togo, West Africa

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Biological invasions and changes in land use are two components of global change affecting biodiversity worldwide. Both contemporary and historic land use may influence the spread of invasive plants by altering landscape patterns, soils, and biotic communities. Indeed, invasion within land uses is often associated with the historical legacy of changes in land use. Like in most West African regions, Togodo Protected Area (TPA) and its peripheries experienced notable land use change over the past few decades. These changes led to the spread of many invasive plants that threaten the biodiversity of the TPA and are chores for local farmers. However, despite the legacy of current and past land uses on plant invasion success, few studies have investigated the mechanisms triggering invasion credit and, in Togo, plant invasion ecology has not yet gained enough attention.

In this study, we investigated the influence of the current and historic land uses on the diversity of invasive plants in and around TPA. Firstly, we defined land use change trajectories using land use maps performed from Landsat images acquired in 1974, 1986, and 2003 and from Sentinel 2 image acquired in 2016. Secondly, we conducted botanic surveys in the different land use types and, 198 quadrats of 50 x 50 m were laid to make an inventory of all plant species.

Biological Invasions

In total, 483 plant species were recorded including 95 aliens, 1 uncertain, 71 invasive or potentially invasive. On average, old croplands are richer in invasive plant species than younger croplands and old vegetation. Croplands and fallows are the richest in invasive plant species. Overall, our results suggest that contemporary land use and past land use change trajectories influence invasion at the local scale. These results can offer insight into the invasion process and help identify areas of greatest risk for the protected areas.

*Speaker

Spatio-temporal evolution of life history traits: Brown trout colonization of the sub-Antarctic Kerguelen Islands

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During a colonization process qualifying the invasiveness of a species and its adaptive potential to new environmental conditions remains of major interest. The brown trout (*Salmo trutta* L.) display a considerable variation in life history strategies. It is a facultative anadromous species with only a fraction of fish migrating at sea (i.e. partial migration). Introduced in the late 1950s in the Kerguelen Islands, the ongoing colonization of the archipelago presents a unique opportunity to understand underlying causes and mechanisms of biological invasions. This study aims at quantifying variation in freshwater growth and age at first marine migration at various spatio-temporal scales with respect to the colonization process. The analysis of age and growth information contained in the scales of fish has become a standard technique in fish population dynamics model. However, inferring growth for fish is dependent upon an accurate description of the age-length relationship, which may be undermined by ageing errors that arise either from disagreements between scale readers or inability of scales to reflect true age (i.e. erosion, false growth ring). Von Bertalanffy growth function (VBGF) that explicitly accommodate ageing errors from scales was used to compare freshwater growth of population colonized at different times and located at different distances from the colonization front. Associated fish life history (i.e. growth curve and age at first marine migration) is discussed with respect for the role of initial stage, evolution and local adaptation.

*Speaker

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Trophic niche divergence between native amphibians and an invasive crayfish promotes their coexistence in pond ecosystems

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Invasion theory suggests that biological invasions are responsible for large changes in species interactions in natural communities, because invasive species have large trophic niches and alter the diet of native communities, notably due to their competitive superiority. The non-native red swamp crayfish, *Procambarus clarkii*, is considered to dramatically alter aquatic food webs and especially to prey upon larval amphibians and outcompete adults. However, to date, this issue has been poorly studied using biomarkers such as stable isotopes, especially because sampling muscle (the reference tissue) is lethal and inappropriate for the vulnerable amphibian species. This work aimed at (1) testing the relevance of sampling the fin of amphibians as a surrogate to the muscle to estimate isotopic ratios of carbon and nitrogen, and (2) exploring the type and extent of trophic interactions between the red swamp crayfish and four species of the amphibian community in natural ponds. We predicted that the sympatry with the invader would change the niche width of amphibian populations and result in substantial niche partitioning. Food webs were studied in 20 ponds selected over a gradient of crayfish densities and habitat features (1810 samples including 1230 amphibians and crayfish), in western France.

Fin and muscle isotopic ratios were strongly related for the four amphibian species, validating the use of non-lethal fin punches for stable isotope analyses given specific correction factors. Large variations in amphibian niche width were recorded, especially for anuran tadpoles when compared to urodele adults. Niche overlaps of amphibians and crayfish were very limited and shifts in the trophic niches of amphibians were mainly contingent upon environmental pond conditions. Our results highlighted that the high flexibility in trophic niche of amphibians would facilitate their co-existence with the invasive crayfish in pond ecosystems.

*Speaker

Inventory of Culicidae in the region of Kabylia and confirmation of the presence of *Aedes albopictus* in Larbaa-Nath-Irathen

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Summary in order to confirm the presence of *Aedes albopictus* and deepen our knowledge of culicidian fauna in the region of Kabylia, we conducted a sampling every 15 days in 3 regions (Taksebt, Larbaa Nath Irathen, Mâatkas) between April and the month of July 2016. A female *Ae. albopictus* was captured, identified and confirmed by the Algiers pastor institute confirming its presence or importation. At total of 4723 mosquitoes were identified belonging to 17 species and 4. *Culex pipiens* is the most abundant species in the area in the region with 2546 specimens followed *Culiseta longiareolata* with 944 specimen, the first station Larbaâ Nath Irathen account it 13 species.

*Speaker

The Increasing Threat of Biological Invasions for Antarctic Biodiversity

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Most ice-free habitats on land in Antarctica and the sub-Antarctic are. Antarctic terrestrial ecosystems are extremely isolated, in effect often islands surrounded by hostile ice and ocean, and have developed unique and striking features. True terrestrial vertebrates are generally absent, except for a small number of native birds on some sub-Antarctic islands, meaning that most foodwebs consist only of invertebrates. Ecosystem structure is generally simplified. Decomposition processes are slow, while few true native herbivores or predators are present, and the predators in particular have very limited impact on their prey species. Over the last two centuries human activities have led to the accidental introduction and establishment on land of many non-indigenous species of vertebrate, invertebrate and plant, particularly to the ecosystems of the sub-Antarctic islands, but also increasingly to the Antarctic Peninsula and Scotia archipelagoes. These introductions have encompassed a range of trophic functions, some of which are poorly or not represented in indigenous ecosystems, in some cases leading to drastic alterations in ecosystem structure and function. Although the number of introductions currently known in parts of the Antarctic Peninsula is small, the sub-Antarctic provides a direct warning of the likely trajectories of these and any future establishment events. This presentation will consider the impacts of non-indigenous biota in Antarctic ecosystems to date, and their implications in a future where these ecosystems are also faced by some of the most rapid rates of environmental change on the planet. It will also identify urgent challenges faced by the authorities responsible for conservation and governance in the sub-Antarctic and Antarctic regions, if the Antarctic is to remain the only continent globally that is largely unaffected by biological invasions.

*Speaker

100 articles every ecologist should read

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Reading scientific articles is a valuable and major part of the activity of scientists. Yet, with the upsurge of currently available articles and the increased specialization of scientists, it becomes difficult to identify, let alone read, important papers covering topics not directly related to one's own specific field of research, or that are older than a few years. Our objective was to propose a list of seminal papers deemed to be of major importance in ecology, thus providing a general 'must read' list for any new ecologist, regardless of particular topic or expertise. We generated a list of 545 papers proposed by 147 ecology experts (journal editorial members) and subsequently ranked via random-sample voting by 368 of 665 contacted ecology experts, covering six article *types*, six *approaches*, and 17 *fields*. Most recommended papers were not published in the highest-ranking journals, nor had they the highest number of mean annual citations. The articles proposed through the collective recommendation of several hundred experienced researchers probably do not represent an 'ultimate', invariant list, but they certainly contain many high-quality articles that are undoubtedly worth reading - regardless of the specific field of interest in ecology - to foster understanding, knowledge and inspiration of early-career scientists. I will discuss the content of this list, including the biases it contains.

Key words: bibliometrics, scientometrics, ecology, expertise, early career, career development

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Benthic aliens in the plankton: investigating life cycle dynamics using metabarcoding on the larval stage

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The number of marine non-indigenous species (NIS) has never been so high and is still rising due to globalization and an ever-increasing international trade. Marine NIS are mainly reported in harbours and aquaculture sites, both being primary entry points for introduced species. As compared to these artificial environments, the proportion of NIS is low in natural habitats. This pattern might be due to ecological processes, such as limitations to dispersal or resistance of native communities, or to our inability to efficiently detect them. Most sessile marine NIS display a pelagic larval phase, the main dispersal agent. Studying this phase is, thus, of great importance to investigate NIS reproductive cycles, spread potential, connectivity between artificial vs. natural habitats, and its role in the pelagic ecosystem. Identifying larvae using morphology is notoriously difficult, sometimes even impossible, because of the lack of diagnostic criteria for many species. DNA metabarcoding, successfully used for species detection in various environments, could be a powerful tool to identify NIS larvae within pelagic communities. Here we assessed the efficiency of this approach to detect and monitor seasonal variations of benthic NIS larvae, by analysing plankton samples collected over 22 months in the Bay of Morlaix (Brittany, France). The DNA extracted from ‘bulk’ plankton samples was amplified for 18S and COI markers. Using metabarcoding, ten NIS were identified by at least one marker (5 with both markers). All were previously reported from the study area and displayed clear temporal variation patterns. For two species (the molluscs *Crepidula fornicata* and *Ruditapes philippinarum*), the temporal variations observed through metabarcoding agreed with those revealed by morphological identification or standard barcoding on individual larvae. This study indicates that DNA metabarcoding might be a suitable tool to assess the dynamics of NIS at the larval stage using semi-quantitative data.

*Speaker

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Importance of phenotypic plasticity in the invasive success of *Drosophila suzukii*

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Biological invasions, largely related to human activities (development of international trade and intercontinental transport), are causing increasingly strong ecological and economic damages. From an academic point of view, invasions represent "natural experiments" that allow investigating evolutionary processes in real time. A process that is supposed to play a fundamental role in the success of an invasion is phenotypic plasticity. Phenotypic plasticity is the ability of a genotype to express different phenotypes depending on environmental conditions. Adaptive phenotypic plasticity allows organisms to express advantageous phenotypes in a broader range of environments at very short time scales (within single generations). It is often assumed that populations of invasive species present greater phenotypic plasticity in their new invasive range compared to populations within the native range. To test this hypothesis we have investigated phenotypic plasticity of wing size in invasive pest species, *Drosophila suzukii*. We have investigated two amongst the most relevant environmental factors for a successful invasion, temperature and nutrition: temperature because it is tightly associated with the latitudinal cline of the invasion, and one of the best-studied environmental factors affecting *Drosophila*; and food substrates because *D. suzukii* is unique amongst *Drosophila* for its ability to exploit unripe rather than rotting fruits and because nutrition influences many traits and individual fitness. By comparing native and invasive populations, we will be able to investigate the genetic variability of the plasticity of size in this species.

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Evaluation of the impact of the invasion of *Baccharis halimifolia* on saltmarshes

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Biological invasions are considered as one of the main causes of the biodiversity erosion of at the global scale, even if on a local scale the impacts are sometimes difficult to quantify. Locally the phenomena of invasion are often very fast and difficult to control when the populations are strongly implanted. The fight is then difficult and requires the deployment of important means. This implies a strong mobilization of the local stakeholders.

The Ria of Étrel in Brittany is particularly concerned by the presence of *Baccharis halimifolia* which occupies more of 20ha of salt marshes. Considering this, a program of fight based on the organization of participative works was set up. This program of fight comes along with a program of follow-ups and with evaluation including several aspects: quantification and mapping of the population, evaluation of the impact of the invasion on several ecosystem components (flora, fauna, soils...) and evaluation of the management efficiency. The presentation will concern the two first points.

Population mapping made in 2017 allowed to underline the evolution of the invasion since 2009 date of the previous evaluation, with an increase of 4.1 ha. New populations were observed, which should be primarily eradicated.

On the base of this map, analyses are made to evaluate the impact of the presence of *Baccharis halimifolia* at local scale on vegetation and arthropods communities and soil characteristics. Links will be made between them and the population characteristics (density, age, ...). The results will allow to precise the strategy of control of the invasion and also to evaluate the efficiency of this strategy. This last point will be implemented in 2019.

*Speaker

Synthesis on Biology, Ecology and Management of terrestrial forms of invasive Water Primroses on meadows

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Invasive Water Primroses (*Ludwigia grandiflora* subsp. *hexapetala* and *L. peploides* subsp. *montevidensis*) are amphibious plants native in subtropical Southern American areas. They become a weed problem in wet meadows along rivers and in marshes, because they are highly competitive over native plants. These forms appear on winter-submersed meadows mainly due to cuttings that settle when water level decreases. They affect pasture productivity, biodiversity and marsh landscapes as well as their use for cattle breeders. Effects on farmers' exploitations are very bad: loose of EU grants, reduction of grazing area and impossibility to use the colonized pastures, leading to land abandonment and marsh agriculture decrease.

We have performed detailed studies in Western France both at the site level and over France. Recently we achieved a 4 years Research program focused on these terrestrial forms.

They can be as productive in terrestrial habitats than in aquatic ones, around 2 kg dry weight per m², up to 5 kg dry weight per m² at a maximum. Both species can grow altogether but *L. peploides* is more hydrophilic and *L. grandiflora* is more competitive and resistant to emersion, eliminating progressively *L. peploides*.

Aquatic plants are dense, longer with poorly branched stems with few roots, while terrestrial ones in wet meadows are shorter, with a bushy form and more roots anchored into the substratum. At the beginning of colonization, populations do not form fruits, at least for *L. grandiflora*, but after some years, fruits are observed. *Ex situ* germination studies point out seed fertility. Seedlings begin to appear in some sites.

Two steps of weed management were distinguished. To avoid colonization, use of naturally brackish water and landscape management practices have been successfully tested. To restore pastures many mechanical of hand pulling methods have been applied leading to recommendations to reduce colonization.

*Speaker

Invasive species influence migration rates in a facultatively migratory fish

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Invasive species are a global threat to native assemblages on tropical islands where their effects on depauperate native species communities can be profound. Across the Hawaiian archipelago, species invasions are a key factor in the degradation of stream conditions; dozens of aquatic invasive species affect the five endemic freshwater fishes, all of which are considered imperiled despite their capacity to disperse via a migratory life-history. These invaders threaten native fishes through predation and may affect the demography of native fishes by influencing migration behavior, which may directly or indirectly influence the fitness consequences of alternative life-histories. Some of the native species exhibit partial migration; one subset of individuals within a population migrate to the ocean as larvae and return to a stream to mature, while another remains as a lifelong resident of the natal stream. We hypothesized that the proportion of migratory contingents of adults in a stream would be affected by the abundance of invasive species through predation on hatchlings and returning post-larvae and competition of resources. We tested this hypothesis by comparing migration rates in populations of an endemic stream goby (*Awaous stamineus*) across an invasive species gradient on the Hawaiian island of Oahu. We found that the proportion of stream-residents was significantly lower when invasive live-bearing fish (Poeciliidae) were abundant, when both live-bearers and armoured catfishes (Loricariidae) were abundant, and when stream flows were more stable. These findings underscore the importance of understanding invasive species effects to conserve imperiled native species in Hawaiian streams.

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How diversity, density and maturity of restored plant communities influence invasion success

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Active restoration of native plant cover is increasingly being advocated as a method to reduce invasive alien plant species (IAPS) establishment and spread. Of all the processes underlying invasion resistance, competition for resources is a major process that could be manipulated by restorationists to combat invasion. Tipping the competitive balance in favor of natives could be achieved by giving a time advance to the restored community, generating "priority effects". Through priority effects, the restored native community benefit of a fitness advantage by which they better resist invasions. How priority effects are influenced by community characteristics is still unknown, but could be very useful to practitioners to improve invasion resistance of restored communities. We designed a pot experiment to simulate a situation in which seeds of three IAPS in France (*Ambrosia artemisiifolia*, *Bothriochloa barbinodis*, *Cortaderia selloana*) reach soil covered with restored native communities composed of commercial plant varieties. We assessed how species diversity (1, 3 or 9 sp.), density (4 or 15 g.m⁻²), and age of the community (1 or 5 months) influence germination, survival, growth and phenology of the three IAPS. In addition to global community characteristics, we also analyzed how soil nutrient content, community cover, and the features of the immediate neighborhood at the time of introduction (i.e. canopy density and the distance to-/the identity of the closest neighbor) affect the performance of each IAPS individual. This study provides new useful insights to elaborate revegetation strategies effective against IAPS.

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*Speaker

Don't move a Mussel! Conservation dogs saving European Waters

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A critical issue in biodiversity is that of invasive species like the ZEBRA and QUAGGA mussel in waters worldwide, referred to as the 'most troublesome freshwater bio-fouling organisms'.

Zebra and Quagga mussels out-compete European native fish for food causing wide-spread decline. They also cause algae outbreaks because of increased water clarity. A further result is bird die-off.

These mussels quickly colonize and clog water pipes, causing extensive and often irreparable damage to hydro turbines and reservoirs, agricultural irrigation, drinking water systems and boat engines. Once a colony of Zebra and Quagga mussels is established, it is nearly impossible to prevent them from spreading elsewhere - further accelerated by watercraft and other vessels. Once boats are infected by infested waters, lengthy quarantine is almost always required - at a great economic loss. Through learning from countries that have tackled this before Ireland, we can assist with setting up detection dog check-points to inspect boats and other watercraft, and give boat owners clearance ID.

Year after year, the cost of fighting these invasive mussels is staggering and an almost futile, ongoing exercise, with bio-pesticides giving disappointing results.

In managing invasive species, early detection is key. Zebra and Quagga mussels live up to 3 years and release close to 1 million eggs each year. Conservation Dogs Ireland are trained to sniff out Zebra and Quagga mussels at the earliest possible larvae stage - which is still invisible to the human eye.

At Conservation Dogs Ireland, we take pride in our research and learning from the best in the world. Governments and organizations in Canada and New Zealand have been successfully employing conservation detection dogs for this purpose.

No other method is as cost-effective, environmentally friendly, thorough and efficient as detection dogs, with them covering areas 40 times faster than humans and their efficiency impossible to quantify.

*Speaker

The environmental filter causing local scale heterogeneity of marine communities – a reciprocal transplant approach

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Urban structures are becoming common around our coastlines, with hard engineering dominating as much as 50% of coasts in some parts of the world. Refuges for boating activities like harbours and marinas are often highly contaminated environments and are known hotspots for invasive species. Previously we have demonstrated that within these habitats, local scale heterogeneity of contaminants is responsible for structuring communities. As such, we hypothesised that the environmental filter is acting to regulate communities, and therefore the presence of invasive species. In these locations, areas furthest from the entrance are likely to be the most contaminated and therefore only habitable to the most resistant species. It is widely theorised that invasive species are more tolerant to a wider range of conditions than equivalent native species, thus enabling them to survive transport and become successful invaders. Through measurement and analysis of community, respiration and the metabolome of selected key species, we investigated the tolerances and the implications of the environmental filter in structuring marine fouling communities. Using a reciprocal transplant approach within Brest, France, settlement panels were deployed at and transplanted among 3 distinct regions of the Chateau Marina. Regions were dictated according to the distance from the single entrance of the marina, corresponding to sampling points closest to and furthest from the entrance, and a midpoint. Previous studies have shown significant differences between these regions in terms of pollution (e.g. heavy metals, pesticides) and community. Further tolerance experiments on dominant ascidians were conducted to determine if invasive species were more tolerant than comparable native species to common stressors. Through this approach we discovered that, at this local scale, the environmental filter is prevalent in acting to shape communities and metabolome, however, evidence also suggests that prior colonisation history within localities is also a determining factor relevant to future colonisation.

*Speaker

Phenotypic and genetic variability of an invasive species within a meta-ecosystem: patterns and drivers

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The functional importance of intraspecific variability in modulating the ecological impacts of invaders on recipient ecosystems has been recently demonstrated. During the biological invasion process, environmental filters and selective forces act synergistically to shape intraspecific variability. Yet, our understanding of the historical and environmental drivers promoting this variability within and between invasive populations remains extremely limited. Here, we used a meta-ecosystem formed by a dynamic mosaic of heterogeneous freshwater ecosystems (artificial gravel pit lakes) colonized by a highly invasive species (red-swamp crayfish *Procambarus clarkii*) to i) first quantify phenotypic and genetic variability and ii) assess its potential drivers. Functional phenotypic variability was measured using body shape (geometric morphometric analyses) and trophic niche (stable isotope analyses: $\delta^{15}\text{N}$ and $\delta^{13}\text{C}$), while genetic diversity was quantified using neutral markers (14 microsatellites). The role of environmental conditions (e.g. hydromorphology, predation, competition) and invasion history (e.g. ecosystem age, dispersion patterns) in shaping patterns of both phenotypic and genetic variability within and between populations was then tested. We first demonstrated that intraspecific variability was high, both within and between populations, and strongly influenced by the environmental and historical contexts. For example, we observed significant phenotypic variability within some invasive populations without any significant genetic differentiation between individuals inhabiting the littoral and pelagic habitats. We also demonstrated the existence of a genetic structuration ('isolation by distance') of invasive populations in the studied meta-ecosystem associated with the colonization history of the species. Finally, we found some associations between morphological and trophic traits related to resource exploitation that varied among populations, indicating a strong context-dependency of intraspecific variability among invasive individuals and their ecological impacts.

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Climatic regeneration niche of an invasive species (*Ulex europaeus* L.) assessed by a reciprocal transplant experiment along an altitudinal gradient

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Biological invasion is an important component of global change, as invading species can alter the biodiversity and functioning of ecosystems. For the efficient allocation of management of invasive species, we need to understand why these species succeed in becoming established, and which factors limit or prevent them.

Assessing the climatic niche of invasive species is a first step to predict species invasion at regional scale.

Reciprocal transplant experiments according to altitudinal gradients have been used to investigate the limits of climatic range tolerance of invasive plant species, and to detect local adaptation and phenotypic plasticity.

As a species model we used gorse (*Ulex europaeus*, L.), one of the most invasive plant species in the world outside its native European range.

We studied the survival and the relative growth rate (RGR) of gorse seedlings from populations of both native (France and Spain) and invasive (New Zealand, Tenerife -Canary islands- and Reunion island) origins.

To accomplish this, we set up a reciprocal transplant experiment with seedlings from all these regions, one in a native area (Asturias) and another in an invasive area (Tenerife). For each transplant experiment 4 common gardens were installed along an altitudinal gradient: 100, 400, 800 and 1100 meters above sea level with four blocks in each site. Growth and mortality measures were taken monthly. The same experimental design was set up in Tenerife (779

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individuals) and Asturias (928 individuals). Comparisons taking into account the origin of the seedlings were done. Mortality in both experiments was quite low and showed no differences according to seedlings origins. For both experiments, RGR was higher for invasive populations than from native ones. Any home advantage had been found for Canarian population suggesting that phenotypic plasticity in RGR has a genetic origin; it should have contributed to the invasiveness character of *Ulex europaeus*.

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Unravelling the worldwide invasion history of the highly invasive red swamp crayfish *Procambarus clarkii*

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Biological invasions are one of the most devastating threats to global biodiversity. Propagule pressure (i.e., the size and number of introduction events) is thought to be one of the key elements driving invasion dynamics. Over the last 45 years, European freshwaters have been widely invaded by the red swamp crayfish, *Procambarus clarkii*. It is generally reported that European invasion was originated from only two large crayfish batches, legally introduced from Louisiana (US) to southern Spain in 1973 and 1974. In order to confirm this "official" history, we aim to: (1) determine whether there have been unrecorded introductions into Europe and where they came from; (2) establish the genetic structure of European populations; and (3) compare their genetic diversity to that of the native area. To do this, 1416 crayfish from 122 sampling sites in the Northern Hemisphere (22 native populations) were analysed using the mitochondrial gene (COI). Some genetic structuring was found in the native area allowing us to putatively identify Louisiana as the main area of origin for introduced populations worldwide. Diverse hotspots in some invaded areas, such as South-Western Spain (Extremadura and Andalusia) or Central Italy (Tuscany) did not show strong bottlenecks, likely due to the high propagule pressure (either large size inoculum, many introduction events or both). Our results showed some genetic homogeneity across Europe, suggesting multiple secondary events mediated by humans. The finding of one haplotype only present in Northern Europe, but not in Spain, also suggests additional translocations of crayfish. These mitochondrial results will be compared to microsatellite results from the same dataset. Any additional *P. clarkii* introductions have, so far, not been well-documented in the literature.

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Living in windy environments: new insights on mechanisms supporting the invasion success of alien plant species at the Kerguelen Islands

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Invasions of native communities by alien plant species constitute a major driver of biodiversity changes, inducing modifications of ecological networks and ecosystem functioning. Due to their geographic isolation and simplified native communities, insular ecosystems are particularly vulnerable to invasions, and are often strongly relevant for investigating mechanisms supporting the establishment and spread of introduced plants. In addition to cool thermal conditions, terrestrial flora of subantarctic islands, including at the Kerguelen Islands, must often thrive in moderate to highly windy habitats, thus imposing strong mechanical constraints to individuals. While native subantarctic plants have evolved in these supposedly harsh abiotic conditions, many alien plants at the subantarctic islands are of tropical or temperate origins, where they were exposed to less stringent wind conditions. As wind likely represents a strong environmental filter for the successful establishment and further geographic spread of the plants, they may have then developed adaptive or phenotypic responses to resist and successfully colonize the Kerguelen Islands.

To test this assumption, we studied the ecological responses to wind exposure in three alien plants that are particularly invasive at the Kerguelen Islands: *Taraxacum ruderae*, *Poa pratensis*, and *Dactylis glomerata*. We sampled plant individuals of these three plants at three different locations, under wind exposed and sheltered conditions. Traits related to avoidance (height), resistance (stem density, flexibility), and performance (individual, and flower biomasses) to windy conditions were measured.

We demonstrated similar patterns of responses in the three studied species. Plant individuals were overall smaller, and displayed stems with a higher flexibility when they are thriving in windy habitats, regardless of the sampling location. This abiotic resistance to wind exposure may have helped alien plants to efficiently colonize habitats of the Kerguelen Islands. Further investigations are nevertheless needed to determine whether these responses are heritable (adaptation) or not (phenotypic plasticity).

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The changing face of invasion science

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The phenomenon of biological invasions has intrigued naturalists and biogeographers since at least the mid 18th century. Charles Elton's 1958 book on *The Ecology of Invasions by Animals and Plants* is widely acknowledged as the foundation publication for what became "invasion ecology" and has now morphed into "invasion science". The study of invasions increased rapidly in the 1980s, and has grown exponentially since the turn of the century (e.g. Web of Science lists 67 papers on "invasive species" published in 2000, and 1809 in 2017 – a 27-fold increase). The extent of biological invasions is growing rapidly in all parts of the world, with no sign of saturation in the accumulation of alien and invasive species in most taxonomic groups. Impacts are also increasing in all ecosystems and many invasive species have caused extinctions, triggered regime shifts, and led to radical changes in ecosystem functioning and the delivery of ecosystem services.

Challenges involved in managing invasions are becoming increasingly complex due to interactions of many factors, including: the large number of invasion pathways for the intentional and accidental movement of species between and within regions; the growing numbers of invasive species that have clearly negative impacts; complex (and often synergistic) interactions between biological invasions and other facets of global change; and the increasing number of stakeholder groups and complex conflicts of interest pertaining to alien species that benefit particular sectors of society but cause negative impacts to others.

Invasion science seeks to understand many things: the pattern of human-mediated movements of species around the world; the factors that mediate the invasiveness of alien species and the invasibility of ecosystems; how humans perceive invasions, attach value to the benefits and costs incurred by alien species, and integrate many factors to decide on management options.

*Speaker

Considering evolutionary processes and connectivity to design control strategies for the invasive amphibian *Xenopus laevis*

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Managing cryptic invasive species is challenging because their range is hard to determine, and little information is available about their dispersal behaviour. The African clawed frog *Xenopus laevis* is considered one of the most harmful invasive amphibians in the world. This southern African species was accidentally introduced in western France more than 30 years ago and is now expanding and threatening amphibian and invertebrate pond communities. Although urgent control actions are to be taken, their design needs to be based on scientific knowledge, especially considering that this species is particularly difficult to detect through visual observations and trapping techniques. In the context of the Life project CROAA, we updated the colonised range using environmental DNA. We then built a connectivity model of the range based on a resistance cost map that we derived from the classification of satellite images. Resistance costs for the main types of land uses were obtained from experiments on juveniles and adults. We then associated the connectivity map with a distribution map of ecological value for local biodiversity across the colonised range to generate alternative control strategies. The cost-efficiency of each strategy will be assessed to implement large scale control operations. We also assessed the evolutionary processes on each stage of this invasive population. We have observed an increase in the dispersal propensity and a change in the locomotor morphology of adults during expansion. For the larval stage, we investigated the variation in larval development, measured the change in thermal acclimation between native and invasive populations of *X. laevis*, and quantified anti-predator response of *X. laevis* tadpoles to predators present in the colonised range. We discuss how information about evolutionary processes may help to gain insight into applied conservation programs and better forecast the expansion of invasive populations.

*Speaker

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Genetic reconstruction of *Aedes albopictus* invasion history in Europe

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The Asian tiger mosquito, *Aedes albopictus*, is currently the most invasive mosquito in the world. Native to South-eastern Asia, it has rapidly spread across all continents over the past 30 years. In Europe, the first record of *Ae. albopictus* is dated in 1979 in Albania, with a second introduction in Italy in 1990. Although an increasing number of studies revealed the possible sources of the recent invasion in Europe, they were based on a small number of populations. In this study, we sampled a broader range of invasive mosquito populations, representative of the current species range in Europe. We used genome-wide single nucleotide polymorphism (ddRADseq SNPs) to explore patterns of genetic variation and infer the most likely colonization scenario. We found evidence for different and independent introduction events in Albania and Italy. China emerges as the most probable source of populations in Albania, and United States, from an ancestral Japanese source, is the most probable source of populations in Italy. The spatial genetic structure suggests dispersal from established populations in Albania to neighbor countries but most of populations in Western Europe are genetically similar to those in Italy, supporting that Italian populations have played a major role in the rapid demographic expansion of populations throughout Europe. The high levels of genetic diversity observed in most recently invaded populations support that they result from genetic admixture from multiple sources of introduction, which probably accelerated the rapid range expansion of *Ae. albopictus* in Europe.

*Speaker

Modelling landscape connectivity in an aquatic invasive frog

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Connectivity models are widely used to locate corridors for species of conservation interest and give recommendations for management actions. However, these models are also useful tools for invasion biology, especially in case of large-scale invasive populations for which eradication cannot be achieved. Identifying the main dispersal corridors of an invasive population may help to predict its future spread and test efficacy of different management strategies based on containment or local extirpation. Here, we build a connectivity model around the largest invasive population of the African clawed frog *Xenopus laevis* in France. This species is considered "principally aquatic", spending most of its life in water but adopting overland locomotion to disperse. The invaded area, estimated through trapping effort, eDNA surveys and opportunistic observations, is about 4300 km² and extends across four departments in western France. We used IGN data and multispectral remote sensing images captured by Spot6/7 satellites to classify the invaded landscape into discrete land cover types (such as forest, bare soil and pastures). Then, we performed laboratory and field experiments on juveniles and adults of *X. laevis* to investigate species-specific behavioural and physiological responses to each land cover type. Empirically derived resistance surfaces were thus obtained by integrating the classified landscape with experimental data to depict functional connectivity between water bodies. A connectivity model was built using the Python-based tool UNICOR, which combines the obtained surfaces with a grid-based resistance kernel. The model visualizes dispersal pathways, identifies areas with high risk of invasion and tests efficacy of some proposed management strategies such as the removal of invasive individuals from invasion hubs, biodiversity hotspots and riparian zones. The output of the model is also used to estimate to what extent the main dispersal corridors of the species overlap with zones of maximum ecological potential/high ecological status across the invaded area.

*Speaker

The population genetics of hybrid zones between introduced and native mussels at the sea-port interface

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Anthropic activities are creating new contacts between genetically differentiated lineages that start to exchange genes again before our eyes. These contacts provide the opportunity to investigate the importance of demography, environmental conditions, reproductive isolation and contingency on the outcome of hybridization between introduced and native lineages. In the opposite direction, a better understanding of the importance of those parameters is essential to hope to control invasions with hybridization, both spatially and genetically. We studied the population genetics of non-indigenous mussels in French ports. The blue mussel species complex (*Mytilus* sp.) is composed of three species distributed in the Northern hemisphere (*M. edulis*, *M. galloprovincialis* and *M. trossulus*), that naturally hybridize each time they meet. *M. galloprovincialis* is also found worldwide due to its invasive potential (e.g. in South Africa, the US West coast or Asia). Using a set of ancestry informative markers we recently uncovered that the mediterranean lineage of *M. galloprovincialis* has been introduced in multiple French ports (Le Havre, Cherbourg, Saint Malo, Brest) and has been extensively introgressed by *M. edulis*. Sharp genetic shifts are observed at a very fine spatial scale at the sea-port interface where the native population is *M. edulis*. In the roadstead of Brest however, where the native population is

^{*}Speaker

Biological Invasions

the Atlantic lineage of *M. galloprovincialis*, we found that the invading lineage started to spread and to introgress the native background. We used adjustment to the migration-selection tension zone model to better understand the relative importance of connectivity, reproductive isolation and adaptation to the port environment in maintaining the spatial structure.

Effect of the temperature increase and the neighbour density on the development of two invasive species: *Ludwigia hexapetala* and *Ludwigia peploides*

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Global warming and invasive species have been recognized as two of the major threats to biodiversity in freshwater ecosystems. Temperature and species interactions are two factors that may influence the success or failure of an invasion. Field observations noticed a displacement of *L. peploides* by *L. hexapetala*. To test the effect of temperature increase and competition on the plant development, we ran an experiment in outdoor mesocosms setting up a 5 different competition scenario between *Ludwigia hexapetala* (Lh) and its conspecific species *L. peploides* (Lp). The experiment spanned from may until mid-october. We studied the effects of a small temperature increase (*ca.* 1°C) of ambient temperature and of varying density of each species. The experimental setup included two controls with only one species, and 5 experimental treatments with varying densities of each specie, keeping a constant density of 6 plants. We used a split-plot design with 5 replicated mesocosms for each temperature (ambient *vs.* heated). Experimental treatments effects were tested on the plant vigour, by measuring morphological traits as, biomass, main shoot length, the production and length of lateral branches and roots, the number of flowers and capsules. Additionally, four physiological traits (Chlorophyll a, NB index, Flavonols and Anthocyanins) were also measured upon leaves. Density treatment did not have significant effect on none of both species morphological traits. On the other hand, *L. hexapetala* increased significantly its growth in the heated mesocosms, but *L. peploides* growth was not affected by temperature treatment. Only *L. peploides* produced fruits with viable seeds. There was no significant effect of plant density and temperature increase on the physiological leaf traits. Our results pointed out that *L. hexapetala* better performed than *L. peploides* under rising temperature scenario, therefore temperature may play an important role in driving the invasive potential of all two species

*Speaker

Tracking the hunting range of *Vespa velutina* by RFID or radio telemetry

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Vespinæ are very invasive, predatory insects that feed their young with proteins, typically other insects. *Vespa velutina*, also called yellow-legged hornet, was accidentally introduced to Western Europe (South West France) in 2004. Since its introduction, it quickly expanded its geographical range to Spain, Portugal, Italy, very recently to Great Britain (2016), and flying individuals have been noticed in Belgium, Switzerland and close to the German border. Where established, it dramatically predated on colonies of *Apis mellifera* which, contrary to the Asian honeybee *Apis cerana*, are rather inefficient at defending themselves. In areas suffering heavy hornet populations, predation is now suspected to contribute to the decline in bees. Research urgently needs to focus on understanding the hornet's dispersion capacity and developing sustainable control methods with limited impact on the environment. Since eradication in some areas is no longer possible, the control of this predator should target the colony itself and should involve understanding the action range of the foragers. We thus used Radio Frequency Identification to evaluate the action range of a nest's workers, and their homing capacities – typically over a few kilometers. This also revealed the capacity of some hornet workers to take long trips, not unlike 'scout' bees. Recently, we successfully used radio telemetry to track workers returning from foraging sites back to their nest. Equipping 8 workers with such tags enabled the rapid discovery of 5 nests in urban landscapes. Those nests were well camouflaged in the upper part of trees and never detected by any monitoring. These approaches offer significant progress in understanding the foraging behaviour of this invasive predator and for early nest detection, which can thus be destroyed.

*Speaker

Chemical Ecology

Tomato Leaves Under Biotic Stress: Can We Detect Specific VOC Blends in the Greenhouse?

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Plants emit specific blends of organic volatile compounds when attacked by herbivores (herbivory-induced plant volatiles; HIPV) or pathogenous fungi (pathogen-induced plant volatiles, PIPV). The majority of previous studies has been conducted under laboratory conditions. Hence, we conducted two greenhouse experiments to investigate specificity and resilience of volatile blends in a more challenging environment. In a comprehensive approach, using solid-phase microextraction (SPME) to collect samples, we detected a total of 89 compounds and gathered very detailed information on constitutively emitted volatiles, HIPV associated with two sap-feeding insect herbivores, *Macrosiphum euphorbiae* and *Bemisia tabaci*, and PIPV associated with the biotrophic fungus *Oidium neolycopersici*. Using orthogonal projection on latent structures discriminant analysis (oPLS-DA), we could distinguish the various blends. This was partly due to absence and presence of certain biomarker compounds, partly due to changed ratios. Our greenhouse experiments confirmed results from laboratory studies regarding species-specificity: distinct *B. tabaci*-HIPV were emitted from infested plants and their composition changed over time, correlating with the presence of different developmental stages of the herbivore. *O. neolycopersici*-infection lead to the emission of PIPV distinct from the sap feeder HIPV and from constitutively emitted blends, although they share the majority of compounds. Between the two experiments, HIPV were more similar than constitutive blends, indicating a high resilience of HIPV and high phenotypic plasticity regarding constitutive blends. The latter may be more sensitive to biotic and abiotic changes. Ecologically, a variable constitutive blend may impede detection by herbivores while resilient HIPV blends should support indirect defense by natural enemies.

*Speaker

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Understand the male effect to an ethical breeding of small ungulates

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Small ungulates (sheep and goat) display seasonal breeding characterized by successive periods of sexual activity and sexual rest. During sexual activity, the female ovarian cycle is active (oestrus) and ready for reproduction, whereas females are in deep anoestrus during the sexual rest period. In order to synchronize anovulatory females at the end of sexual rest, breeders are mostly using exogenous hormones. An alternative to these hormones is to expose females to a sexually active male or its fleece/goatee. Indeed, it is well known that fleece/goatee odors can reactivate the female gonadotropic axis, leading in most cases to ovulation. This is called the male effect. Ram and goat odors act as primer pheromones, even if their molecular components are not precisely identified.

Numerous studies have focused on the physiological effects of male odors perception in the female brain, but never at the peripheral level of odors reception. Our previous work on pig has shown that the olfactory secretome, mainly composed of Odorant-Binding Protein (OBP) isoforms is modified under control of endogenous hormones (Nagnan-Le Meillour *et al.*, 2014). We wondered if the olfactory secretome could also be modified by exogenous factors, such as male odors, hypothetically showing an adaptation and a specialization of the peripheral sensory equipment of the females. As there is a strong inter-individual variation in chemical signals and olfactory proteins patterns in mammals, we followed the same flocks of ewes and goats along their cycles during 3 years and during a male effect protocol, we collected their nasal mucus by using a non-invasive manner. The olfactory secretome was analysed by 2D-electrophoresis, and the proteins were identified by high-resolution mass-spectrometry. Our results suggest that the olfactory secretome is a marker of a particular physiological status, and constitutes a phenotype of female receptivity, which can be used by breeders.

*Speaker

How do climate warming affect *Sphagnum* secondary metabolites?

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Sphagnum genus have a key role in peatland functioning by creating the conditions for the accumulation of one third of the world's soil carbon. However, *Sphagnum* secondary metabolites are poorly quantified compared with vascular plants. Recent works has shown that total phenolic compounds produced by living *Sphagnum* influence microbial communities, fungal enzymatic activities and vascular plant mycorrhizae. They also vary according to the season and are reduced by global warming. It is then timely to better understand how *Sphagnum* secondary metabolism responds to global change.

We investigated how climate warming affect *Sphagnum* specific phenolics (*Sphagnum* acids) using a metabolic profiling approach. Two *sphagnum* species (*S. magellanicum* and *S. fallax*) were collected along an experimental site in a peatland of Jura (Frasne, 25) within two microhabitats (wet lawn versus dry hummock) submitted to an increase of +1°C thanks to the installation of Open top chamber since 2008. *Sphagnum* acids of ethanolic extracts (v/v20/80%) were evaluated by UHPLC MS-Qtof.

Our results identified four sphagnum acid forms (i.e. a simple sphagnum acid, a glycosylated form, a conjugated form with uronic acids and an ethylester form). Their production was majoritary in the capitulum and varied between months and species. Global warming had little effect on the production of sphagnum acids for both species. Interestingly, the microhabitat influenced only the production of glycosylated and conjugated with uronic acids forms in *S. fallax*. For this species, the sphagnum acids production was positively correlated to the air temperature and mire water pH. For *S. magellanicum*, they were negatively correlated to air temperature and water level but positively to the *Sphagnum* pH. These results underline the importance to study the production and regulation of sphagnum acids among *Sphagnum* species. Allelopathic roles of these metabolites between *Sphagnum* species, vascular plants and microbial communities offer interesting perspectives.

^{*}Speaker

The multiscale fluid mechanics of olfaction in insects: Particle Image Velocimetry (PIV) around 3D-printed models of antennae

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Volatiles perception by insects is a multiscale phenomenon. We present here our first results on the dynamics of flow around a multiscale antenna of a moth, *Samia Cynthia* (Saturniidae). Because of the multiscale aspects of these antennas, which span four orders of magnitude (from the 3- μm diameter of the sensillae to the 1-cm length of the whole antenna), no single additive technology able to print a whole antenna. Thus, we built two 3D physical models of different architectures, focusing either on the scale made of the main branch and the secondary branches (called ramis), and on the scale made of the ramis and the hair-like sensillae (see picture). For the same reasons as above, the overall antenna and the sensillae on it are living in very different Reynolds numbers (from 0.001 to almost 1000) for a single air flow so we decided to use Particle Image Velocimetry, both in water and oil, at different speeds to understand the structure of the flow around the antenna. From these flow profiles, we calculated the proportion of volatiles reaching the antenna and derived the efficiency of the antenna in terms of molecule capture.

*Speaker

Pollination in a drier world: how climate change affects pollination networks via the alteration of floral traits

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Pollinator decline is ubiquitous, yet pollinators are essential for the reproduction of the vast majority of plants, and hence they play a major role in the stability of terrestrial ecosystems. They also contribute to the productivity of 75% of human cultivated crops. Among the causes of their decline is habitat fragmentation and climate change, but how precisely environmental changes affect wild pollinators and their interactions with plants is unknown. One way to bridge this gap is to extend studies to entire plant-pollinator communities, and to incorporate functional traits that are relevant to plant-pollinator interactions, such as floral signalling traits. Although floral scent is considered a major communication channel between flowering plants and their pollinators, it is currently underrepresented in community-level studies. We measured how experimentally drier conditions affect floral traits, including floral scent, and how this alteration may in turn affect the pollination network, in a Mediterranean shrubland community. Using the drought-mimicking CLIMED experimental in the garrigue near Marseilles, we measured floral scent, floral colour and nectar production of the most abundant species in experimentally drier areas, as well as in control areas. We also measured the frequency of visits of the different pollinator guilds (mostly bees) on those abundant plant species. We then built the pollination networks in the different climatic treatments and incorporated the floral traits as explanatory variables on networks' structure. With this dataset, the first of its kind, we will answer fundamental questions on the resilience of plant-pollinator communities in a drier world.

*Speaker

Deciphering molecular cross-talks during kelp-endophyte interactions

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Kelps are important primary producers in temperate to cold northern hemisphere shores and key species in the formation of coastal marine habitats. As sessile organisms, these large brown algae are able to actively respond to external biotic stress by regulating transcription and metabolic pathways in order to cope with various associated micro- and macroflora. In kelps, small endophytic filamentous algae are known to invade stipes and fronds. For instance, the endophyte *Laminarionema elsbetiae* is highly prevalent in European populations of the sugar kelp, *Saccharina latissima*, but has also been found occasionally in *Laminaria digitata*. The presence of algal endophytes coincides with morphological changes in the hosts- such as dark spots, galls, twisted stipes and deformation of the blades. However, little is known about the molecular and chemical bases of this interaction, its physiological impacts on the hosts and its ecological role. To get further insight into host-endophyte interactions, we set-up an experiment to monitor the impact of the endophyte on growth of laboratory-grown kelp sporophytes. First results revealed that co-cultivation of *L. elsbetiae* does not induce strong oxidative responses of its main host *S. latissima*, neither affect its growth. On the contrary, growth of the occasional host *L. digitata* decreased significantly when co-cultured with the endophyte within less than a week. The molecular detection of endophytes associated with the kelp tissue by qPCR showed a lower prevalence in *L. digitata*, suggesting that defence reactions against *L. elsbetiae* were triggered in *L. digitata*, but not in *S. latissima*. Large-scale transcriptomic analysis of endophyte-induced early responses in both kelp species will help us to decipher the molecular and metabolic cross-talks during kelp-endophyte interactions.

*Speaker

Use of ecometabolomics in chemical ecology to disentangle plant-environment interactions on various scales

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Ecometabolomics tools, ranging from untargeted metabolic fingerprinting to profiling of target compounds, offer a great potential to gain a deeper understanding of the huge variation in the chemical composition of organisms on various scales and its relevance in driving interactions between species. A large variation can be found not only between species, but also within species and even within individuals. Challenging various plant species with an identical treatment (i.e., the same arbuscular mycorrhizal fungus species), species-specific versus general phytochemical plant responses to this mutualism could be revealed in systemic leaf tissues. Within the plant *Bunias orientalis* (Brassicaceae), we used metabolomics tools to disclose the phytochemical variation between populations of this range-expanding and partly invasive species, which likely experienced different selection pressures across its distribution range. Chemical differences in leaf quality found in plants of different populations growing under common garden field conditions had pronounced effects on herbivores and pathogens interacting with this species. Finally, within the species *Tanacetum vulgare* (Asteraceae), chemical differences between tissues (i.e., flowering stems versus leaves of different age) were enclosed which may explain, why herbivores show distinct preferences for certain plant parts. Analyses of phloem exudates of these tissues revealed a high intra-individual variation in plant chemistry that may be an important driver for plant-aphid interactions determining niche differentiation. I will demonstrate examples on these various scales to highlight the advantages of ecometabolomics approaches in chemical ecology.

*Speaker

Evolution of the NUDX1 gene in wild roses

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Previously, a new enzyme involved in geraniol biosynthesis has been characterised in modern roses. This enzyme, named NUDX1, does not belong to terpene synthases but to Nudix hydrolases (Magnard et al. 2015 Science 349, 81-83). In other organisms like *Escherichia coli*, *Arabidopsis thaliana* and *Homo sapiens*, NUDX1 homologs are involved in cellular sanitization, hydrolysing 8-oxo-dGTP to avoid mutations. In modern roses, it hydrolyses geranyl diphosphate into geranyl monophosphate. This compound is then probably hydrolysed into geraniol by an unknown enzyme. To gain knowledge about this new function of NUDX1 and its evolution, we have begun the characterisation of *NUDX1* gene orthologs in wild species of roses and in other *Rosaceae*. We would like to know whether this function has appeared during domestication (30,000 cultivars created by growers since the XVIIth century), during evolution of the genus *Rosa* (120 species all around the world), or during the evolution of *Rosaceae* and closed families.

*Speaker

Oviposition induced plant volatiles act as warning cues of herbivory to neighbouring plants

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Plants can respond to environmental cues that predict impending herbivory by priming appropriate defences; yet, we have limited knowledge about how priming cues that change plant defence phenotype, can also influence plant fitness. Here we show that volatiles induced by herbivore eggs-prior to any feeding damage-can prime defences in neighbouring plants. Working with both an annual, black mustard (*Brassica nigra*), and a perennial, Brussel sprouts (*Brassica oleracea*), we found that volatiles induced by the eggs of a specialist herbivore, the large cabbage white butterfly *Pieris brassicae*, elicited enhanced defence responses to subsequent herbivory that reduced herbivore performance. Interestingly, *Brassica nigra* plants exposed to oviposition-induced plant cues also showed significantly higher flower and seed numbers compared to non-exposed plants, indicating that priming cues can also influence plant fitness. These findings provide evidence for an unexplored role of plant-insect interactions to fitness benefits from insect-derived olfactory cues, even before actual herbivory is present.

*Speaker

Evolution of floral scents in a nursery pollination mutual

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Flower scents have a well-demonstrated role as major signals in structuring pollination interactions. Most studies of chemical mediation between plants and pollinators highlight the direct impact of pollinator-mediated selection on the composition of flower scents. Nevertheless, phylogeny may also constrain flower scent composition and thereby the evolution of the emitted signal. Using a model system with obligate pollination interactions, the mutualism between figs and their species-specific pollinating fig wasps, we tested whether phylogenetic history constrains the composition of plant chemical signals that mediate interactions with pollinators. We collected floral scents from receptive figs using *in situ* headspace extraction from 25 species of several subgenera of *Ficus* from different tropical and subtropical regions, and analyzed their chemical composition using gas chromatography / mass spectrometry. Using a previously reconstructed phylogeny of the genus *Ficus*, we analyzed the phylogenetic signal exhibited by semi-quantitative flower scents data by applying phylogenetic principal component analysis (pPCA) and Kmult tests. When considering only the major compounds emitted by each species (*i.e.* compounds representing more than 5% of the total scent), no phylogenetic signal was revealed. By contrast, when we considered all the VOCs emitted by figs, a significant phylogenetic signal was detected. Our results therefore suggest that there is a significant phylogenetic conservatism in the VOCs emitted by figs, probably due to constraints in the evolution of some biosynthesis pathways, but this signal is mainly due to minor compounds, while closely related species tend to emit different blends of major compounds, probably as a consequence of pollinator-mediated selection.

*Speaker

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Optimal foraging at small scales: deciphering the intra-plant foraging pattern of an herbivorous insect

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According to the optimal foraging theory, diet selection by herbivorous insects should result from a trade-off between costs and benefits associated with feeding. Costs include energy loss during resource location and handling, as well as negative effects due to plant defenses. Benefits are nutrient and energy gains. Optimization of food choice by balancing nutrient intake while minimizing toxicity from defense compounds has been studied for many years, especially in the framework of diet mixing between different plant species. However, both nutrients, defenses and morphological characteristics are known to vary also within a plant, for example, depending on organ age. The optimal foraging theory is then as much relevant to understand intra-plant foraging strategies of herbivorous insects. We applied these concepts to the pollen beetle (*Brassicogethes aeneus*), a florivorous insect that feeds on pollen of many plant species including oilseed rape (*Brassica napus*). Prior to blossoming when pollen is only accessible by piercing flower buds, this insect shows a stereotypic intra-inflorescence pattern of resource exploitation. Indeed, the youngest (i.e., smallest) buds are almost systematically preferred over older buds. We tried to decipher the bases of such foraging behavior in a series of experiments focusing each on an important variable predicted by the optimal foraging theory: resource availability, resource accessibility, nutrient content, defense level and energy gain. Our results show interesting interactions between these variables.

*Speaker

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Do anal gland scent of Alpine marmots encode genetic relatedness?

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Chemical signals are omnipresent in sexual communication in the vast majority of living organisms. To enhance their fitness benefits, choosy individuals should be able to obtain information about the genetic makeup of conspecifics. The use of chemical signals as indicators of genetic compatibility (relatedness) could facilitate inbreeding avoidance and help in identifying the best mate. This implies that choosy individuals are able to discriminate genetically compatible mates and orientate their mate choice towards them. We tested this prediction in the Alpine marmot, a cooperatively breeding species, which social and extra-pair mate choice were previously reported to be based on genetic characteristics. In Alpine marmots, the proportion of extrapair paternity has been shown to increase with both high similarity and dissimilarity between the social pair suggesting a choice for an optimal outbreeding variant. We predict that odour of anal gland should encode chemical information about pairwise genetic relatedness within and between the sexes which should use as cue in mate assessment. We sampled anal gland scent of 154 Alpine marmots and we couple gas chromatography and mass spectrometry data with genetic analyses to test whether the chemical composition of anal scent provides information on genetic compatibility. We expect that anal scent provide these genetic information and so that chemical signals have the potential to act as effective signals for mate assessment.

Conservation Biology

Guiding decision-making to mitigate lynx-vehicle collisions using spatially-explicit individual-based models

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Large carnivores are wide-ranging species, highly mobile and live in human-dominated landscapes where habitat destruction and fragmentation are important threats. In parallel, the terrestrial transportation network is getting denser and acts as a barrier for the movement of these animals as well as it increases the risk of collisions. The Eurasian lynx (*Lynx lynx*) is no exception and its populations in the Vosges and Jura mountains in France are at risk, with vehicle collision being the main source of mortality.

Transportation planners and land managers need models to assess the current situation and the consequences of potential future management actions. Integrating previous works on the Eurasian lynx, we developed a spatially explicit individual-based model to estimate lynx population viability. The model simulates lynx movement and demography accounting for its habitat and the risk of collision with cars and trains. The model is implemented with the new R package NetLogoR (<http://netlogor.predictiveecology.org/>) which provides classes and functions to easily create spatially explicit individual-based models in the R platform.

We show how to run different scenarios (e.g., adding a new road segment, reducing traffic in a specific area, or adding a road overpass) and assess the changes in lynx viability compared to the business-as-usual scenario. Overall, we provide new modelling tools to guide decision-making to mitigate wildlife-vehicle collisions.

*Speaker

Floristic study and preservation of the biodiversity of the Macta wetland (north-west of Algeria)

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The work dealing with the wetlands of the Oranie are few and that studying the Floristic cortège is even rarer. Among the wetlands of the west Algeria, that of the Macta, remains one of the most interesting areas to study.

The Macta, is constituted by a rich ecosystem and specific. It is characterized by the presence of water during almost the entire year, by a diverse wildlife and by vegetation subservient (vegetation halophyte). Of this fact, it is a site where the protection and the preservation of this biological diversity is more than necessary on both the national and international level.

In terms of climate, the exploitation of Weather Data Highlights average elevation of the temperature of 1.5°C and a decrease of the tranche of rainfall annual average, with impacts on the floristic composition of this space.

The pedological approach confirms the clayey texture of the ground where the majority of the surveys have been carried out. In addition, the electrical conductivity shows the saline character of the soil, with an alkaline pH.

The floristic study has made it possible to Inventory 83 species say halophytes to broad distribution and abundance high enough. Among the halophytic species, include *Sarcocornia fruticosa* , *Atriplex halimus* , ... We also note the presence of species of land uncultivated and brownfield sites, as well as some of the introduced species by reforestation as *Pinus halepensis* , *Acacia horrida* , ...

The statistical study, through a factorial analysis of correspondences (AFC) has helped to establish a correlation between the vegetation and environmental factors studied. The vegetative mat of the Macta wetland rest conditioning, in addition to the climate, by the edaphic factor and by the time and the intensity of flooding by the water.

Key words: wetland – biodiversity - Climate - Soil - halophilic vegetation- western Algeria

*Speaker

Combining an innovative monitoring method and a hierarchical bayesian model to estimate diadromous fish run

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Over decades, diadromous fish have strongly declined and many species are now protected through national and international regulations. They account for less than 1% of worldwide fish species; however they are one of the most tangible linkage between freshwater and marine ecosystems, and can reveal changes in the functioning of both ecosystems. Juvenile and adult migrations are key transitions of their life cycle, during which the abundance estimates is of critical interest for managing the populations. Fish counting facilities such as traps, video or resistivity counters, have been installed for decades on many rivers to provide abundance time series. However, the number of fish counted does not necessarily reveal real fish run (limited coverage, detection efficiency dependent on turbidity, ...). Here we propose a two-step approach to assess the efficiency of fish counting facilities and to estimate diadromous run in streams. First, an acoustic camera (ARIS) is implemented in complement of the current counting facility during a short period of the fish run. Secondly, the acoustic data produced and the usual fish counts are analyzed jointly thanks to a hierarchical Bayesian model to estimate detection efficiencies. To that end, a generalist model has been developed and can be applied to various species and counting systems. Simulated data were used to test the model robustness. The approach was then performed in the Touques River (France) to estimate the silver eel run. The relevance of this approach and its potential transfer to managers is discussed.

*Speaker

Plant communities' responses patterns in wet grasslands: an investigation of management-driven contrasts versus uncontrolled drivers

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In situ datasets are compulsory to identify the actual drivers of biodiversity and thereafter to efficiently design conservation strategies. They are especially badly needed when stakeholders harshly opposed as in many wetlands where debate concerns water level management. Indeed, valuable croplands surrounding wetlands required low water levels in early spring for sowing corn while conservationist considered that typical wetland biodiversity depends on long flooding durations and high water levels in spring. Despite a long-standing debate, very few proper data are available to shed light on 1) the actual dependency of wetland plant biodiversity on flooding duration and 2) how much flooding duration depends on water-management control and on natural elevation settings.

This study aims to answer these questions while taking into account shortcomings associated to field data, i.e. their limitation to distinguish the effect of management-controlled conditions *versus* the effects of uncontrolled environmental conditions.

Focusing on the various plant communities in 110 wet grasslands, an intensive sampling was conducted for 4 years, together with a large multi-dimensional environmental characterization in 11 sites in the Marais poitevin, western France.

The results showed, as expected from previous studies, that the flooding duration and water table's conductivity impacted the plant diversity and composition. Less expectedly, the between-sites elevation contrasts, resulting from natural settings, were found of lower importance for vegetation pattern than water level management. Plant composition significantly responded to the severity of summer drought and this unexpected result could not have been achieved without the year-round and multi-dimensional *in situ* environmental characterization. We showed that the spatial pattern of plant communities matters much for diversity pattern: the vegetation composition was indeed more contrasted within-sites than between-sites (differing by the water level management) due to natural elevation contrasts. This result advocates for considering ecological contrasts underpinning beta diversity when designing conservation strategies.

*Speaker

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Investigating protected areas effectiveness using North-American Breeding Bird Survey

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Protected areas are one of the main tools for conserving biodiversity worldwide, yet their effectiveness in doing so has been studied to a limited extent. Previous studies mainly used pairwise comparisons between a protected versus an unprotected site, but the choice of the unprotected control site is often poorly defined and thus rather subjective, which can introduce important biases (*e.g.*, differences in altitude, productivity, or habitat). In practice, the choice of the control is key, as it is tangled with the very definition of protected areas effectiveness. For example, very different conclusions will be obtained when considering as the control for a protected forest an unprotected cultivated area that was previously a forest, or an unprotected forest with higher intensity of human activities, or an unprotected forest with similar level of human activities.

In this talk, I will argue that large biodiversity monitoring datasets provide a major opportunity for investigating protected areas effectiveness at large scales, as analysing these datasets forces us to define together control site and expected effects. I will illustrate this using an analysis of the effectiveness of North-American protected areas in conserving bird biodiversity. We found no effects of protected areas on species richness or total abundance. However, we show that in a given habitat, protected areas favour species typical from this habitat (*e.g.*, forest species are more abundant in protected forests than in unprotected forests), making the assemblage more typical. Moreover, we show that protected areas are beneficial to species that avoid human presence, hence effective in protecting species that are potentially the most affected by human activities.

I will conclude that measuring protected areas effectiveness is not only crucial in order to understand how they are affecting biodiversity, but also to think about the expected effect of conservation in a context of biodiversity crisis.

*Speaker

Media coverage of the wolf recovery in France: how newspapers' social-ecological values impact conflict mitigation

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The return of large carnivores in Europe has increasingly led to environmental conflicts, mainly due to their impact on breeding activities. By extensively covering stakeholders' debates, mass media have shaped a specific representation of human-wildlife conflicts, and have thus contributed to influence public perception of predator recovery issues. In this communication, we focus on the media coverage of the wolf return and management in France. Using a linguistic approach based on lexical and syntactic discourse analysis, we compared the evolution of the wolf conflict treatment in a French national (*Le Monde*, n=338) and regional (*Nice-Matin*, n=942) newspaper, from 1992 to 2014. As generalist newspapers have to maintain a large readership, they are likely to build a less sliced conflict representation than involved stakeholders. However, we observed that social-ecological views of both newspapers had an impact on the properties attributed to human and non human stakeholders. Along the period, *Nice-Matin* emphasized an empathetic description of livestock breeders' experience of the wolf, and tended to exclude the predator from a well balanced social-ecological system. Before the establishment of quotas allowing wolf removal (2004), *Le Monde* expressed its support for the wolf conservation essentially by associating deceitful attitudes to livestock breeders, and rational properties to institutional officials. The establishment of wolf removal policy was associated with a progressive rehabilitation of breeders and a focus on the emotional aspects of predation. Properties of violence and intentionality were then attributed to the wolf. Our study shows that in each newspaper, media coverage of the conflict induced the exclusion of either the wolf or the breeder from a well balanced social-ecological system. We finally discuss the critical impact of printed press' unbalanced treatment of human-wildlife issues. Instead of contributing to mitigate the conflict, media coverage emphasizes the representation of polarized positions in the public debate.

*Speaker

Place of invertebrates in individuals' minds and hearts

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Invertebrates are everywhere: they represent 95 % of the world's animal diversity, and being linked to every ecosystem function, they have key roles in biodiversity resilience. However, are we conscious about this? Do we value such diversity? Therefore, it is important to investigate how to "show" this animal diversity, through words or pictures, to elicit a positive attitude for biodiversity, which may sustain protective behaviors. In this presentation we have focused on students' perceptions in a French University, who are representative of the society, as more than 80% of a class age has access to University in France. Two studies have been carried out, the first one focusing on what student think about what is animal diversity, the second one on how students "feel" diversity.

Through study 1, we demonstrate that what students think as "animal diversity" is more likely to be a list of more or less well-shaped vertebrate fauna dominated by domestic mammals and birds. Insects are a mix of invertebrates with an overall negative perception. Moreover, sympathy for invertebrates was correlated to the "quality of the human environment" of the person only: being surrounded by influent persons (parents, best friends) actively involved in nature conservation increase awareness of insect diversity, insect knowledge and positive perception of the group.

Through study 2, we focused on a relatively unknown invertebrate group of species living in the soil: Springtails. French university students were invited to evaluate their feelings while watching a series of pictures, each showing one species of Springtails. This study enabled us to identify what are the visual cues that induce positive emotions and those that induce negative ones.

Through both studies, we highlight the importance of invertebrates' perception studies as a crucial question to develop useful conservation tools.

*Speaker

Human activities explain the degradation status of a marine ecosystem. Which use for management?

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During the last fifty years, there has been a dramatic increase in the development of anthropogenic activities, and this is particularly threatening to marine coastal ecosystems. The management of these multiple and simultaneous anthropogenic pressures requires reliable and precise data on their distribution, as well as information (data, modelling) on their potential effects on sensitive ecosystems. Focusing on *Posidonia oceanica* beds, a threatened habitat-forming seagrass species endemic to the Mediterranean, we developed a statistical approach to study the complex relationship between human multiple activities and ecosystem status. We used Random Forest modelling to explain the degradation status of *P. oceanica* (defined herein as the shift from seagrass bed to dead matte) as a function of depth and 10 anthropogenic pressures along the French Mediterranean coast (1700 km of coastline including Corsica). Using a 50 x 50 m grid cells dataset, we obtained a particularly accurate model explaining 71.3 % of the variance, with a Pearson correlation of 0.84 between predicted and observed values. Human-made coastline, depth, coastal population, urbanization, and agriculture were the best global predictors of *P. oceanica*'s degradation status. Aquaculture was the least important predictor, although its local individual influence was among the highest. Non-linear relationship between predictors and seagrass beds status was detected with tipping points (i.e. thresholds) for all variables except agriculture and industrial effluents. Using these tipping points, we built a map representing the coastal seagrass beds classified into four categories according to an increasing pressure gradient and its risk of phase shift. Our approach provides important information that can be used to help managers preserve this essential and endangered ecosystem.

*Speaker

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Functional Rarity of Four Major Taxas in Mainland France

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Biodiversity has been the long focus of ecology. Less attention is generally devoted for rare species. Recently the idea of functional rarity of species, i.e., the rarity of their traits locally and regionally, has been proposed.

Conservation science traditionally focus on species that are rare in abundance but neglect species that are rare in terms of traits, while species with original traits may fulfill original functions locally and regionally.

We quantified the functional rarity of species and its relation to conservation measures (IUCN status, protected areas) across mainland France on four major taxa using field relevés: birds, herbs, trees and fishes.

Most species were geographically rare while functionally common for all taxa. Their regional and local trait rarity was highly correlated. Threatened species were functionally rarer on average than non-threatened species for all taxa. We pinpoint several functional rarity hotspots at the scale of France, where the concentration of functionally rare species was highest for all taxa.

These results suggest that better conservation measures could be taken for additional protection of functionally rare species. More research is needed to understand the origin and importance of functional rarity as a new facet of biodiversity.

*Speaker

Seed banks across floodplains: a study in five major habitats of the Middle Loire River (France)

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The role of seed banks in the assembly of plant communities has been a rising topic within recent years. Goodson et al. (2001) identified riparian seed banks to be a neglected area of river research, and seed banks in riparian systems a poorly investigated ecosystem type in seed bank research. Since then, a series of studies concerning riparian seed banks have become available. Most studies however concentrate on only a small range of habitats or low-energy lowland rivers of moderate size. The present study investigates seed banks in relation to standing vegetation in the floodplain of a great river with high-energy floods and over the whole range of floodplain habitats, i.e. over a wide disturbance and successional gradient. It aims to test current hypothesis on seed bank density, composition, spatial variability with regard to disturbance gradients and seed bank persistence.

The study took place on the Loire river floodplain in the Center of France and concerned its five most frequent habitats types: 1. sand banks or sandy river shores with scarce pioneer vegetation, 2. Softwood (*Populus nigra*) shrubs, 3. Softwood forest, 4. Mature forest, 5. *Elytrigia*-dominated grasslands. While seed banks from different habitat types showed clear differences in species composition, they were rather similar with regard to average values of most other descriptors. The most frequent species occurred at a limited portion in the standing vegetation but over a wider range of the floodplain gradient, thus illustrating the extent of lateral dispersion, the local species pool and effect of environmental filters. Significant differences in intra-habitat variability of seed bank characteristics suggest different processes in seed bank formation. Those processes will be discussed.

Goodson, J.M., Gurnell, A.M., Angold, P.G. & Morrissey, I.P. (2001) Riparian seed banks: structure, process and implications for riparian management. *Progress in physical geography*, 25, 301-325.

*Speaker

Ecological interactions between wild bee species and the managed honeybee: towards practical decision rules in protected natural areas

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As modern farming practices make agro-ecosystems less suitable environments for sustainable honey production, professional beekeepers now commonly migrate their bees. They periodically move large apiaries to natural areas, either to exploit temporary mass-flowering resources or to escape chemical hazards and seasonal food shortages. But in recent years, conservation biologists have raised awareness about the risk of ecological interference between massively introduced managed honeybees and the native wild bee fauna in protected natural areas. Here we show that high-density beekeeping in natural mass-flowering areas triggers foraging competition which depresses not only the occurrence and foraging success of local wild bees but also nectar and pollen harvesting by the honeybees themselves. This intraspecific competition among the honeybees has practical implications for beekeepers. It shows that the local carrying capacity has been exceeded and raises concerns for honey yields and colony sustainability. It also offers an effective ecological criterion for pragmatic decision-making whenever conservation practitioners envision progressively reducing beekeeping in protected areas. Regardless the considered competition criterion, setting distance thresholds among apiaries appeared more tractable than setting colony density thresholds for beekeeping regulation. Overall, honeybee-induced competition spanned distances of 600–1.100m around apiaries, i.e. covering 1.1–3.8km² areas. Although specific to the studied area, those distance estimates may help raise consciousness about the threat high-density beekeeping may pose to local nature conservation initiatives.

*Speaker

Southern European common lizard populations are threatened by global warming

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Gene flow is one of the most important factors determining the evolution of a species, since it directly affects population structure, species' adaptation, and evolution. The European common lizard (*Zootoca vivipara*) is the terrestrial reptile with the widest and farthest north distribution of the world. For this reason, this species has been highly studied, but the lack of a large, reliable and highly variable panel of microsatellite loci has hindered the study of its population genetics. Here we produced highly variable microsatellites and investigated for the first time the population genetics of the Ibero-Pyrenean common lizard (*Zootoca vivipara lousislantzi*). We analysed gene flow among populations of this sub-species by employing 34 newly developed polymorphic microsatellite markers. The analyses unravelled the presence of isolation by distance, inbreeding, bottlenecks, genetic differentiation, and low levels of gene flow among most populations, in line with physical barriers hindering longitudinal migration and climatic conditions being probably the reason for differences in gene flow on the Southern and Northern Pyrenean slope. The results point to isolation of *Zootoca vivipara* populations, especially those located on the Southern Pyrenean slope, which may be threatened by global warming, if temperatures continue increasing in the future.

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Development of a non-lethal method to detect the parasite *Anguillicola crassus* for the conservation of the endangered European eel

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Anguillicola crassus is a parasite nematode of the eel swimbladder, endemic in East Asia. Since its recent introduction in Europe, *Anguillicola crassus* became a predominant parasite in the European eel, *Anguilla anguilla*. The *A. crassus* life cycle depends upon predatory-prey interactions. Eels are infected by ingestion of the third-stage juveniles present in intermediate hosts (copepods, fish...). Then the ingested parasite will infest its host's swimbladder until maturation. Parasites eggs are then, released in the eel's intestinal tract and are then evacuated with feces in the water. This nematode may impair the capacity of European eels to complete the spawning migration and shorten the life cycle. So far, the only method to detect this infection implies dissection of the swimbladder, which is lethal for the fish. The present study describes the development of a new detection method from eel's feces using molecular biology protocol. Using parasite-specific molecular markers, we aimed to detect the parasite's DNA in eel's feces. Positive results showed that the method allows a non-lethal way of assessing the prevalence of *A. crassus* from the feces with comparable or better rates to swimbladder dissection. However, this method has some limitations that will be discussed during the presentation.

*Speaker

Is my SDM good enough? Insights from a Lucanoidea citizen science dataset in a Point Process Modeling framework

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Citizen science programs, and particularly atlas schemes, are very important sources of data for species distribution models and conservation. Nevertheless, this data is prone to bias, particularly when it comes to "not-so popular" or hard to detect/identify species such as insects and it represents the challenge of presence-only datasets (lack of absence data). Moreover, how do we know if the model predictions are trustworthy?

In recent years, Point Process Models (PPM) have shown their strength as a unifying frame to fit presence-only species distributions models (SDM) with many advantages in model implementation and interpretation. Based on the French citizen science program - "Stag Beetle Quest", we illustrate different methods to assess "model reliability" within the PPM perspective fitted with a lasso penalty and bias corrections. To do this, we randomly subsampled different sets of locations from the whole dataset and compared fitted intensities and model coefficients. All of the developed measures are congruent and can be used to identify at what number of point locations the model stabilizes, which will be dependent on the dataset.

Thereby, our work presents new tools to explore questions around model stability based on the number of locations in the context of PPMs with a lasso penalty and confirms once more the use of PPM framework as flexible and unifying framework to model presence-only species distribution models.

key-words: *Lucanus cervus*, citizen science, atlas, diagnostic tools

*Speaker

Revisiting conservation limits for Atlantic salmon: a new risk based definition

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The North Atlantic Salmon Conservation Organisation recommends a fixed escapement strategy for population management, including freshwater fisheries regulation. It is based on a benchmark reference point, i.e. a conservation limit (CL), defined as the spawning stock size that maximizes the long term average of potential catch. This widely applied international recommendation implicitly considers that ensuring conservation is equivalent to maximizing exploitation potential. Although these two management objectives are not necessarily incompatible, they must be separated and prioritized because maximizing catches can be conflicting with conservation. We propose a new CL definition based on the premise that conservation should aim at avoiding, i.e. controlling the risk of, low recruitment. We demonstrate the applications of this definition by means of a case study on the salmon populations (18) of Brittany (France). For each population, the CL is derived from river-specific stock-recruitment (SR) relationships, relating the number of eggs produced by pre-spawning females (stock) to the abundance of the resulting young-of-the-year juveniles (recruitment). A hierarchical SR model, based on a Beverton-Holt type relationship with a mixture of lognormal process errors, is used for the joint analysis of all populations. Relying on the Bayesian framework for statistical inference, the risk associated to the CLs fully integrates the major sources of uncertainty: recruitment stochasticity, measurement errors of the stock and the recruitment, estimation of the SR relationship.

*Speaker

Effects of harmful algal blooms on juvenile green turtle (*Chelonia mydas*) foraging ecology and habitat use

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Anthropogenic pressure has led to extensive impacts on the coastal environment. Harmful algal blooms (HABs), often linked to anthropogenic impacts, can cause ecological damage and die-offs of flora and fauna. Successful marine conservation requires an understanding of how organisms respond to environmental changes. As harmful algal blooms are predicted to become more common and severe in the future, it is necessary to evaluate their impacts on marine turtles. The Indian River Lagoon (IRL) along the east central coast of Florida has experienced an increased frequency of HABs in recent years, causing severe reductions in seagrass cover and drift macroalgae, key food resources for juvenile green turtles (*Chelonia mydas*). While our long-term data (1982-present) indicate decreased juvenile green turtle abundance during and after severe HABs of 2011 and 2012, we hypothesize that HABs also resulted in changes in diet and/or habitat use among the turtles that remained in the IRL during the HABs.

To evaluate this hypothesis, we conducted stable isotope analyses on skin samples from 250 juvenile green turtles captured in the IRL between 2010 and 2015. Briefly, stable isotope ratios in an animal's tissues reflect isotope ratios of what and where that animal has been eating. In our study, it is necessary to account for potential changes in baseline isotope ratios as a result of algal blooms in the IRL. Therefore, we compared turtle isotope signatures to those of 130 samples collected from fish resident in the IRL, enabling us to disentangle changes in baseline ratios from potential behavioral and foraging changes exhibited by the turtles. Initial results indicate that juvenile green turtle stable isotope signatures were more variable before the HABs of 2011-2012 than during or after, indicating more restricted diets and/or reduced turtle recruitment to the IRL as a result of the blooms.

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Saving the threatened terrestrial biodiversity in the French Overseas tropical islands: which research strategy?

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70% of the ca. 18,000 endemic plant and animal species known in France are found in the French Overseas tropical islands, formed by 11 territories located in three oceans (Atlantic, Indian and Pacific) and comprising an area of only 4 % of the French nation. This "mega-biological" diversity hold France responsible for both the study and the conservation of this unique natural heritage at the European and international level. Moreover, these island biota are highly threatened by local and global anthropogenic changes (e.g. loss and degradation of natural habitats, invasive alien species, overexploitation, pollutions, and climate change) with exacerbated impacts in the more vulnerable island ecosystems, and with record numbers of extinct or endangered endemic species. Those challenges justify that particular efforts in conservation sciences should be conducted on both the endemic species and the particular ecosystems and habitats found in these tropical island territories. In this talk, we illustrate their relevance in crucial ecological issues (colonization, speciation and radiation, extinction and rarity, biological invasions and biotic interactions, forest dynamics and restoration, impacts of temperature and sea-level rise) through some research and conservation programs recently conducted or planned in the next future. We urge that more concerted efforts between research scientists, managers and local island communities, and between territories sharing the same challenges, are developed. They should lead to common strategies and demonstrate the importance of these French Overseas tropical island territories at the national, regional and international scales.

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Towards the restoration of the Mesoamerican Biological Corridor for large mammals in Panama: a multispecies approach

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Habitat fragmentation is a primary driver of wildlife loss, and the establishment of biological corridors is a conservation strategy to mitigate this problem. A key example is the Mesoamerican Biological Corridor (MBC), established to connect protected forest areas between Meso- and South America to allow dispersal and gene flow of forest organisms. However, its effectiveness has been questioned, and recent studies indicated that it is dysfunctional for large terrestrial mammals in Panama, the narrowest section of the MBC. While most corridor planning initiative focus on single species, here, we used a combination of methods to identify important corridors within the Panama portion of the MBC for an assemblage of nine large mammals. We divided the nine species into two groups depending on their sensitivity to habitat disturbance, and hypothesized the multispecies connectivity scenarios to be different between the two groups. For each group, we estimated landscape resistance using (i) resource selection functions from empirical occupancy data collected across Panama, and (ii) step selection functions with GPS telemetry data from white-lipped peccary *Tayassu pecari*, puma *Puma concolor*, and ocelot *Leopardus pardalis*. Based on the resistance surfaces modeled, we estimated connectivity with circuitscape algorithm. Finally, we compared the different multispecies connectivity scenarios, and assessed their performance. On the basis of our results, we propose areas to conserve in priority for establishing effective corridors that would facilitate the movement of large mammals in Panama. This study represents the first effort to assess the effectiveness of the MBC (i) at a country scale, and (ii) for several species simultaneously, to accurately inform the local authorities in conservation planning. The approach we present can also be used in other sites, and/or for other species.

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Strong increase in Red kite adult mortality resulting from a vole poisoning campaign using anticoagulant rodenticide

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A recent upsurge of wildlife poisoning has been described worldwide, threatening many species of conservation concern. Poisoning can be used as an illegal mean to eliminate predators. Evidence for secondary poisoning, i.e. when the poisoned target species is consumed by another non-target species, is growing and scavenger species (obligatory or not) are particularly affected. The use of anticoagulant to fight against rodent farmland pests, such as voles, has led to the recording of secondary poisoning for many non-target species. However, estimating the genuine impact of poisoning on non-target population dynamics from the partial recovery of dead animals is difficult. Failure to make strong inferences regarding poisoning impact hampers the set-up of effective management responses. An intensive poisoning campaign, using Bromadiolone rodenticide, occurred in 2011-2012 in response to a water vole outbreak in ‘La Chaîne des Puys’ (Massif Central, France), and resulted in the discovery of an unusually high number of dead red kites ($N = 25$), a Nearly-Threatened IUCN-list species. We analysed capture-recapture data from a wing-tagging program conducted on this species since 2006, and found a severe reduction in adult survival (-19%) over the two years of the poisoning campaign. First-year survival was not affected, young birds being less exposed than adults to Bromadiolone, the latter being mostly spread in early spring (before birth) and late autumn (after their departure for migration). Adult survival in two ‘control’ study areas from Massif Central, lacking poisoning campaign, was not reduced over the same period, reinforcing the putative link between additive mortality and poisoning campaign. We further explored the impact of repeated, large-scale water vole poisoning campaigns on red kite population growth rate at the regional level using projection matrices.

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Relevance of the multifaceted approach of biodiversity for conservation

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Since the early 2000s, scientists have called for a more integrative approach of diversity that encompasses functional and phylogenetic components beyond the traditional focus on species richness. Application of this approach to spatial conservation strategies has been then advocated through the analysis of the mismatch and congruence between the different dimensions of biodiversity with protected area networks for several groups in different regions. These papers have challenged existing conservation strategies in suggesting that important biodiversity facets were excluded from protected areas. However, the contribution of these facets to ecology and conservation science is still unclear. Overall, the justifications for developing new conservation strategies based on multi-faceted approaches must be clarified. Here, we conducted an exhaustive review of the articles integrating a multifaceted approach of the diversity for conservation, including the taxonomic, functional, and phylogenetic components. We reviewed the questions addressed in each paper as well as the spatial and thematic extent covered. We examined and explained the potential caveats and advances of using such multifaceted approaches for conservation strategies. This synthesis provides an overview of commonly used multifaceted frameworks and most promising agendas in this direction.

*Speaker

Conservation Biology

*Speaker

Spontaneous recovery of functional diversity and rarity of ground-living spiders shed light on the conservation importance of recent woodlands

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Secondary forests, whose development is favoured by massive farmland abandonment, are increasingly seen as promising habitats that limit losses of biodiversity and ecosystem processes. The importance of temporal forest continuity (i.e. the duration of an uninterrupted forest state) for conservation of the forest fauna has been demonstrated for several taxa, but its influence on functional diversity and conservation importance of communities remains unclear. We studied how temporal continuity can shape taxonomic and functional composition and structure of forest-ground spider communities at a regional scale. According to broad-scale ecological site characteristics – among which forest continuity ranks uppermost –, species composition substantially diverges between ancient and recent forests. Yet, we did not evidence any significant differences for functional composition as well as for community structure and conservation importance of the two forest categories, except for functional originality (which quantifies the average functional uniqueness of species within an assemblage). Thus, in a conservation perspective, our study provides evidence that (i) as each forest harbours unique species combinations, each of them is irreplaceable, (ii) this is mainly true for ancient forests, which are functionally more original, but (iii) secondary woodlands have likewise a high potential to spontaneously recover typical forest fauna communities with very similar structural and functional profiles to those of ancient forests.

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Embracing phylogenetic uncertainty in prioritising species conservation: sensitivity of HEDGE scores to species split

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The number of described species has been increasing rapidly over the last 30 years, a phenomenon which may result from a shift in species concept ("taxonomic inflation") and/or real taxonomic progress enhanced by the advances in DNA-based taxonomy and phylogeny reconstruction of the past decades. This increase in species numbers goes together with the split of single species into several ones. The consequences of such species split are the delineation of post-split species with restricted ranges and potentially increased extinction risks, which may have pronounced impacts on the establishment of conservation priorities based on extinction risk. Species split also leads to a re-evaluation of phylogenetic trees, with post-split trees having more species but species that are less evolutionary distinct species than pre-split trees. Therefore, species split may also impact the establishment of conservation priorities based on species phylogenetic originality. Consequently, predicting how species split will affect conservation priorities that incorporate both species extinction risk and phylogenetic originality is challenging. The HEDGE score is one of the criteria according to which such conservation priorities may be established. This score incorporates the evolutionary distinctiveness of a focal species, its extinction risk and those of its close relatives. Here, we evaluated the influence of a hypothetical species split on HEDGE scores. We showed that such split do not affect HEDGE scores for the close relatives of the split-species. However, it can dramatically increase the score of the split-species itself. These results suggest that ignoring cryptic species within a lineage underestimates its HEDGE score. In such situations, the estimated ranking does not capture the real ranking and some lineages may not receive the conservation attention they deserve. Overall, this work demonstrates the need for quantifying phylogenetic uncertainty in the establishment of species conservation priorities and challenges the use of species as relevant conservation units.

*Speaker

Paying for conservation: a bioeconomic analysis of land use effects on the viability of an endangered species, *Eryngium alpinum*

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Land management is critical for biodiversity conservation in mountain grasslands. It should be both ecologically effective and economically efficient. We provide an economic analysis of different options (spring and autumn grazing, mowing and abandonment) and their effects on population viability of a rare plant species, *Eryngium alpinum* (Apiaceae), in two French mountain grassland sites (Fournel and Pralognan).

Using data collected in a ten-year, individual-based demographic study, we estimated the effects of land management options on the population growth rate and simulated the effect of combinations of options. Income earned through each option was estimated using data on associated costs (price of consumables, working time, wages) and benefits (forage production, quality and price), and we assessed the economic effects of agri-environment subsidies (AESs). We also simulated the effects of increased frequencies of extreme climatic events (such as the 2003 heatwave). Spring grazing was the worst option for *E. alpinum* demography but the best in economic terms, as it provided net positive incomes. Autumn grazing was the best option, resulting in positive

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growth rates and incomes. Mowing was the second best option for demography but resulted in economic losses for farmers. Abandonment provided zero income and was not favourable to population growth.

In Fournel, AESs allowed for economically and ecologically near-optimal combinations of management options. In Pralognan, alternating years of grazing with mowing resulted in an acceptable compromise, with positive growth rates and incomes, but AESs were not sufficient to cover the opportunity cost of spring and autumn grazing.

Simulations with increased frequency of extreme climatic events resulted in negative growth rates in Pralognan.

The conservation effectiveness and economic efficiency of grassland management could be improved by alternating practices over several years. However, existing agri-environment subsidies are barely sufficient to increase uptake of the most favourable land management options for biodiversity.

Large microclimatic variations do not affect breeding success in artificial nests occupied by an obligate secondary cavity breeder

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Recent development of environmental impact assessment policy has led to the multiplication of mitigation processes such as biodiversity offsetting. These are largely based on direct human interventions, which raise ethical questions. Furthermore, created or restored habitats may at first appear identical to good natural habitats but might however be of lesser quality. They may lead to low survival or reproduction of individuals that occupy them and thus be so-called ecological traps. This risk is particularly strong in case of the use of artificial tools such as nest boxes for vertebrates.

In this study, we tested the hypothesis that artificial nest boxes might be ecological traps. To do that, we compared reproductive parameters of European rollers *Coracias garrulus* in natural cavities (n=22) versus nest boxes (n=17) by monitoring its reproduction in each nest from egg laying stage to chick fledging. We also compared microclimate conditions in cavities (n=41) and nest boxes (n=33), using temperature and humidity loggers placed inside the nest as well as temperature loggers placed outside each nest. We then explored potential effects of microclimate on breeding parameters.

We found strong microclimate differences between natural and artificial nests, with cavities buffering temperature much better, and having a much higher humidity rate. However, we found no significant differences in breeding parameters between rollers occupying both nest types. Our results on breeding parameters suggest that, despite providing microclimate conditions very different from natural cavities, artificial nest boxes are not ecological traps for European rollers in South of France. However, other fitness parameters such as chick development should be explored in order to conclude for the innocuousness of artificial nests for rollers. The low temperature buffering capacity of nest boxes suggests that, – in Mediterranean regions – they should be placed in shaded conditions and built using materials with good insulation properties.

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Spatiotemporal variation of the greater horseshoe bat (*Rhinolophus ferrumequinum*) diet in Western France: applications to chiro-surveillance and conservation strategies

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A detailed knowledge of the diet composition of insectivorous bat species is of primary importance to understand their ecology, and to evaluate their role as agents of biological pest control in farmlands. It is also critical in terms of conservation needs as insectivorous bats are exposed to toxins (pesticides, antihelminths...) by ingestion of pollutants through foraging. Because of their high trophic level, exceptional longevity and large amount of preys ingested per night, bats are very sensitive to this issue. We have developed a rigorous high throughput metabarcoding approach based on a universal COI minibarcode that enables to simultaneously identify bats and their preys from guano samples. This parallel identification of predators and preys provides a rapid, resolute and cost-effective screening tool to accurately describe the spatiotemporal variation of insectivorous bat diets. We have applied this approach to the greater horseshoe bat (*Rhinolophus ferrumequinum*), a near-threatened species that experiences high anthropic pressures because it roosts in buildings during summer and it uses agricultural fields as foraging sites. Guano samples were collected in six maternity colonies in Western France every two weeks throughout the maternity period, when the greater horseshoe bat females gather to give birth and raise the young. It is a very energy-intensive period, where the females and the newborn are very fragile. This study provides a detailed description of the greater horseshoe bat diet and of its variability throughout contrasted landscapes (hedgerows, crops, meadows ...) and during a critical period for reproduction. Our results highlight the possibility of using the greater horseshoe

Speaker

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Conservation Biology

bat as a sentinel for chiro-surveillance and as a natural biological pest control agent. They also give insights into the links between landscape, ecotoxicology and diet, what will lead to improved recommendations for further design of conservation strategies.

Speaker

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Temporal patterns of plant endemism in world islands

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A key feature of islands is their high level of endemism. In plants, more than 70,000 species are endemic to islands. Endemism is both relevant for biodiversity conservation and to understand how biodiversity has been shaped. Yet endemism has mostly been studied at the species level and some important features of endemism may have been missed. Especially current approaches do not inform about the age of endemic species. This topic has been widely discussed for more than a century as it may reveal the diversification process at the origin of endemic species. In this context a distinction should be made between neo-endemism, which shed light on areas where are confined recently diverged species, and paleo-endemism, which reflects areas of range-restricted and ancient taxa. Here we took advantage of the recent development of dated phylogenies to measure phylogenetic endemism in world islands. We then used null models to identify centers of endemism and whether they belonged to the neo, paleo or mixed endemism categories (areas neither dominated by paleo or neo endemism). We focused on Monocotyledons in 4,306 islands across the world. We then explored, thanks to Boosted Regression Trees and multi-model selection, how geographic, bioclimatic and historic factors may have shaped temporal patterns of endemism. We observed that centers of endemism, a majority of them being mixed endemism islands, were found at a higher concentration in the southern hemisphere. Abiotic variables driving temporal patterns of endemism varied with the category of endemism. Nonetheless we found that high elevation, high number of ecosystems, low latitude, low wind speed may have highly contributed to shape centers of endemism. This study thus provides new insights on patterns of insular diversity and its formation. Besides, estimating relative endemism age may guide conservation through the identification of potential museums or cradles of biodiversity.

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Dealing with heterogeneous data

Global evaluation of the impacts of storms on freshwater habitat and structure of phytoplankton assemblages

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The GEISHA/Storm-Blitz group has been studying the impact of storms on the diversity and community structure of freshwater phytoplankton communities, including taxonomic and functional composition. The project has involved significant challenges related to the acquisition of appropriate high-quality temporal data, and the standardization of phytoplankton datasets based on diverse and ever-changing taxonomic nomenclature. Although protocols that clearly define the format for datasets and the development of a controlled vocabulary are necessary and helpful, there are additional challenges presented by biological datasets with a diverse and spatially variable taxonomy. We will discuss lessons learned and best practices for working with data contributors and standardizing heterogeneous datasets, including the benefits of taking a functional approach to analyses of diversity and community composition. We will also describe open-source software tools that we have developed to facilitate the analysis of phytoplankton community data.

*Speaker

Saturnid and sphingid moths as novel models for the study of insect diversity and macroecology

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Invertebrates are keystone species in the global ecosystem and the consequences of their loss are anticipated to be considerable. In particular, there is little understanding of invertebrate assemblages in tropical forests, let alone their response to climate change. Using the saturnid and sphingid moths as models, the group has conducted an ambitious program combining museum, genetic (Bar Code of Life), and environmental data to answer this question. We will present results of macroecological studies at global scale for these moths, with an emphasis on the approach used to combine records from various sources.

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Integrating weed community assembly rules to agroecosystem sustainability: insights from the FRB CESAB DISCO-WEED project

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Arable weeds play a key role in agroecosystems by supporting pollination services and trophic networks, but have drastically decline as a result of intensive chemical control for ensuring crop production. Designing sustainable cropping systems therefore requires a greater understanding of the structure, dynamics and functions of weed communities. In this objective, the DISCO-WEED project mobilizes four databases from France and UK gathering surveys on weed flora, agricultural practices and crop yields, collected at spatial scales ranging from 1m² to the national

scale over nearly 4000 agricultural fields sampled during the last 15 years. From this compilation,

175 taxa were added to the *ca.* 1400 weed species of the comprehensive flora from Jauzein (1995). This extended weed pool encompassed species originating mainly from Mediterranean areas and related to ruderal habitats (56.6%), mesic grasslands (11.4%) and mesophilous fringes (4.6%). To functionally characterize arable weeds, traits of weeds and grassland species were compared using functional spaces: even if weed and grassland species hypervolumes largely overlapped, weed species with high fidelity to arable fields showed a strongly reduced spectrum of ecological strategies, thereby identifying a trait syndrome providing tolerance to arable field conditions. Spatial dynamics analyses also accord with a metacommunity functioning of weeds as both local dispersal from field margin and mass-effect from source habitats in the landscape were demonstrated as major drivers of weed diversity. A meta-analysis of *ca.* 60 articles revealed that while the presence of weeds generally decreased cereal yields, the strength of this effect highly varied between studies. Additional investigations include the modelling of weed community dynamics, the assessment of weed sampling strategies, and the ecological mechanisms linking weed regional frequency to local abundance. Overall, this project provides new elements to design an innovative conceptual framework aiming to promote farmland biodiversity maintenance and agroecosystem sustainability.

Dealing with heterogeneous environment, species and trait data to analyse the functional diversity of food webs at multiple spatial scales

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It is often challenging to collect taxonomic and functional diversity data on biological communities, as many communities are too diverse or spatially diffuse to allow adequate sampling. By focusing on the aquatic communities within "tank" bromeliads (plants that form water reservoirs within their leaf axils), we took advantage of a food web that is small and contained, widely distributed over the Neotropics, and viewed by ecologists as a model system for testing ecological theory. Over the past 20+ years, the bromeliad invertebrate fauna has been sampled by several teams of researchers at 22 locations from Mexico to Argentina. Environmental variables and functional traits were associated to the communities and taxa recorded, respectively. The data was originally collated and read in from the Bromeliad Working Group database, and combined with other data stored separately (e.g., taxonomic and climate information from global databases). Inevitably however, data collected by different researchers at different times and within different scientific contexts were heterogeneous in terms of consistency and quality. We therefore designed a workflow which allowed us to continuously update both the data (e.g., reconstructing missing values from allometric equations) and the data-cleaning process (unit conversions, consistency in trait data across taxonomy), so collaborators could work on analyses even while the data underwent changes. We illustrate the various means by which our dataset was improved within this framework, given our aim to examine the evolutionary and ecological determinants of invertebrate functional traits from individual bromeliads to biogeographic regions.

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Rescuing old ecological data (before it's too late): from the coffee machine to FAIR data

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Identifying consistent and predictable associations between vegetation and environment is one of the oldest quest of ecology, which has been boosted by the need to improve our understanding and modelling of global change impacts on vegetation. A wealth of data has been collected in various places over the last century that could potentially be synthesized to address this timely and pressing issue.

As a researcher at the Centre d'Ecologie Fonctionnelle et Evolutive in Montpellier, one of us (EG) had heard (in corridors and during discussions at the coffee machine) of a vegetation transect that had been intensively studied in the 1960ies, that ran from the Mediterranean Sea to the foothills of the Mont Aigoual. This corresponds to a 60 km transect over a steep rainfall (and temperature, to a lesser extent) gradient that could be used to improve our understanding of relationships between vegetation and environment. But where the hell are the data?

This talk will present the detective investigation that allowed us to save the data collected from this transect from certain death. It involves library and garage cabinets, a retired researcher of goodwill, a dead researcher, his wife and daughter. The story ends well, and we believe these data are now in a FAIR – Findable, Accessible, Interoperable and Reusable – state. On the path from the coffee machine to the PostgreSQL data base, we will discuss the FAIR principles and data management issues, including the use of metadata standards and semantic resources, that have been designed to prevent the next generation of ecologists from spending too much time on rescuing data collected during this century, supposed to be that of "Big Data".

*Speaker

Origin and congruence of taxonomic, functional, and phylogenetic diversity of the Mediterranean trees

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The WOODIV project aims to describe and understand the spatial distribution patterns of three facets of tree diversity in the European part of the Mediterranean basin: taxonomic, functional, and phylogenetic. Botanists have identified the status of 209 tree species and 244 subspecies in 13 Mediterranean countries. We gathered available data on current distribution of tree taxa from many sources and designed a long-lasting database of tree occurrences. We also collected functional traits and built a species-level phylogeny by completing available sequences from sequencing of new samples. This challenge of collecting data has been addressed by scientists and botanists from five Mediterranean countries. From these data and a strong conceptual basis provided by a literature review, we are analyzing the congruence and mismatches of these diversity components and discuss the implications for conservation of Mediterranean woody diversity.

*Speaker

Retrospective Analysis of Antarctic Tracking Data (RAATD) to identify areas of ecological significance in the Southern Ocean

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The SCAR Retrospective Analysis of Antarctic Tracking Data (RAATD) project aims to undertake a multispecies assessment of habitat use of meso- and top predators in the Southern Ocean, using existing animal tracking data. This will identify Areas of Ecological Significance - regions that are important for foraging to a range of predators, thereby signalling high prey abundance and diversity. The dataset contains data from 17 predator species, 4060 individual animals, and over 2.9 million observed locations. The data for the project were derived from over 70 contributors across 12 national Antarctic programs, and the challenges of getting people to join up and contribute data were considerable. Animal tracking data themselves present challenges for analysis, with data across several dimensions, some of which may have gaps. Tracking data are integrated with environmental data, leading to further challenges. The RAATD group has developed methods and workflows that deal with these challenges to produce habitat use predictions for 17 marine predator species across the Southern Ocean. The synthesis of these data provides an unprecedented view of biodiversity in the Southern Ocean.

Functional Rarity in Ecology and Evolution

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The importance of rare species is well recognised in law (e.g. IUCN Red list), but their ecological importance is poorly understood. Beyond the rarity of a species, the rarity of the functions played by a species (functional rarity) is key to understanding the impact of biodiversity decline on ecosystem function.

Rarity has always fascinated conservation and evolutionary biologists with the goal of discovering the characteristics of species that are at risk of extinction. Recently, some results suggest that rare species make a high contribution to the diversity of traits within communities, and they have irreplaceable roles, while other results show that rare species are functionally redundant.

Beyond the rarity of species, the rarity of functions played by species, known as functional rarity, is the key to understand the impact of biodiversity decline on ecosystem functioning. However, functional rarity still lacks a clear definition and a quantitative framework and its emergence and maintenance within communities is largely unknown.

The aim of the FREE working group is to explore the concept of functional rarity and examine the causes and consequences of functional rarity at local to global scales. We first analysed the distribution of functional rarity at community, regional, biome and global scales using a cross-taxonomic comparative approach (plants, microbes, mammals, birds, fishes) and an identified set of inter-operable databases. Next, we explored the theoretical causes of the maintenance of functional rarity in communities using simulations. Finally, we evaluated the theoretical consequences of functional rarity loss on ecosystem functioning and quantify them using a database of biodiversity-ecosystem functioning experiments in plants.

*Speaker

What about the data quality used for assessing the ecological status? The example of uncertainty on the French Macrophyte index for rivers (IBMR) related to taxa misidentification

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Since the implementation of the European Water Framework Directive in 2000, the assessment of water bodies ecological status is closely based on hydrobiological methods, including several biological elements. However, the assessment using bioindicators is subject to a range of uncertainties that may occur at each stage of the protocol.

The application of sampling protocols allows the calculation of hydrobiological metrics from taxonomic lists. A first source of variability, related to the surveyor effect, can be identified at this stage of the protocol as species identification mistakes.

The aim of this project is to evaluate the impact of the taxa identification errors on IBMR (French standard NF T90-395), officially used in the national river assessment

The first stage was the construction of a confusion matrix, used to model and evaluate the impact of a random introduction of taxonomic confusions on the IBMR score and on the resulting assessment of rivers. An initial approach allowed to analyse the weight and impact of each pair of confusion on the index score. Secondly, new floristic lists were generated by randomly introducing several confusions, to reflect the reality on the field.

Among all paired confusions identified, 56 lead to a shift of the index value of 1 to over 2 points (23 lead to a reduction, 33 to an increase). The modelling of the impact of multiple confusions on 5.400 surveys showed an average difference of 0.05 points, but the maximum can be much higher, mainly for the low richness sites. These shifts lead to a misclassification for 24% of the surveys.

Finally, the uncertainty due to taxonomic confusions can vary significantly depending on the river type concerned. It is then possible to determine weighted coefficients for the impact of confusions between ecoregions.

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Eco-Evolutionary Dynamics

The dynamics of adaptive response under strong selection regime in small populations

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Climate changes are affecting plants at an incredible pace leading to major life-cycle shifts with complex consequences. The capacity of plants to cope with the rate of predicted climate changes will ultimately determine their survival. Here we investigate the rate of life-cycle shifts in maize using two independent divergent selection experiments (DSEs), conducted for more than 20 years under natural conditions in the Plateau de Saclay. Within each DSE, we applied a strong selection pressure (1%) for phenological shifts by choosing and selfing at each generation the 10 earliest- and 10 latest- flowering genotypes among thousand observed ones. The resulting Early and Late evolved populations exhibit pronounced phenotypic divergence for flowering, while preserving original characteristics of the initial inbreds. Using genetic markers and transcriptomic data, we identified a number of (epi)genetic differences. In order to address questions related to the role of new mutations versus standing variation in the response to selection, and to the rate and limits of adaptation, we have implemented a revised version of the animal model that explicitly accounts for new mutations. In this model, the observed response to selection is treated as a quantitative trait, driven either by shifts in average phenotype or plastic changes. From the dynamics of the selection response, we quantified the input of new mutations over generations, and indicated the most likely mutational events along the pedigrees. In addition, we implemented a population genetic model that describes the fate of a new mutation, in this high selection-high drift design. We discuss how, in these conditions, drift can accelerate fixation of adaptive mutations.

*Speaker

Evolutionary pathways to cooperative breeding in Mammals: The role of ecology

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In cooperatively breeding species, non-breeding helpers assist in raising young produced exclusively by dominant breeders. Such species also display delayed dispersal, as helpers are usually previous offspring produced by breeders. Ecological constraints are widely thought to have a major role in the emergence of cooperative breeding, by increasing the costs of dispersion and the benefits of cooperation. Several studies linked the severity of ecological constraints to the prevalence of cooperative breeding in birds. In mammals, previous research focusing on abiotic variables has linked cooperative breeding to low annual rainfall. However, little attention has been paid to the role of habitat variation, and the resulting variation in predation pressure and resource availability. Yet the impact of such variables on the costs and benefits of group living, delayed reproduction and delayed dispersal may make them key factors in the evolution of cooperative breeding. Here, we investigate the role of variation of habitat specialization, predation pressure, food availability and climate in explaining why cooperative breeding has evolved in some lineages of mammals but not in others. We aim at identifying which ecological characteristics are overrepresented in cooperatively breeding species, and are therefore susceptible to have played a role in the evolutionary pathway to cooperative breeding. Ultimately, our work aims at investigating the directionality of the evolutionary relationships between cooperative breeding and ecology: Has cooperative breeding enabled species to specialize in habitats, or has it evolved in response to specific ecological characteristics?

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How species interactions affect species responses to climate change ?

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Most studies aiming to predict species response to climate change consider single species in isolation, whereas in nature, species interactions may have a profound impact on a species' ability to adapt to a changing environment or track new suitable habitats. To make forecasts more realistic, we integrate species interactions into an eco-evolutionary dynamic model to predict species responses to climate change. We consider two types of interactions: 1) competition, where phenotypically similar individuals or species compete more strongly than phenotypically divergent ones, and 2) predation, where the predator trait evolves to match the mean prey trait which evolves to match the changing environmental optimum. By increasing the selective pressure on maladaptive individuals and the rate of selective events, predation and competition may speed the adaptation of species to climate change and enhance the persistence of population. Nevertheless, such phenomena are observed only when the positive effects of interactions on species adaptation overcome the reduction of population density, in part from the direct impact of competition and predation and in part from the departure of species from their phenotypic optimum due to character displacement. We discuss the mechanisms and conditions that lead to positive and negative effects of competition and predation on species responses to climate change and emphasize the implications of our results for species conservation practices and policy.

*Speaker

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Does the long incubation period of *Zymoseptoria tritici* result from ecological constraints?

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Zymoseptoria tritici causes a damaging foliar disease on wheat. This hemibiotrophic fungus has an unusually long, symptomless incubation period, during which the pathogen remains in the apoplast at low densities, hidden from the plant’s immune system. Why does *Z. tritici* have such a long incubation period? Based on ecological theory, we propose that an advantage of a longer incubation is a delay of leaf damage, favouring host growth. To test this hypothesis, we developed a consumer-resource-based epidemiological model. When fungal symptoms appear at the end of the incubation, we assume that locally photosynthesis is reduced and therefore resources available for plant growth as well. The incubation period also determines the onset of pathogen sporulation. For the pathogen, the cost of permitting plant growth is hence late sporulation. We show that there is an optimal incubation that maximizes spores production over the season. We further show that the optimal incubation depends on the pathogen’s ”virulence”, in its ecological definition as the level of host damage caused by the pathogen. Our model predicts that more virulent strains have a longer optimal incubation in order to maintain enough plant growth for developing epidemics. However, due to the pathogen’s limited dispersal distance, the optimal incubation also depends on plant architecture as taller plants favor a shorter incubation to avoid newly emerging leaves escaping disease from the lower infected leaves. The optimal incubation thus results from a tradeoff between delaying host damage and colonizing the growing plant. We argue that the long incubation of *Z. tritici* may be a so-called ”milker” strategy to delay host damage and thereby increase fungal fitness. This work is a first step to increase our understanding of the evolution of such hemibiotrophic fungi, which we argue is essential in the agroecological context of developing sustainable strategies for crop disease control.

*Speaker

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Forecasting eco-evolutionary changes in natural populations: which species' traits matter?

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How can we characterize a species' ability to withstand rapid environmental changes? Which species' traits allow for rapid evolution and escape from extinction, and which do not? Although models investigating conditions for evolutionary rescue and adaptation to a changing environment have addressed some of those issues, we still miss a general framework to evaluate which species are most at risk of population decrease and ultimate extinction. In this talk, I will present a modeling work mixing classical species distribution models (SDM) with a simulation-based dynamical eco-evolutionary model (DEEM) to forecast the change of species' range under climate change for a set of species that vary in their adaptive capacity (plastic and evolutionary), life history strategies, dispersal capacity, and reproductive systems, among other key species' traits. This approach allows us to characterize which species' traits are most important for species' persistence. As an illustration, I will present a recently published eco-evolutionary model of the response to climate change of endemic alpine plant species and the Austrian alps. This work compares SDMs and DEEMs prediction of species' range shifts until the next century. We show that, by taking precise account of the demographic and evolutionary dynamics of the perennial plants modeled, we predict a rapid demographic decline caused by a delayed evolutionary answer of local populations. Overall, the SDM predictions show a faster decline of the species' ranges compared to the eco-evo approach, in part because of the positive effect of migration in the later. I will show how variation in a few key species' traits can deeply modify those predictions.

*Speaker

Investigating the dynamics of a partially migratory fish population

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In a context of global change, phenotypic plasticity is considered an advantage in dealing with environmental variability. Partially migratory populations, which reflect plasticity in migration, should take advantage of positive environmental changes and better buffer negative conditions compared to solely resident populations. The intraspecific diversity in migratory tactics could be the key element driving a stronger resilience in these populations. Brown trout (*Salmo trutta*) is a typical example of a partially migratory fish, where both resident and migratory tactics coexist. Migrant fish benefit of the highly productive marine habitat to achieve higher body growth and fecundity than fish residing in freshwater for their whole life. This advantage is counter-balanced by a high mortality risk in migrant fish due to physiological changes upon entry to the sea and predation in the marine environment. We analyzed 18 years of capture-mark-recapture data from brown trout (*Salmo trutta*) in the river Oir (Normandy) to study the role of this phenotypic plasticity and its consequence on the dynamics of this partially migratory population. Firstly, we investigated whether ecological factors may trigger migration in juvenile trout and highlighted the key role of density dependence. Secondly, we compared the reproduction success of both resident and migrant trout on the same spawning ground and found that body size mattered more than migration decision. Finally, we combined these trait-based approaches into a joint population model to quantify the influence of resident and migratory tactics on the population growth rate. Using simulations, we investigated how changes in the environment may affect the proportion of migrant and the population growth rate.

*Speaker

Evolutionary response to coexistence with close relatives: increased enemy defence, different response to climate, but no costs for climatic tolerance.

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Plants face climatic stress and herbivore pressure. Herbivore pressure is highest in a conspecific or phylogenetically proximate neighbourhood because such a neighbourhood may be a reservoir of co-evolutionary shared phytophagous species. We hypothesize that, first, trees in phylogenetically proximate neighbourhood adapt by increased anti-herbivore defences. Second, a strong investment in such anti-herbivore defences could be traded off against the ability to tolerate climatic stress, and a phylogenetically proximate neighbourhood might hence indirectly select against climatic-stress tolerance. Finally, enemy pressure in a phylogenetically proximate neighbourhood might interfere with the selection by climate for defences. We studied oak (*Quercus petraea*) genotypes from provenances of contrasting phylogenetic neighbourhoods and climates in a common garden. We measured traits related to herbivory and climatic-stress tolerance. We found that genotypes from the populations that had evolved in phylogenetically proximate neighbourhood have tougher leaves and are better defended against leaf miners than genotypes that evolved in phylogenetically distant neighbourhood, but without inducing cost to climatic stress tolerance. We found that in phylogenetically proximate neighbourhood, the selection pressure for chemical traits promoting climatic tolerance are opposites from that in a phylogenetically distant neighbourhood. The results suggest that tree populations are not passive victims of herbivory pressure in a closely related neighbourhood but can adapt. This adaptation has no costs in terms of climatic-stress tolerance but interferes with the way populations adapt to climate.

*Speaker

Macroevolutionary processes can drive species richness patterns at very small spatial scales

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A common paradigm in ecology is that macroevolutionary processes become increasingly unimportant for explaining species richness at smaller and smaller spatial scales. However, few studies (if any) have actually tested whether these processes do help explain richness patterns at very small scales. Here, we study richness patterns in plants from small-scale local plots in The Netherlands. We hypothesize higher richness in plots from habitats having greater estimated age and/or faster diversification rates among the sampled species. We inferred high age from high average distances among all species and faster diversification rates from low average distance among most closely related species. We find that local richness of habitats increases with both the evolutionary age and the speed of diversification represented in local species communities. Richness of species pools of habitats increases with age, in particular if diversification is low. Our results show that macroevolutionary processes can matter at very small spatial scales.

*Speaker

Effects of heterogeneity of crop fertilisation at the landscape scale in epidemics and pathogen evolution

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Agroecology suggests that spatial heterogeneity can be a lever for crop protection. Using a model we study whether landscape-level heterogeneity in cultural practices can sustainably hamper crop pathogen epidemics. We focus on crop fertilisation in the wheat-leaf rust pathosystem. We use a spatially explicit model in which the agricultural landscape is a mosaic of individual fields, with either high or low crop fertilisation. Fertilisation determines crop growth dynamics and therefore resources available for epidemic development. Within each individual field, we use a SEIR epidemiological model. Fields are linked together through pathogen dispersal. We study the epidemiological and evolutionary dynamics of the pathogen in this context, concentrating on the latent period as the evolving trait.

Using methods from adaptive dynamics, we find that spatial heterogeneity is likely to induce pathogen maladaptation: the occurrence of pathogen strains that are significantly less competitive than the optimal strain in a given environment. When such maladaptation occurs, certain landscape configurations reduce the quantity of inoculum released into the landscape and slow down the colonization of the landscape by the pathogen. But we also demonstrate that these beneficial effects of spatial heterogeneity are not sustainable: after a period of maladaptation, pathogens may undergo a process of evolutionary branching, thereby filling all available resources niches in the landscape.

Even if resource heterogeneity at the landscape scale alone may not be sufficient to sustainably limit crop pathogen epidemics, it may prove useful in combination with other types of spatiotemporal heterogeneity that promote local pathogen maladaptation. These results further emphasize the need to take pathogen evolution into account when addressing questions about sustainability in agriculture, even for "soft" regulation methods such as fertilisation practices, as opposed to "hard" methods of pesticides and resistance.

*Speaker

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AraBreed: testing ecological theories with experimental evolution in a model plant species

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Experimental evolution combined with modern genomic tools provides a great opportunity to examine the dynamics and strength of selection in real time as well as to test the validity of prominent ecological hypotheses. For instance, ecological theory states that plants cannot simultaneously be efficient at certain tasks, such as acquiring and conserving resources, or be both competitive and stress tolerant. Resulting trade-offs between traits are described as major constraints that drive plant diversification across large taxonomic scales. However, the role of these trade-offs on the rapid adaptation and differentiation of populations within species remains to be elucidated. Here we present AraBreed, a project that aims at exploring the evolution of complex trait variation and covariation with the development of new approaches at the interface between ecology, evolutionary biology and genomics. In AraBreed, we monitor the evolution of the model plant *Arabidopsis thaliana* over several generations in four environments, which

*Speaker

Eco-Evolutionary Dynamics

differ in resource availability (nutrient and water), and herbivores abundance. Each experimental

population consists of 17,500 recombinant lines, previously generated from 350 random crosses between 400 natural and fully sequenced accessions. This has the advantage of breaking up ancestral gene complexes and recreating phenotypes thought to be purged in natural populations. Experimental populations are replicated seven times per environment (28 populations for 500,000 genotypes in total). Each year during the project, multiple samples will be collected to perform population genetic analysis with pool-seq, and plant traits will be phenotyped to analyze the evolution of major ecophysiological trade-offs. With AraBreed, we aim to assess the evolution and the underlying allelic changes of complex traits and trait-trait relationships in response to controlled selection pressures. Here we present the first results of AraBreed, from the data collected in spring 2018 on the first generation of plants.

Eco-evolutionary dynamics in plant-pollinator systems: implication for diversity maintenance

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Recent pollinator population declines raise concerns for the future of the pollination service. It also strongly affects the evolution of plant-pollinated species. We wonder here if plant evolution can help maintain plant-pollinator coexistence in this pollination crisis context. We build a simple pollinator-plant model that assumes an allocation trade-off between the attractiveness of the plant (e.g. nectar production, flower shape and size) and its intrinsic growth rate. Using eco-evolutionary dynamics, we investigate the evolution of plant investment in attractiveness (as a proxy for pollination services) and its consequences on species persistence and biomass production. Especially, we study the role of the allocation trade-off shape and the mutualistic interaction asymmetry on the eco-evolutionary dynamics. First, we show that only a concave allocation trade-off allows the existence of evolutionary stable strategy with coexistence of both the plant and the pollinator. Second, a decline in pollinator population is most likely to result in a plant-driven disappearance of the mutualistic interaction accompanied by the extinction of the pollinator population. However, asymmetry in mutualistic interaction that is beneficial for the pollinator might help maintaining its population. Therefore, our model underlines that in addition to the direct effects due to changes in ecological dynamics, pollinator populations may be further weakened by the evolution of attractiveness in plant populations. Our results also suggest that if actions are taken to save endangered pollinator populations, they need to be enforced early enough to prevent potential negative effects of plant-driven evolution. Finally we discuss impacts of plant flowering phenology on pollinator foraging phenology evolution.

*Speaker

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Variation in competitive ability with mating system, ploidy and range expansion in four *Capsella* species

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Self-fertilization is often associated with ecological traits corresponding to the ruderal strategy in Grime's Competitive-Stress-tolerant-Ruderal (CSR) classification of ecological strategies. Consequently, selfers are expected to be less competitive than outcrossers, either because of a colonization/competition trade-off or because of the deleterious genetic effects of selfing. Range expansion could reduce further competitive ability while polyploidy could mitigate the effects of selfing. Although suggested by meta-analyses, these predictions have not been directly tested yet. We compared the competitive ability of four *Capsella* species differing by their mating system and ploidy level. For vegetative traits we found no difference in competitive ability neither among species nor among populations. For flower production, we found that the two diploid selfing species (*C. rubella* and *C. orientalis*) were more sensitive to competition than the diploid outcrosser (*C. grandiflora*), and that the tetraploid selfer (*C. bursa-pastoris*) was intermediate. Within *C. bursa-pastoris*, we also found that sensitivity to competition increased in parallel to range expansion. A complementary analysis in the tetraploid *C. bursa-pastoris* suggests that reduced fitness along the expansion front could be due to the accumulation of deleterious mutations and/or to a trade-off with flowering time allowing to avoid competition. These results highlight the possible roles of ecological context and ploidy in the evolutionary trajectories of selfing species.

*Speaker

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Ecological Interactions

Importance of the soil food web in the functioning and services of Mediterranean forest ecosystems submitted to climate change

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Plant litter decomposition is an essential process for ecosystem functioning since it determines carbon and nutrients cycling. Among involved factors in litter decomposition process in Mediterranean forests, collembola and mites appear as important groups, especially through their trophic interactions. Indeed, it is well known that microorganisms are grazed by collembola communities that are also preys of predatory mites. Climatic parameters such as soil temperature and humidity, strongly mediate abundance, diversity and trophic interactions of these soil organisms. However, climatic change expected for the current century, particularly the increase of temperature and the number of dry days in Mediterranean region, may directly impact collembola communities and their responses to predation. Moreover, these responses could vary among species depending on their morphological and physiological traits (e.g. body or furca sizes). A 2-month microcosm experiment was carried out to study the impact of the increase of air temperature (+10°C) coupled with the decrease of soil humidity (-30% of soil field capacity) and the presence or absence of a predatory mite (Acari: *Stratiolaelaps scimitus*) on i) the abundance and the biomass of collembola community, i.e. *Folsomia candida*, *Proisotoma minuta* (Collembola: Isotomidae), *Protaphorura fimata* (Collembola: Onychiuridae) and *Mesaphorura macrochaeta* (Collembola: Tullbergiidae), ii) the microbial structure and composition (PLFA) and iii) the litter mass loss (*Acer monspessulanum*).

*Speaker

Coastal phytoplankton community dynamics and coexistence

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A major puzzle in ecology is the continued coexistence of species-rich communities of primary producers, such as phytoplankton, in spite of the likely competition for shared resources, that in theory often leads to competitive exclusion. To investigate what drives phytoplankton community dynamics and allows coexistence, we translated the hypotheses of population dynamics models for phytoplankton communities into multivariate time series models, allowing interactions between species or genera, as well as forcing by abiotic variables. We then performed a statistical analysis of a long-term (> 20 year) coastal survey of phytoplankton, with counts every two weeks. The statistical models reveal that net competition (for nutrients or other resources) between groups seems rather weak in the field, unlike what is found in more controlled environments. While fluctuating environments rather than niches differences are usually invoked to solve the "plankton paradox", more elaborate statistical models specifically developed for fluctuating environments, mimicking the storage effect or relative nonlinearities, seem also inappropriate for this coastal community. Here, strong intragroup density-dependence dominate while interactions between groups (genera) are weak, often positive, and fluctuate little over time. This points to other drivers of coexistence such as predation or microscale spatial structure, for which we highlight the modelling and data collection implications.

*Speaker

Prey diversity and selection by two generalist mammalian predators in suburban habitats

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In urbanized areas, some species (synurbic species) may take advantage of the access to new resources and habitat types in urbanized areas. In these human altered habitats, the decreased of large predators, leads to the increase of wild medium-sized predators. In addition, the presence of domestic predators, commensal prey species and anthropogenic refuses modify trophic interactions in urbanized areas. Domestic cats and red foxes are among the most abundant medium-sized carnivores in European urbanized areas. Although their diets were described in these areas, neither their concomitant predation pattern nor their prey selectivity were studied yet. Here, we monitored prey availability (in richness, diversity and density) and cat and fox diets in three suburban habitats (park, agricultural land and forest) during 2-years to evaluate the prey selectivity by both predators. We detected significant differences in prey richness and diversity inter- and intra-habitats. In addition, lagomorph, small mammal, bird and invertebrate densities were significantly affected by habitats, seasons and habitat: season. The overall cat diet richness was lower than fox diet richness, while cat diet diversity was higher than fox diet diversity. We assess significant differences in cat and fox diet richness and diversity according to habitats and seasons. Overall both predators positively selected vertebrate prey (mammals and birds). Thus, fox and cats may have a synergetic effect on those prey populations. Within habitats and across seasons, predator scat composition was significantly more specialized than the average predator diet suggesting the existence of individual trophic specialization. We strongly recommend to simultaneously monitoring prey availability and predator diets to be able to model concomitant predator impacts, particularly in disturbed areas where small changes in species abundances can lead to strong trophic cascades.

*Speaker

Oak genotype and chemical defences as drivers of the performance of two insect herbivores

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Ecological research on plant-herbivore interactions has long recognized that plant genotypic identity plays a key role in shaping insect abundance and herbivory, as well as in determining plant defensive levels. However, how plant genotype influences herbivore feeding behaviour, and which plant defensive traits are associated with such genetic effects on herbivore feeding behaviour, remain poorly understood.

We investigated how pedunculate oak genotype affects feeding behaviour of two insect leaf chewers, the generalist *Lymantria dispar* and the specialist *Thaumetopoea processionea*. We further tested whether leaf chemical defences were associated with genetic effects on insect feeding behaviour. We collected leaves from oak trees consisting in four replicates of 30 genotypes randomly distributed in a common garden. With these leaves we performed laboratory feeding trials to estimate performance of both herbivore and quantified the concentration of constitutive phenolic compounds.

Oak genotype significantly predicted leaf consumption by the specialist herbivore species only. In contrast, oak genotype did not significantly predict growth rate of both herbivore species or concentration of leaf phenolic compounds. We found positive significant genetic correlations between all phenolic compounds and growth rate of the generalist herbivore species only. Consumption by both herbivore species significantly increased in leaves with higher concentrations of condensed tannins. Such increased leaf consumption in highly-defended leaves could be due to a compensatory feeding response. We found significant positive genetic correlations between the both herbivores, for leaf consumption and growth rate. These results suggest the existence of oak genotypes with multiple resistance against insect herbivores.

Overall, our results indicate that oak genotype and chemical defences partly explain variability in leaf consumption and growth rate of insect herbivores. These results stress that further studies investigating genetic control of plant-herbivore interactions should focus simultaneously on both plant and insect herbivore points of view.

*Speaker

Plant-insect networks in French calcareous grasslands: how does phenology affect the probability of interaction and the number of visits?

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Plant-pollinator networks are one of the most studied types of mutualistic networks. On latitudinal gradients, plant and pollinator abundance, richness and presence are expected to vary, with potential impacts on network structure. Moreover, temporal and phenological mismatch could have an impact on the probability of interaction between species. Despite considerable theoretical advances, there are still few models available to predict the probability of interaction in such networks. I will present results of a project aimed at understanding the consequences of environmental gradients on species interactions in calcareous grasslands. The presentation will focus on networks involving hoverflies (Diptera: Syrphidae), using taxonomically precise data from observations of pollinator visits obtained during monthly samplings from April to October in six different sites in France. To predict the probability of species interaction and how it can vary in time and space, we used a Bayesian Structural Equation Modeling approach with latent variables and random species effects linking the number of visits to abundance and phenology. We tested 16 models with varying numbers of parameters and we used the leave-one-out cross-validation criterion (LOO) for the purpose of comparing models. We found that insect and plant abundances are strong determinants of the expected number of visits. The strength of the effect of phenology overlap on both the probability of interaction and the expected number of visits varies with network modularity and along the gradient. We also found that two models better predict the probability of species interaction. Our results highlight the importance of taking into account both species relative abundances and phenology to better assess their interactions in pollination networks. Our findings could foster reflection towards conservation policies while accounting for both community structure and species co-phenologies. The next step of our research is to extend this analysis to native bee species (Hymenoptera: Anthophila).

*Speaker

Host specificity in the species complex of the brown alga *Pylaiella littoralis*

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Ecological speciation is an evolutionary process by which a change of habitat (or resources) leads to the formation of two new species exploiting different ecological niches. This phenomenon generally leads to a divergent selection leading to the formation of two lineages. *Pylaiella littoralis* is a filamentous brown algae that usually develops as an epiphyte on different host species of brown algae. Our study, combining barcoding and population genetics methods, revealed the existence of at least two new cryptic species (or semi-species) developing on specific hosts depending on the season. The first species occurs mainly in summer on *Fucus vesiculosus*, the second in spring and summer on *Ascophyllum nodosum* and the third in autumn on *Fucus serratus*. However, genetic analysis using microsatellite markers suggests that reproductive isolation is not complete and that these different groups are able to hybridize when individuals are found together in the field. Limited spore dispersal and close reproductive system ($F_{is} > 0$) may favor the specificity of the host. Although the interactions between *Pylaiella spp* and the hosts remain to be elucidated, we can think that the ecological specialization could play a role of accelerator in the diversification of these groups.

*Speaker

Can African elephants influence predator-prey interactions through vegetation modification?

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Interspecific interactions, such as predation or competition, are key drivers of the structure and functioning of communities. While interactions between two species have been widely studied, there is an increasing awareness that natural communities are complex systems and that there is a need to consider the network of interspecific interactions operating in a community and the effect of interaction modification. This is typically the case for ecosystem engineers, which modify the structure of the environment and thus have the potential to influence the interspecific interactions occurring in the environment they modify. In this work, we studied such environment-mediated interaction modifications by investigating the role of African elephants as modifiers of predator-prey interactions in savanna ecosystems. We first analyzed data from 12 long-term vegetation plots (2001-2015) in the savanna ecosystem of Hwange National Park (Hwange LTSER), Zimbabwe, which is an ecosystem characterized by one of the highest elephant population density to assess elephant-induced vegetation structure changes. We showed that elephants mainly modify the canopy structure of the understory of the vegetation, i.e. in the < 2m height stratum that is relevant for large mammalian interactions. We then used data from GPS-collared African lions to detect lion kill sites (n=209) and measure vegetation characteristics at these sites to assess whether elephant induced vegetation changes can influence the hunting success of lions. We revealed that lion kills are located mainly in areas modified by elephants (an unexpected result as these sites have a higher visibility and less ambush site opportunities) but at the microhabitat scale, they killed close to a potential vegetation ambush site. Our study suggests that ecosystem engineers can indirectly mediate trophic interactions, but that mechanisms are scale-dependent.

*Speaker

Soil fauna communities are facilitated by plant nurse species in coastal sand dunes

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Facilitation is an ubiquitous biotic interaction which has been well extensively studied by plant ecologists in many ecosystems. Most of these studies demonstrated that nurse plants might directly or indirectly improve environmental conditions for beneficiary plants. This ecological process is particularly important to maintain biodiversity in stressful environments (c.f. Stress Gradient Hypothesis). However, the facilitation by plants on soil fauna has been rarely explored although both plant canopy and rhizosphere might directly and indirectly influence belowground organisms. This positive effect of plant on soil fauna could be modulated both by plant functional traits and stress level. Thus, to explore these interactions, we tested in a coastal sand dune environment whether soil fauna communities (Nematodes, Collembola and Mites) better establish under the protection of 3 nurse species (*H. stoechas*, *C. canescens* and *A. arenaria*) comparatively to adjacent open gaps. This sampling was repeated along 330 km of the Atlantic French coast, from Vendée to south of Landes. Our results revealed a strong and positive effect of nurse species on soil fauna communities (density and diversity). The intensity of these effects depends both on functional traits and species identity (i.e. nurse plants and soil fauna). As a consequence, the functional characteristics of the belowground communities might in turn modulate core ecosystem processes, such as nutrient cycling with positive feedback on nurse growth and plant-plant interactions. We thus will discuss the concept of facilitation and mutualism in the context of plant-soil interactions. Lastly, in such constraint habitat, the role of plants in soil processes is so relevant that they can be considered as ecosystem engineers since they create suitable habitats for other organisms.

*Speaker

Significance of studying spatial ecology and behavioural patterns of urban rhesus macaque in conservation science and management

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Rhesus macaque (*Macaca mulatta*) is commonly known as ‘weed species’ and ‘pest primate’ for its damaging activities and creating nuisance in urban landscape, agricultural areas and forest-urban mosaics. Increasing human-macaque conflict has spread threats to human societies in urban and suburban areas of major cities in India and wildlife managers need an urgent action plan for mitigation of rising conflict and maintaining sustainable population of macaques. Translocation of primates, construction of electric fences and barriers around the sanctuary or enclosures and sterilization have become popular methods of reducing conflict incidences. But our intervention suggests that studying ecology and behaviour of macaques will help in mitigation of negative interactions between human and macaques and to achieve conservation goals. We studied 21 troops of urban rhesus macaques which have been translocated into Asola-Bhatti Wildlife Sanctuary, Delhi for rehabilitation and recorded their ecology and behavioural patterns using focal and scan sampling techniques from 2016 to 2017. We designed our study in two parts studying ecology and behavioural patterns of rhesus macaques in and around the sanctuary assessing the nature and extent of conflict behaviour outside the sanctuary. The aim of this study was to combine the result of both the study aspects and plan effective mitigation controls for this urbanized, commensal and non-domesticated primate species. Our study results showed that rhesus macaques have flexibility in behavioural adaptation to cope with new environment for long-term species persistence and their population dynamics showed consistency in higher female: male ratio and female: juvenile ratio indicating a growing population structure in the sanctuary. Understanding behavioural ecology of macaques is essential to manage this least concerned (LC) species in urban settings with human and we can no longer neglect the importance of studying macaques to reduce human-macaque conflict and conservation in urban landscape.

*Speaker

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Are forest reserves or deadwood retention key elements for bryophyte diversity?

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Extending the network of strict forest reserves is one of the conservation measures promoted by the French National Strategy for Biodiversity. It is based on the worldwide literature, according to which strict forest reserves may help preserving a part of the biodiversity that is threatened by forestry. However, this strategy is based on poor knowledge in the temperate context. In a national-scaled project based on data from 213 study plots set up in 15 forest sites throughout France, we analyzed the effect on forest management cessation and associated forest structure variables on the richness of 7 taxonomic groups: bats, vascular plants, birds, carabids, bryophytes, lignicolous fungi, saproxylic beetles. Bryophytes and lignicolous fungi appeared as the more favored by forest reserves and stand variables linked to deadwood or large old trees. Focusing on bryophyte groups, and distinguishing between all species and strict forest species, we here present further analyses including the additive or interactive effects of other variables known as important for bryophytes, namely humidity, light, temperature, precipitations or altitude. Although some of them enhanced the models in addition to deadwood variables, their additional effect was low compared to the strong positive effect of deadwood variables.

*Speaker

Can we improve floral resources in agricultural and urban landscapes to support plant-pollinator networks ?

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Projects and methods are developed in Europe to mitigate species decline, both for entomophilous plants and for pollinating insects. In urban and agricultural landscapes, increasing projects concern the maintenance and restoration of plant-pollinator networks. For example, in agricultural landscapes, among AES methods, the managed flowered strips (and to some extent the hedges) aim to provide floral resources for pollinating insects. In cities, street trees are questioned for their potential benefits. The efficiency of such land planning needs to be evaluated. We performed mid-term studies on plant-pollinator interactions, based on the evaluation of the floral resources quantities and qualities and on direct observations of the interactions. For in several case studies of such practices, I propose to review and compare the most visited plant species and their resources for insect visitors. We will focus on the main pollinators in Western Europe, i.e. bees (Hymenoptera) and syrphids (Diptera).

*Speaker

New databases on orchid-pollinator interaction and fruit set in the Euro-Mediterranean region

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Biotic interactions have played a major role in the generation of biodiversity in both the plant and animal kingdoms. One of the major challenges in the study of plant-pollinator interactions is to determine what factors underlie similarity in pollination niches between plants, a question that is relevant both to ecology and evolutionary biology. In addition, the relative contribution of plant-pollinator interactions and other environmental factors in determining plant reproductive success is important both to predict the evolutionary outcome of pollination interactions and to set up appropriate conservation strategies. In this context, we present here two new databases concerning Euro-Mediterranean orchids: 1) one on orchid-pollinator interactions (1278 interactions between 243 orchid and 773 pollinator species) and 2) one on the fruit set of these orchids (171 orchid species from 1750 populations). By analysing the first database using a network approach, we show that specialization in orchid-pollinator interactions depends on orchids' pollination strategy, but also on their geographical range. We further demonstrate that the number and identity of insect families with which orchids interact depend on their pollination strategy and phylogeny, while the number and identity of insect species with which they interact depend on their spatio-temporal distribution. This suggests that if there are consistent associations between some pollination strategies or phylogenetic groups and some insect families, at a finer scale, orchid-pollinator interactions may be more opportunistic than previously thought. By analysing the second database using generalized linear mixed models, we show that orchid fruit set varies among pollination strategies and may be influenced by floral display traits, while ecological preferences of orchid species seem to have no impact on their reproductive success. These two databases on orchid-pollinator interactions and fruit set will allow comparative analysis on reproductive ecology of Euro-Mediterranean orchids and provide relevant information for population dynamics and conservation studies.

*Speaker

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Microbial community assemblies and interspecific interactions in wheat sourdough

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Microbial community assemblies are largely studied in complex environments such as ocean, gut or soil communities. Although our knowledge of microbial communities' diversity has been largely enhanced by the use of -omics technics in the last decade, observations as well as experimental and theoretical works are needed to decipher the ecological processes governing their patterns of biodiversity and how the species forming these communities interact together.

Here, we address these questions in the case of wheat sourdough microbial communities. Sourdough communities are always composed of an assemblage of lactic acid bacteria and yeasts but species composition vary between sourdoughs. As these communities are relatively simple in terms of species richness, they can represent a good opportunity to study the role of abiotic conditions and biotic interactions on community assemblies.

It has been hypothesized that yeasts and LAB interact together mainly in a non-competitive way through mutualistic supply of important metabolites, such as glucose release by LAB, or vitamins release by yeasts to the benefits of each other. However interspecific interactions in sourdough have not been extensively studied. We used two kind of approaches to investigate these interactions: i) an analysis of the network of sourdough yeast and LAB species documented in the literature to determine whether some species tend to co-occur more (or less) often than expected in the absence of interactions, ii) mono and co-culture of yeast and LAB strains sampled in natural sourdough to characterize yeast-LAB interactions. We have shown that LAB presence tends to decrease yeast density whereas yeast presence tends to decrease LAB density although results are contrasted depending on species and strains. Further work is needed to unravel the mechanisms shaping these interactions.

*Speaker

The Secret Lives of Himalayan Wolves: Diet, Predation & Movement in High Elevation Himalaya

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The Himalayan wolf was only recently distinguished as one of the most basal lineages within *Canis lupus*. However, little is known about its ecology and behaviour. We investigated the diet of wolves in the western Himalayan region of Spiti above 4000 a.m.s.l and compared the diet and prey preferences of the wolves through available literature (n =20). We also, investigate the ranging and movement pattern of wolves in the region (n=3). We also conducted a social survey based on open and close ended questions (n = 200) to assess depredation and perceptions of local communities towards wolves as well as other large carnivores in the area.

Wolves primarily relied on large domestic prey. GLM showed that prey choice of wolves was significantly related to length and home range. Cattle (Jacob's Index = 0.8) was the most utilized prey (n=41), while poultry was the least preferred. NMDS analysis (k=5, Stress = 0.025) showed regional prey preferences in wolves showed wolves utilised domestic, small ranging, medium to large prey in Quinghai Tibet region while in the Central Asia and Himalayan region preferred wild prey as well. Himalayan wolves were perceived to be a large threat to local agro-pastoral livelihood though respondents reported fewer encounters with the species.

GPS satellite telemetry showed, Himalayan wolf movement was restricted to elevations of of 3000-5000 m. Movement of Himalayan wolves showed greater distances traversed during winter periods than warmer summer movements. Individuals ranged well beyond national boundaries traversing linearly along the valleys and but probably rendezvoused close to human dominated patches in the valley. In Spiti, the survival of the species has depended largely on socio-religious settings of the region but future efforts must strive for a coordinated trans-boundary strategy to sustain wolf populations and their prey.

*Speaker

From deer gut to deer fear: the underappreciated consequences of predator absence on ecological interactions

Jean-Louis Martin * ¹

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We document the profound effects of absence of predation risk on the foraging ecology, behavior and ecological trophic effects of a large mammalian terrestrial herbivore, the Sitka black-tailed deer. We used a unique natural experiment provided by deer introduction to a remote archipelago in western Canada. We combined behavioral, ecological and isotopic data from a natural and manipulative long-term experiment to produce coherent evidence on the links between predation risk, selection pressure on deer behavioral profiles, and changes in their diet and habitat use.

In a nutshell, we suggest that the absence of predation risk was key to explain the magnitude of loss in plant and animal diversity caused by abundant deer populations. Absence of predation risk facilitated behavioral changes that allowed deer to adjust to a habitat their browsing had progressively impoverished in quantity and quality of available forage.

* author intending to deliver the talk

*Speaker

An integrative study of host response to parasite: from molecular bases to phenotypic alterations

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Ecological interactions can be analyzed at different levels of biological organization, from molecular to ecosystem levels. However, studies generally focus on one or a few levels of organization at a time, hence limiting our ability to generate integrative predictions. Here we aimed at measuring the responses of a host to an ectoparasite, from the molecular level to the population level using a set of complementary approaches. We used the rostrum dace (*Leuciscus burdigalensis*, a freshwater fish species) and its ectoparasitic copepod *Tracheliastes polycolpus* as model species, and we tested whether -and how- this parasite generates cascading effects from molecules to populations. Specifically we tested whether *T. polycolpus* altered the whole gene expression (in three different tissues), the competitive ability, the functional responses and the trophic niche of *L. burdigalensis*. We showed that parasitized host -compared to healthy ones- over-expressed genes related to immune processes at the expense of genes related to metabolism, suggesting an energetic trade-off imposed by the parasite. We further showed that parasitized hosts were poorer competitors (i.e. they had a lower access to feeding resources) compared to healthy hosts, although the functional response of host was not affected. Finally, the parasite modified the trophic niche of its host, which suggests potential impacts of the parasite at biological levels higher than the population. We concluded that *T. polycolpus* has a strong effect at the molecular level (with a costly immune response expressed in parasitized hosts) that generated cascading effects on other biological levels, notably those concerning interactions with the prey community of the host. By using complementary tools, this study is one of the first at demonstrating how a parasite can affect the host biology at multiple biological scales, which illustrates the usefulness of integrative studies for dissecting the complexity of ecological interactions.

*Speaker

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Parasites on the move: the large scale circulation of seabirds, ticks, and their associated infectious agents

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The capacity of birds to disperse infectious agents at large spatial scales is now widely recognised. Among birds, colonial seabirds include the most wide-ranging species and are characterised by a suite of life history traits that renders them ideal hosts for parasites and pathogens. Surprisingly, however, little is known about their role in parasite and pathogen circulation at different spatial scales. Using a series of examples from the different areas of the globe, we highlight the different factors that affect seabird movement and dispersal, outline how different types of seabird movements can alter patterns of dissemination of their associated parasites, and discuss potential feedback loops that can affect seabird population dynamics and favour pathogen emergence.

*Speaker

Facilitation by nurse plant *Juniperus communis* subsp. *hemisphaerica* and its role on natural regeneration of cedar forest on the southern slope of Djurdjura (Algeria)

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The main objective of this study is to determine if *Juniperus communis* subsp. *hemisphaerica*, a nurse plant, plays a facilitating role in the dynamics of cedar forest in the massif of Djurdjura. In order to highlight the possible effect of the presence / absence of cedar seed trees on vegetation dynamics and natural regeneration of this species, the choice of study sites meets the criterion of representativeness and takes into account three different phytoecological situations: a dense stand of cedar, a cedar-pasture ecotone area and a juniper formation without cedar seed trees. In each type of these sites, we sampled 13 tufts of hemispherical juniper, each one representing a floristic record; the dimensions of each record are those of the patch itself. To appreciate the various correlations that may exist between the nurse plant, its biological characteristics and the facilitated species, through different parameters, as specific diversity of the flora, number of tall scrubs and recovery of individuals of *Cedrus atlantica* within juniper thickets, we used multivariate analysis for the handling of the data collected. The dataset table contains 39 surveys and 16 dendrometric and biological variables of juniper individuals measured at the three study sites. The results obtained allow to highlight the nature of positive interactions of this juniper in the dynamics of the cedar forest. These interactions, rendered by the role of shelter provided by the tufts of hemispherical juniper, favor the emergence of a microhabitat adequate to the installation of the plant species linked to the cedar stand, thus protecting them from ecological stress in mountain and anthropogenic disturbances. Among these latter, overgrazing remains the major problem threatening the biological recovery and biodiversity of the Djurdjura massif. It would be conceivable to use this facilitation process for ecological restoration of the degraded cedar forest in Djurdjura.

*Speaker

Can we use plant form to explain the coexistence of woody plants and elephants in the thicket system?

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While the notion that elephants topple trees is well recognised, little is known about factors determining the coexistence of elephants and woody plants. This is of particular interest if we are to understand the impacts of elephants, particularly in systems where this coexistence may have been disrupted. Plant growth form (tree - stem with distinct canopy cover vs multitemmed shrub) may influence elephant tree pushing, and such growth forms may be altered by goat browsing. The Karoo Thicket Mosaic provides an ideal opportunity to explore the impacts of elephants after their return to this system, which has been transformed by goat browsing. We predicted that woody plants in areas exposed to prolonged goat browsing will occur in the tree form. Conversely, woody plants exposed to elephant browsing will occur in shrub form owing to resprouting or coppicing following damage. Additionally we predicted that plant form will play an important role in influencing elephant tree toppling. We tested these hypotheses, using *Pappia capensis* as a dominant model for thicket woody trees. We sampled in a site with a relic elephant population (Addo Elephant National Park Main Camp), a site where elephants were recently re-introduced (Kuzuko) and a site with domestic livestock but no elephants (a livestock farm adjacent to Kuzuko). As predicted, in the presence of goats, woody plants are converted to umbrella shaped trees, with the tree form predominating in sites with long periods of goat browsing, but not elephants. Further, woody trees suffered higher levels of elephant toppling than shrubs of comparable size. However, toppled *P. capensis* is able to persist, either through coppicing or resprouting and these forming shrubs not trees. The result explains the patterns of woody plants persistence in the presence of elephants, this through change in growth form.

*Speaker

Harbour and grey seals' foraging ecology in the Eastern English Channel highlight potential competitive trophic interactions

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Harbour (*Phoca vitulina*) and grey seals (*Halichoerus grypus*) are sympatric species occurring in the Eastern English Channel (EEC). Harbour seal colonies are established since the 1990's and increase (+21%/year), reaching nowadays around a thousand individuals. Several hundreds of grey seals were also observed in recent years (+30%/year) and may result from movements from the North Sea. In a context of potential competitive trophic interactions, we assessed their foraging ecology in the EEC by using a multi-disciplinary approach combining telemetry, stable isotopes and scat analyses. We analysed 283 harbour seal scats and 143 grey seal scats containing the remains of 6509 and 1388 individual preys respectively. Harbour seals' diet was mostly composed of juvenile and small flatfish (86% of ingested biomass [CI95%: 68-100]) including sole and plaice. Grey seals' diet was characterized by a higher variety of prey including 61% [38-87%] of the same flatfish species but larger in size, as well as 29% [13-54%] of round fish (mainly herring, whiting and pout) and 10% [1-23%] of squids. Carbon and nitrogen stable isotopes analysis of whiskers from 38 seals suggested a trophic overlap between the two seal species although grey seals generally fed on higher trophic level prey. The estimated total biomass consumed from 2015 to 2017 increased from 592 [490-701] to 750 [632-878] tons year for harbour seals, and increase from 422 [369-476] to 750 [675-827] tons for grey seals respectively. Lastly, telemetry showed that foraging areas of both species partly overlapped. Although some spatial and trophic partitioning was highlighted between the two species, harbour seals' trophic niche is included within the grey seals' one. The abundance of grey seals and their prey consumption will probably overtake that of harbour seals in the next years, potentially leading to an increase of competitive interactions which could affect harbour seal population dynamics.

*Speaker

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Insect herbivory on trees: untying the effects of tree diversity, leaf traits and climate

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Increasing the diversity of tree species in forest stands can lead to both associational resistance or susceptibility to insect herbivory. Discrepancies among existing studies remain largely unsolved, which prevent the development of a predictive framework of associational effects. Although several studies report that plant-insect interactions may change along large scale climatic gradients as a result of direct effects on herbivores or indirect effects on plant investment in chemical defenses, the potential role of climate in mediating associational effects has been overlooked.

We measured leaf insect herbivory and the foliar chemical defenses of birch (*Betula pendula*) in twelve long-term tree diversity experiments belonging to the Tree Diversity Network (TreeDivNet). Experiments covered temperate and boreal biomes, spanning a latitudinal range between 44.7 (France) and 61.7 (Finland) decimal degrees. Age of trees in experiments ranged from 5 to 57 years. We extracted climatic data (temperature and rainfall) for each study site from the CHELSA high resolution global climatology dataset. We modeled the response of chemical defenses and herbivory as a function of tree diversity and climate and explored whether the leaf insect herbivore responses were mediated by leaf traits.

Our results do not support the view that there is a general effect of tree diversity on insect herbivory. Instead, we show that the strength and direction of associational effects vary among sites, likely according to stand age and density, and are partly mediated by climatic factors and variability in leaf chemical defenses. Further work is required to elucidate factors underpinning resistance to herbivory in mixed forests, and in particular to explore the dependency of the biodiversity-resistance relationships to environmental context.

*Speaker

Parasites affect their hosts through many ways: virulence, vulnerability, behavior and energy

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Parasites are important components of ecosystems, altering life history trait and many interactions among species. Such modifications imply different types of mechanisms. Parasites are known for their effects on fecundity and mortality of hosts (virulence effects) that affect basic parameters of population dynamics. Parasites also modify the vulnerability to predation (interaction effects) thereby affecting ecological networks. Previous modelling works showed that these two effects may constrain coexistence and stability within trophic systems. However works rarely study these effects simultaneously. In the present study, we investigate their relative importance for a host-parasite interaction. We use *Daphnia magna*, infected by iridovirus DIV-1 that induce the White Fat Cell Disease (WFCD), a parasite known for their virulence effects, and undergoing predation by European minnow (*Phoxinus phoxinus*). We measure how parasites modify fecundity, mortality, activity (speed, time of activity), energetic content (carbohydrate, lipids and proteins) and vulnerability to predation (preference and search time of predator) in short experiments and/or in ponds. Results show that WBD reduce survival of *Daphnia*, but have little effects on their fecundity, and reduce their activity. Thus, it may be caused by or the cause of energetic contents modifications. Therefore, we may expect that parasite increase vulnerability of host due to effects on appearance and behavior. We predict alteration in the diet of predators as prey profitability is affected by the parasite. Consequently, parasites may have important effects in trophic systems, involving bottom-up effects (parasited-prey becoming more or less profitable) and trophic cascades (by modulating trophic interactions). Parasite effects therefore go beyond those expected based on simple virulence effects.

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Ecological Interactions

*Speaker

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Mistletoe infection in mixed and pure pine stands: a special case of associational resistance

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Increasing evidence is showing that tree diversity contributes to forest ecosystem functioning and the provision of ecosystem services. The fact that a given tree species suffers less damage when growing with heterospecific neighbors than amongst conspecific plants, i.e. associational resistance, seems a common pattern for herbivore insects and root pathogens. However, the effect of tree diversity on abundance of parasitic plants, such as mistletoes, has to our knowledge never been studied. And yet, mistletoes can affect tree growth, possibly leading to decline in conjunction with water stress. In this study, we tested the effect of tree diversity on the presence of European mistletoe (*Viscum album*) on Scots pine (*Pinus sylvestris*) and maritime pine (*Pinus pinaster*) in pure and mixed stands in northern Spain. Since only 1.2 % of maritime pines were infected by mistletoe, we considered it a non-host species. The infestation level of Scots pines was significantly higher in pure Scots pine plots (45.1%) than in mixed plots of Scots pines and maritime pines (25.4 %). Scots pine trees that were taller than the surrounding trees had a higher infestation probability. Since in mixed plots Scots pine trees were slightly lower than maritime pines, tree apparency whereby host trees were partially dominated by non-host trees may partly explain the observed associational resistance. However, plot type remained significant after the effect of tree height was accounted for, indicating that other factors additionally contribute to lower mistletoe infestation on Scots pine in mixed plots. This associational resistance may be related to the behavior of seed dispersing birds (e.g. Mistle thrush) that may prefer to land on taller trees or to spend more time in infested pure stands thereby provoking new infections. The association with maritime pine thus allows diminishing the negative effects of *V. album* on growth and survival of Scots pines.

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Plants versus herbivores: synchronization matters

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Plants can escape herbivores either by building up defenses such as plant secondary compounds, or by shortening their life-cycle so that they become mature before herbivores attack them. In France, a first generation of herbivores such as European corn borers occurs in spring. A second generation occurs in summer. Sewing of early maize varieties is recommended because maize stems are stronger when the second-generation larvae arise and better resist invasion, but it is still not known if this is simply due to their age.

To analyse how plant phenology shifts interfere with *Lepidoptera* stem borers, we used the maize lines selected for early or late flowering, coming from two independent Divergent Selection Experiments (DSEs). The two initial populations arose from two inbred lines, F252 and MBS. At each generation, we selected and selfed early and late flowering genotypes. The resulting Early and Late evolved populations exhibited pronounced phenotypic divergence for flowering, while preserving original characteristics of the initial inbreds. We expect thus that these lines differ mostly by the timing of their growth rather than by the quality of their secondary compounds. DSEs experimental designs were used to measure the prevalence of corn borers in Early and Late populations. Altogether flowering time varied between 1300 (Early F252) and 1900 (Late MBS) degree-days. Pyralids prevalence was more important in Early than in Late MBS populations. For F252, there was no difference between populations, but the average prevalence depended on the date of arrival of the second generation (year effect). In our plant material, synchronization between insect and plant life cycles appeared more important than the trade-off between growth and defense. We further discuss the setting-up of an experimental design to measure differences of leaf consumption rates between plant genotypes attacked by pyralids.

*Speaker

Genome-wide identification of plant host invasion traits in *Agrobacterium tumefaciens* using transposon-sequencing

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Ecological niche construction, which ensures a preferred access to resource, represents a recurrent strategy evolved by pathogens and symbionts. Identifying metabolic pathways involved in the exploitation of resource and evaluating their involvement in the fitness of microbes colonizing their host represent an important issue in ecology and evolution. In this work we used transposon-sequencing (Tn-seq) for identifying the fitness genes in the niche-constructing pathogen *Agrobacterium tumefaciens* when it is exploiting plant host. Tn-seq combines both transposon insertional mutagenesis and massively parallel sequencing of the transposon insertion sites. We will present two approaches:

1/ using metabolomics, we determined the enriched plant metabolites in the ecological niche which is constructed and exploited by the pathogen, and then we used transcriptomics and Tn-seq for identifying the fitness genes that are important for exploiting these metabolites;

2/ using Tn-seq, we directly determined the fitness genes that are important for exploiting the constructed niche on plant host.

These two complementary approaches will be discussed. This work also highlights the advantage and limits of Tn-seq to decipher the microbial genetic determinants that are involved in ecological niche exploitation on plant host.

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*Speaker

Sex makes them sleepy: host sexual morphs induce parasitoid diapause

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When organisms coevolve, any change in one species can induce phenotypic changes in traits and ecology of the other species. To overwinter successfully, parasitoids have to synchronize their life-cycle to both abiotic conditions and their hosts' phenology. Although winter diapause in parasitoids has been shown to be mostly induced by photoperiod and temperature, seasonal host phenotypic variations may also constitute induction cues. To test the effect of host reproductive strategy on parasitoid diapause induction, we used a holocyclic clone of the pea aphid *Acyrtosiphon pisum* producing both asexual and sexual morphs, the latter being only present at the end of the growing season. *Aphidius ervi* parasitoids from contrasted climatic origin (harsh *vs.* mild winter areas) were allowed to parasitize each morph and developing parasitoids were next reared under either fall-like or summer-like temperature-photoperiod conditions. We next examined aspects of the host physiological state by comparing the relative proportion of forty-seven metabolites, using gas chromatography, and lipid reserves in sexual and asexual aphid morphs. We found that sexual aphids are cues *per se* for diapause induction; parasitoids entered diapause at higher levels (19.4 ± 3.0 %) when developing in oviparous aphids than in viviparous aphids (3.6 ± 1.3 %), but only under summer-like conditions. This pattern was only observed in parasitoids from the harsh winter area since no diapause was observed in the other population under summer-like conditions, suggesting local adaptations to overwintering cues. Metabolomics analyses suggest parasitoids' response to be mainly influenced by sexual aphids' physiology, with higher proportion of polyols and sugars, and more fat reserves being found in oviparous aphids. Our results underline strong coevolutionary processes between hosts and parasitoids in their area of origin, leading to phenological synchronization.

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[†]Speaker

Insect herbivory and herbivore predation in newly established oak forests

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Forest ecosystems form a network of more or less connected patches of woody habitats that can alter the relationships among organisms such as insect herbivores and their predators. However, little is known about how these organisms and their interactions are affected by woody patch size and isolation. We addressed oak-herbivore-predator interactions in 18 oak stands in Aquitaine, south-western France, chosen along a gradient of patch size and isolation (i.e., abundance of oak forests in a 500 m radius buffer around patches). We measured leaf insect herbivory on four oaks per patch. We used artificial caterpillar larvae to estimate the activity of bird and arthropod predators and recorded the abundance and diversity of insectivorous birds within patches. Leaf-miner abundance increased with patch isolation but was not affected by patch size. The percentage of leaf area removed by chewing insect herbivores increased with patch size, and this effect was stronger in isolated patches where herbivory was higher. Overall predation rate (by both birds and arthropods) increased with patch area, but was not affected by patch isolation. In contrast, abundance and diversity of insectivorous birds surveyed in oak patches increased with both patch area and isolation. Predation rate and bird diversity were unrelated and either predation rate nor bird diversity had a significant effect on herbivore damage. Altogether, our results indicate that the size and isolation of oak stands has the potential to affect trophic interactions among trees, herbivores and predators, but that their effects on insect herbivores and predators were independent. Our results therefore have important implications for the management of small isolated and expanding forest patches in complex landscapes.

*Speaker

Ecotoxicology and Environmental Pollution

Pollution exposure amplifies the effects of predation risk on cell-mediated immune response in a passerine species

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Immune systems have evolved to counteract the negative impacts of pathogens on host fitness. However, mounting immune responses is costly, and may be traded-off against resource allocation to other fitness-related functions. In this study, we used the Hybrid sparrow (*Passer domesticus* x *hispaniolensis*) to experimentally explore how cell mediated immune response (CMI) might vary according to the levels of experienced predation risk and prior exposure to metallic pollution. To do so, we captured a sample of sparrows in the surroundings of Gabès–Ghannouche factory complex of phosphate treatment (high exposure to metallic pollution) and another sample in a less polluted site, situated 12 km to the north (low exposure to metallic pollution). Each sample was divided into two subsamples that have been exposed to either a cat (high predation risk) or a rabbit (no predation risk). Subsequently, we assessed the intensity of CMI in each sampled sparrow, using the Phytohaemagglutinine (PHA) test. Generalized Linear Mixed Models (GLMM) were then conducted to investigate CMI as a function of exposure to pollution (two classes), predation risk (two classes) and their interaction. We found that the intensity of exposure to pollution and the level of perceived predation risk had interactive effects on the amplitude of CMI. Sparrows from the less polluted site showed overall higher levels of CMI compared with those from the polluted site. More interestingly, CMI intensity decreased with increasing predation risk in sparrows from the less polluted, while no significant change was recorded in those from the less polluted site. These results suggest that predation risk induced a reduced allocation priority of resources in immune function, which might be in turn weakened by the previous long term exposure of the prey to metallic pollution. Further investigations including additional measures of immune function are needed for better understanding of this issue.

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Assessing the impact of farming practices and landscape heterogeneity on ground beetles' exposure to pesticides

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In the nineties, John Cairns emphasized the importance of developing a field of "landscape ecotoxicology". Indeed, landscape features influence both abiotic and biotic processes, such as pollutant transfers in the different compartments of the environment, or population dynamics of beneficial organisms. Realistic ecotoxicological scenarios therefore require a spatially explicit assessment of the exposure of mobile non-target organisms to pollutants, but so far this research field has received poor attention. The present study aims at investigating the impact of farming practices (pesticide applications) and landscape heterogeneity (proportion of semi-natural habitats and organic fields in the surrounding landscape) on ground beetles exposure to pesticides. In 2016 within the RESCAPE project, we sampled carabid beetles in hedgerows, grasslands and cereal fields in 60 different 1km² agricultural landscapes in western France (LTER site "Zone atelier Plaine et Val de Sèvres", 46°11N – 0°28W). 180 carabid beetles individuals (*Poecilus cupreus* and *Harpalus dimidiatus*) are currently being analyzed for 31 pesticide residues commonly used on the study area. We will establish quantitative links between pesticide residues concentration in animals, type of habitat, local farming practices, and landscape heterogeneity. We aim at generating spatial exposure maps to identify "at-risk" landscape contexts to pesticides transfers (i.e. landscape contexts where exposure of non-target organisms is enhanced) versus "resistant" landscapes. Such a knowledge is a prerequisite to guide scientists and land managers in identifying management tools to improve agroecosystem resistance to pesticide effects and would allow getting original insights into landscape ecotoxicology and ecology.

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Invertebrates facing environmental contamination by phthalates: novel evidences and recent insights

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Phthalates are synthetic contaminants released into the environment notably by plastic waste. Semi-volatile and highly lipophilic, they adsorb to organic matter into sediments and stick to volatile organic compounds, getting distributed in all ecosystems. Effects of this major anthropogenic pollution on human and on economical species have attracted large interest, leading to the recognition of phthalates as endocrine-disrupting chemicals. However, very few studies have focused on wild unexploited populations. In two independent studies on wild invertebrate models, we highlight the fact that terrestrial invertebrates and especially insects are more exposed to phthalates than previously thought: the lipophilic nature of the cuticle makes it a good trap for atmospheric phthalates, leading to permanent presence of these molecules onto the insect body. We showed that such basal chronic contamination probably has deleterious effects on the ant *Lasius niger*, reducing queen fertility and disturbing immune functions in workers. Furthermore, we evidenced subtle effects of living in a phthalate-contaminated milieu in the sand-dwelling marine worm *Hediste diversicolor*. While chemical analyses of the sediments predicted no acute toxicity for the worms, and phenological studies evidenced no direct cost for the studied populations, we evidenced that both populations exposed to multiple pollution (high phthalates + high metals) or to phthalates alone (medium levels of phthalates) showed a significantly reduced survival upon infection with a local pathogen, compared to a reference population (low levels of phthalates). Moreover, the females living in polluted areas (medium and high) seem to protect less efficiently their descent: their oocytes contain less antibacterial molecules active against local bacterial strain. Generalized exposure and subtle negative effects should prompt us to deeper investigate the consequences of such ubiquitous environmental contaminants on invertebrate natural populations.

*Speaker

Multiple stressors in freshwater ecosystems: antibiotic mixtures and temperatures

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Interactions among different anthropogenic stressors are at the core of unexpected ecological impacts on ecosystems as they can provoke complex effects that lessen or amplify the direct effect of each stressor. One of the most important stressors in freshwaters are pharmaceuticals, including antibiotics. Antibiotics have been used in large quantities for some decades but it is only in recent years that they have been investigated to assess the environmental risk they might pose. We performed two different laboratory-based experiments to explore the effects of antibiotic mixtures and temperature together. Firstly we used the bacterium *Pseudomonas fluorescens* and in a second experiment, we used a natural bacterial community coming from a leaf litter biofilm. We exposed them to a mixture of ciprofloxacin, ofloxacin and sulfamethoxazole at low concentrations (under 100 $\mu\text{g/L}$) and under different temperatures treatments. We measured the bacterial fitness of the final bacterial population - exposed to antibiotics for 7 days – by assessing its growth under the different temperature and antibiotic treatments, and by comparing it to the growth of the ancestral bacterial strain or community - which was never exposed to antibiotics. While *P.fluorescens* growth was negatively affected by the presence of antibiotics – in particular ciprofloxacin and ofloxacin alone - the natural bacterial community growth was positively affected. Metabolic alterations caused by the resistance mechanisms can increase the growth of the bacterium in the presence of the antibiotics, even sometimes causing dependence to the antibiotics. In both experiments, all antibiotic combinations induced bacterial resistance after 7 days, especially at lower temperatures. Because of the constant release of antibiotics in the environment, we do not expect antibiotic resistance in stream biofilms to be reduced in the near future and we need to follow up with experiments looking at the combined effects of stressors in short and long-term scenarios.

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Biological vs. Chemical monitoring of freshwater ecosystem and assessment of water pollution level

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Introduction: Water pollution due to urbanization and anthropogenic causes has risen in India in last few decades and aquatic species survival and persistence face challenges and threats as the consequence of environmental pollution. River Mahanadi is one of the major river systems in India and carries over 66 km³ water from Chhattisgarh to Bay of Bengal via Odisha state covering all the main cities.

Materials and methods: We conducted field study Mahanadi river, Cuttack (85°46'21.29" E 20°28'15.81" N & 85°49'45.23" E 20°30'50.00" N) during 2013-2014 and collected aquatic invertebrate samples from 13 different stations and stored in 70% ethanol in tubes. Later the species were sent for identification. To compare biological method to chemical monitoring technique, we have also collected water samples and fixed immediately and later analyzed in our laboratory following standard APHA methods.

Results: We analyzed the samples for biological monitoring working party (BMWP) score, average score per taxa (ASPT) method and macro-invertebrate based index (MBI) value. Chemical parameters were tested to find correlation with the presence of macroinvertebrates.

We developed macro-invertebrate based biotic index for biological assessment of water quality and pollution level. Our result showed significant correlation with high value of Dissolved oxygen, nitrate, chloride and phosphate with presence of macroinvertebrates in various sampling stations.

Discussion: This study showed relationship between water parameters and presence of macroinvertebrates and biological indicators showed more accurate result of aquatic ecosystem health. Species abundance and richness of pollution tolerant taxa and pollution sensitive taxa indicated elevated risk of pollution in Mahanadi river. Macro-invertebrate based biotic index has been proven as a very efficient tool to assess freshwater quality over chemical monitoring of water. We explored diverse families of aquatic invertebrate species which were endemic to Mahanadi belt and increased the knowledge about biodiversity and faunal composition of river of concern.

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*Speaker

Ecological risk assessment of heavy metal pollution of river ecosystems in the Debed River catchment area, Armenia

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Investigating the mechanisms behind the impact of heavy metal pollution on aquatic ecosystems is urgently required. Due to increasing growth in the mining sector, pollution in the Debed River catchment area located in the north of the Republic of Armenia has become a serious threat to water resources and aquatic biodiversity. The aim of the present study was to investigate and assess the environmental risks of heavy metal pollution of river ecosystems in the Debed river catchment basin. Water and hydrobiological (macrozoobenthos and fish) samples were taken from the risky and non-risky river sites of the Debed river catchment area in April, July and September of 2017. Heavy metal and hydrobiological analyses were done by the standard methods. The results of the study showed that heavy metal concentrations in the waters of the investigated rivers were conditioned by both lithogenic and anthropogenic sources, as the concentrations of different heavy metals in all the investigated observation sites of the rivers exceeded the background level (BL). In the river sites being at the risk of mining impact, all the investigated heavy metals exceeded the BL, and heavy metal content was mainly formed by anthropogenic influence. In the mining impact zone, a noticeable increase in heavy metal content was also registered in the tissues and organs of aquatic organisms (macrozoobenthos and fish). Hydrobiological investigations showed that the degree of heavy metal pollution of the river waters in mining areas negatively affected the growth of aquatic communities. In the mining impact zone, a decrease in the quantitative parameters and diversity of benthic macroinvertebrates and fish was observed.

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*Speaker

Two populations of *Temnothorax nylanderi* display differential adaptation in response to heavy metals exposure

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Cities are unique opportunities for scientists to study the adaptation of species to environmental changes. Indeed, cities are quite recent, they involve strong modifications of the environment, and each city constitutes an independent replicate. The urban environment has specific features including warm temperatures, fragmented habitat, human presence and light, noise and chemical pollutions. Species that manage to live in such environment often have generalist or opportunistic diets, tolerate human presence and display bold behavior. Species that are not adapted can also maintain urban populations through migration from non-urban source populations. Adaptive traits can result from either genetic evolution or phenotypic plasticity. Most of those traits have been found by comparing different closely related species living either in urban or non-urban environments, however studies comparing population of the same species from different environments are lacking. Our study were aim to determine whether there is adaptation to urban chemical pollution at the level of the population. We used different population of the same ant species, *Temnothorax nylanderi*, that is commonly found both in cities and forest. We reared colonies collected from forest (unpolluted) or urban (polluted) habitats (3 replicates) under either a normal or cadmium-supplemented diet. Cadmium is a heavy metal pollutant found at high concentration in cities. We measured several traits of laboratory-born workers (size, immunocompetence) as well as mortality rate of both workers and larvae and compared them between treatments and habitats. Our results allowed us to discuss whether colonies from urban habitats are more adapted to heavy metal pollution than colonies from forest habitats.

*Speaker

Effects of Titanium Dioxide Nanoparticles on the Antioxidant System of *Galleria mellonella*

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The nanoparticles which rapidly release to the environment could cause adverse effects on living organisms. Titanium dioxide nanoparticles (TiO₂-NPs) are extensively used in a wide range of products. The physiological effects of TiO₂-NPs are still not completely understood. Hence, the influence of TiO₂-NPs should be investigated by establishing experimental model organisms. For this aim, we examined the effects of different doses of TiO₂-NPs (100, 500, 1000, 3000 and 5000 ppm) on total protein amount, antioxidant enzyme activities and malondialdehyde (MDA) amounts in the hemolymph of the greater wax moth, *Galleria mellonella* (L.) (Lepidoptera: Pyralidae). Exposure with dietary TiO₂ NPs caused a significant increase in the total protein amount and content of MDA and glutathione S-transferase activity in the hemolymph at 100, 500 and 1000 ppm compared with control and other doses of TiO₂ NPs. While the activity of catalase increased by 1000, 3000, and 5000 ppm and superoxide dismutase activity increased at all doses of TiO₂ NPs when compared with control. Our results indicated that TiO₂ NPs have dose-dependent toxic effects on the *G. mellonella* larvae and can enhance the stress resistant capacity of insects at low concentrations.

Key words: Antioxidant enzymes, *Galleria mellonella*, Model insect, Nanotoxicology, Titanium dioxide nanoparticles

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*Speaker

Association between agricultural practices and small mammal blood bacterial assemblages

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Agricultural intensification, characterised notably by field enlargement, reduction of perennial (wooded) habitats, and increased use of chemical inputs, can have strong consequences on the biodiversity and ecological functions of agroecosystems. If direct responses of many taxa to this agricultural intensification are already documented, the indirect effects are still little studied. For instance, the use of pesticides may reduce the populations of non-target species, which may cause a collapse of wildlife populations that feed on them, and thus change trophic web structure. At the same time, the exposition to pesticides may disturb the immune system of animals, altering their resistance to infectious agents. While crucial and urgent in the current debate about the use of these chemical compounds in agriculture, identifying and quantifying the different impacts of pesticides among other factors remains a complex task. In this study, we aimed at characterising the blood bacterial assemblages of small mammals trapped before and after seeding around maize fields cultivated with different agricultural practices (with or without pesticide inputs, *i.e.* neonicotinoids coated seeds), and in different landscape contexts (*i.e.* proportions of surrounding woodland cover). High-throughput sequencing of the bacterial 16SrRNA gene from DNA extracted from small mammal blood samples should allow us to identify the bacteria present in small mammal blood. The composition of bacterial assemblages will be then compared with a dataset of blood analyses, chemical clinical plasmatic analyses, and the analyses of pesticide residues in small mammal hair. This study is an initiating step to assess the impact of agricultural practices (here neonicotinoid use) on small mammal communities, small mammal physiological state, and the blood bacterial assemblage they host together. The first results will be presented and discussed with regards to some pathogenic infectious agents of human health and veterinary concern (*e.g.* *Bartonella* sp., *Borrelia burgdorferi* s.l.).

*Speaker

A new imperative for the life sciences not to be ignored by ecotoxicology

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Increasingly evidence is accumulating that microbial communities form an integral part of the physiology, ecology, and evolution of animals. Using next generation sequencing, our knowledge on microbial diversity associated with animals is rapidly growing. Over the last years, life sciences have acknowledged that (1) microbes associated with animals are much more diverse than previously thought, (2) microbes communicate with their host in many different ways, (3) microbial communities support essential host functions, and (4) microbial pathogens play an important role in the population dynamics of both vertebrates and invertebrates. It is interesting though, that interactions with microbes are rarely considered in ecotoxicology. If microbial communities form an integral part of the ecology of an animal, and if, as some have said, it is imperative to include them in any study on animal functioning, they cannot be ignored by ecotoxicology. It is useful to consider the interaction between environmental pollution, animals and microbial communities as a triad. In some cases, microbial species act as symbionts providing essential nutrients to their hosts, in other cases, the role of microbes is unclear, even though their association with animals is sometimes quite specific. Regarding the assessment of toxicants, the important question is whether microbes make the host more vulnerable to toxicants or may protect the host from intoxication. The latter seems to be the more common phenomenon, arguing from the very limited evidence available to date. Environmental management should be aware that preserving ecosystem health requires consideration of animal-microbe interactions. EU's 7th Environment Action Program aims to safeguard the Union's citizens from environment- related pressures and risks to health and wellbeing. A one-health perspective including humans, animals and plants, plus microbial communities and all the interactions between them and the environment is the best way to achieve this aim.

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Environmental Genomics

Population genomics of the red coral *Corallium rubrum*: from local adaptation to conservation

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The recent methodological advances in molecular ecology allow renewed study of adaptive processes in heterogeneous environments for non model organisms. The precious red coral, *Corallium rubrum*, is a long lived species, present in very contrasted thermal conditions, from shallow to deep environments. Due to its life history traits, its ecological role and the anthropogenic (harvesting) and climatic (mass mortality events) pressures impacting its populations, this species is an original model to characterize the interaction of neutral and selective microevolutionary processes in the population response to global change. The first population genetics studies, combined with field experiments, allowed defining pertinent study scale in this species, and emphasized the importance of local processes in the population maintenance. The use of NGS, through RNA and RAD-sequencing, allowed a deeper investigation of local adaptation to thermal regime in this species, explaining potentially the differential mortalities observed in the field during mortality events. Nevertheless, a lack of convergence in gene candidates or functions was reported. A by-product of this study was the demonstration, for the first time in a non-bilaterian species, of a XX/XY sex determination system. These results have important implications for the management of red coral populations ranging from the design of marine protected area to potential restoration actions.

*Speaker

Pollination network analysis by environmental metagenomics

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Plant-Pollinator interactions are organized in bipartite, mutualistic complex networks with two organism groups: for plants, pollinators are essential pollen vectors required for their reproduction, while plants provide vital food resources to pollinators. Studies of plant-pollinator networks are traditionally based either on field observations of pollinator visits to plant species or pollen identification by microscopy, both having strong limits. Recently, a new innovative approach has been developed; it consists to identify the pollen of the various plant species carried by insects or deposited on plant stigma by using DNA metabarcoding, high throughput sequencing and bioinformatics tools. Compared to traditional approaches, metabarcoding provides a striking different picture of pollination networks. Moreover, the approach allows investigating intraspecific networks and upscaling the impacts of individual behavior on species networks.

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Ecological networks of microbial plankton influence the biological carbon pump processes in the oligotrophic ocean

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The biological pump corresponds to the combination of biologically driven processes encompassing the production of organic matter via photosynthesis, its export to the deep and its remineralization. Phytoplanktonic composition in surface influences the strength of carbon export. Besides, key players involved in the biological pump have been identified, such as diatoms because of their large size and fast sinking rates and copepods by the production of fecal pellets while migrating in the water column. However, the functions handled by micro-organisms in the biological pump are yet poorly characterized, and results suggest that the biological carbon pump is the result of their interactions rather than their independent actions. Here we defined three different states of the water column corresponding to situations where primary production, carbon export or flux attenuation is dominant over the two other processes. We used environmental and genomics data from the *Tara* Oceans project to disentangle planktonic interactions and functions involved in the variability of the biological carbon pump. Using ecological network inference methods, each of the states were analyzed to determine their underlying system organization at the level of prokaryotic species and functions. The states were then compared to check how their structure may differ or whether transitions between them can be detected. As the results suggest that the taxonomic and functional composition of prokaryotic plankton in the euphotic zone correlates with those states, we anticipate our results to be a starting point for monitoring the biological carbon pump over time and space and improve global carbon cycle models.

*Speaker

The hybrid zone theory, a universal framework for population genomics

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Most species are subdivided by hybrid zones. Overwhelming evidence support this claim and recent analyses of genome sequences have strengthened it as a ubiquitous result of population genetics. Surprisingly, the consequences for the interpretation of population genetics data have remained mainly ignored. I intend to highlight the generality of the hybrid zone framework for population genomics. First, I will argue that hybrid zones of the pre-genomic era, studied with a few markers, represented only a small fraction in the gradient of genomic differentiation between interacting genetic backgrounds. Genome analysis allowed identifying many new cryptic hybrid zones between more loosely differentiated lineages (younger divergence) or more loosely isolated taxa (more porous genetic barriers). Refraining to call them hybrid zones is unfortunate and distracts us from interpreting them in the light of the hybrid zone theory. Second, I will recall two important predictions of the hybrid zone theory that well explain how genetic diversity is structured in space and within genomes. (i) Hybrid zones are expected to be trapped by barriers to dispersal or by ecotones. This explains genetic-landscape associations, even when past vicariance and/or partial reproductive isolation best explain the genetic differentiation. (ii) Hybrid zones are expected to act as semi-permeable barriers to gene flow between heterogeneously differentiated genomes. This explains the usually much higher observed variance of differentiation than the neutral expectation, and the correlation with recombination rates. I will seize the opportunity to dispute against the mistaken belief that selection against migrants could be an effective genome-wide barrier to gene flow. Finally, I will argue that introgression tails emanating from hybrid zones should be accounted for to interpret population genomic data within apparently well-mixed biogeographic regions. There are good reasons why introgression gradients should better correlate with ecological variables or with least cost path connectivity maps than with geographic distance.

*Speaker

Development of genetic tools to study the phenotypic heterogeneity of a marine pathogen

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Marine organisms are facing a dual and cumulative threat, *i.e.* pathogenic microorganisms reinforced by global warming. Bacteria belonging to the genus *Vibrio* are one of the most common pathogens in oceans and are responsible for massive death of molluscs. However, despite these ecological and economical concerns, virtually nothing is known about the behaviour of bacterial individuals during infection. Does every single cell of an isogenic pathogen behave the same, or is the bacterial population composed of different sub-populations, behaving differently to divide the labour and conquer its new ecological niche. This "divide and conquer" strategy is the focus of a new field of research in microbiology, but this field remains typically restricted to mammal pathogens.

Here, the aim was to start unravelling the behaviour of *Vibrio harveyi* ORM4, a pathogen infecting the abalone, working at the single cell level to account for the phenotypic heterogeneity. The major limiting step was to genetically modify this strain, as the genetic tools typically available for model organisms are not necessarily valid for environmental and marine bacteria. An electroporation protocol was developed to introduce exogenous DNA in various *Vibrio* strains. Moreover, we constructed bioreporters to follow the expression of genes at the single cell level, targeting relevant virulence genes. Importantly, we could demonstrate for the first time that an isogenic population of *V. harveyi* is composed of 2 populations with varying expression states of a flagellar promoter.

This work is a fundamental step to understand the behaviour of marine pathogens, and will deepen our understanding on the extent of microbial phenotypic heterogeneity during microbial infections.

*Speaker

Comparison of Bacterial Communities Found in Villa Luz Caves of five different underground sites

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Villa Luz caves (VLC), in the southern Mexican state of Tabasco, which are interconnected by an aquifer network that spans hundreds of kilometers in a region lying North of the Sierra de Chiapas, with by at least 26 groundwater inlets and the Chichonal volcano, containing 300-500 mg L⁻¹ H₂S and < 0.1 mg L⁻¹ O₂.

We extracted environmental DNA for metagenomic analysis of collected samples in five selected Villa Luz caves sites, with pH values of 2.5 to 7. Foreign organisms found in this underground ecosystem that oxidize H₂S to H₂SO₄ include the following bacterial associations: biovermiculites, which grow on the rock walls; snottites, which are whitish, viscous biofilms hanging from the rock walls; and sacks or bags of phlegm, which live within the aquatic environment of the springs. Amplification products in V1 and V3 hypervariable regions of 16S rRNA bacterial gene generated 20,901 readings, by TEFAP pyrosequencing.

Seven bacterial phyla were identified, Proteobacteria was more frequent than Acidobacteria. Finally, acidophilic Proteobacteria was detected in UJAT5 sample.

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Genomic diversity of *Dickeya* species associated to potato

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Blackleg and soft rot diseases caused by soft rot enterobacteria provoke important losses in potato production worldwide and are the cause of up to one third of the rejections of seed tubers lots in Europe. Modifications in the structure of pathogenic bacterial populations causing blackleg disease have been observed these last decades with the emergence of two *Dickeya* species, *D. dianthicola* and *D. solani*. To tackle the putative genetic traits involved in this emergence, we undertook both intra- and inter-species genomic comparisons. While *D. solani* appeared to be mostly clonal (Khayati et al, 2015), *D. dianthicola* strains are more diverse. Both species harbour more than 3,000 interspecific common genes including the virulence genes characterized in the model *D. dadantii* 3937 strain. Each species also possesses hundreds of specific genes that are often regrouped in genomic regions that may present signatures of horizontal transfer. To deepen our comparison of the two *Dickeya* species, we performed a transcriptomic analysis of one strain of each species after growth either in rich medium or on potato tubers. Several genes included in species-specific genomic regions were activated on tubers pointing to a possible role in interactions with plants. Interestingly, a few hundreds genes common to both species, including virulence genes, presented different expression profiles in the two species suggesting different adaptations to similar environmental conditions.

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Phytoplankton's taxonomic and functional diversity patterns over a coastal tidal front

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Oceanic communities of photosynthetic organisms (*ie* phytoplankton) with various ecological strategies are responsible for about 50% of the earth's primary production and shape global biogeochemical cycles. Understanding the dynamics in the taxonomic and functional composition of this bulk of organisms is thus a great challenge. The factors brought forward to explain phytoplankton's distribution involve, 1) Advection and dispersion (*eg* water currents, mixing), 2) resource availability (here light and nutrients) and 3) biotic interactions; whether trophic (*eg* predation), symbiotic (*eg* parasitism) or competitive (here competitive exclusion for light and nutrient).

The Ushant tidal front (Iroise Sea, French Brittany), is a zone of high primary production where all those confounding effects takes place. A recent application of trait-based modelling in the Iroise Sea highlighted a hotspot of diversity in the location of the front. Two hypotheses were highlighted to explain a higher phytoplankton diversity in the front: 1) the advection of ecological strategies adapted to the distinct biotopes surrounding the front (*ie* ecotone) and 2) the local decrease in competitive exclusion due to better resource availability.

These mechanisms shaping phytoplankton's taxonomic and functional diversity in the front were studied by coupling metabarcoding and a biological trait analysis. The Ushant tidal front was sampled three times during 2015 and protists (*ie* unicellular eukaryotes) were targeted and identified by sequencing methods. Based on their taxonomy, Operational Taxonomic Units (OTUs) were annotated with 13 traits to select and infer phytoplankton ecological strategies. We will first highlight the physicochemical factors influencing the formation of distinct biotopes and protistan communities in the Iroise Sea. Then, in a focus on phototrophic protists (here considered to represent phytoplankton), will discuss the maxima in diversity at the front and compare the two hypotheses previously highlighted, with respect to taxonomic and functional diversity.

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Linking Allele-Specific Expression and Natural selection in wild population of *Oithona similis*

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Allele-specific expression (ASE) is now a molecular mechanism widely studied at the cell and organism-levels. However, population-level ASE and its evolutive impacts have still never been investigated. Here, we deciphered the potential link between ASE and natural selection. As a model, we used metagenomic and metatranscriptomic data of seven wild populations of the marine copepod *Oithona similis* from Tara Consortium sampling in the Arctic Seas. We were able to (i) Study the structure between these populations, (ii) Detect variants under local adaptation, (iii) Develop a method to detect variants under ASE. We found a significant amount of variants under ASE in at least one population and under selection across all the populations, proving that a link exists between these two molecular mechanisms. The next step of this work is to determine the nature of the link between ASE and selection.

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A hierarchy of ecological filters acts at a hierarchy of phylogenetic resolutions to shape arbuscular mycorrhizal fungi spatial distribution

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Traditionally, species is the taxonomic unit used to quantify the importance of ecological factors shaping communities of arbuscular mycorrhizal (AM) fungi, but it may not provide the appropriate resolution. Using an Illumina amplicon dataset of large subunit (LSU) ribosomal DNA (rDNA) sequences from a chronosequence of soil agricultural recultivation, we tested whether the correlation between soil parameters and AM fungal community composition changes across phylogenetic resolution. We inferred amplicons sequence variants to resolve phylogenetic diversity at resolutions finer than provided by traditional sequence clustering methods, and we used a phylogenetic framework to cluster variants into operational taxonomic units at coarser resolution. Clustering variants up to a genetic distance of 0.03 substitutions per site increased the correlation between community composition and soil plant-available phosphorus (P) and nitrate (NO₃⁻). Furthermore, P better correlated with community composition at a broader phylogenetic resolution compared to NO₃⁻. Our study suggests that a hierarchy of ecological filters acts at a hierarchy of phylogenetic resolutions in shaping AM fungal communities. By informing on the ecological preferences of AM fungal clades at multiple phylogenetic levels, our approach can address the challenges of assessing functional complementarity and predicting the consequences of environmental changes on AM fungal diversity.

*Speaker

Epigenetics and stress tolerance in polyploid *Spartina* (Poaceae)

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Investigating epigenetic mechanisms in non-model species confronted to challenging environments is an important question in evolutionary ecology, but needs the development of adequate resources and methodologies. We present here the approach we developed in the salt-marsh genus *Spartina* (Poaceae) which is notorious for its recurrent hybridization and genome duplication events that resulted in highly successful invasive species. *Spartina* species play an important ecological role in the sedimentary dynamics of coastal saltmarshes in several continents where they are able to tolerate several hours of immersion under seawater. Some species exhibit particular tolerance and resilience to chemical pollution (e.g. heavy metals, polycyclic aromatic hydrocarbons PAHs) which make them excellent candidates for phytoremediation. The most complex genome (namely the invasive allo-dodecaploid *Spartina anglica*) arose recently in Europe *c.a.* 150 years ago, by genome duplication of the homoploid hybrid *S. x townsendii* resulting from an interspecific cross between the introduced *S. alterniflora* ($2n=6x=62$) as maternal parent and the European native *S. maritima* ($2n=6x=60$). Allopolyploidy was accompanied by significant DNA methylation alteration following hybridization, mostly in regions flanking transposable elements, and gene expression evolution. We used massive parallel sequencing technologies to explore the genomes and transcriptomes of these species, and we developed bioinformatic approaches and tools for detecting the different putative orthologous copies originating from the parents (duplicated homoeologs) in *S. anglica*. We also evaluated the repetitive compartments and annotated repeats, which allowed us to identify small RNAs (siRNAs and miRNAs) involved in epigenomic response to PAH-induced stress and/or in parental species, hybrid and the highly tolerant allopolyploid.

*Speaker

DNA metabarcoding to quantify the response of insect diversity to mountain forest die-offs in the French Pyrenees

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Mountain forests suffer from an increase in frequency and severity of summer droughts and infestations of pathogens and insects. Those factors are causing high mortality of some keystone tree species (forest die-offs). Yet, how tree diebacks and associated changes in forest composition will affect local diversity and ecosystem functions remains unknown.

Here, we aim at quantifying the impact of climate-induced forest decline on biodiversity by measuring changes in taxonomic structure of invertebrate communities along gradients of silver fir (*Abies alba*) dieback in the French Pyrenees.

We use DNA metabarcoding to analyse 224 samples of Malaise traps placed on 56 silver fir dominated plots in the French Pyrenees from May to September 2017. Samples were sequenced using Illumina MiSeq and analysed using the DAME twin-tagging pipeline approach. We conducted taxonomic assignment against reference DNA barcode libraries to streamline identification and recover biological information for ecological analysis.

We discuss the results of our metabarcoding analysis and the utility of our approach to conduct biomonitoring across a large geographical scale.

*Speaker

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Innovative tools to diagnose the impact of land use practices on soil microbial communities

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Preservation and sustainable use of soil biological communities represent major challenges in the current agroecological context. Indeed, most of soil ecosystem services results from biological functions mainly driven by taxonomic and functional assemblages of microbiological communities (*i.e.* nutrient cycling, soil aggregation, depollution, etc.). Consequently, soil microbial communities are logical candidates as effective indicators of soil quality and sustainability. But, good biological indicators must be associated with references that encompass an operating range of measured values that are positioned in order to perform the desired diagnosis. Even if numerous studies have focused on soil microbial communities over the last two decades, due to the variety of ecosystems, sampling designs and methods, we still lack reference databases and diagnosis tools allowing the robust evaluation of agricultural practices impact on soil microbial communities. To attain this goal, we used an extensive set of samples originated from the French Soil Quality Monitoring Network (RMQS). This monitoring network is based on a 16-km regular grid across the 550,000 km² French territory representative of its pedoclimatic diversity. We determined: (i) the microbial biomass by quantifying the DNA extracted from soils, and (ii) the bacterial taxonomic richness. Both measures are good microbial indicators as they satisfy technical, practical and economic prerequisites. Based on the database encompassing thousands of values, two diagnosis tools were developed, using statistical predictive models according to environmental parameters (soil physico-chemical, climatic characteristics). Indeed, they provide reference values fitted for a given pedoclimatic condition, which is to be compared to the corresponding measured data for a robust diagnosis of soil biological quality. These tools were validated on external datasets and their applicability directly in the field was demonstrated on a farm network. In conclusion, these innovative tools providing reference values for a given pedoclimatic condition allow a robust diagnosis of soil biological quality.

*Speaker

Epigenetics, Phenotypic Plasticity and Physiological Ecology

Overwintering strategy of different populations of *Aphidius colemani* from Chile

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Overwintering strategies are essentially an ecological adaptation to face environmental variability. To survive winter, ectotherms can stay active or enter diapause; the selected strategy depends on winter harshness at a given location, and the capacity to enter diapause must thus be assessed for each insect population. Short photoperiods and low temperatures are the main factors inducing winter diapause in insects. Response to photoperiod and temperature in two different Chilean geographic populations originating from cereal fields (Talca 35°26'S; 71°40'W and Temuco 38°45'S; 72°40'W) of the aphid parasitoid *Aphidius colemani* (Hymenoptera: Braconidae) was studied. The aim of this study was to determine the effect of different combinations of day lengths and temperatures on diapause incidence in *A. colemani*, and to evaluate if cold storage in complete darkness (extreme conditions) may induce diapause at the highest level. We examined the potential effects across four constant conditions: 8:16 LD (Light:Dark, h) at 10°C, 10:14 LD at 14°C, 16:8 LD at 20°C (control), and cold storage at 4°C in complete darkness after one day of mummification for seven days. Besides, immature developmental time, survival and longevity were measured. Neither of two populations of *A. colemani* expressed diapause at any tested condition. Our results showed that the shortest photoperiods and the lowest temperatures prolonged the development time of immatures. However, there were no significant differences among emerging individual performance in terms of survival and adult longevity. These results suggest that *A. colemani* remain active during the winter and may therefore act as biological control agent against aphids (also active during the winter) in winter cereal fields from Chile.

*Speaker

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Effects of environmental constraints on the fitness and physiology of a tenebrionid beetle, *Alphitobius diaperinus*

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Insects must cope with a combination of naturally and anthropogenically changing conditions in their environments. To successfully maintain fitness and performance throughout their life, they have developed behavioral and physiological responses that allow them to try to maintain their performance when the conditions are largely suboptimal. Nowadays, however, insects are increasingly exposed to stressful conditions, and new environmental stressors, including pollutants. Investigations of the effects of environmental variations, and combination of environmental stressors, on the physiological responses of insects are rare. In particular, the long term consequences of physiological adjustments and energetic costs developed during stress exposure on the subsequent fitness are understudied. Here, we investigated the effects of environmental variations (daily heat periods), and anthropogenic pollution (exposure to the insecticide Cyfluthrin), and the combination of these two stressors, on the survival, physiology (antioxidant capacity and metabolite composition), and reproduction (number of offspring per female) of *Alphitobius diaperinus*. We hypothesized that repeated heat or insecticide exposures would cause body reserves to decline with increased number of stress exposure events, as body reserves should be used for fueling the repair of injuries. These costs are expected to have a negative effect on the number of offspring, but as stressful environments can result in an increased reproduction response, the outcome can be driven by the nature of the counteracting effects at play. This study therefore shows not only the physiological response to environmental changes in these insects, but increases much needed knowledge of the fitness effects of such changes.

*Speaker

ATP synthesis and mitochondrial efficiency: the forgotten elements in the metabolism – body mass relationship

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In ecology, a lot of studies have been conducted on the relationship between body mass and metabolism, using oxygen consumption as proxy of metabolism rate. They showed in mammals, that specific oxygen consumption (per mass unit) negatively correlates with body mass. In cells, oxygen is used by mitochondria via the oxidative phosphorylation to provide cellular energy (ATP), essential for individual performances (growth, survival and reproduction). Nevertheless, 20 – 30 % of all the oxygen consumed are not converted in ATP but serve to compensate energetic losses arising from this biochemical process, known as "proton leak". Consequently, it seems obvious that oxygen consumption without considering intensity of this proton leak does not allow the best estimation of the real quantity of ATP produced, available for individual performances. The aim of our study is to revisit the relationship between metabolism and body mass. We measure ATP synthesis and oxygen consumption of mitochondria isolated from mammalian muscles (bull, boar, nutria, golden and European hamsters, wild rat, African mice...) in order to estimate their mitochondrial efficiency (ATP/O) and study its dynamic with body mass. Many authors found in mammals that proton leak negatively correlates with body mass, suggesting that smallest ones have lower mitochondrial efficiency combined with a weaker ATP synthesis. After phylogenetic correction (Phylogeny Independent Contrast), our data reveal that oxygen consumption and ATP synthesis decrease with increasing body mass in mammalian muscle mitochondria. Mitochondrial efficiency, on the other hand, remains surprisingly constant, implying that it could be one of rarely metabolic functions independent with body mass. These results highlight the necessity to incorporate both ATP synthesis and mitochondrial efficiency in the relationship between metabolism and body mass and to revisit theories based only on oxygen consumption to estimate metabolic rate of individual.

*Speaker

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Eco-physiological aspects of cold tolerance plasticity in *Drosophila suzukii*

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The Spotted Wing *Drosophila* (SWD) is a major invasive insect pest of soft fruits in Europe. The knowledge gap regarding its low temperature biology and overwintering strategies prevents the construction of accurate population dynamics models. In particular, the mechanisms by which SWD modulates cold-tolerance during lifetime in response to environmental variables (i.e. acclimation response) are still largely unknown. We studied how pre-exposures to low temperature during ontogeny and/or during adult stage affected subsequent cold tolerance of SWD. We found that acclimation induced high plasticity in cold tolerance of SWD. Here, we synthetically report some of the physiological mechanisms underlying these acclimatory responses (based on Omics data). Metabolomics revealed that metabolites with supposed cryoprotective functions (sugars, polyols) were mobilized in acclimated SWD. Time-series metabolomics showed that acclimated SWD had the capacity to maintain metabolic homeostasis under cold stress situation, while chill-susceptible counterparts did not; this suggests that acclimation allows metabolic robustness. Loss of metabolic homeostasis in chill-susceptible phenotype may be partly explained by cold-induced protein degradation that releases free amino acids (through proteasome activity), a phenomenon not observed in acclimated flies. Lipidomics showed that acclimated flies modulated phospholipids composition of membranes, likely to better deal with cold-induced rigidifying effects. As found in many species, SWD exposed to prolonged cold stress displayed a typical and gradual loss of ion homeostasis (K⁺). RNAseq comparing cold acclimated vs control SWD detected extensive transcriptional changes and functional annotation found many GO-terms, among which the most significant were linked to ions' transport. Altered expression of genes functionally related to ions transport during cold acclimation is likely an adaptive response to prevent loss of ions homeostasis at low temperature. Collectively, these data show that SWD possesses a great toolkit of strategies to deal with low temperature stress via plastic and physiological responses.

*Speaker

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Adaptive and non-adaptive divergence in wild fish populations under global change

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One major aspect of global change is the rapid change in land use around aquatic systems, causing strong alterations of habitat and water quality for fish. However, it remains unknown whether fish populations could show adaptive phenotypic divergence in response to such new environmental conditions. First, we compared the level of population divergence in 17 wild populations of gudgeons *Gobio occitaniae* from urbanized, agricultural and natural rivers of the Garonne watershed in France. Comparisons of their morphology, coloration, body condition, and parasite load highlighted a significant phenotypic divergence on several traits, such as a more robust body shape and a higher body condition in gudgeons from disturbed areas compared to non-disturbed areas. Interestingly, a *Pst-Fst* approach showed that this divergence was higher than the neutral genetic divergence expected under a neutral scenario for most traits. This confirms that divergent selection might influence phenotypic but also physiological variation among populations at a small geographical scale. However, it is not possible, at this stage, to disentangle the genetic and plastic components of this divergence. In a second part, we used a reciprocal transplant experiment in four populations from disturbed and non disturbed sites to compare the plastic responses of populations having evolved in contrasted environmental conditions. Results show some population-by-environment interactions, suggesting that the level of phenotypic plasticity also differ between populations exposed to contrasted anthropogenic disturbances in rivers, although further work is needed on F1 and F2 fish to confirm these results. With this study, we hope to bring new insights in the consequences of local anthropogenic disturbances on the evolutionary trajectories of wild fish populations.

*Speaker

Torpor-Migration convergences and emerging rules about adaptation to seasonality

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A component of climate change is the decrease in the predictability of climate, with an increase in climatic variations between years, and more unusual (extreme) events. Organisms capable of rapidly modifying their characteristics (phenotypic flexibility) in response to changes in environments are likely to be endowed with physiological and behavioral mechanisms that make them less sensitive to climatic anomalies. I will explore this hypothesis from a synthesis of the literature on the regulation of two extreme adaptations of endothermic vertebrates to seasonal climatic harshness: torpor use and migration. Heterothermic endotherms are able to reduce their metabolism and body temperature during episodes of energy stress, such as reductions in food availability, either optionally from one day to the next (daily torpor) or in a sustainable manner (hibernation). A completely opposite strategy is to migrate, i.e. to avoid the energetic constraint by movement, again either optionally (partial / differential migration) or systematically (long-distance migration). A systematic comparison of torpor and migration is currently missing, although both seasonal adaptations involve strikingly similar physiological convergences. I will present a review of torpor-migration main convergences (and divergences), with extensions about their potential role (particularly as source of phenotype flexibility) for the compensation of climate-driven environmental fluctuations.

*Speaker

Metabolic flexibility and tracheal morphology impacts on newly invasive insect thermal limits under oxygen limitation

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The recent host shift of the indigenous longhorn beetle *Cacosceles newmannii* (Coleoptera: Cerambycidae) from indigenous vegetation onto sugarcane in the KwaZulu-Natal Province of South Africa has resulted in widespread concern surrounding its pest status due to severe crop damage and significant economic losses for growers.

This dramatic host shift can be attributed to several potential mechanisms that include both abiotic and biotic factors. Since temperature is a key environmental driver of insect population dynamics and distribution, it is important to characterize the thermal tolerance of this emerging pest.

Here we tested a predominant hypothesis about the mechanistic cause of death at high temperature (i.e. oxygen- and capacity-limited thermal tolerance theory). To understand the scope of support for this hypothesis, we used insect life stages variations as a model system (larva vs adult). We first examined the upper critical thermal limits (CT_{max}) to activity and survival of insects in a set of respirometry experiments using two different gas mixtures (normoxia and hypoxia). This study shows that despite a supposedly less constrained environment, adults have a much greater flexibility than larvae. Although similar in their thermal maxima at normoxia, larvae have a more pronounced hypoxia-induced reduction in CT_{max} than adults, but seem to be able to maintain a similar maximum metabolism under both gas mixtures. Further, we investigated the scaling relationship between tracheal structures and thermal resistance under hypoxic conditions. These results were linked with preliminary measurements of total tracheal volume using high-resolution micro-CT scans of adults and larvae.

Part of the ongoing research is now to investigate the physiological mechanisms behind hypoxia tolerance using several molecular techniques such as metabolomics or RNAseq.

*Speaker

Ecophysiological modeling of the impact of light quantity and quality on microalgae growth in high-density open ponds

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Light is one of the main factors affecting the growth of phytoplankton, both at a quantitative level (total irradiance, usually measured by the photosynthetically active radiation or PAR) and at a qualitative level (spectral composition). In aquatic environment, both light quality and quantity vary through the water column, due to light attenuation by water molecules and suspended organic matter, including phytoplankton itself. This attenuation also affects the light quality since all the wavelengths are not attenuated in the same way. In open ponds dedicated to the production of high-density microalgal cultures, a similar process occurs but at a much shorter spatial scale (few cm). Although light is a crucial factor for improving microalgae cultivation technics, studies dedicated to the impact of light quality on phytoplankton growth remain scarce. In this study, we perform experiments on *Dunaliella salina* cultures in open ponds (raceways) placed in a greenhouse. In order to estimate the impact of light quality on microalgal growth, the cultures were exposed to different light conditions using coloured filters. In parallel, we developed a growth model for microalgae cultivated at high density in open ponds. The originality of this model was to take into account both quantity and quality of incoming light. The experimental data were used to calibrate the model. For each spectral light condition, the model was able to reproduce the temporal evolution of algal biomass. The variability observed between the different light conditions was also reproduced. Our results show that the highest productions were reached in the open ponds with the strongest incoming light intensity. Moreover, the model predicted a better conversion yield of light energy under green light conditions. In the future, this model could be used to choose filters allowing an optimal growth of microalgae, to enhance the production of valuable chemical compounds.

*Speaker

Phenotypic plasticity of arctic charr *Salvelinus alpinus* at the individual and population scales in response to co-occurring environmental stressors during development

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Temperature is a key driver of many biological processes in aquatic ecosystems and plays as such a determinant role in development, growth, and metabolic rates of ectotherms. Although temperature is of crucial influence, freshwater biota is facing numerous distinct pressures that ought to be considered combinedly as the co-occurrence of several stressors might lead to additive or synergistic interactions.

The arctic charr (*Salvelinus alpinus*) is a stenothermic cold-water salmonid that is widely distributed in subarctic regions. In alpine and peri-alpine lakes, the charr lives at the Southern edge of its native range and seems highly vulnerable to climate change. Due to their inability to migrate to find more suitable environments, charr eggs and juveniles are particularly exposed to an array of environmental pressures such as pollutants or fine sediments that temperature might interact with.

Here we use a common garden approach to i) investigate individual phenotypic variation in early life in response to environmental constraints, and ii) explore how temperature might modulate the impacts of fine sediments, another common stressor in freshwater environments, on life history traits. We compare four arctic charr populations originating from thermally contrasted lakes by rearing embryos at an optimum or stressful temperature and in the presence or absence of a realistic sediment load. We link inter- and intra-population differences in fitness-related traits at hatching and physiological markers related to oxidative stress in order to investigate existing trade-offs between life history traits.

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We report a synergistic interaction between our stressors such that temperature exacerbates strongly the negative effects of sediments on survival and energy expenditure during development. Charr populations respond differently to temperature increase, exhibiting differences in life history traits plasticity although the performance of individuals seems globally reduced.

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*Speaker

The expression of phenotypic plasticity of different fitness related traits in multi-dimensional environments

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Understanding the way individuals react to new environmental pressures has become crucial to assess the impacts of global change. Phenotypic plasticity is recognized as a central factor in mediating individual fitness, by allowing organisms to rapidly adjust to a wide array of new environments. Yet, understanding the role of environmental drivers in determining phenotypic plasticity remains largely unclear, especially in natural populations. Indeed, the phenotypic expression of traits results from the influence of multiple environmental gradients in interaction with individual genotype. In this study, we aimed at disentangling the effects of two environmental variables (temperature and nutrient level) and the genotype, as well as their interactions, on the expression of phenotypic plasticity. In microcosms, we submitted 15 distinct, clonally reproducing genotypes of ciliate protists (*Tetrahymena thermophila*), to a combination of 5 temperature and 5 nutrient levels, and quantified phenotypic traits linked to the demography (growth rate), the morphology (size and shape) and the movement (speed and linearity) of the individuals. Statistical models including these factors explained more than 70% of the variance in the phenotypic response and allowed us to compute three-dimensional reaction norms representing the overall impact of both environmental factors. The mean plastic responses to temperature and nutrients were consistent with the literature, but their impacts were largely independent, and their interaction was systematically negligible. However, their respective interaction with genotype was significant for several traits, indicating that phenotypic plasticity was indeed variable. We also found that the response of traits linked to movement varied greatly with genotype, while those of traits linked to demography or morphology, which are subject to stronger selection pressures, were more consistent across all genotypes.

*Speaker

Effect of the environment on life-history traits in *Drosophila suzukii*

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The life-history traits of organisms can be driven by the environment. Specifically, the nutritional composition of resources can influence life-history traits in insects. In *Drosophila*, the ratio of protein to carbohydrate (the P:C ratio) strongly influences life history traits. However, natural resources used by *Drosophila* species vary in many other factors. We compare how well P:C ratios of fruit resources predict life history traits in *D. suzukii*, relative to other measures of fruit composition and fruit identity, which integrates all aspects of the resource. We evaluate how 12 different fruit purees influenced life-history traits in *D. suzukii*. Fecundity (eggs laid in 24 hours) on each fruit medium was measured in a choice and a no-choice environment. We also evaluated development time, the rate of survival from egg to adult, and the total number of adults as an estimate of total fitness. We then test whether fruit identity, composition or P:C ratio best predict *D. suzukii* life history. Fruit influenced the entire life cycle, including oviposition and larval performance as well as the number of adults produced in the next generation. Variation in these traits is best explained by fruit identity, then

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composition, and lastly by the P:C ratio. These results highlight the importance of considering a resource as a whole. Considering only the ratio of protein to carbohydrates is not sufficient for understanding variation in key life-history traits.

Variability of fish population responses to multiple stressors

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Aquatic organisms face multiple challenges in human-altered rivers such as abiotic (e.g. contamination) and biotic (e.g. pathogens) stressors. Defense mechanisms against these stressors are likely to interact strongly but their interacting effects are still understudied, hindering our ability to predict the responses of wild populations to multiple stressors. In addition, recent studies bring very variable results depending on the populations and biological level of organization studied. In this study we hypothesized that populations of fish would display contrasted sensitivity to stressors depending of their past history in their natural environment (local adaptation). More specifically, we tested: i) how an experimental exposure to trace metals could affect the response of wild fish across biological levels (immunity, body condition, behavior) and, ii) how the past history of exposure to metal pollution would affect their plastic responses to the experimental contamination? To address these questions we selected 5 wild populations of gudgeons (*Gobio occitaniae*) along a contamination gradient of trace metal elements (TM's) in the Garonne watershed. Fish immune and behavioral responses were measured throughout exposure to an environmentally relevant mixture of TM's (Cd, Cu, and Zn) and standardized antigen injection mimicking a parasite attack (full factorial design).

We predict that the exposure to combined immune and contaminants stressors would influence mostly labile traits such as behavior and physiology through shifts in energy allocation for investment in detoxification process and immune responses, which could lead to immunotoxicological effects. We also predict that populations originating from the most contaminated areas will be better able to cope with the experimental contamination than control unpolluted populations. Such studies will improve our understanding of the high variability in sensitivity to contamination observed in wild populations and will help anticipating the effects of human-induced stressors in aquatic organisms.

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Do aphids alter leaf surface temperature patterns during early infestation?

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Arthropods at the surface of plants live in particular microclimatic conditions that can differ from atmospheric conditions. The temperature of plant leaves can deviate from air temperature, and leaf temperature influences the eco-physiology of small insects. The activity of insects feeding on leaf tissues may, however, induce changes in leaf surface temperatures, but this effect was only rarely demonstrated. Using thermography analysis of leaf surfaces under controlled environmental conditions, we quantified the impact of presence of apple green aphids on the temperature distribution of apple leaves during early infestation. Aphids induced a slight change in leaf surface temperature patterns after only 3 days of infestation mostly due to the effect of aphids on the maximal temperature that can be found at the leaf surface. Aphids may induce stomatal closure, leading to lower transpiration rate. This effect was local since aphids modified the configuration of the temperature distribution over leaf surfaces. Aphids were positioned at temperatures near the maximal leaf surface temperatures, thus potentially experiencing the thermal changes. The feedback effect of feeding activity by insects on their host plant can be important and should be quantified to better predict the response of phytophagous insects to environmental changes.

*Speaker

Understanding mechanisms of response to complex environmental conditions using model and non-model plants

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Understanding how organisms are able to respond to environmental challenges at different time scales is an essential component of deciphering the impact and long-term consequences of changing environment. This session on "Epigenetics, phenotypic plasticity and physiological ecology" provides examples of a variety of studies using classic experimental design to examine the importance of phenotypic plasticity and divergence under different conditions. In particular, the session highlights ecophysiological responses such as response to nutrient, temperature, light, and seasonality. Several studies describe the complexity of multiple environmental stressors and take advantage of the context of biological invasions or other components of global change. As an introduction, I will briefly show how our work uses similar experimental design to investigate the molecular level response to complex environmental challenges. Our recent studies rely on rapidly developing genomic tools from model plants grown in controlled conditions, which can now be used to examine the mechanisms of phenotypic response in a broad array of wild organisms and biologically relevant conditions. My lab group uses reduced representation bisulphite sequencing and transcriptomic approaches to explore the potential role of genetic and epigenetic processes in natural and controlled studies of native and invasive salt marsh species like *Spartina alterniflora* and Japanese knotweed. We also leverage the power of the eudicot *Arabidopsis* and monocot *Brachypodium distychum* model plant species to confirm our findings in these non-model plants. Combined these studies will enhance our understanding of how genetic and epigenetic variation interact in response to environment on different time scales, and ultimately contribute to adaptation.

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Artificial light at night causes stress and disturbs reproduction of common toad during breeding period

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Since the last century, the terrestrial globe is facing a "global decline of biodiversity": its sixth mass extinction. Such losses are considerable, as they may have profound consequences on ecosystem's function. Among these, amphibians are particularly affected in terms of population size and diversity. The global Amphibian Assessment revealed that one third of amphibian's species are currently threatened with extinction. Several anthropogenic factors have been identified likely to contribute to such a decline, but one of the currently fastest growing, +6% increase per year, is nocturnal artificial light at night (ALAN). ALAN, resulting from cities development, industrialization and transport infrastructures, is a worldwide phenomenon, as 18.7% of the Earth surface is exposed to brightness levels higher than natural thresholds (Gaston et al., 2013). ALAN leads to alterations of photoperiod, the main driver of daily and seasonal rhythms synchronization. As a consequence, it may affect individual's behavior and physiology by altering processes, such as endocrine regulation, metabolism, motor activity and foraging rhythm. In a previous study, we showed a 75% decrease motor activity of common toads (*Bufo bufo*) exposed to ALAN, which could impact their reproductive behavior (Touzot et al., submitted). Here, we experimentally exposed breeding male toads to three low realistic intensities of ALAN (0.01, 0.1 and 5 lux) and measured the effects on stress level, testosterone and fertilization rates. After twelve days of exposure, corticosterone levels significantly increased when light intensity was above 0.1 lux. Moreover, male pairing success, exposed to ALAN, was delayed. Finally, at 5 lux, toads testosterone rate dropped by about 10%, which triggered a drastic reduction (25%) of the fertilization rate. Those results may have a major ecological impact on the reproductive success at populations scale, emphasize the impacts of ALAN on organisms and bring novel insight into the mechanisms involved in amphibian's global decline.

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Evolution

Small scale spatial variation in the patterns of ageing in a wild population of the meadow viper (*Vipera ursinii ursinii*).

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Senescence, the inexorable and progressive deterioration of an adult organism with advancing age, has been found to affect many organisms and it was considered to be almost universal until recently (1). Under certain conditions, natural selection may be sufficient to delay or render undetectable this degradation with age (2). Snakes may be good candidates for the evolution of negligible senescence because reproductive output usually increases with age while some extrinsic causes of mortality can decline with adult size.

We use data collected during 38 years on a meadow viper (*Vipera ursinii ursinii*) population (3²⁵) to study if negligible senescence can be detected in the wild in this species. The effects of age on reproduction have been studied by taking into account the effect of body length, which varies with age. The effect of age on adult survival has been studied using Bayesian survival trajectory analyses (6).

We found that most reproductive traits benefit from negligible senescence and found that senescence on survival was either negligible or positive depending on sex and small scale spatial variation of environmental conditions.

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Hybrid speciation, reproductive isolation and adaptive radiation along an elevational gradient in an alpine butterfly

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Speciation with gene flow is more common than previously thought, but the mechanisms by which phenotypic divergence and reproductive isolation arise are poorly understood. Furthermore, the role of hybridization in species diversification and adaptive radiation is debated. Approximate Bayesian Computation procedures based on a large SNP dataset suggest that the Darwin's Heath (*C. darwiniana*) is a hybrid species between the Pearly Heath (*C. arcania*) and the Alpine Heath (*C. gardetta*) with different parental contributions, dating back $\simeq 10,000$ years ago. The hybrid lineage presents an intermediate morphology between the parental species, while its climatic niche is more similar to the alpine species *C. gardetta*. Unexpectedly, although the hybrid genome is mostly constituted of the lowland species genome (70% *C. arcania* and 30% *C. gardetta*), introgression rates in contact zones were much higher between the hybrid lineage and the high altitude species *C. gardetta* than with the lowland parental species *C. arcania*. Interestingly, the alpine species emit volatile compounds (Octadecanal, Octadecanol and Eicosanal) that are also present in the hybrid lineage, but absent in the lowland species, suggesting pre-mating isolation mechanisms between the alpine and lowland species through olfactory cues. Evidence for local adaptation to cold temperature was found by measuring higher warming-up rate (thorax temperature in controlled conditions) with increasing elevation in the lowland and hybrid species. The alpine species *C. gardetta* had the highest warming-up rate, suggesting that temperature is a main driver of adaptive radiation along elevational gradient in this butterfly alpine species complex.

*Speaker

Contagious asexuality in the pea aphid and its evolutionary consequences

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Asexual lineages occur in most groups of organisms and arise from loss of sex in sexual species. Yet, the genomic basis of these transitions in reproductive modes remains largely unknown. We addressed this issue in the pea aphid where both sexual and obligate asexual lineages coexist in natural populations. These lineages may occasionally interbreed because some asexual lineages maintain a residual production of males potentially able to mate with the females produced by sexual lineages. We combined quantitative genetic and population genomic approaches to unravel the genetic control of shifts towards permanent asexuality in the pea aphid. We found that permanent asexuality was determined as a recessive character by a single locus and identified a 2.5 Mb genomic region responsible for this transition located on the X chromosome. Also, our population genetic data indicated substantial gene exchange between these reproductively distinct lineages, potentially leading to the conversion of some sexual lineages into asexual ones in a contagious manner. We are currently narrowing down the size of the control region and investigating patterns of coding and non-coding polymorphisms within and outside the causal locus in sexual and asexual lineages. This genetic system provides insight into the mechanisms of coexistence of sexual and asexual aphid lineages and on the genomic footprints of reproductive mode variation.

*Speaker

Parthenogenesis in ladybirds (Coccinellidae: Coleoptera): a new model for the study of asex?

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Parthenogenesis, the development of eggs without fertilization resulting in the exclusive production of female offspring, is rare in animals and found predominantly in invertebrates. Polyploidy and hybridization of parents with different genomes as well as endosymbiont infections are often considered as its major causal events but the mechanisms triggering off asexual reproduction remain unclear.

Here we study the proximate causes at the origin of parthenogenesis in a first reported case of asexuality in the Coccinellidae (Coleoptera). The asexual populations were found in distant insular regions – the Macaronesia and the Mascarene – and were identified as *Nephus voeltzkowi* Weise, a bisexual species widespread in sub-Saharan Africa. Specimens from each population are diploid but present different karyotypes, composed respectively of 14 and 17 unmatchable chromosomes that evoke different hybrid origins. However, the great proximity of their genomes (99.8 % homology for the complete mitochondrial genome and 99.9 % for the complete nuclear ribosomal cluster), discards this interpretation. We propose that they belong to a single chromosomally polymorphic species undergoing Robertsonian fusions. It remains to be studied if these translocations are a pre- or post-parthenogenetic event. Furthermore, specimens from both populations are infected with *Wolbachia* bacteria, contrary to bisexual species of the same genus. Although *Wolbachia* was shown to induce parthenogenesis in haplo-diploid organisms, it has been recently suggested it could induce parthenogenesis in hosts with other sex determination systems.

Parthenogenetic individuals from the South-Western Indian Ocean might have attained the

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Macaronesia by the hand of man: the two regions have been in contact since the 16th century, as they housed important ports of call of the Portuguese mythic round ward voyage "*Carreira da Índia*".

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Recovering the complexity in scientific knowledge: towards automatically reconstructing the maize floral transition gene regulatory network

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In annual plants, flowering time is a highly integrated life-history trait which summarizes growth and development. We used plants issued from two independent divergent selection experiments on flowering time in two maize inbred lines. One of the trait that was targeted by selection was the timing of floral transition, that occurs early during maize life-cycle. RNA-Seq data from shoot apical meristems of Early and Late genotypes sampled before, nearby and after floral transition revealed thousands of genes that changed their expression throughout time. The inventory of these genes was different between ancestral genetic backgrounds, but also between Early- and Late-flowering genotypes derived from the same ancestral inbred. The number of differentially expressed genes was much higher than expected from the level of genetic polymorphism between Early and Late populations, suggesting the existence of hubs in the maize floral transition Gene Regulatory Network (GRN).

The description of the GRN cannot be achieved through statistical analyses because of lack of power in transcriptome data, nor by functional analyses of gene ontologies, that do not account for regulations and interactions. Here we present a text-mining approach that aims not only at automatically collecting data from the scientific literature, but also at organizing them in terms of causal relationships. This approach relies on the design of a model of knowledge that enumerates possible entities like genes, metabolites, phenotypes and environmental factors that could belong to or alter the GRN, and describes their possible interactions. In collaboration with computer

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scientists, we are adapting an existing knowledge model developed for *Arabidopsis thaliana* seed development to address the question of *Arabidopsis* floral transition, the GRN of which is well known. After having proved the concept in *Arabidopsis*, the next step will be to adapt the model to maize.

Life history traits impact the nuclear rate of substitution but not the mitochondrial rate in isopods

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Life history traits are expected to be a major driver of substitution rate variation among species. However, the relative contribution of each trait to this variation is poorly understood. Here, we intend to disentangle the relative influence of life history traits using a group of isopod species that have made multiple independent transitions from surface to subterranean environments. Species having undergone this ecological transition have evolved a lower metabolic rate, a longer lifespan and a longer generation time. We assembled the nuclear transcriptomes and the mitochondrial genomes of 13 pairs of closely related isopods, each pair being composed of one surface and one subterranean species. Based on a total of 382 nuclear and 12 mitochondrial orthologous genes, we found that subterranean species have a lower rate of nuclear synonymous substitution while the mitochondrial rate did not show any consistent trend in rate variation. This unexpected result suggests that the rate of molecular evolution of these two genomes is influenced by different factors. We propose that this decoupling between nuclear and mitochondrial rates comes from different DNA replication processes in these two compartments. In isopods, the nuclear rate is probably tightly controlled by generation time alone. In contrast, mitochondrial genomes would replicate and mutate at a rate independent of life history traits. These results are incongruent with previous studies, which were for the most part devoted to vertebrates. We suggest that this incongruence can be explained by developmental differences between animal clades, with a blockage during female gametogenesis in mammals and birds, as opposed to a continuous gametogenesis in most arthropods.

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Reproduction in kelps: consequence for resource management and aquaculture

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In the coasts of Europe, habitat-forming brown seaweeds like kelps often dominate marine habitats, creating highly productive and diverse communities comparable to forests. Environmental changes and human activities seem to threaten critically these marine forests resulting in wide populations' declines and distribution shifts. We used different complementary approaches on large brown seaweeds from the different fields of ecology, genetics and evolution to address the questions of local adaptation, landscape genetics and ecology. Kelps are characterized by a two-phase reproductive life cycle: A generation of large diploid individuals (the sporophytes) produces by meiosis spores that will differentiate into microscopic dioecious haploid individuals (male and female gametophytes). A direct consequence of this type of cycle is the effect of selection that will tend to purge rapidly the deleterious alleles within the haploid generation. Our study aims to deepen knowledge about the reproduction of this species. The question that arises here is that of the variation of the compatibility of crossbreeding between individuals according to their similarity and of the selective value of their descendants since the reproduction between genetically too similar individuals would suffer from an accumulation of deleterious mutations (Inbreeding depression) whereas the crossing between too different individuals would cause a rupture of the adaptive complexes (outbreeding depression). While the effect of genetic distances between parents on reproductive success is commonly studied in higher plants, this is still very little known in algae. In addition, kelp responses to temperature at range limit compared to core populations were compared both in the field and under controlled conditions suggesting that parthenogenesis is more likely to arise at the range limits, where populations are sparse, fragmented, and more prone to local extinctions. This knowledge has important consequences on the management of natural resources and on the development of aquaculture.

*Speaker

Highly convergent co-evolution of bacterial predators and prey

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Predation is widespread in all ecosystems and is integral to many ecological and evolutionary processes including population dynamics, extinction rates and speciation. Beyond large eukaryotes, predation is also found among bacteria and may play a major role in shaping the composition and evolution of microbial communities. Among bacterial predators, *Myxococcus xanthus* preys upon a wide range of microbial species using a unique predation strategy based on the combination of several social behaviors. Experimental evolution is a powerful way to explore the evolution of bacterial interactions and to investigate the resulting genetic and phenotypic adaptations. We established an experimental co-evolution system with *M. xanthus* as predator and *Escherichia coli* as prey in which the prey grew on a carbon source (glucose) that the predators cannot utilize, such that they depend solely on prey consumption for survival. After ~200 prey-generations of evolution we found evidence of adaptation by both predators and prey, which exhibited fitness advantages over their ancestors and evolved controls. Such adaptation appears to be specific to the predator-prey interaction as the coevolved populations were not fitter compared to controls in the absence of their partner. Moreover, both prey and predators exhibited strong signatures of convergent genetic evolution. In *E. coli*, the gene coding for the protease *ompT* was mutated or deleted in all but one coevolved populations and in none of the control populations that evolved in the absence of predators. Deletion of *ompT* in the prey ancestor resulted in a fitness advantage only in the presence of predators. Reciprocally, in *M. xanthus*, the uncharacterized gene *Mxan_5760* was mutated or deleted in all coevolved populations but not in control populations. These experiments highlight the importance of predatory interactions in microbial evolution and open opportunities for more complex experimental studies of microbial food-web evolution at multiple trophic levels.

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Global Changes and Biodiversity

Temporal turnover in weed biodiversity in highly anthropogenic habitats

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During the last decades, agricultural intensification has led to a loss of biodiversity in farmland landscapes, with a decline in all taxa. Despite a general increase in yields, this intensification has also affected ecosystem functioning and the provision of services such as pollination and pest regulation. In this context, studying the temporal dynamics of weed diversity in farmland landscape is interesting as weeds are the basis of food webs, providing resources to many living organisms. In this study, we address two questions: (1) what is the underlying level of weed temporal turnover in a community, and (2) is weed biodiversity changing relative to this background turnover, due to a local management in fields (e.g. herbicides use or crop rotation) and/or to change in landscape composition and structure (e.g. loss of semi-natural habitats or presence of organic fields)? We use flora surveys performed in arable fields in the LTSER Zone Atelier 'Plaine & Val de Sèvre' from 2006 up to now (more than 2000 surveys). Since distinguishing among the various sources of change is challenging, we assess weed temporal turnover through combining several diversity indexes such as Simpson index, species-exchange ratio and dissimilarity matrices. We discuss our results in the context of global change.

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Biodiversity and ecosystem functioning under global change - Meta-analysis of litter decomposition and consumer diversity responses across global change drivers

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Environmental change affects ecosystem functioning through both biotic and abiotic processes. The biodiversity-mediated effect of global change on ecosystem functioning has received a lot of attention in ecological literature, mostly based on experiments manipulating biodiversity directly and randomly. Yet, under the influence of environmental change, the importance of the biodiversity-mediated effects could be offset by non-random shifts in biodiversity, changes in community composition and in species contributions to function, and abiotic processes. It is thus crucial to re-introduce environmental change into biodiversity-ecosystem functioning research.

In this synthesis, we focused on litter decomposition as a key process fueling ecosystems, and jointly determined by the diversity of saprotroph organisms and by abiotic factors sensitive to the influence of environmental change drivers. We aim to quantify the relative magnitude of the biodiversity-mediated effect on litter decomposition of a range of global change drivers, including chemical stressors that are currently overlooked drivers of global change. We used data from published records that measured the impact of two contrasting types global change drivers; resources (nutrient, CO₂) and stressors (chemicals, acidification, warming, drought) on both consumer diversity and litter decomposition. We assume that the two types of drivers have different effects with stressors decreasing both biodiversity and function, while resources are predicted to decrease biodiversity but to increase function.

Using the correlation between biodiversity and decomposition within study as an effect size, preliminary results show the contrasting impacts of resource enrichment (no overall diversity-function relationship) and chemical stressors (significant positive relationship). We will use structural equation modeling of the responses of decomposition and diversity to environmental change intensity to quantify the relative magnitude of the biodiversity-mediated effect. These findings represent an important conceptual advancement in biodiversity-ecosystem functioning research by re-introducing the environmental factors that drive biodiversity in the first place, providing crucial insights for both scientific and management purposes.

*Speaker

Rethinking Ecology, a new journal fostering new thinking in ecological research

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Rethinking Ecology is a new open access, peer-reviewed journal that aims at fostering both forward-thinking and the publication of novel ideas in all aspects of ecology, evolution and environmental science. *Rethinking Ecology* is an opportunity to publish novel ideas and hypotheses prior to fully testing them. Our aim is to encourage scientists to share and discuss their novel ideas with their peers without fear of losing the credit they deserve. The publishing of these ideas at an early stage has the potential to draw attention from the scientific community, help create research networks with other interested parties, support grant proposals, and help refine the idea before testing it experimentally. The aim of *Rethinking Ecology* is therefore to be an incubator for novel ideas, and a catalyst for new thinking. This role is particularly important in conservation science where urgent innovation is required to stem biodiversity loss.

During its first year of existence, *Rethinking Ecology* has published papers contributing to advancing ecological research by recommending new definitions, proposing new avenues of research, exploring new tools for conservation, fostering discussions on previously published research, and proposing better ways to fund scientific research.

This presentation will outline and discuss the core values of the journal which have been hot topics in recent the past two years, in particular the tackling of biases associated with single blinded reviews, the gender bias, the issues with peer-review funding panels, or the co-authorship black box.

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Subalpine grass species are directly fertilized by atmospheric nitrate

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Mountainous grasslands are vulnerable to nitrogen (N) atmospheric deposition because of little acidification buffering capacity in soils and optimized N uptake strategies of native plants in response to historical nutrients limitation. Here, we investigated the sources of N to two typical grass species in the French Alps meadows (*F. paniculata*, *D. glomerata*), using the triple isotopes ($\Delta^{17}\text{O}$, $\delta^{18}\text{O}$ and $\delta^{15}\text{N}$) of plant-tissue nitrate (NO_3^-). We demonstrate that this technique help to quantify, in the field, the direct contribution of atmospherically deposited NO_3^- to plant NO_3^- pool (up to 33% in our study). Distinct temporal patterns in NO_3^- isotopic composition in leaves and roots reflected the seasonal evolution of plant N uptake. Direct foliar uptake of atmospheric nitrate accounted for 3-16% of plant NO_3^- demand, a non-negligible pathway for N uptake in plants under natural conditions especially when growing on subalpine nutrient poor soils. We observed ^{15}N gradual enrichment of NO_3^- from soils to leaves which suggested the importance of NO_3^- assimilation in contributing to plant total N. This multi-isotopic approach has a unique potential to decouple atmospheric N input pathways into plant species and to better constrain its fate in the environment.

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Body size and climate change: contrasting effect of temperature anomaly along species thermal range in French birds

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Besides distributional and phenological shifts, body size reduction was recently proposed as one of the major ecological responses to climate change. However, the mechanisms underlying body size change are still poorly understood, and the direction of size change varies between studies (with reports of body size decrease, increase, or stasis). This may be because the direction of the thermal stress may differ between climatic regions. We predicted that morphological response to temperature fluctuations should vary within species ranges, depending on the relative position of the population within species' thermal niche. We tested the effect of spring temperature anomaly on juvenile body size, and whether this effect varied along an 11°C-thermal gradient in France (204 sites, representative of $58\% \pm 13$ SD of species thermal niches), for 9 songbird species ($n = 34,101$ individuals). For all species, warmer temperatures induced body size increase in juveniles that were located towards the cold edge of their thermal niche. As expected, this effect decreased towards the hot edge, becoming negative for two species. This may be due to the differing consequences of temperature change on both organismal thermoregulation, and ecosystem production and food availability. We therefore predict that warming should induce body size increases more frequently at the cold edge of species distribution ranges, and rather body size declines at the hot edge. Hence, future studies focussing on climate-driven changes in body size should consider the possibility of non-uniform responses within species ranges.

*Speaker

Adaptation to climate change and biodiversity in French forests: a love-hate relationship?

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France is highly covered by forests, upon which rely numerous jobs and natural habitats. Therefore, the country adopted a strategy of adaptation to climate change, leaning on a rich silviculture history to offer foresters various means to adapt (rotation shortening, species mixes, ...). Still, different adaptations can be interesting in a given forest, depending on the trade-off between ecosystem services: timber production, biodiversity conservation, water quality preservation, ... Hence, how do French foresters decide of the adaptation to implement? What are the impacts of their choices on biodiversity?

The following explores how adaptation in the field occurs – a complementary approach of providing better understanding of the impacts of climate change on forest biodiversity. It analyses how biodiversity is included in field adaptations, and how this concords with guidelines of sustainable forestry. Results come from semi-structured interviews led in two French forests differing in anthropization, making use of ecology and geographic sciences. The analysis discriminates two non-exclusive positions on biodiversity: "utilitarists" adapting thanks to biodiversity and "conservationists" adapting for biodiversity. Utilitarists rely on species selection or introduction of allochthonous species to resist windstorms or biological attacks for instance, a potential threat for local populations. On the opposite, conservationists favor Darwinian adaptation over interventionist strategies. Conservationists would for example prioritize spontaneous evolution, at the risk of tree species running short of time because of the speed of climate change.

These results are integrated in a wider project including natural parks managers for decision-taking in forest management. Because elements of biodiversity are deeply rooted in adaptation discourses, a serious game is currently being designed in order to assess what adaptation strategies foresters project – or not– in an uncertain climatic future.

*Speaker

Relationships between human activity and biodiversity in Europe at the national scale: spatial density of human activity as a core driver of biodiversity erosion

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Many empirical studies have analyzed the relationship between human activity and the environment. Some of these have focused on the potentially negative impacts of human activity on the environment. Some others have tried to identify socio-political variables that could be at play in this relationship. Herein, we used well-adapted statistical methods to study the relationship between human activity and biodiversity in Europe at the country level; we worked with classical biodiversity indicators (two state indicators, two pressure indicators and one re- sponse indicator) on the one hand, and socio-economic variables on the other hand. We found strong relationships between economic variables and pressure indicators (related to soil sealing) as well as state indicators (related to the proportion of extinct and threatened species). However, there was no relationship between economic variables and the response indicator (related to the proportion of protected area). Though we did find significant relationships between some sociological variables and biodiversity indicators, the best models all included economic variables. These results cast a new light on an old issue: first, they reveal the pertinence of a set of variables related to the spatial density of human activity – either through economic growth or population levels; they also show that the impact of the spatial density of human activity on biodiversity indicators tends to decelerate – but not to decrease – as the spatial density of human activity increases; finally, since past and current levels of biodiversity erosion are best explained by the spatial density of human activity more than one century ago, they indicate that development of human activity may affect biodiversity after a long delay. These results reveal the need for further studies involving these metrics.

*Speaker

Carbon stocks and fluxes across ecosystem and climate types

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Global changes impact different aspects of ecosystem functioning, such as biomass, or fluxes and rates of ecological processes, that likely cascade on each other. To understand how ecosystem state might move within a multifunctional space, we conducted a global quantitative synthesis of a wide range of ecosystem functioning metrics related to carbon stocks and fluxes. We gathered a total of about 4000 values from the literature of metrics including biomass and detritus stock, biomass production, ecosystem respiration, and decomposition rate across eight major ecosystem types (e.g., forest, grassland, stream) and five broad climatic zones (e.g., arctic, boreal, tropical). We analysed the global relationships among variables emerging from the variations of stocks, fluxes and rates across ecosystems and climates. Within this three-dimension space, average ecosystems align along a gradient from fast rates-low flux and stocks (freshwater and pelagic marine ecosystems) to low rates-high fluxes and stocks (forest). Moreover, fluxes and rates decrease from warm to colder climates, consistently with the metabolic theory of ecology. However, the strength of climatic effects differs among variables and ecosystem types, resulting, for instance, in reversed effects on net ecosystem production between terrestrial and freshwater ecosystems (positive versus negative effects). This large-scale synthesis provides new insights on ecosystem multi-functionality and useful information to eventually predict the inter-dependence among ecosystem stocks, fluxes, and rates, and their sensitivity to global change.

*Speaker

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Ecological functioning and Ecosystem evolution in mosaic forest-savanna and human presence context for 2000 BP at Lope National Park (Gabon)

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Lope National Park (LNP) is within the Guineo-Congolian phytogeographical region. This region is today probably one of the least known of the African continent in term of floristic composition and biodiversity, as well as its environmental settings. Surface sampling within many marshes showed that if it is possible to distinguish from pollen rain closed canopy signal and opened canopy signal, it is difficult to distinguish all the vegetation types. Davis Index gives us the following groups: **Associated taxa**: Those taxa are common in both vegetation assemblages and pollen assemblages. They are predominantly pioneer taxa such as *Aucoumea*, *Anthocleista*, *Barteria*, etc. Those taxa grow at the margin of the marsh, where there is the maximum of light; **Over-represented taxa** They are most predominant in the pollen assemblages than the vegetation assemblages. Those taxa are often synonym of a perturbation/shift in the environment such as savannah (*Cnestis*, *Annonaceae*, *Asystasia*), an anthropogenic opening in the canopy such as a road (*Alchornea*, *pentachletra*, etc), or an human establishment such as a village (*Elaeis guineensis*, *Pycnanthus angolensis*, etc.); **Weakly associated taxa** Those taxa are a mix of over-represented and under represented taxa. They are (*Asteraceae*, *Cassia-type*, *Cyperaceae* indéterminé, etc.). They correspond to taxa which grow together as a population, controversially to the other taxa mentioned above. Preliminary cores studies show a strong presence of taxa common in opened canopy landscapes.

*Speaker

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Lyallia kerguelensis, a Kerguelen endemic cushion plant from extreme environments in the face of climate change

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Rapid climate change is occurring in sub-Antarctic islands, mostly with temperature increase and loss of precipitations. The native sub-Antarctic flora is poor and composed of perennial and often long-lived plants, potentially more vulnerable to rapid environmental changes. Endemic species should be even more at risk. *Lyallia kerguelensis* (Montiaceae), an endemic cushion plant in sub-Antarctic Iles Kerguelen is particularly infrequent on the archipelago and specialized in certain habitats. Many cushions show more or less important necrosis. Our research aims at understanding the ecological and physiological limits of *L. kerguelensis* in its current range and predict the plant potential to respond to climate change. We aim to determine which environmental factors (abiotic, biotic) are most limiting for plant performance. Field studies covered wide distribution and ecological ranges of the species in Kerguelen. Plant performance was described by the extent of necrosis within cushions. In each studied population, we quantified topographic and geomorphological features, climate (meteorological and local climatic recorders), edaphic parameters (soil profile, water content, conductivity, pH, texture, elemental composition and nutrients), epiphytes in cushions and composition of the neighbouring community. To characterize the performance and morphology of cushions we developed a photointerpretation method using ArcGis. We made calibrated pictures on a sample of individuals from each population. Several views by individual were used to extract phenotypic traits. Morphological traits such as shape and compactness were calculated. Trait variability at intra- and inter-population levels and correlations to environmental factors were investigated. Finally, morphology and flowering phenology were monitored across 10 years in one population. The results are interpreted in the light of climatic data and provide a hint for the temporal scale of morphological changes in the cushions. As a whole, we found correlations between the proportion of plant necrosis in the populations and several abiotic factors all resulting in water stress.

*Speaker

Mass extinctions on the Earth in the past and hereafter: combined use of the progress in paleontology, cosmology, science on food, and engineering for their explanation and forecasting of the impending dangers and the ways of minimization of their harmful effect

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The Earth's species diversity from unicells to mammals depends not only on the time-scale but also on the natural conditions critically varying repeatedly over the Earth's history as a result of alternation of the periods favorable for flora and fauna development and periods of global or regional damaging natural phenomena of the terrestrial, solar, or cosmic origin. During the last 542 My, in the most devastating extinction, 80-90% of Earth's species disappeared and, in two most widely-known extinctions, dinosaurs and mammoths and many other plant and animal species were destroyed. The events, which had occurred repeatedly in the past, will surely happen hereafter, because no principal changes happened in nature. Basing on the PFO-CFO Theory of Solar System Formation and Transformations developed by us step by step in the last decade [1-3], we give a common explanation for these catastrophic phenomena [4, 5], predict the natural events that will precede the arrangement of conditions fraught with harmful consequences hereafter, and consider here the necessary prior scientific and engineering activities capable of minimizing the devastating effect of the next dangerous natural event.

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*Speaker

Global Changes and Biodiversity

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Struggling despite anthropogenic subsidies: Northern gannets in the English Channel

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Fisheries modify ecosystem balance, fishing through marine food webs, and producing large amount of discards subsidizing scavengers. Among them, seabirds are the most conspicuous and have been benefiting from anthropogenic food sources generated by fisheries. Yet this alternative feeding behaviour also exposes seabirds to new threats, such as accidental bycatch on fishing gear. Seabird-fishery interactions have been the focus of numerous studies, with a recent emphasis on seabird behavioural responses to fishing vessels. However, little is known about multi-annual dynamics in seabird-fishery interactions. To explore this facet, we performed GPS-tracking and stable isotopic analyses in Northern gannets (*Morus bassanus*) across a decade, during which they coexisted with fisheries in the English Channel. This allowed us to demonstrate that gannets favored fishery wastes when their natural prey (pelagic fish) became scarce, but that this dietary shift induced enhanced seabird foraging effort and reduced body condition. These changes were concomitant with reduced gannet reproductive success, and reduced growth rate of their breeding colony. Our work provides essential, novel understanding of scavengers-fisheries interactions, and confirms the detrimental effect of anthropogenic subsidies on seabirds. The ongoing discards

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reform of the European Union aiming at strongly reducing at-sea dumping of fishery waste will modify the foraging environment of marine scavengers. It seems essential to combine this discard ban with efficient rebuilding of pelagic fish stocks, which are a pivotal element of marine trophic networks and an irreplaceable food source for vulnerable seabird populations such as Northern Gannets in the English Channel.

Insular threat associations within taxa worldwide

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The global loss of biodiversity can be attributed to numerous threats. While pioneer studies have investigated their relative importance, the majority of those studies are restricted to specific geographic regions and/or taxonomic groups and only consider a small subset of threats, generally in isolation despite their frequent interaction. Here, we investigated 11 major threats responsible for species decline on islands worldwide. We applied an innovative method of network analyses to disentangle the associations of multiple threats on vertebrates, invertebrates, and plants in 15 insular regions. Biological invasions, wildlife exploitation, and cultivation, either alone or in association, were found to be the three most important drivers of species extinction and decline on islands. Specifically, wildlife exploitation and cultivation are largely associated with the decline of threatened plants and terrestrial vertebrates, whereas biological invasions mostly threaten invertebrates and freshwater fish. Furthermore, biodiversity in the Indian Ocean and near the Asian coasts is mostly affected by wildlife exploitation and cultivation compared to biological invasions in the Pacific and Atlantic insular regions. We highlighted specific associations of threats at different scales, showing that the analysis of each threat in isolation might be inadequate for developing effective conservation policies and managements. Nevertheless, human-driven species’ declines and extinction are usually evaluated solely from the taxonomic perspective missing both evolutionary and functional species’ characteristics. Considering complementary diversity components is a next crucial step to better assess and understand the structure and composition of species assemblages, and also to determine relevant conservation priorities for maintaining ecological processes in a global change context.

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Global biogeographical regions of freshwater fishes

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Two centuries ago, early biogeographers outlined six major biogeographic regions (Nearctic, Neotropical, Palearctic, Ethiopian, Oriental and Australian) on the basis of the distributions of organisms across continents. During recent years, these major regions have been confirmed by an upsurge in bioregionalisation studies. However, this upsurge befell exclusively on terrestrial vertebrates, which represent but a fraction of continental organisms. Here, we propose to investigate global biogeographical regions for a group of organisms with very peculiar and limited dispersal abilities: freshwater fishes. We define for the first time the hierarchy of kingdoms, regions and subregions of freshwater fishes by applying network methods on the recently published global database on freshwater fish occurrence. We compare freshwater fish regions to the well-known regions of other groups and discuss the processes that generated the observed regions. Specifically, we investigate transition zones between regions in order to determine whether freshwater fish were subject to the same processes of vicariance-dispersal as other continental life forms. Our results suggest that freshwater fish regions were shaped by similar events of vicariance and geodispersal than other groups but with freshwater-specific processes of isolation that led to extremely high degrees of endemism, specific boundary locations, and limited extent of transition zones. The extremely high endemism and diversity of freshwater fish regions urges their high vulnerability, and we show here, by comparing the historical (excluding introduced species) versus current (including introduced species) regions the consequences of the current global and massive rates of species introductions.

*Speaker

Characterisation of salvage logging as a concatenation of interacting ecological/anthropogenic disturbances

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Large disturbances increasingly affect forests around the world. As a result, increasing amounts of forest are subject to salvage logging –an intervention aimed at salvaging economic value of the forest and sometimes considered a means of ecological restoration. Understanding and managing the world’s forests thus increasingly hinges upon understanding the combined and interactive effects of natural disturbance and logging disturbance, including interactions so far unnoticed. Here, I disentangle and describe the mechanisms through which natural disturbance (e.g. wildfire, insect outbreak or windstorm) can interact with anthropogenic disturbance (logging) to produce unanticipated effects. For this, I apply recent advances in disturbance-interaction theory. First, many ecological responses to salvage logging likely result from interaction modifications–i.e., from non-additive effects between natural disturbance and logging. However, a systematic review encompassing 209 relevant papers showed that interaction modifications have not been the focus of empirical research to date. Second, salvage logging constitutes an interaction chain because natural disturbances increase the likelihood, intensity and extent of subsequent logging disturbance resulting from complex socio-ecological interactions. The existence of such an interaction contrasts with the typical plot-level research. Both interaction modifications and interaction chains can be driven by nonlinear responses to the severity of each disturbance. Sampling at different natural disturbance and/or logging intensity levels is necessary to understand such nonlinearities. Whereas many of the effects of salvage logging likely arise from the multiple kinds of disturbance interactions between natural disturbance and logging, they have mostly been overlooked in research to date. Interactions between natural disturbance and logging imply that increasing disturbances will produce even more disturbance, and with unknown characteristics and consequences. Disentangling the pathways producing disturbance interactions is thus crucial to guide management and policy regarding naturally disturbed forests.

*Speaker

How and how much does vegetation in drainage ditches depends on current environmental conditions ?

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Floodplains are currently heavily managed due to human occupation, uses for agriculture and tourism. Old histories of management include flood management and complex combinations of drainage and irrigation. Moreover, recent intensification may have caused changes in century old agro-systems. However, they often remain cases of human made systems where remnants of wetlands, extensively used and/or temporarily favourable areas combine into rich landscapes. Improving management for biodiversity considering all other uses requires a better understanding of the relationships between biodiversity and a complex set of environmental characteristics with strong internal interactions, and temporal and spatial variability.

The Marais poitevin on the French Atlantic coast has been managed for several centuries but major changes occurred in the 1950-60ies. A field approach of biodiversity patterns was developed and combined to inter-annual monitoring of environmental variables in order to address this challenge. Here we document patterns in biodiversity of the vegetation of ditches, a relatively simple community chosen because composed of a limited number of rather well known species, with strong relationships with fauna, and because users, via tourism and fishing activities particularly, are sensitive to its changes. It is highly impacted by all uses via water management. Four year monitoring data of the community allowed to assess the relevant scales of patterns and changes of biodiversity and determine the main relationships with environmental variables. Diversity resulted in both broad patterns due to the geological history of the flood-plain that determine soil and groundwater characteristics, and local processes. The predictive ability of models based on current conditions was limited, possibly due to interactions among factors, temporal lags, and unrecorded human activities. Results are discussed in relation to the management of the area, and strategies for agro-environmental schemes.

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§Speaker

Surviving in southern Mediterranean refugia: *Veronica aragonensis*, a rare endemic from the Iberian Peninsula

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The Mediterranean basin harbours the most important glacial refugia for flora and fauna. In particular, southern mountain systems have played an important role for the survival of plant biodiversity during the Quaternary **glacial** periods. In turn, these mountains provided numerous microhabitats that may help many cold-adapted species to survive to warmer conditions reached during **interglacial** periods. Thus, understanding the adaptive potential of cold-adapted species to respond to climatic oscillations is fundamental to predict the consequences of contemporary global climate change.

The species *Veronica aragonensis* Stroh, endemic to the Iberian Peninsula, was selected as a model for our study. This perennial herb inhabits calcareous scree-slopes from Pyrenees and the Baetic System, usually between 1,000–2,300 m. Microsatellite markers were characterized to investigate genetic diversity and structure of the species. Our main aim was to elucidate how the biological and historical processes shaped the evolutionary history of this cold-adapted species.

Our results suggest the existence of genetic bottlenecks during postglacial colonization together with long periods of isolation and high levels of inbreeding that could affect the future survival of some populations of *V. aragonensis*. Conservation of the evolutionary process that originates genetic variability within the species is the basis for the long-term biodiversity conservation. Thus, our understanding of genetic patterns in *Veronica aragonensis* will help to the implementation of effective conservation plans for this relict species. Additionally, glacial and inter-glacial refugia in which the species could survive to the glaciations have been identified. These southern populations at the edge of the distribution range are clear potential candidates to define micro-climatic refuges for cold-adapted species under the present climate-change scenario. Protection of these habitats would allow the conservation of many other threatened taxa which constitute plant communities on this type of rocky mountain habitat.

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Response of reindeer breeding time to a warming spring in Finnish Lapland

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The breeding time of many taxa has changed over the past two to three decades in response to climate change. In order to predict how climate change will affect species' viability, it is crucial to understand how species base their reproductive efforts on environmental cues since breeding time in animals is a key reproductive trait affecting individual's reproductive success and therefore the population's recruitment rate and dynamics. Using long-term datasets of 45 years of birth dates, and mating behaviours and copulation dates recorded since 1996 of a semi-domesticated reindeer population in Kaamanen, North Finland, we show that calving season has advanced by $\simeq 7$ days between 1970 and 2016, the males' mating time by 11 days over 16 years and the females' copulation dates by 14 days over 18 years. The advancement of those phenological events were found to follow the climatic changes reported in the study area since earlier calving dates were associated with lower snowfalls and a reduced snow cover in April and warmer temperatures in April-May and males began to display mating behaviours earlier and observed copulation dates also occurred earlier following a warmer weather in May. An improved physical condition of individuals in response to warmer temperatures in early spring, facilitating availability of late winter food and early green-up of vegetation probably accounted for such observed advance in reindeer breeding time. That both calving and mating seasons were affected by climatic conditions at the same period of the year confirmed that timing of calving season appears to be the ultimate cause of the timing of the mating season. The plastic response of breeding time to climatic conditions in spring most likely allowed reindeer to adapt to climate change in Finnish Lapland and indicates that reindeer populations may be more resilient to climate change than previously acknowledged.

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Towards well-informed species distribution models to reconstruct species' past distribution

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Climate change pushes species to redistribute or evolve to adapt to new conditions. To hindcast and forecast species redistribution under past and future climate, the state-of-the-art is to use all available information (e.g., presence-absence data, range maps) about the current species' distribution and relate it to climatic conditions, an approach known as species distribution models (SDMs). Traditional SDMs use all populations of a given species to encapsulate the species' climatic niche, an appropriate approach for interpolation purposes. However, when hindcasting a species distribution into the past based on current data for extrapolation purposes, the use of all extant populations of a given species to calibrate SDMs can be misleading as it may inflate the species' climatic niche width. Here, we hypothesize that SDMs calibrated either with (H1) basal lineages more likely to represent the common ancestor or (H2) populations from the migration front (i.e., leading edge) that are most likely to show higher levels of niche conservatism should lead to better reconstruction of the past distribution than SDMs calibrated with all populations. To test those hypotheses, we analysed distribution data from two species for which there is established phylogeographic structure: the brown snail *Cornu aspersum* and the European beech *Fagus sylvatica*. We calibrated and compared model performances between three types of SDMs: (i) a baseline SDM for all populations; (ii) a lineage-specific SDM based on basal lineages most likely to represent the common ancestor occurring during the last glacial maximum (LGM); and (iii) a leading-edge SDM based on populations from the postglacial re-colonisation front. All SDMs were calibrated with present data before hindcasting the past distributions during the LGM. Our preliminary results suggest that focusing on populations from the leading edge (H2) may contribute to more realistic reconstruction of species' past distribution.

*Speaker

End-of-century habitat model forecasts suggest potential redistributions of marine predators around the Prince Edward Islands, southern Indian Ocean

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One of the most important effects of climate change is the redistribution of biodiversity and this is occurring rapidly in marine systems. Marine top predators are regarded as ocean sentinels because they occupy high trophic levels and therefore integrate environmental signals into their behaviour and demography. They also play an important functional role in ecosystems. Projections of the future distribution of these predators can: 1) indicate future potential biodiversity patterns and rearrangements, such as changes in community structure; 2) form the basis for hypotheses about the future structure and functioning of marine communities; and 3) generate spatial scenarios for conservation and management planning. We used tracking data from 14 species (3 seals, 10 seabirds and 1 cetacean, totalling 538 tracks) to model the habitat use of top predators around the Prince Edward Islands in the southern Indian Ocean. Using ensembles of 5 machine learning algorithms, we modelled habitat preference as a response to 4 static environmental covariates and 11 dynamic environmental covariates obtained from the Max Planck Institute Earth System Model, an IPCC-class climate model. To forecast the potential distribution of the predators in 2070-2099, we used the climate model projections that assume the 'business as usual' greenhouse gas emissions scenario RCP8.5.

Analogous climates are projected to predominantly shift to the south-east and south-west. Species potential range shifts varied in direction and magnitude, but overall shifted slightly to the south-west. Cluster analyses indicated potential changes in future community

*Speaker

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composition. Overlap scores – indicating areas of common use among the predators – were higher and more concentrated at $\simeq 47^{\circ}\text{S}$. This means that marine predator biodiversity will likely be redistributed, and that some areas might be more intensively utilized by multiple predator species in the future. This would affect ecological processes that require consideration in terms of conservation and management.

Linking C Sequestration Service and High Arctic ecosystem multi-trophic functionality

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The mechanistic response of Arctic terrestrial ecosystems to ongoing climate changes is a key of carbon (C) sink status of the soil. The assessment of the sustainability of Arctic soils C sequestration service requires deeper understanding of the ecological mechanisms leading to C accumulation in the soil. We explored the links among plant, soil invertebrate and microbial communities, and the C biogeochemical cycle along environmental gradients in different valleys of central Svalbard. This multi-trophic functional approach integrates the holistic aspect of the ecosystem structure and aims at stressing the association of ecosystem service resilience with the functional links among the compartments. We sampled (1) plant composition, abundance, above and belowground traits, (2) soil invertebrate composition, abundance and feeding traits, (3) soil microbial communities functional composition and activity; and (4) soil C organic and inorganic contents. Our preliminary analyses showed functional clustering across the compartments and also different levels of sensitivity to environmental gradient depending upon the compartments. Analyses need to be deepened and completed with manipulative experiments to disentangle the mechanisms but our results already illustrates a breakthrough in functional ecology with an explicit consideration of multi-trophic response-effect framework.

*Speaker

Germinating in a warmer world: Tropical plant species are at greater risk from climate change

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Since Janzen's 1967 paper "Why mountain passes are higher in the tropics", tropical species have been hypothesised to withstand a narrower breadth of temperatures than species at higher latitudes. While this is true for animals, this assumption has yet to be tested for plants. We used 7721 records for 866 species from the Kew Gardens' global germination database to quantify global patterns in germination temperature. Surprisingly, we found no evidence for a latitudinal trend in the range of temperatures across which plant species can germinate. However, tropical plants are predicted to face the greatest risk from climate change, because they are closer to their upper thermal limits. By 2070, over half (84/149) of tropical plant species are predicted to exceed their optimum germination temperatures with some even exceeding their maximum (35/190). Conversely, 97% of species at higher latitudes (above 45°) are predicted to benefit from warming, with temperatures shifting closer to the species' optimal germination temperatures. Thus, the prediction that tropical species would be most at risk under future climate change was supported by our data, but through a different mechanism to that generally assumed.

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Using $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ of present and past otoliths to monitor the effects of climate change and fishing activities on the marine food web of Faroe Islands

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It is widely accepted that climate change and fishing activities can modify the structure of marine food webs due to their effects on species assemblages, phenologies and life history traits. On the contrary, changes in trophic functions, i.e. prey-predator interactions, created by these perturbations remain largely unexplored. However, monitoring these changes is crucial for understanding marine population dynamics and enabling sustainable stock management. So far, this monitoring has been a challenging task, primarily due to the complexity of assessing trophic relationships over time in a natural habitat. Recent findings suggest that these limitations can now be overcome by using $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ from otolith organic matter to reconstruct diet characteristics. In this study, we take advantage of this new method to understand the effects of climate change and fishing activities on food web structures and functions. Towards this goal, we used otoliths from three co-occurring gadoids experiencing different degrees of fishing pressure and belonging to different trophic niches (the saithe, the cod and, the haddock). For each species, we assessed the annual $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ of otoliths from individuals caught in Faroe Islands between 1955-2014 and modeled the temporal variations of these signatures according to fishing pressures, environmental parameters, and climate indices. The results of this study, the first one investigating the long term changes in marine trophic functioning, will allow for a better understanding and better predictions of the impacts of climate change and fishing activities on marine ecosystems.

*Speaker

Energy efficiency drives the global seasonal distribution of birds

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The uneven distribution of biodiversity on Earth is one of the most general and puzzling patterns in ecology, and many hypotheses have been proposed to explain it. However, previous studies investigating these hypotheses have been mainly descriptive as controlled experiments are hardly feasible at such large geographical scale. Here, we use bird migration – the seasonal redistribution of about 20% of bird species across the world – as a natural experiment for testing the species-energy relationship, the hypothesis that animal diversity is driven by energetic constraints. We develop a mechanistic model of bird distributions across the world and across seasons based on simple ecological and energetic principles reflecting Lotka's maximum power principle. Using this model, we show that bird species distribute as to optimise the balance between energy acquisition and energy expenditure while taking into account competition with other species. These findings support, and provide a mechanistic explanation for, the species-energy relationship. They also provide a general explanation of migration as a mechanism allowing birds to optimise their energy budget in the face of seasonality and competition. Finally, our mechanistic model provides a tool for predicting how ecosystems will respond to global anthropogenic change, and we used it to reconstruct the global seasonal distribution of birds back to the Last Glacial Maximum.

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The effects of climate change and the collapse of the shrimp fishery on fish communities' diversity and functions in a tropical context: the case of the continental shelf off French Guiana

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For more than two decades, describing and understanding the spatio-temporal dynamics of fish communities has been subject to increasing attention from scientists and fisheries managers. Such dynamics are crucial for ecosystem functioning and productivity which provide goods and ecosystem services. Most of the works based on fishing and climate change effects on fish communities' ecology and functions are focused mainly on temperate and boreal ecosystems. There is a lack of information concerning the adaptation capacity of the fish communities to warmer waters in tropical regions. Our study is based on datasets from surveys conducted from 1993 to 2017 using a bottom shrimp trawl between 10 and 60m depth in a tropical continental shelf (French Guiana) which is characterized by a significant increasing of SST and a declining fishing pressure (shrimp fishery by bottom trawl). We firstly compared the functional richness of the fish communities to values obtained from a null model that enabled us to identify the relative importance of the assembly rules (niche filtering hypothesis versus limiting similarity hypothesis) using a trait-based approach. Then we analyzed the ground fish communities' spatio-temporal structure and functional diversity. Subtropical species occurring at the upper limit of their thermal range are disfavored with warming waters provoking potential changes in the fish communities' structure. Moreover, individual observed sizes were larger in the recent years probably due to the decrease of the fishing pressure. The consequences of such alterations are discussed.

*Speaker

Drought impacts on leaf functional and hydraulic community traits in grasslands: A matter of timing

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Drought events can occur at different periods during the vegetation growing season, likely having contrasting effects when happening early or later in the season. However, knowledge about the interacting effects of the timing of drought and the stage of the vegetation along the growing season is still scarce, thus limiting our ability to accurately predict forage quantity losses.

To investigate plant community responses to drought seasonality (during or after the peak of biomass production), we established a drought experiment in two semi-natural grasslands of the Swiss Jura Mountains. We measured three plant functional traits including two leaf traits reflecting drought tolerance (SLA, LDMC) and one hydraulic trait (predicted percentage loss of hydraulic conductance, PLCp) and plant aboveground biomass. Plant species composition was also determined to calculate community weighted mean traits.

First we observed that community weighted mean trait values strongly varied along the growing season. Second we found that the effects of drought occurring during the peak of growing season had lower intensity than when occurring after this peak. We also found that the plant hydraulic trait was more plastic than the leaf traits.

Using a structural equation model (SEM), we also showed that reduction in soil moisture had no direct impacts on aboveground biomass production. Instead, we observed that the diminution in aboveground biomass production was partially due to a lower PLCp under drought, which directly and indirectly affected changes in SLA. Change in SLA in response to drought was the best predictor of community aboveground biomass production.

The stochasticity of extreme drought events is likely to increase in the future and knowledge on the effects of different drought timing together with the choice of plant traits used to assess community response to drought are thus important for improving mechanistic model predictions of climate change impacts.

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Forest tree recruitment in the margin of the distribution range: a question of forest canopy and microclimate for *Fagus sylvatica*

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As a mesophilic tree species, beech (*Fagus sylvatica*) is highly threatened in the southern margin of its distribution range. Its recruitment decreases with mild winter temperatures, but also with water stress and extreme heat events in summer. At the edge of their distribution range, marginal populations can persist locally in areas with favourable site conditions. In order to understand how these populations persist, 49 pairs of mesocosms have been installed in the Ciron Valley in the south-west of the distribution range, using a factorial design of canopy structure (open environment, pinewood, mixture, hardwood). The microclimate has been quantified along our gradient of canopy cover: hemispheric pictures were taken in winter and summer to assess light resource availability, and climate sensors have been measuring air temperature and humidity under the tree canopy. Canopy effects depend on the season and the type of cover. As for light availability, the results show a significant difference between open environments and all other forest canopies during the winter. In summer, pine forests show intermediate levels of light between open and broad-leaved environments. Preliminary results for two-year old plants show a lower growth in height, diameter and number of branches in open environments, but no difference between the various forest canopies. Similar results for survival and growth of tree seedlings are observed, and no difference can be noticed for seed germination. Our results suggest that in the margin of its distribution range, conditions for *Fagus* are favourable for germination, and the presence of forest plays an essential role in the recruitment of trees, irrespective of the canopy type.

*Speaker

A Model Analysis for the Regime Shift in Alpine Vegetation

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In alpine ecosystems, global warming may accelerate the time of snowmelt in spring, which shortens the duration of snowmelt-water supply in alpine regions, resulting in drier soil conditions in mid-summer. This may influence the species composition of alpine vegetation especially inhabiting moist habitat. Using a dynamic mean field model, the regime shift of vegetation change in alpine ecosystem under warming is theoretically analyzed.

Our model is based on the observed vegetation change, rapid expansion of dwarf bamboo (*Sasa kurilensis*) into snow-meadow vegetation, in the Daisetsuzan National Park, Northern Japan. A positive feedback mechanism is considered in the model, that is, dwarf bamboo favorably expands the distribution area under early-snowmelt conditions and soil water contents are more suppressed due to high transpiration ability of dwarf bamboo. This feedback mechanism is formulated as two equations. First, the effect of dwarf bamboo B on soil water content W is introduced through a differential equation in which a decreasing period of snowmelt-water supply caused by an increase in air temperature T is contained. Secondly, the effect of W on B is represented by a function $B = B(W, T)$, which is based on the empirical photosynthesis responses of B to W and T . The former gives an indirect effect of T on B via a change in snowmelt period due to a change in T , while the latter gives a direct effect of T on B .

It is found by our model analysis that a regime shift, i.e., quasi irreversible drastic change from snow-meadow to bamboo shrubland, can occur substantially not through the direct effect of temperature but through indirect effect of temperature via early snowmelt followed by soil aridification. This result suggests that drastic change in alpine vegetation may occur by small shift in snow regime.

*Speaker

Halieutic and MarineEcology

Investigating demogenetic consequences of spatial dispersal on Atlantic salmon populations using an Individual-based metapopulation model

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Organism stability and resilience is driven by the diversity of responses of populations to the environment and the connectivity between these populations. Indeed, populations are spatially structured, connected by the movement of individuals between patches via spatial dispersal. Dispersal influences dynamic systems (from genes to community) so that local population dynamic can be strongly influenced by local conditions (environment, adaptation, selection, ...) but also by metapopulation dynamic. Thus, local population can not be treated as isolated system and management and conservation strategies should consider connectivity between populations, i.e. the role of metapopulation. Using an Individual-based metapopulation model, we investigate the demogenetic consequences of environmental and anthropogenic perturbations (e.g. fisheries, connectivity) on an exploited metapopulation of Atlantic salmon (*Salmo salar*). Our approach allows to integrate ecology, evolution and demography at once to better understand the demo-genetic responses of A. salmon populations to perturbations. First, we explore the demogenetic consequences of connectivity on A. salmon populations. Second, we investigate how environmental (climate change) and anthropogenic perturbations (e.g. selective fisheries, alteration of connectivity) affect local population dynamic and the whole metapopulation functioning. By doing so, we aim to define management/conservation strategies in a metapopulation framework which mitigate the effect of perturbations by protecting diversity.

*Speaker

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Deep-sea bioregions based on network analyses

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The definition of bioregions based on assemblages of species or communities is fundamental in ecology and biogeography but also in evolution and conservation biology where conservation policies often imply spatially based measures such as protected areas. Hence, spatial units should be biologically and ecologically relevant. In the deep sea, the definition of bioregions faces different constraints and limits. First, only a small percentage of the biggest realm on Earth has been explored. Second, species description rates are continuously increasing, highlighting the scarcity of our knowledge on deep-sea marine species. Here, we aimed at delineating bioregions of the Indo-Pacific region, based on two major (and well documented) taxa of the deep sea benthos: the Galatheids and the Ophiuroids. To cope with data of limited quantity and variable spatial coverage, we first tested aggregating of occurrence data at multiple scale to investigate the impact of the scale used for bioregion delimitation and chose the optimal scale. Then, we applied an innovative method to find bioregions based on bipartite networks. This method allows identifying bioregions but also biodiversity hotspots and transitional zones, which represent an interesting and challenging concept in the open marine environment. We compared our results to existing marine regions classifications (shallow, pelagic or deep-sea ones). Finally, we discuss our results under the perspective of the opportunities and caveats of museum data for such applications.

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Do green tides affect the trophic ecology of juvenile flatfish? Response through the combination of two complementary methods

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Coastal zones are some of the most productive and diverse ecosystems in the world and play key roles as nursery grounds for many commercially valuable fish species like sole, plaice, turbot and brill. They are also subject to numerous anthropogenic disturbances, such as excessive nutrient inputs which can cause green tides (GT) that have been shown to modify zoobenthic communities. One can question their effects on higher trophic levels particularly juvenile flatfish which prey on macrobenthic invertebrates. Our study concerned two macrotidal sandy beach systems located in Brittany (Western Europe), one representing the undisturbed site (no-GT) and the other representing the impacted site (GT). Young-of-the-year individuals of flatfish species (*Pegusa lascaris*, *Pleuronectes platessa* and *Scophthalmus maximus*) were sampled at no-GT and GT sites before, during and after the eutrophication event (*i.e.* the algal bloom). Their feeding ecology was studied through gut content analysis (GCA) and stable isotope (carbon and nitrogen) analyses (SIA). The results of GCA showed that young flatfish did not feed on algae but adapted their feeding strategy when the macrobenthic community was modified by green tides. No diet overlap was evidenced whatever the site. SIA results showed a ¹³C enrichment at the GT site. The isotopic niche (given by the Surface Ellipse Areas) of Particulate Organic Matter as primary source, invertebrate prey and of *P. lascaris* or *P. platessa* were reduced in GT compared to those in no-GT sites. Isotopic niche overlaps were only observed at GT site suggesting part of feeding on the same source. These results tend to demonstrate that green tides affected the trophic ecology of young flat fish through modification of the base of the food web.

*Speaker

Targeted studies to decipher humpback whale genetic diversity

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Humpback whales are a typical example of a highly mobile marine mammal species, and yet show strong intra-specific genetic structure. Fidelity to feeding and breeding grounds may strongly influence the population structure. In particular, regional differences in mitochondrial DNA (mtDNA) could mirror cultural transmission of the migration route, thus leading, over generations, to fidelity to specific feeding and breeding grounds. We attempted to decipher the complex structure of humpback whale genetic groups in the Madagascar breeding ground (in collaboration with the NGO Cetamada, CNRS and University of Paris XI), and in two feeding grounds: in the Bering Sea (with the University of Moscow, the Pacific Geographical Institute and FEROP project) and around Saint-Pierre-et-Miquelon Island (in collaboration with the NGO FNE SPM, DTAM, CNRS and University of Paris XI). Our results support those of other studies and shed light on the actual levels of genetic diversity in humpback whales and their local variations. Comparative analysis of nuclear and mitochondrial DNA polymorphisms is highly informative, and can lead to contrasting results. For instance, we showed that two groups of humpback whales from Russian Pacific waters, separated by approximately 500 km within what has been considered the same feeding ground, are unexpectedly genetically different. In contrast to nuclear DNA polymorphisms, which show no differences between humpback whales sampled in the two groups, a significant difference in mtDNA was observed between the two areas. Fidelity to specific feeding sites, maternally learned and corresponding to a cultural transmission between generations, could therefore occur at smaller geographic scales than generally thought, and reflect some heterogeneity in feeding grounds. Such diversity should be taken into account with regard to conservation since the loss of a specific site used by humpback whales, even at a small geographical scale, could well correspond to the loss of genetic heritage.

*Speaker

Low connectivity in a nursery-dependent fish metapopulation revealed by modeling mark-recapture data may hide seasonal variability of movements

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Quantifying connectivity within fish metapopulations is critical to understand population dynamics and to provide an evidence base for assessment and management. Connectivity determines the colonization of new habitats, population resiliency to harvest, and consequently should influence the design of spatial management strategies. The common sole (*Solea solea* L.) in the Eastern Channel (EC) is an ideal case study to assess metapopulation connectivity. The life cycle typology determines the spatial structure of the metapopulation. Adults spawn offshore in spring. Eggs and larvae drift passively for several weeks before settling in coastal nursery grounds, where the juveniles spend their first two years. When approaching maturity, juveniles migrate offshore to deeper waters where they recruit to the exploited adult population. Based on results from neutral genetic markers, EC sole is currently considered as a single, spatially homogeneous population. However, larval drift models and limited in situ movement of larvae and juveniles within nurseries suggest very low connectivity between EC sub-populations. However, connectivity induced by adult movements remains effectively unknown. To fill this knowledge gap, extensive tagging experiments have been carried out since 1955, covering a large area from the Celtic Sea in the west to the North Sea in the east, including the EC. We developed a state-space mark-recapture model, designed to estimate seasonal movements of fish between pre-defined sub-areas, and considering three seasons corresponding to three biological states. Our results suggest that few movements occur at the adult stage, supporting the hypothesis of segregated population subunits within the EC. Our results did, however, reveal high variability of seasonal movements, with cyclic migration patterns that may conceal intra-annual seasonal migration related to the inshore-offshore life cycle strategy.

*Speaker

Response of food-web structures to the re-oligotrophication of a deep lake and implications for the fisheries

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Lake Geneva, which lies on the border between France and Switzerland, is the largest lake in Eastern Europe. It suffered a strong eutrophication from the 1960s until the late 1970s with total phosphorus concentrations reaching more than 80 $\mu\text{gP.L}^{-1}$. Management measures to reduce phosphorus loading into the lake have been successful (deployment of water treatment plants, prohibition of phosphorus in detergent ...), and nowadays the phosphorus concentration dropped down to 20 $\mu\text{gP.L}^{-1}$. According to the OCDE categorization, Lake Geneva has reached a mesotrophic status. Such strong diminutions in phosphorus loads were associated with significant decline of fisheries in several Swiss lakes and the question is now: what is the future of Lake Geneva fisheries if this concentration keeps on declining? Actually, decrease in phosphorus concentration can affect primary production and then fish production through food web amplification. However, the processes are poorly described and a holistic approach is necessary to understand how trophic flow distribution in the Lake food web is modified during re-oligotrophication process. We calibrated several mass-balanced food web Ecopath models at different periods during the re-oligotrophication (from 1980 to 2015). Flow distributions were compared and Ecological Network Analyses were performed in order to assess the evolution of Lake Geneva food web functioning and properties facing these changes in phosphorus concentration. Assumptions regarding the potential future of fisheries will then be proposed and a first attempt of dynamic Ecosim modelling will be proposed to foresee the effects of an ultra-oligotrophication on Lake Geneva fisheries.

*Speaker

A definition of the thermal niche of spawning for a French metapopulation of Allis shad in a global warming context

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All around the world, diadromous fish are facing multiple anthropogenic pressures resulting in a global decline of these migratory species. In Europe, the allis shad (*Alosa alosa* L.), is no exception and has dramatically declined since 2000. Although the decline of this species in Europe is documented, the potential disruptive force of global warming is sparsely studied. To estimate the consequences of these perturbations, we explored ways in which individuals from the population in the Gironde watershed, sheltering the most abundant population in Europe, can adapt the reproduction to thermal heterogeneity. We used 14 years of daily reproductive surveys associated with river temperatures to define the thermal niche of reproduction for allis shad in the Gironde watershed. The low variability of realized thermal niches, despite fluctuations in thermal habitat, demonstrates that allis shad is a thermal generalist. Therefore, the allis shad can reproduce in a wide range of temperatures and is assumed to be weakly affected by the present thermal heterogeneity in river. Nevertheless, electivity index demonstrated a thermal preference for reproduction, slighted shifting to lower bound of the thermal tolerance of early stages. In a context of rapid warming of river temperature, the adaptability of this generalist strategy will be tested using an individual based model.

*Speaker

Structure of the megabenthic communities of the ” Grande Vasière ” of the northern Bay of Biscay: a system adapted to chronic disruptions by bottom trawling?

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Bottom trawling is a widespread fishing activity, worldwide. Countless studies have reported its adverse effects on the benthic environment, including sharp declines of the benthic biodiversity and changes in the species composition. Reiss et al. (2009) argued that, beyond a certain threshold of trawling intensity, benthic communities might reach a new state of equilibrium so that an additional source of disruption would have no supplementary impacts. Nevertheless, this hypothesis has not been verified because most of the studies have been performed in low to moderately trawled areas. The ” Grande Vasière ” (GV) of the Bay of Biscay is fished for more than 90 years for Norway lobster (*Nephrops norvegicus*) and hake (*Merluccius merluccius*). It currently exhibits a remarkably high trawling intensity compared to the other European fisheries. Despite this, the benthic communities and their structuring factors remained poorly known. Our study aimed at filling this gap of knowledge. We first described the environmental characteristics (outputs of the Mars 3d model) and the distribution of the trawling intensity (data from the Vessel Monitoring System) within the GV. Then, on the basis of a three-years halieutic survey, we drawn the first map of the megabenthic communities structure (> 10mm) at the GV scale. Finally, the correlations between the megabenthic communities structure and the environmental characteristics along with the trawling intensity have been investigated. Fishing appeared to be a poor predictor of the megabenthic communities structure and our results contrasted with those of several studies performed in moderately trawled areas. Our conclusions comfort the hypothesis of Reiss et al. (2009): we suggested that decades of intensive trawling have irremediably removed the vulnerable organisms, such as seapens, and that the megabenthic communities have been adapted to chronic disruptions. So, an increase of the trawling intensity has no more detectable effects.*Speaker

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Holobiont and Extended Phenotype

Evidences for a core microbiota resulting from earthworm-plant interactions

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The core microbiota concept has been proposed to describe the subset of a microbiota associated with a given host and going beyond macroenvironment differences. In soils, there is an overlap between the so-called rhizosphere and the drilosphere (burrows and casts), defined as the functional domains under the influence of plant roots and earthworms respectively. Plants and earthworms have been sharing the same soils over geological times, thus microbial communities living at the congruence of rhizosphere and drilosphere could be specific of plant-earthworm interaction, as a consequence of their coevolution. Here we tested the hypothesis that a specific core microbiota exists in rhizosphere in the presence of earthworms and in drilosphere in the presence of plants, that remains consistent in three different soils. We grew barley in microcosms in the presence/absence of the endogeic earthworm *Aporrectodea caliginosa* and investigated the structure of microbial communities (16S rRNA gene amplicon sequencing). We found that (i) rhizosphere community assembly was always impacted by the presence of earthworms and (ii) cast communities were controlled by earthworms in the rich soil, but mainly under the influence of plants in the poor soil. We observed a core microbial co-occurrence network of plant/earthworm interactions, shared in cast and rhizosphere and absent from the bulk soil, with a modularity corresponding to the type of soil. Tracing back the origin of microbial taxa according to a hierarchical model, we established that microbial communities from rhizosphere in the presence of earthworms and from casts in the presence of plants were mainly originating from (1) the bulk soil and (2) microhabitats shaped by plants or earthworms alone. A significant remaining proportion of the microbial community was strictly due to the plant-earthworm interaction, justifying the claim that a core microbiota can be specific of an interaction between macroorganisms such as plants and earthworms.

*Speaker

Lignocellulose degradation at the holobiont level: teamwork in a keystone soil invertebrate

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Lignocellulose is the main component of plants and is composed of cellulose, lignin and hemicellulose. Its degradation requires the collective action of diverse Carbohydrate-Active enZymes (called CAZymes). Many invertebrates express few lignocellulose-degrading enzymes, but in most of them efficient degradation of lignocellulose is only possible thanks to mutualistic associations with endosymbionts.

Due to their important role in the decomposition of organic matter, terrestrial isopods are recognised as keystone species in terrestrial ecosystems. Past studies have shown that they can digest cellulose and are able to produce some endogenous cellulases (Kostanjsek et al. 2010). Although marine isopods like *Limnoria quadripunctata* secrete all the enzymes necessary for cellulose digestion in the absence of gut microbes (King et al. 2010), terrestrial isopods would not be able to digest cellulose without the help of their microbiota (Bouchon et al. 2016). Similar to termites, it has been suspected that several hepatopancreatic symbionts may be involved in the lignocellulose degradation in terrestrial isopods completing the CAZyme repertoire of their hosts (Zimmer et al. 2002).

To test this hypothesis, transcriptomic and metagenomic approaches have been used in the pillbug *Armadillidium vulgare*. We identified the CAZyme repertoire from both the microbiome and the isopod host. Depending on CAZyme families, complementary as well as redundancy between host and microbiome repertoires were recorded. Tissue specific expression of some representative of the host CAZymes were shown. Experimental diet manipulations showed that the expression of these CAZymes was modified in correlation with the modification of the microbiote. Our results provide an insight into the role of the microbiome in the evolution of terrestrial isopods and their adaptive radiation in terrestrial habitat.

*Speaker

Diversity patterns of the microbiota associated to *Laminaria digitata*, a kelp with an iodine defense metabolism

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The microbiota of the seaweed holobiont plays an important role in host health and physiology and it is affected by interactions with the host. The kelp *Laminaria digitata* possesses a unique defense metabolism, associated with the production of toxic iodine compounds. *L. digitata* gradually concentrates iodine in its tissues depending on age, thallus areas, and season. Iodine is highly concentrated in the peripheral cell layers, creating specific niches for the associated microbiota during iodovolatilisation. This microbiota is thus expected to vary along the alga according to these characteristics. Here, we investigate (*i*) the acquisition mode of the associated microbiota of *L. digitata*, (*ii*) the stability of the microbiota according to different maturation stages of the sporophyte, (*iii*) correlations between fluctuations of the microbiota according to varying concentrations in iodine in the algal tissues. The associated microbiota of cultivated and harvested wild plantlets, blade and stipe samples from four wild adult *L. digitata* sporophytes was determined using metabarcoding. Analyses of the microbial community composition and structure showed that the microbiota from the field plantlet was different from the laboratory plantlet but similar to the blade, and the four stipe samples strongly clustered together. This suggested (*i*) an environmental acquisition of the associated microbiota; (*ii*) the relative stability of a core microbiota at the kelp blade surface, and (*iii*) an associated microbiota specific to the thallus area. In the context of *L. digitata*'s defense metabolism, cross-kingdom interactions in the kelp holobiont may determine the composition and the distribution of the associated microbiota.

*Speaker

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Role of earthworm-gut microbiota in pesticide tolerance ?

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Earthworms are important drivers of soil biological properties. Due to their burrowing activities, they are considered as "soil ecosystem engineer". In agricultural fields, they are exposed to insecticides such as organophosphates (OP), which display a high acute toxicity by inhibiting acetylcholinesterase, affecting their nervous system. Moreover, pesticides pose a serious threat to soil microbial processes. Both the assessment of health status of earthworms and the impact of OP on soil enzyme activities has been investigated. However little is known concerning the impact of burrowing activity on the microbiota of the ingested soil during the gut transit. The earthworm digestive tract could be considered as an environmental filter that favors the growth of some microorganisms at the expense of others, possibly controlling activities involved in the degradation of OP. We studied *Allolobophora chlorotica* and *Aporrectodea caliginosa*, two soil-dwelling species abundant in the studied agro-ecosystem. We have previously shown that both the behavior and biochemical responses of *A. caliginosa* are more sensitive to OP than for *A. chlorotica*. Here, we aimed to assess the effects of OP on soil, earthworms' intestinal microbiota and casts microbial communities. Both species were exposed for 1-week to parathion. The soil was sampled as a control (day 0), the bulk-soil, and the casts were sampled after 4 and 7 days exposure, then after 5 additional days of gut voiding, the intestinal tract and the fresh casts were collected. We used DNA metabarcoding approach to analyze bacterial and fungal community diversity and we measured their abundances through quantitative PCR. Our results show particular community composition of the digestive microbiota that differ between earthworm species and evidence the environmental filter related to the transit of the soil into the gut. We verified an effect of OP mainly on the fungal community composition of the gut microbiota.

*Speaker

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How does urbanization affect the human gut microbiome? A case study in Cameroon

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The gut microbiota (GM) seems strongly associated with human health status, as illustrated by a number of lifestyle-related diseases that have been linked to a loss of diversity and to a disruption of GM community structure (dysbiosis). These "modern" diseases, such as obesity and allergies, are on the rise in industrialized countries and understanding the mechanisms behind their increase in prevalence is vital for restoring and maintaining health. The higher GM diversity observed in multiple non-industrialized countries indicates that there is something about the industrialized lifestyle that causes impoverishment of gut microbial communities. Is this effect linked to diet, sanitary conditions, medical practices, latitude or other yet unexplored factors? It is so far unclear as previous studies have compared geographically distant populations that differ in a variety of ways. Moreover, gut protists, which have likely shaped human-GM interactions throughout their coevolutionary history but are virtually absent from industrialized populations are rarely taken into account. To address these limitations, we examined the GM diversity and composition in Cameroonian populations along an urbanization gradient at a local scale. Apart from GM metagenetic (SSU gene) and metagenomic data from 140 subjects, we recorded a number of ethnological, medical, sanitary and parasitological parameters in order to disentangle diverse urbanization-related factors that influence GM diversity. Our results shed light on the link between various aspects of urbanization and GM structure and question the hypothesis that GM diversity declines along the urbanization gradient.

*Speaker

Influence of the symbiont *Wolbachia* on life history traits of the cabbage root fly (*Delia radicum*)

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Wolbachia is an endocellular bacteria infecting arthropods and nematodes and only transmitted vertically by females via the cytoplasm of the egg. It is often a manipulator of host reproduction, causing cytoplasmic incompatibility, thelytokous parthenogenesis, feminisation or male killing, which all increase the proportion of infected females in the population. However, *Wolbachia* can modify life history traits of the host without causing the above phenotypes and each species illustrates the variability of relationships between this remarkably versatile symbiont and its many hosts. We have measured maternal transmission and the impact of a natural *Wolbachia* infection in the cabbage root fly *Delia radicum*, a major agricultural pest. We used a population that is polymorphic for the infection to ensure identical genetic and microbiome backgrounds. Maternal transmission of the infection was 100% in our sample (n = 707 offspring of 70 females assayed by PCR). We found no evidence of cytoplasmic incompatibility, thelytokous parthenogenesis, feminisation nor male killing. *Wolbachia* infection significantly reduced hatch rate in infected eggs (by 10%) but improved larvo-nymphal viability sufficiently so that infected eggs yielded 5% more adults as uninfected ones in our sample (the difference is NS), albeit with a 1.5% longer total development time. Starved females laying eggs suffered a significantly reduced viability (-20%) when infected, but this effect was not found in starved virgin females nor in starved males, suggesting that the energetic cost of the infection is only revealed in extreme conditions. *Wolbachia* had no effect on egg hatch time or offspring size. The perfect vertical transmission and the significant but mutually compensating effects found suggest that this infection might be close to neutral for the host and might only drift slowly, which would explain why the infection rate has been stable in our laboratory (approx. 50% individuals infected) for at least 30 generations.

*Speaker

What are the ecological drivers of symbiotic microbiome assemblages? The case of an antic affair between an iconic Mediterranean fruit tree and its symbiotic microbiome

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Holobiont and Extended Phenotype

The root symbiotic microbiome, notably arbuscular mycorrhizal (AM) fungi, is a key factor of plant ecology and agro-ecosystem functioning, but the relative contribution of multiple ecological factors driving their diversity and assemblage are poorly assessed. Moreover, few studies have approached this question with a wide geographical perspective, which is important when dealing with domesticated fruit trees characterised by diverse cultivated, feral or wild populations, and consequently subjected to a wide range of environmental constraints and selection pressures.

In the framework of the international project DYNAMIC (Deciphering sYmbiotic Networks in cArob-based MedIterranean agro-eCOsystems), a metabarcoding approach was developed to assess the specificity of tree-symbiotic microbiome associations and to characterise the relative contribution of main ecological drivers of symbiotic microbiome associated with the carob tree in the Mediterranean basin.

The carob tree (*Ceratonia siliqua*) is a multi-use tree of high socio-economical added value with a major place in the traditional rural landscapes of Mediterranean regions. It belongs to the highly diverse family of legumes (Fabaceae) but does not nodulate. However, the carob tree is highly dependent of arbuscular mycorrhizal (AM) symbiosis, and bacterial endophytes were hypothesized as a second major symbiotic partner.

Domestication in the Middle-East around 6,000-4,000 BC may have caused extensive genetic and physiological modifications in carob, conducting to potential changes/adaptations of its associated symbiotic microbiome. These impacts have been investigated for domesticated cereals but rarely for trees.

The results provide new insights into the characterization of a Mediterranean core and accessory "SymbiOme" of the carob tree, highlighting geographical patterns, as well as the contribution of host genetic diversity, habitat and edaphic parameters. The better understanding of ecological rules controlling the specificity of interaction in tree symbiotic associations opens up promising perspectives for the development of more efficient strategies in conservation and agroecology based on plant microbiome symbiosis.

*Speaker

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Ecological and evolutionary transmission of gut mutualistic symbionts in wood-feeding termites

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While host-microbe symbiotic mutualisms are widespread and play major roles in the functioning of many ecosystems, the mechanisms by which these associations persist and diversify in the course of evolution are poorly understood. In many cases, it is assumed that mutualism stability is insured by a strict vertical transmission of the symbionts (from host parents to offspring). To test this hypothesis, symbiont transmission needs to be characterized at both ecological (from one host generation to another) and evolutionary (from one host lineage to others) timescales.

The present study aims to characterize symbiont transmission patterns in the nutritional symbiosis between *Reticulitermes* termites (Rhinotermitidae) and their mutualistic gut protists of the genus *Trichonympha* (Trichonymphidae). Phylogenetic reconstructions of *Trichonympha* symbionts based on 18S rRNA and ITS sequences revealed that *Reticulitermes* termites have acquired independently 3 to 4 distinct lineages of *Trichonympha*, most probably from another termite group through horizontal transmission. In addition, although congruence tests between the host and symbiont phylogenies were significant, reconciliation analyses suggested numerous host shifts.

Molecular characterization of *Trichonympha* has revealed the coexistence of two *Trichonympha* species (A and B) in the host *R. grassei*. Interestingly, the screen of these symbionts in host populations showed variation in the composition of *Trichonympha* assemblage. Some colonies harbour both A and B symbionts whereas other colonies harbour only B. Furthermore, results showed that future reproductives (i.e., alates) that swarm from their parental colony to found new colonies harbour all possible combinations of *Trichonympha* assemblage (i.e., AB, only A, only B, neither A nor B).

Together, these results suggest that the diversification of *Reticulitermes* ² *Trichonympha* symbioses not only includes co-speciation events, but also many host-shifts and symbiont losses. A strict vertical transmission pattern insuring partner fidelity is thus probably not the only mechanism allowing mutualism stability in this system.

*Speaker

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Why do hosts need their symbionts?

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A revolution in biology in the last decade or so is the broad recognition of the importance of host-associated microbial communities in the lives of multicellular organisms. A main cause of this revolution has been new technologies that enable the study of non-cultivable organisms. For the first time, we can survey most biodiversity, including the once-hidden players living inside and on the surfaces of ourselves and other animals. These organisms are finally getting credit for their roles in ecology and evolution. What evolutionary forces drive the effects of symbionts on hosts? In some cases, hosts and their associated microbial communities, sometimes called holobionts, have shared fitness interests, and natural selection has pushed microbes towards phenotypes that benefit host fitness. In extreme cases microbe and host are essentially fused into a single entity. But, just as genes within a single genome undergo evolutionary conflict, components of an intimate symbiotic association also can be at odds. Observing that host fitness drops when associated microbes are experimentally eliminated does not imply that those microbes evolved to benefit hosts, though it may reveal ecological importance of the association. Such associations, or "holobionts", range from pairwise interactions with high fidelity over generations to complex communities that engender both competition and cooperation. The topic of levels of selection has a long history in evolutionary biology, and this work has lessons for those considering how selection acts on holobionts. These themes are illustrated with examples of insect-associated microbial communities showing different levels of complexity, different levels of conflict, and different degrees of persistence over generations.

*Speaker

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Characterization of *Wolbachia*-infected *Drosophila suzukii* lines for the development of a combined SIT and IIT approach

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Drosophila suzukii, the Spotted Wing *Drosophila* (SWD), fly originated from South East Asia, has recently invaded western countries and it has been recognized as an important threat for a wide variety of commercial soft fruits both in open field and greenhouse production systems. The shape and length of the females' ovipositor allows *D. suzukii* to infest a wide range of ripening fruits, leading to substantial yield and revenue losses in the affected regions. The species demonstrated a rapid and widespread expansion in America and Europe, and it has escalated into a major invasive insect pest. The development of an efficient environmentally-friendly control approach to fight against *D. suzukii* is necessary.

An encouraging way out of the chemical control is to employ species-specific and environmentally-friendly control methods, like the Sterile Insect Technique (SIT), which is based on the mass-rearing and release of males sterilized by ionizing irradiation to suppress populations of a target pest species. The SIT has been successfully applied for about 60 years in controlling various insect pest and disease vector species worldwide. As a contingency plan, we suggest exploiting *Wolbachia*, a bacterium able to manipulate its host reproduction through cytoplasmic incompatibility (CI), to develop a combined Sterile and Incompatible Insect Technique (SIT / IIT). In this study we aimed at characterizing two candidate *Wolbachia*-infected *D. suzukii* lines. We concluded that both *Wolbachia* strains induce strong, but not 100%, CI in *D. suzukii*. Both *Wolbachia*-infected lines suffered from reduced fecundity compared to the uninfected line. Our currently available data suggest that low irradiation doses can be combined with *Wolbachia* infections to produce fully sterile males. We plan to perform experiments to assess the production and quality profiles of these lines, as well as the mating compatibility and male mating competitiveness in field cages.

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Can soil microbial diversity influence plant metabolites and life history traits of a rhizophagous insect? A demonstration in oilseed rape

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Interactions between plants and phytophagous insects play an important part in shaping the biochemical composition of plants. Reciprocally plant metabolites can influence major life history traits in these insects and largely contribute to their fitness. Plant rhizospheric microorganisms are an important biotic factor modulating plant metabolites and adaptation to stress. While plant-insects or plant-microorganisms interactions and their consequences on the plant metabolite signature are well-documented, the impact of soil microbial communities on plant defenses against phytophagous insects remains poorly known. In this study, we used oilseed rape (*Brassica napus*) and the cabbage root fly (*Delia radicum*) as biological models to tackle this question. Even though *D. radicum* is a belowground herbivore as a larva, its adult life history traits depend on aboveground signals. We therefore tested whether soil microbial diversity influenced emergence rate and fitness but also fly oviposition behavior, and tried to link possible effects to modifications in leaf and root metabolites. Through a removal-recolonization experiment, three soil microbial modalities ('high', 'medium', 'low') were established and assessed through amplicon sequencing of 16S and 18S ribosomal RNA genes. The 'medium' modality in the rhizosphere significantly improved insect development traits. Plant-microorganism interactions were marginally associated to modulations of root metabolites profiles, which could partly explain these results. We highlighted the potential role of plant-microbial interaction in plant defenses against *Delia radicum*. Rhizospheric microbial communities must be taken into account when analyzing plant defenses against herbivores, being either below or aboveground.

Studying host pathogen interactions by a mutagenesis approach: the case of *Vibrio tapetis* type IV secretion system (T4SS) in the brown ring disease (BRD) affecting the Manila clam *Ruditapes philippinarum*

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BRD is a disease affecting the Manila clam *Ruditapes philippinarum* due to the Gram-negative bacterium *Vibrio tapetis*. Recently, Dias et al. (2018) demonstrated the high level of conservation of the gene cluster coding for the T4SS in strains of *V. tapetis* pathogenic to clams. This system is well known to be responsible of pathogenicity in multiple diseases and can deliver proteins directly into host cells to cause infection. Our approach is to delete genes potentially linked to pathogenicity in order to improve knowledge on the mechanisms associated to the infection by *V. tapetis* in the context of BRD.

For our first study, we choose to target the gene *VirB4*, encoding an ATPase subunit of the T4SS, in order to prove its role in BRD. Our approach is based on a mutagenesis technique by two homologous recombinations enabling to delete only the targeted gene. To test pathogenicity of our *Delta-VirB4* strain, we performed an *in vitro* standardized virulence test based on the ratio of non-adherent hemocytes in exposed samples (to the WT strain or the *Delta-VirB4* strain) / in control samples.

We succeeded to construct a *V. tapetis* strain lacking the gene *VirB4* by optimizing the conjugation protocol in order to improve the efficiency of our technique. Our virulence test shows a loss of adherence properties of clam hemocytes in the presence of the WT strain but not in the presence of the *Delta-VirB4* strain, revealing then a loss of *V. tapetis* cytotoxic activity in absence of the gene *VirB4*.

These results strongly suggest that the T4SS plays an essential role in the pathogenic capacity of the bacterium. With this technique we have developed, we will be able to better understand the genes and thus the mechanisms related to the pathogenicity of *V. tapetis* in the context of BRD.

*Speaker

Microbial warfare between competing *Drosophila* species shapes niche partition

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Deciphering the mechanisms of niche separation between species is a central question in ecology. However, the influence of symbiotic microbes on competitive interactions remains seldom studied. Microbe-mediated niche partitioning may be particularly important in *Drosophilid* flies, which larvae rely on exo-symbiotic microbes for fruit consumption. We previously demonstrated how the invasive pest *Drosophila suzukii* facilitates fruit infestation by *D. melanogaster* through the wounding of fruits by ovipositing females, and the subsequent cultivation of bacteria and yeast by offspring larvae.

We now demonstrate that ovipositing *D. suzukii* females avoid fruits previously exposed to *D. melanogaster*. Using axenic strains, we further show that microbes carried by *D. melanogaster* are responsible for this repellency. Additional experiments reveal that the avoidance of *D. melanogaster* by *D. suzukii* relies on short-scale taste perception. Comparison among *D. suzukii* populations indicates the behavior is present in populations from both the native and invasive ranges but depends on previous fly experience. On-going experiments test the hypothesis that *D. suzukii* females avoid fruits infested by *D. melanogaster* because its symbionts would create conditions unfavorable for *D. suzukii* progeny.

Our study highlights how symbiotic microbes may determine interspecific interactions and niche partitioning through facilitation and competition; the results further suggest natural repellents may provide innovative and sustainable biocontrol solutions against agricultural pests.

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Do bacterial symbionts influence the foraging behaviour of their insect hosts?

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The majority of eukaryote species are involved in durable and intimate associations with symbiotic microorganisms. Microbial endosymbionts are able to modify the ecology and the evolution of their host by inducing various effects on its phenotype. More recently, an increase body of evidence on different animal species indicates that microbial symbionts can also influence the behaviours of their hosts. Such effects would have profound consequences on organism's fitness when affecting behaviours associated with resources foraging.

In Behavioural Ecology, the Optimal Foraging Theory has been developed by considering individuals as 'unique' organisms. As almost all animal individuals harbour symbiotic microbes, it is important to study how those symbionts influence the host foraging behaviours and their optimality. For this purpose, we investigate the impact of bacterial symbiosis on nutritional resources foraging in the pea aphid (*Acyrtosiphon pisum*). This insect hosting simple and easily manipulable symbiotic associations, it is a good biological model to study the effects of symbionts on foraging behaviours.

By considering aphid lines differing only by their bacterial secondary symbionts consortium, three experiments were conducted. Depending on environmental conditions, aphids can produce two different morphs in their offspring: winged or wingless individuals. We first tested whether symbionts have an impact on dispersal capacity by comparing the proportion of winged offspring in lines with or without symbionts. Secondly, we studied symbiont's influence on the time needed to reach a nutritional resource (a plant) in different challenging environment. Finally, we investigated whether symbionts affected their plant preference and acceptance in a choice test experiment by using different aphid lineages with distinct host plant preferences. All the results obtained will be discussed in the light of the 'historical' Optimal Foraging Theory.

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Interaction of Ecological and Social Aspects in the Categorization of Spaces and Species

The values of biodiversity in a non-market context

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Subantarctic islands are regions without permanent inhabitants and where nature is not exploited. The values of biodiversity is thus not directly linked to its utility for humans or the ecological services provided. The aim of this research was to detail the non-utilitarian intrinsic values of biodiversity, and to investigate their articulation with other values in relation to different social factors. In most situations, such identifications are made difficult by the fact that utilitarian values are predominant and closely intertwined with other types of values. Insofar as values depend both on individuals and on their situations, this analysis can be done in situations where non-utilitarian values do not risk being overshadowed by utilitarian values. This is the case of the subantarctic islands. Furthermore, these islands mobilise a small but diverse number of actors: between scientists, military, logistics personnel, volunteers and the staff of the reserve, the social actors have widely diverse trajectories, affiliations and socializations. We made surveys in 2016 and 2017 on the Marion Dufresne and at Kerguelen, consisting in series of semi-directive interview realized with all the types of people present. The interviews were analyzed with by the qualitative method of thematic analysis of content and a multivariate quantitative statistics. The particular context of the Kerguelen and the diversity of the people surveyed made it possible to identify a large number of values, mostly non-utilitarian and non-economic, and to begin to analyze how they relate to one another. We defined a dozen categories of values (authenticity, singularity, responsibility, scientific, aesthetic, memorial, affective, existence, spiritual, ...), and related them to the different attributes of nature, and different situations. We also analyzed which ones are shared or divisive, and linked these values and their emergence context with the context of socialization to nature.

*Speaker

Towards "no net loss" of biodiversity in urban development: adapting the mitigation hierarchy to a territorial scale

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Human activities, in particular urban spread, are a major cause of biodiversity erosion. In this context, the mitigation hierarchy of avoidance, reduction and offsetting impacts made by development projects has become an international regulatory tool whose aim is to achieve a "no net loss" of biodiversity. However, the efficiency of this tool has been increasingly questioned, in particular the ecological efficiency of the offset step.

In this study, we analyse how biodiversity is concretely included within the whole mitigation hierarchy with a multi-scale approach. To do so, we combine two complementary approaches: a quantitative analysis of biodiversity integration into the environmental impact assessment of small-scale, multiple development projects and a qualitative analysis of stakeholders' organisation and interactions through project development. Despite significant policy-related improvements at the project scale, ruptures in ecological connectivity and cumulative impacts on biodiversity are not correctly identified in environmental impact assessment. In addition, the avoidance step is totally neglected. The analysis of stakeholder interactions illustrates how biodiversity is streamlined by stakeholders and how interests, negotiations and power relationships can make the inclusion of biodiversity in project development difficult. At the "project scale", procedures lack flexibility concerning the localisation and opportunity of a project, indicative of why avoidance is not correctly implemented.

Upscaling the implementation of the mitigation hierarchy towards a territorial and strategic approach to biodiversity conservation at a "land-use planning scale" could help fill the current gaps associated with a project-by-project approach. In this perspective, we propose an anticipation framework for the mitigation hierarchy to set ecological priorities for avoidance and identify ecological similarities for offsetting in order to potentially reach "no net loss" objectives.

*Speaker

Anthropogenic opportunities and constraints for tropical savanna social-ecological systems: the CASEST project

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Ecological and Social Drivers of the Categorization of Spaces and Species

Protected areas (PAs) constitute the keystone of the conservation strategy throughout the world. However, the increasing landscape and habitat changes occurring around PAs have raised new conservation challenges. In many regions, including tropical savannas, interface areas (IAs) between PAs and the outside world are transformed by the expansion and industrialization of agriculture. These changes represent a major threat to biodiversity and induce the loss of key ecosystem services (ES) for local people's livelihood and wellbeing. Yet, if correctly managed, IAs may have positive impacts on biodiversity and on local development. The CASEST project aims to (i) build a conceptual framework for analyzing IA social-ecological dynamics, (ii) identify the anthropogenic drivers and leverage points of positive landscape connections and trade-offs at different temporal and spatial scales, and (iii) model IA social-ecological dynamics. In a first step, a quantitative literature review highlighted main research outcomes and challenges about IA social-ecological dynamics. From this work, we are building a conceptual framework for IAs that will be tested in three tropical savanna PAs, in Zimbabwe (Zone Atelier CNRS INEE Hwange), Brazil (Bodoquena National Park) and South Africa (the Garden route). In particular, we will combine (i) remote sensing analyses in order to quantify and map landscape changes at different spatio-temporal scales, and (ii) interviews with local and regional stakeholders in order to map ES demand and trade-offs, and uncover how stakeholders handle trade-offs. Finally, the two approaches will be integrated to model the feedbacks between local and regional anthropogenic drivers (e.g. demography, land uses, infrastructures, ES demand, social networks) and landscape changes at different scales, and therefore address the relationships between social and landscape connectivity. As a final outreach, the CASEST project aims to deliver an operational model for supporting local and regional policy making in the sustainable management of IAs.

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Categorizing spaces and species in the Anthropocene

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Two approaches for categorization can be contrasted.

On one hand, categorization can rely on scientific concepts issued from the internal dynamics of natural sciences, ecology. Variables, categories, used in the Madingley model can be considered as such an attempt.

On the other hand, categorization can be associated to concepts created by Conservation Sciences, the civil society, in particular environmental NGOs, rather documented by citizen sciences. Biodiversity indicators like species conservation status and red-list index, common bird index, flows and bundles of ecosystem services, are such categorizations.

These two categorizations differ in the way they consider the place of humans, their institutions, in ecological systems. While these are used in different models, scenarios, their combination should bring new knowledge, concepts. That might require deeper interactions with social sciences and humanities, integrating the logics of different institutions and representations.

*Speaker

Plural values associated with soil biodiversity among farmers in Europe

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Soils provide a wide range of ecological, economic, social functions, and many of them depend on soil biota. Human activities, such as agriculture, take profit from these functions, hence considered as ecosystem services, but some cultural practices widely spread threaten soil biodiversity.

In the context of the Biodiversa program "SoilMan", we investigated to what extent and how farmers include biodiversity into their soil management, comparing five European countries. Following the environmental pragmatism theory developed by John Dewey we investigated farmer's values associated to soil biodiversity by analyzing the arguments for their management decisions. Using the concept of plural values, we then assigned values to various categories besides instrumental values.

We used existing literature, in order to get first insights in values underlying farmers' management decisions. We conducted five focus groups, one in each country, and exploratory interviews to investigate soil biodiversity values within the variety of expressed values.

According to the traditional literature on farmers' behavior, we have found that instrumental values are of main importance in their management strategy. However, depending on their cultural background, our results suggest that other valuation processes can also play a role in farmers' management choices. Farmers can for example favor their well-being, try to get independent from advisory institutions or protect biodiversity for itself.

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Delayed behavioral shifts undermine the sustainability of social-ecological systems

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Natural habitat destruction and fragmentation generate a time-delayed loss of species and associated ecosystem services. As social–ecological systems (SEs) depend on a range of ecosystem services, lagged ecological dynamics may affect their long-term sustainability. Here, we investigate the role of consumption changes for sustainability, under a time-delayed ecological feedback on agricultural production. We use a stylized model that couples the dynamics of biodiversity, technology, human demography and compliance with a social norm prescribing sustainable consumption. Compliance with the sustainable norm reduces both the consumption footprint and the vulnerability of SEs to transient overshoot-and-collapse population crises. We show that the timing and interaction between social, demographic and ecological feedbacks govern the transient and long-term dynamics of the system. A sufficient level of social pressure (e.g. disapproval) applied on the unsustainable consumers leads to the stable coexistence of unsustainable and sustainable or mixed equilibria, where both defectors and conformers coexist. Under bistability conditions, increasing extinction debts reduces the resilience of the system, thus favouring abrupt regime shifts towards unsustainable pathways. Given recent evidence of large extinction debts, such results call for farsightedness and a better understanding of time delays when studying the sustainability of coupled SEs.

*Speaker

Ecosystem services: a new form of considering ecological interactions in the categorization of spaces and species ? From the perspective of law science

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With the arrival of the term "ecosystem services" in policy discussions and then in positive law has changed the legal categorization of spaces and species. First, the attractive effect of ecosystem services, including in law, is or will not be without consequence on the place reserved for the legal protection of species. The legal consideration of ecosystem services will not be neutral with respect to species: it will be complementary to it, by addressing species that do not benefit legal protection as such. It can also create tensions by competing in a certain way, legal devices hitherto reserved for species. It can also create tensions by competing in a certain way, legal devices up to now reserved for species. Secondly, the territorial scope of the law cannot be indifferent to the legal consideration of ecosystem services. In fact, on the one hand, ecosystem services allow an opening to ordinary biodiversity; new areas of legal protection are and can be created. On the other hand, to the extent that ecosystem services are intended to create a bridge between nature and society, putting into perspective socio-ecosystems could also influence the determination of biodiversity conservation areas.

*Speaker

Does complexity improve viticulture landscape aesthetics? A comparison between different perceptions across Europe

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Ecosystem services related to biodiversity, including cultural services such as landscape aesthetics, are essential for agricultural production such as viticulture.

The European research BiodivERsA project VineDivers aims at linking ecosystem services and vine production, in an integrative approach including both landscape structure and cultural practices (cover-crops *versus* bare soils), in vineyards of Austria, France, Romania and Spain.

In this study, we investigated if landscape complexity and soil management practices (1) provide cultural ecosystem services and (2) influence people willingness to buy wine, comparing the obtained results between the four countries.

We implemented a questionnaire based on photographs about biodiversity perception and visual aesthetic evaluation in each country. Each questionnaire used representative pictures of the respective studied area. Inhabitants of the studied areas, including local winegrowers, as well as visitors were asked to answer our questions.

While differences can be observed between the countries, overall, our results highlighted the effect of landscape complexity and soil management intensity on cultural ecosystem services provision. This allows us to discuss the global importance of biodiversity for wine-producing regions on both cultural and economic perspectives.

As consumers are more and more aware of ecological issues in viticulture, cultural ecosystem services associated with environmentally-friendly wine production could be an economic and social asset for rural regions.

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Landscape Ecology

Time-lagged response of vegetation communities to agricultural landscape changes along the Sélune river, France

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Scheduled to begin in 2020, the removal of two dams on the Sélune River, Manche (France) will be one of the largest river restoration projects undertaken in Europe. Expected consequences of dam removal include benefits from restoring more natural flow and sediment regimes but also impacts on biodiversity and associated ecosystem services due to changes in landscapes and agricultural dynamics. It can be challenging to discern such shifts while natural ecological and physical processes have been suppressed or altered since the installation of dams in the 1920s. Long-term analysis is a necessary step to provide knowledge on how present conditions came about and understand current patterns before analyzing the consequences induced by dam removal.

Changes in landscape composition and configuration is considered to be one of the main drivers behind biodiversity patterns. An often neglected issue concerns the temporal scale of biodiversity response to landscape change. Here, we investigated the response of vegetation communities to compositional and configurational changes in the landscape, over 10 years. We performed exhaustive vegetation surveys in fields located in 9 1 x 1 km² agricultural landscapes, distributed from upstream to downstream, which are selected to represent a gradient in landscape heterogeneity. In total, 37 fields were sampled pertaining to three habitat types constituting a perturbation intensity gradient: extensive wet meadows, grasslands and cereal fields. First results showed that species richness and diversity were more related to past than to present-day landscape composition.

Our results highlight the importance of taking account of time to explain current patterns of vegetation communities. It emphasizes the importance of long-term observations to understand some ecological patterns that would be missed in short-term studies. We suggest that care should be taken when assessing the effectiveness of the Sélune river restoration as time delays between dam removal and its consequences may occur.

*Speaker

Forest fragmentation shapes the relationship between local and regional richness in plant communities

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Local richness (alpha-diversity) is the result of an environmental filtering of a larger (regional) pool of species available at a coarser spatial resolution (gamma-diversity). This spatial nestedness constrains the alpha-gamma relationship towards either linear (cf. proportional sampling) or curvilinear (cf. community saturation) patterns. Here, we assume that forest fragmentation shifts the AGR from a linear, at low fragmentation, to a curvilinear pattern at high fragmentation, especially so for forest specialists. Across nine 5km x 5km landscape windows in northern France, we surveyed 116 forest patches scattered across three different levels of forest fragmentation: none (fake patches within a forest matrix); intermediate (connected patches within a matrix of grasslands); and high (isolated patches within a matrix of crop fields). Plant species richness of both forest specialists and generalists was surveyed at five nested spatial resolutions: 1m²; 10m²; 100m²; 1000m²; and total patch area. We used linear mixed-effects models to test, for each pair of nested spatial resolutions and for forest specialists and generalists separately, whether the fragmentation level interacts with gamma diversity while controlling for the effect of patch characteristics (size, area and age), habitat quality (soil and light conditions) and heterogeneity (proportion of forests within the landscape). For forest specialists, we found an interaction with a curvilinear pattern at high fragmentation level in two out of ten pairs of nested spatial resolutions (100m² vs 1000m² & 100m² vs total patch area). For forest generalists, the interaction appeared in the other eight pairs of nested spatial resolutions and was reversed, with a curvilinear pattern at low fragmentation level. This suggests that fragmentation influences the alpha-gamma diversity relationship differently for forest specialists and generalists and thus should be taken into account, in addition to patch characteristics and habitat quality and localization, when predicting local richness from the regional species pool.

*Speaker

Landscape genetics of a montane pond-breeding amphibian in ski resorts

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Linear human infrastructures can act as ecological barriers for animals and limit gene flow within a landscape. If effects of roads and railways on animal movement have been widely studied, effects of infrastructures related to mountain activities like ski pistes and ski lifts are less well known. In order to quantify the ecological permeability of ski resorts, we implemented a procedure involving Bayesian clustering methods and circuit theory applied to landscape genetics, allowing to estimate resistance values of the landscape. The model species is a pond-breeding amphibian, the European common frog (*Rana temporaria*), for which we used eleven microsatellite markers. We analyze to what extent genetically different groups can coexist in ski resorts at a very small spatial scale, and test the hypothesis of isolation by distance for distances inferior to 1 km. We quantify the contribution of different variables related to topography (such as slope, wetness index, elevation) or land cover and human activity (presence of ski runs and roads, vegetation) on the genetic distances. Our results are relevant in a perspective of conservation in human-transformed mountain landscapes.

*Speaker

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Scale of community assembly: Small birds in boreal forests

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Spatial scale has a leading role in wildlife ecology and habitat suitability studies. The influential role of scale in ecological interactions has not yet been clarified in previous studies. In this study on a group of small birds in boreal forests of Finland, we found possible patterns of relationships between species composition and habitat characteristics in different spatial scales. Additionally, we recognized the most influential spatial scales for each relationship. We followed a multiscale process of landscape analysis in GIS (Geographic Information System) by quantifying different habitat variables in different size buffers from 50m to 10km around bird count points. We combined habitat data with bird data (abundance and richness) in GIS. This has been provided the possibility of comparing bird composition, as well as their abundances and diversity in comparison to habitat characteristics in different scales. Our calculations resulted in knowing the most important buffer sizes or scales for each habitat variable using AIC (Akaike Information Criterion) calculations in R. For example, some results show the high importance of small (100-250m) buffers in composition and suitability of habitats. We also, achieved interesting results related to patterns of relationships between abundance-diversity parameters and habitat characteristics in different scales.

*Speaker

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How agricultural landscape dynamics have shaped habitat selection in Grey partridge (*Perdix perdix*) over the past two decades?

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Changes in agricultural practices have reshaped agricultural landscapes. They have triggered a drastic decline of spatial and temporal heterogeneity leading to changes in habitat quality and food resources for birds. Consequently, a severe decline in European farmland birds has been observed during the last decades. As studies that have demonstrated changes in habitat selection in response to land cover variation are rare in birds, we investigated whether, and if so, how habitat selection patterns have varied over the last 20 years in Grey partridge, an iconic farmland species, which has experienced a severe decline since the 1950s.

We used a long-term (1997-2017) dataset on Grey partridge occurrences collected in the Long-Term Socio Ecological Research platform (LSTER) "Zone Atelier Plaine & Val de Sèvre", Western France. We investigated changes of land cover across years running species distribution models. We assessed the dynamic of landscape metrics' contributions, the strength of the relationship between landscape features and partridge occurrence, and the dynamic of habitat quality over time.

Our results suggest that over time, Grey partridge occurrence has become less influenced by the distance to predator reserves (woodlands and urban areas) and more by permanent landscape covers (i.e. road/pathway and hedgerows densities). We discuss the shift of habitat selection with the change in the size and quality of suitable patches.

*Speaker

Combining connectivity and habitat suitability models as decision-making tools: a case study in the south of France

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Landscape connectivity, the degree to which a landscape impedes or promotes flows among resource patches, is an essential characteristic to maintain species long-term viability. Connectivity results from the interaction between landscape characteristics (composition and spatial organization of landscape elements) and the capacity of movements of the organisms considered. The spatial elements that influence the landscape connectivity is a central question in conservation ecology with direct implications for land planning. From broad-scale to fine-scale, movements across the landscape matrix are a key ecological process that influences the distribution, the survival, and maintenance of animal populations, especially in fragmented and heterogeneous anthropo-ecological systems. Here, we present preliminary results of spatially explicit habitat connectivity analysis. We analyzed the habitat suitability and the connectivity of the landscape using a set of animal species selected based on their sensitivity to structural and functional connectivity. We used Species Distribution Models (SDMs) in combination with connectivity analysis based on graph theory. The output maps of SDMs were validated by a combination of statistical assessment and expert knowledge. Least-cost corridor analysis was used to develop a resistance map in relation to weighted distance and the probability of connectivity index used to measure the level of connectivity in the landscape matrix. The methodology was applied in a study site located in the south of France, which includes the Etang of Thau and the terrestrial lands adjacent to it. This site is of particular ecological interest due to the presence of several protected areas, and an application interest due to the pressures from development and the upcoming implementation of territorial coherence program. The landscape-based approach used represents an example of decision-making tools useful for stakeholders but also will highlight the necessity to use connectivity models as a complement of SDMs.

*Speaker

Assessing spatial priority of Green Infrastructures using morphological analysis: a European approach

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Landscape connectivity is considered a key issue for the conservation of biodiversity, natural ecosystems stability and integrity, and ecosystem services that depend on fluxes of organisms and matter. Highlighting the spatial elements that influence the connectivity is a central question in conservation ecology with direct implications for land planning. Within this context, we need to gain a better understanding on the role of landscape connectivity for biodiversity by improving our ability to build efficient biodiversity networks (e.g. ”Trame Verte et Bleue” in France). The European project BiodivERsA IMAGINE investigates how sustainably managing Green Infrastructure (GI) can succeed on a regional and landscape level. Networks of healthy ecosystems provide cost-effective alternatives to traditional ’grey’ infrastructure and offer many other benefits for both human dwellers and biodiversity. GI is a strategically planned network of natural and semi-natural areas designed and managed to deliver a wide range of ecosystem services. With the implementation of the GI Strategy by the European Commission, the protection, restoration, and creation of GI become an integral part of territorial spatial planning. As part of the IMAGINE project, we selected six case study sites across Europe to analyze spatiotemporal key trends in the landscape pattern of GI cover. We applied Morphological Spatial Pattern Analysis (MSPA; Soille and Vogt, 2009) to classify GI according to seven categories (core, islet, perforation, edge, loop, bridge, branch) corresponding to different potential functional roles on six study sites across Europe. A productivity index, the Normalized Difference Vegetation Index, was used to provide complementary information on GI. The landscape-based approach used represents an example of decision-making tools useful for local experts and stakeholders to integrate landscape-scale metrics, and processes that could be in the perspective of establishing a comprehensive GI strategy implemented at the EU level.

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Past and current landscape heterogeneity drives functional structure of plant and bird assemblages

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Landscape heterogeneity, characterized by habitat composition and configuration in space, is a major driver of biodiversity. It indeed affects species movement and dispersal, driving species coexistence. Responses may be dependent over time depending on the species ability to persist and propagate after landscape modifications.

This study aims to determine the effects of the current and past landscape heterogeneity on two contrasted groups: plants and birds. We used a functional approach to understand the mechanisms underlying the responses of these organisms to landscape heterogeneity. We recorded landscape heterogeneity for three dates (2000, 1985, 1963) and assemblages of plants (hedgerows and grasslands) and birds in 20 landscape plots of 1km². We characterized the functional diversity and aggregated trait values using a set of functional traits related to dispersion, phenology and life strategy. We used null models to quantify the functional convergence or divergence for each trait and tested then for the effect of landscape composition and configuration on the non-random responses.

For both groups, we detected non-random functional diversity due to changes in species occurrence. Plant and bird assemblages responded rather to the past landscape than the current one, demonstrating a delay in their functional response. Functional diversity in plants generally increased with decreasing heterogeneity of landscape configuration (higher mean area). A high heterogeneity of configuration favored hedgerow species with a short flowering durations and seed persistence and heavy seeds. Landscapes characterized by high percentage of grassland favored grassland species with late flowering and high clonal reproduction. Birds with low a brood number and a long life span were favored by an increase in heterogeneity of configuration. This study offers interesting patterns in two contrasted biological groups and a new understanding on the mechanisms underlying the effects landscape changes on biodiversity.

*Speaker

Ecological monitoring of soil-vegetation cover of minor river basins landscape

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Catchment area is one of the fundamental geomorphological elements and it indicates landscape regularity expressed as systematic and repetitive dependence of slopes, soils, location and activity intensiveness of both fluvial and lithogenic flows. The research objective is to assess the dynamics of soil-vegetation condition of river basins. Research object. The Klyazma river basin area located in European Russia on the East European plain, refers to the Volga basin which belongs to the close Caspian basin. Research methods. Basin approach has been used for the research. The research has been carried out applying geoinformation systems and remote data. For the integrated characteristic of soil and vegetation cover of minor river basins ecosystems soil productive potential (SPP) index, suggested by the authors, has been applied. It characterises the ability of natural or anthropogenic-natural ecosystem under certain soil-climatic conditions to produce phytomass and averages phytomass reserve, produce, crop, humus content, soil-ecological index. NDVI (Normalised Difference Vegetation Index) is suggested to be applied as a generalised, efficient and monitoring index of soil-productive potential determined by remote method. Results: Minor river basins creating the Klyazma catchment area differ in their peculiarities of soil-vegetation cover.

The highest SPP in the Klyazma basin refers to the Nerl river, the largest and the most diverse in landscape. Agricultural land here adhere basically to grey forest soil, possess high SEI and crop, whereas natural ecosystems productivity is low and it is compensated with the considerable phytomass reserve of forest massifs, located on turfy-podzol soil.

A group of minor river basins (the Sudogda, the Kirzhach, the Peksha river basins) can be distinguished which are characterized by maximal and stable values of soil-productive potential (according to NDVI).

The intensity of the Sudogda basin ecosystems transformation is traced through the indices of forest vegetation assessment (area and wood reserve) their dynamics.

*Speaker

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Relationships between landscape structure, host community and the prevalence of tick-borne pathogens (*Anaplasma phagocytophilum* and *Borrelia burgdorferi*) in small mammals

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Land use changes, by reshaping hosts and vectors communities and their dispersal, can modify the circulation of vector-borne pathogens. Understanding how the landscape structure influences the circulation of these pathogens is therefore useful to create vector-borne diseases risk maps and for developing preventive measures.

Small mammals can be important hosts for larval *I. ricinus* ticks, the main vector tick species in Europe. Because small mammals are also reservoirs of tick-borne infectious agents, identifying the main drivers of their prevalence in small mammals is a key issue in understanding the ecology of these infectious agents. In this aim, we investigated the prevalence of two tick-borne infectious agents in small mammals and assessed their relationships with landscape structure and host community.

During two years (2012 and 2013), we trapped small mammals in 24 sites situated in different landscape contexts (in forest, and in agricultural landscapes woodland patches and hedgerows, with various surrounding land covers and hedgerow network densities). We trapped 608 individuals in which *Anaplasma phagocytophilum* and *Borrelia burgdorferi sensu lato* were searched by real-time PCR methods. We used graph theory and least cost paths analyses applied on each studied species in order to compute appropriate landscape connectivity measures. We also computed landscape composition and configuration variables at various scales (from 50 m to 500 m radius buffers around sampling sites).

Landscape Ecology

The prevalence of *A. phagocytophilum* was positively associated with the proportion of wooded habitats in the landscape, whereas the prevalence of *B. burgdorferi* s.l. was positively associated with samplings at forest-pasture ecotones. The small mammal community species richness explained a substantial part of the prevalence of *A. phagocytophilum*, but not that of *B. burgdorferi* s.l. The importance of the life history traits of infectious agents and host-vector meta-communities in relation with landscape structure, and some research perspectives, will be discussed.

Modelling landscape connectivity at local and regional scales using an empirical quantification of resistance: an application for the conservation of the greater horseshoe bat

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In the context of habitat fragmentation, evaluating landscape connectivity for identifying and protecting linkages have become central challenges in applied ecology and conservation. This connectivity is usually assessed with landscape modelling, but several studies pointed out the importance of parameterization with empirical, biologically relevant proxies of factors affecting movements and also the need to validate the models with independent dataset. Here we used the least-cost path analysis (LCP) incorporating quantitative, empirical data about fine-scale behaviour of the greater horseshoe bat *Rhinolophus ferrumequinum* – a widespread bat species in Europe, with major declines recorded this century, particularly in northern Europe – to build up a model of functional connectivity in relation to landscape connecting features. We then validated the accumulated costs surface from the LCP model with two independent datasets, one at an individual level with radio tracking data and one at a population level with acoustic data.

When defining resistance at fine scale, we found that the probability of bat presence in a hedgerow is higher when the distance between hedgerows is below 38 m, and decrease rapidly when gaps are larger than 50 m. The LCP model was validated by both datasets: using acoustics, bat presence was higher in areas with lower accumulated costs, and radio tracked bats foraged more likely in areas where accumulated costs were lower.

Landscape Ecology

Finally, we applied this connectivity model at a regional scale (200 km wide) to identify relevant corridors between important breeding and wintering sites. The model output was tested against data from more than 2180 PIT-tagged greater horseshoe bats controlled in > 300 sites distributed throughout the Nouvelle Aquitaine region and bordering departments, allowing linking individual movements between these sites as a function of their connectivity.

*Speaker

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How do local factors and landscape affect insect-pollination efficiency in oilseed rape?

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More than 70% of the crops depend on insect pollination and the world's area of these crops is increasing while the pollination service is endangered. Pollination service depends on the community of pollinators which is influenced by local (ecological niche) and landscape factors (dispersal) through the support of floral resources (organic farming, oilseed rape, semi-natural habitats), the provision of nesting sites (semi-natural habitats) or the connectivity (length of the boundaries between the habitats).

The aim of this study was to understand how local and landscape factors interact to influence the efficiency of insect pollination in the oilseed rape (*Brassica napus*). Oilseed rape plants used as phytometers (832 since 2014) were placed in the LTSER "Zone Atelier Plaine & Val de Sèvre" in three crop types (oilseed rape, grassland, cereal) which differ in their local floral diversity. Fields were located in landscapes varying in their densities of organic farming (e.g. from 0 to 89% in a radius of 500m), oilseed rape (0-63%), semi-natural habitats (0-40%) and the length of the boundaries (7-30 kms). Landscape variables were quantified in buffers of radius ranging from 500m to 2000m.

We showed that local and landscape factors at a small spatial scale (500m) influence grain production. While grain production is more important in oilseed rape fields, it's negatively influenced by the percentage of oilseed rape in the three crop types and positively affected by organic farming in cereal fields. We further explored how local and landscape factors affect the influence of the pollination processes (entomogamy, autogamy, anemogamy) on grain production using an experimental approach. The flowering stems of the phytometers were subjected to different treatments excluding either wind- and insect-pollination, only insect-pollination, or pollination by the largest insects. Our analysis showed that local and landscape factors influence grain production independently of the pollination process.

*Speaker

Efficiency of conservation biological control depends on interaction effects between landscape and pesticide use intensity

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Control of crop pests by their natural enemies provides a valuable but poorly quantified ecosystem service. Many studies have addressed the multiple scale drivers of pest control but results from such studies appear variable, if not equivocal. The variability of landscape responses can result from its modulation factors by local practices, among which pesticide use intensity which affects pests and natural enemies and could be a major driver of natural pest control. In this study, we examine the relative contribution of pesticide use and landscape on biological control along a double gradient of pesticide use and landscape simplification.

Eighty commercial fields were monitored during three years in four contrasted regions in France. Biocontrol in each field was estimated using three different types of sentinel preys (*Ephesttia kuehniella* eggs, *Acyrtosiphon pisum* aphids and *Viola arvensis* seeds). For each one, the interaction effects of landscape variables with the intensity of pesticide use on predation patterns were analyzed.

*Speaker

Landscape Ecology

The predation of weed seeds was negatively influenced by both pesticide use and landscape simplification, without interaction between the two scales. The predation of *Ephestia* was negatively influenced by landscape simplification only in case of low pesticide use intensity whereas the effect was positive in case of high pesticide use intensity. There was a significant interaction between pesticide use and the length of interfaces between crops and woods on the predation aphids. These landscape variables had a positive effects on the predation of aphids in case of low or medium pesticide use intensity but a negative effect in case of high pesticide use intensity. These results could indicate that in fields with low local pesticide use, landscape complexity enhance biological control whereas in intensive fields, the presence of semi-natural habitat could be unsuitable for natural enemies adapted to intensive situations.

Modeling link complexity between crop yield, ecosystem services and multiple landscape representations in the Coteaux de Gascogne region

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What is the relative influence of landscape and agricultural practices on crop yield? Are landscape effects on yield explained by an indirect effect on biodiversity and ecosystem services such as predation of pests? Which representation of the landscape is most relevant to explain these effects?

We will attempt to answer these questions from a dataset collected in the Vallées et Coteaux de Gascogne by implementing a Path Analysis (PLS-PM, following Sanchez 2013). Twenty plots of straw cereals were measured for various aspects of yield, pollination and predation services, and bird and plant diversity. A compendium of phytosanitary practices has been produced. Four types of representations were used to describe the landscape structure: land use, spatial variations of the vegetation index derived from hyperspectral images, LIDAR data, and the ecological landscape, as perceived through bird communities.

PLS-PM is one of the many statistical methods for combining multiple blocks in a single analysis. Like Puech et al (2015) or Quinio et al (2017) among others, we will highlight the contributions of this statistical approach to landscape ecology, and some limitations.

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*Speaker

Degradation of the Ararat valley ecosystem as a result of change of ground waters level

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The Ararat Valley is situated in the South Caucasus in Armenia republic at an altitude of 800–950 meters above sea level. It stretches from northwest to southeast for 120 kilometers, it is 10–30 kilometers wide. The Araks river and its valley is a significant groundwater reservoir in this region. Since the old days, the Ararat Valley has been regarded as a breadbasket of Armenia, and today it remains a major agricultural region in the country.

The flatland part of the Ararat Valley has a typically semi-desert landscape with its specific semi-desert soils. Its soils range from hummocky sands and alkaline and saline soils to water-logged soils. A significant part of the valley is managed; this part has irrigated meadow brown soils. The non-managed part is covered with xerophilous and halophilous vegetation and *Artemisia* (sage), whereas irrigated meadow brown soils bear fruit orchards, vineyards, and various agricultural plantations.

Currently, in the Ararat Valley, land uses are linked with the enhanced development of fish farming, which requires artesian water in great amounts. As a result of unsustainable management of the natural resources, the water level of the artesian basin has declined by 8–15 meters, and the groundwater level has gone down by more than 3 meters. This has brought about a number of adverse processes: the drainage of agricultural soils, increased irrigation depth, losses of soil organic matter, and so on.

The change in the soil moisture regime has led to soil aridization in some areas of the Ararat Valley. Today it has become evident that the entire ecosystem's environmental capacity has been significantly overused. The main mistake was transforming the area to make it perform functions that were alien to its nature as a desert/semi-desert geographic landscape.

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Additive effects of ecological continuities drive plant assembly rules

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Understanding the influence of landscape connectivity on plant assemblages' structure is a central issue in landscape ecology. So far, empirical studies showed contradictory results, possibly due to (1) an inaccurate assessment of landscape connectivity prioritizing the effect of some habitat types among others, when landscape connectivity may be best estimated accounting for the different ecological continuity types independently and (2) the absence of consideration that plant dispersal vectors may be positively or negatively influenced by the different continuity types.

Here, we studied plant assemblages in agricultural landscapes comprising three main habitat types: woodlands, grasslands, and crops. Using 25 habitat patches per habitat type, we analysed the effect of connectivity on plant assemblages' similarity between pairs of patches for three dispersal modes (animal-dispersed, wind-dispersed and unassisted). Plant response was evaluated relatively to the random similarity expected based on the species pool. We measured connectivity using circuit theory, combining continuities provided independently by wooded, grassland and crop elements.

Plant assemblages' similarity in woodland and grasslands was better predicted by accounting for wooded, grassland and crop continuities together rather than by the continuities of the focal habitat alone. Assemblages' similarity was not related to connectivity in crops. In particular, connectivity provided by wooded continuities increased assemblage's similarity for both wooded and grassland assemblages. Responses were modulated though by dispersal mode. Animal dispersal in woodlands was promoted by wooded but disfavoured by crop continuities whereas in grasslands, it was promoted by crop and woodland ones. Wind-dispersal species was independent of connectivity. Dispersal of unassisted species was promoted by wooded continuities for grasslands.

Our study demonstrates that the simultaneous consideration of the different continuity types to assess connectivity improve our capacity to predict plant community assemblages. Specifically, some assembly rules related to plant dispersal were determined by the additive effects of the different ecological continuities.

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Palaeoecology: How today's ecosystems became
what they are?

Past human occupation of the Guianese forest: what wood charcoals tell us

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Past human impacts on Amazonian forests are now widely and increasingly documented. Whether in terms of floristic composition or of soil structure and contents, testimonies of past occupation and land use are clearly visible. Though still poorly studied from an archeological point of view, the Guianese forests make no exception and reveal their own anthrosols, rich in charcoals and pottery sheds. The LongTime project (**Long Term Impact of ancient Amerindian settlements on the Guianese forests**) aims at defining the impact of pre-Columbian activities on forest structure and composition through a pluridisciplinary approach, including anthracology. Soils under different types of vegetation (bamboo thickets, liana forests and high canopy forests) were sampled in the Nouragues Reserve, French Guiana, in order to detect gradients of pre-Columbian activities. Peculiar sites detected by LiDAR were also investigated: a 'ring-ditched hill' and a 'ring-ditched plateau', which are sites surrounded by ancient manmade ditches. Two sampling protocols were carried out and will be discussed here: the first one is to harvest charcoal on soil profiles, the second one to collect several samples with a soil auger on a 1ha area around each profile, in order to improve the sampling of floristic diversity. The first results given by charcoal identification reveal a high floristic diversity in some of the studied areas and the presence of useful tree species. First 14C datings point several periods of occupation on some sites and give an insight into the burnt vegetal communities present and used by humans at these time periods. These results will be further analyzed in combination with present-day floristic composition and other pedological bio-proxies such as soil structure, micromorphology and phytoliths contents.

*Speaker

Pip shape echoes the origins and history of modern grapevine diversity (*Vitis vinifera* L.)

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Since the Iron Age, grape cultivation became a central aspect of French culture, economy and geopolitics. From an ecological point of view it also deeply shaped agricultural, ecosystem and landscape dynamics. The structure and identity of modern French wine regions started to take form during the first centuries A.D. and were maintained since then. Even if many aspects of ancient wine production are nowadays well documented archaeologically, little is known about the cultivated grape itself: what are the biological, geographical and chronological origins of modern grape varieties, or "cépages" still remain unclear and very little is known if and how they were assembled to produce wine in the different regions. Archaeological excavations provide large number of grape pips, relatively well preserved, due to waterlogged conditions in some structures. Morphometrics, the quantitative description of shape, helps to characterize these ancient pips sampled from different sites and periods, comparing them to reference collections of modern pips of both wild and domesticated grapes. We first explore the shape diversity of modern *Vitis vinifera* seeds in relation to subspecies (wild vs. domesticated), main uses of grapes, geographic origin and various phenotypic and genetic characteristics of varieties. The comparison of ancient to modern morphotypes brings evidence of the cultivation of an important, and unsuspected, varietal diversity in southern Gaul which seems to occur even at the scale of the individual site. For early times of wine production in Gaul, some pips present a wild morphotype. The evolution of "domesticated" morphotypes are quantified in time and space.

*Speaker

Palaeolithic local flora in dry and semiarid Mediterranean regions: an insight from plant macroremains

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Archaeobotanical macroremains are good markers of the local flora and their study improves our knowledge on how human groups used the vegetal resources and how the vegetation has changed through time. Combining anthracology and carpology is essential, since we can obtain more information and improve the interpretation of plant remains. The agents primarily responsible for the accumulation of the material in the archaeological deposits were the human groups who collected plants as firewood for their hearths or other uses. Probably, most of the carpological remains were carried to the cave by humans, with the firewood, as food, etc. In this communication, we present archaeobotanical results for several Palaeolithic sites located in the E-SE dry and semiarid Iberia, covering a wide sequence from MIS 5 to MIS 2.

In general, sequences show that conifer forests dominate Palaeolithic landscapes, especially those species of cold and dry or sub-humid conditions (*Pinus* type *nigra/sylvestris*, *Juniperus* spp.), the warm ones being relegated to southernmost locations (*Pinus pinea*, *Pinus halepensis*) or warm periods (MIS 5e). Open formations of *Juniperus* sp. and Fabaceae, sometimes in association with *Ephedra* sp. and *Artemisia* sp., spread during phases of greater aridity. The low diversity of shrubs and small plants possibly indicates the presence of open herbaceous steppe formations.

This information indicates that during the glacial periods, most of the region had similar bioclimatic conditions to those currently prevailing in the Iberian summits of the supramediterranean belt. Thermophilous species took refuge below the 40th parallel North during the Last Glacial Period, and rainfall regime would be dry in Alicante and semi-arid in the Murcia area.

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Historical dynamics of *Quercus* spp. versus *Fagus sylvatica* in forests of the Lorraine Plateau (France) documented by pedoanthracology

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In central European temperate deciduous forests, *Fagus sylvatica* is among the most competitive tree species. However, locally the oaks stand (*Quercus petraea* or *Q. robur*) are often dominant and beech remains sporadic. These two species are potential trees of the natural forest dynamics, but their distribution and frequency is influenced by on-going and past forest management.

On the Lorraine plateau, we find oak trees on well-drained station where theoretically the beech should dominate, while it is supposed to be limited on hydromorphic soils. The actual ecological niches of these forest species remain unclear. To explore that key issue for forest management we defined two research assumptions: i) Oak species have been favored by past and present forest management ii) while beech has been limited in its expansion.

To test these assumptions, we conducted a soil charcoal analysis on the Lorraine Plateau. We sampled 12 forests in brunisol and luvisol soil types. For each site, one trench (10m) was opened to determine the pedological context and for soil sampling. Macroscopic charcoal assemblages were extracted of the soil samples by wet and dry sieving. The charcoal pieces were then sorted-out and taxonomically identified.

Preliminary results based on 1000 charcoal pieces clearly highlight the anthracological potential for our questioning. *Quercus* is the dominant genus (55% of the identified pieces) of the charcoal assemblages, *Fagus* (15%) is identified in almost all sites. Other occurring taxa are *Carpinus* (12%), *Pomoideae* (1.6%) and *Prunus* (0.65%). The radiocarbon dates indicate that oaks and beech have been growing together at local scale for millennia in well-drained soil conditions. Soil charcoal analyses bring new arguments for the hypothesis that the historical forest management influenced significantly the current distribution of forest species to a state that does not reflect the natural potential of the mature forest of the Lorraine Plateau.

*Speaker

Indicators of past ecosystem dynamic on current soils in Lorraine (France)

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Developed between geological substratum, atmosphere and biosphere, soils have a key role on the biodiversity and are ecological indicators of the ecosystem health. Soils evolve under natural environmental modifications. But the belief of current pristine soils is a fake. Indeed, for at least 8000 years, they are also under human forcing influence with a significant impact trend through the modern time (Anthropocene). The soil resilience may be complex to measure with current markers but soils are important archives. They record past human activities on landscapes and ecosystems dynamics through their development and the material they contain (charcoal, wood, pollen, anthropogenic artefacts...). Archaeology is then a good way to approach those archives, giving a chronological frame to the researches on soil dynamics.

This presentation will illustrate new aspects of the research in Lorraine (north-eastern France).

Recent results highlight a strong erosion phase, related to human and natural factors, at the end of the Iron Age (450-50calBC) and a loamy clayey soil degradation, maybe related to both roman drainage and climatic water stress, at the beginning of our era (100-200c. AD). Ongoing works using paleoclimate research attempt to precise the climatic contribution on both processes.

Multi-disciplinary researches are starting using approaches from archaeology, soil science, geochemistry and botanic. Forested ecosystems areas associated to charcoal production are studied in the Vosges Mountains (Lorraine) to investigate the influence of an historical human activity on current soil pollution and/or fertility.

*Speaker

Did the past and recent human activities affect the Northern Vosges Mountains ecosystems during the last three millennia?

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In the Northern Vosges Mountains, populations have extensively used the forest resources for their daily use as well as to supply xylophagous industries. Several archaeological remains and archives highlight the occurrence of many human activities: old ones as agro-pastoral activities or semi-industrial like glass-making, mines, metalworking, and more recently military activities (Bitcherland). Nevertheless, the beginning of these activities as well as the first human impacts on the Northern Vosges Mountains ecosystems have not been clearly identified or dated. In attempt to highlight the anthropogenic impacts and to identify their beginning in the Northern Vosges Mountains, a multiproxy analysis, with pollen, non-pollen palynomorphs (NPP), seeds analyses and geochemical analyses (XRF), is carried out on several cores sampled in peatlands close to industrial sites. Palynological studies show that the environment in the Northern Vosges Mountains was extremely wooded during the three last millennia. Three phases of human impacts, more or less significant depending to sites, occurred. During the Late Neolithic phase, crops appeared and other anthropogenic indicators - like weeds, ruderal and pastoral taxa - as well as coprophilous fungi and carbonized particles increased, showing the beginning of the agropastoral practices. The Gallo-Roman period is characterized by the increased of pastoral indicators and of *Quercus*, probably privileged to gather acorns. At this period, geochemical analyses show the beginning of the semi-industrial activities with the increase of metallic trace elements inputs in the peatland, especially lead. During the Middle Age, the decrease of all trees taxa and the increase of anthropogenic taxa highlight a very important land use consistent with the establishment of human population with castel or abbaye foundation. Moreover, study of local vegetation in the peatland like mesohygrophilous and aquatic taxa as well as *Sphagnum* shows for example the increase of the water level in the peatland at the Middle Age.

*Speaker

Ecological functioning and Ecosystem evolution in mosaic forest-savannah and human presence context for 3000 BP at Lope National Park (Gabon)

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Pollen collected in surface samples and cores are studied in Lopé National Park (LPN) in Gabon in order to (i) establish the modern pollen-vegetation relationship; (ii) the forest-savannah dynamic and (iii) the human impact on this dynamic. In this aim, Correspondance Analysis (CA), and linear regressions are used in both vegetation survey data and a set of 23 surface pollen samples. The CA results are concordant with published data, distinguishing closed vegetation habitat from opened ones in pollen assemblages, and two vegetation types (savannah and forest) in plant taxa. This last one shows a difference between vegetation near the marsh and the one beyond. The border between the two areas seems to be around 30-40 m from the marsh margin. Unfortunately, even if all the plant associations are well represented in pollen assemblages, those last ones cannot clearly distinguish each of them in term of groups. We also used Davis indices to better understand this modern pollen-vegetation relationship. The results indicate that Associated taxa are predominantly pioneer taxa such as *Aucoumea*, *Anthocleista*, *Barteria*; The Over-represented taxa correspond to taxa often indicators of a perturbation or a shift in the environmental parameters, they are taxa such as *Cnestis*, *Alchornea*, *Pentachletra*, *Elaeis guineensis*, etc. The Weakly associated taxa are a mix of over-represented and under represented taxa. They correspond to taxa wich grow together as a population. They are Asteraceae, Cassia-type, Cyperaceae. Long term pollen and multy proxy analysis show a turn over in environmental settings in LPN.

Keywords: forest-savannah mosaic; marsh; pollen analysis; Davis indices; Central Gabon

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Palaeoecology: How todaysecosystems became what theyare?

Are recent fires unprecedented? Paleoperspectives from the Greater Yellowstone Ecosystem (USA)

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The Greater Yellowstone Ecosystem (GYE), a mountainous region in western North America and home to Yellowstone National Park, is one of the last remaining, nearly intact landscapes in the mid-latitudes. In the summer of 1988, dry conditions led to large fires across 36% of the Park. That single year comprised the largest fire-fighting effort in the US at the time and cost over US\$ 120 million. Since then, the western US has experienced more large, severe fires with costs now exceeding \$2 billion per year. Are current fires unprecedented? Paleoecological data spanning the last 15,000 years allow us to compare recent events with the long-term variability of fire and assess both the drivers of past fires and their consequences on the landscape. Charcoal data from a network of seven sites in the GYE suggest that periods of high fire activity have occurred during times of high temperatures and pronounced drought, such as in the early Holocene and the Medieval Climate Anomaly. Fire thus emerges as a natural component of the GYE greatly dependent on changing vegetation, climate and weather conditions. Calibrated vegetation reconstructions show that, although no single fire has triggered long-term transformation of vegetation composition in the past, shifts in the fire regime coupled with climate variability have led to a spatial reorganization of vegetation, particularly at lower treeline. Recent fires in the GYE, which were seemingly unprecedented in terms of magnitude and impact, can be reinterpreted as the expected outcome of ecosystem dynamics when millennial time scales are considered. The longer perspective highlights the divergence of the societal and ecological definitions of ‘novel’ and ‘surprise’, with implications for conservation strategies in the future.

*Speaker

Woodland usage and fuel wood ecology: Linking historical information and kilns charcoal analyses in the northern Vosges (Pays de Bitche; France)

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Little research has been conducted to the landscape history and woodland usage in the Pays de Bitche area, although local past industries and landscapes indicates the possible importance of anthropogenic use of forest resources in the area. This appears to be a considerable gap for the understanding and management of local ecological systems, especially when considering that wood consumption and charcoal production was one of the main driver for forest degradation in low mountain ranges in central Europe.

Therefore, we developed a study of the past forest use for wood and charcoal. In this study we are presenting first anthracological analyses from charcoal production sites (kiln sites) to get a better understanding of the fuelwood usage and the local scale interlocking of deciduous trees (e.g. *Quercus* sp., *Fagus sylvatica*). And, we compare the anthracological data with historical written sources to link the historical information about wood consumption or protection and charcoal production. Through this innovative interdisciplinary approach, we try to gain a better understanding of the historical forest use and therefore the creation of the current forest system.

468 kiln sites were localized from which 76 sites were chosen for charcoal analysis. All in all, 7700 pieces of charcoal were taxonomical identified and the minimum size were estimated to get information about the used wood diameter.

Information about past wood consumption were gathered from historical records of trees selection by foresters. These records are selected when permitting chronological assessment and solid localisation in landscapes. They provides information for species, size and amount of trees that were harvested or/and maintained for each specific area.

We then compared the anthracological data and the trees selection records on areas where both practices were done. First results of our approach show a relevant complementary of the data. We present here those results.

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Fire, human and vegetation in Corsica during Holocene

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The Mediterranean regions represent less than 5% of the Earth's surface, but contain almost 20% of the world vascular plants species. Within the French Mediterranean area, Corsica houses the higher number of endemics species, and 32% of them are threatened. It is also the region, the most affected by forest fires. Corsica vegetation is in some way adapted to this disturbance but a change in fire frequency or intensity may lead to ecological, economical and human disasters. This paper presents the dynamic of vegetation–human–fire interactions for the past 12000 years as recorded by lake Bastani (Corsica, France). Well-dated sedimentary records of charcoals, pollen and fungal remains have been used to reconstruct past fire regime, land-cover and land-use changes. Fire is almost inexistent before 11 000 cal BP, then biomass burned strongly increases thanks to the development of the arboreal vegetation. After 6800 cal BP, the presence of *Pinus* sp. and *Erica* sp. in the canopy decrease, a mixed oakwood develops and fire signal returns low. From the Late Neolithic and Chalcolithic periods (ca 5500 cal BP) onward, fire regime changes meaningfully, according to the development of human activities: it is characterized by a high frequency and intense episodes whereas fuel is mostly herbaceous. At the end of the Iron Age (ca. 2300 cal BP), biomass burned decreases until the end of the Medieval period. A short-term increase in fire signal is recorded around 500 cal BP and then decreases for the last three centuries. Along the entire record, pollen richness increases with an acceleration from 5000 cal BP and human impact. However, we also found a negative correlation between the pollen richness and the fire signal. At the same time, the species turnover increases during periods of intense and more frequent fires.

*Speaker

Global fire history of grassland biomes

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Grasslands are globally extensive; they exist in many different climates, at high and low elevations, on nutrient-poor and -rich soils. Their distribution today is closely linked to human activities, fire, and herbivores, but they have frequently been converted into urban areas, forests, or agriculture fields, depending on the region.

Roughly 80% of global fire activity takes place in grasslands each year, for management or for agriculture purposes, making fire a critical component of grasslands dynamics. Given that the locations of grasslands have changed over time, we compare fire history reconstructions based on alternative classification schemes highlighting: 1) sites from modern grassland locations; 2) sites that were likely grasslands during the mid-Holocene; and 3) sites based on author-derived classifications. We also compare the grassland fire histories with forested sites only (mid-Holocene classification) and a global biomass burning reconstruction.

Taken together, the reconstructions indicate that burning in grasslands has followed a different trajectory than burning in forests during the Holocene. Globally, grassland burning increased from the early to mid-Holocene, reaching a maximum about 8000-6000 years ago; it subsequently declined, reaching a minimum around 4000 years ago. In contrast, fires in forests tended to increase during the Holocene until about 2000 years ago.

Additional research focusing on calibration, integrated vegetation, climate, and fire history analyses, and model experiments could greatly improve our understanding of grassland fire globally. It is already evident, however, that the different trajectories of burning in grassland versus forests globally during the Holocene has large implications for understanding changes in the global carbon cycle, as well as biodiversity, conservation, and land management in grasslands.

*Speaker

Biodiversity dynamics, land use and Holocene landscape of Northwest France

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Palaeo-ecology makes an important contribution to the understanding of biodiversity dynamics. Various studies using pollen stratigraphies have demonstrated significant correlations between Holocene plant diversity, climate and human activities.

This study aims to reconstruct and explain spatio-temporal trends in past plant diversity (alpha, temporal, spatial beta diversity) of Northwestern France during the Holocene period. This area is rich in high-resolution palaeo-botanical data. About fifty well-dated and high-quality pollen records from four different regions in the Armorican peninsula (Western Brittany, Morbihan Gulf region, Loire region, Eastern Brittany) were taken into account. All sampling contexts consist of peat bogs. Therefore it is possible to reconstruct the vegetation changes of the main long-term trends in great detail.

Studies in past plant biodiversity research have significantly increased after the introduction of the rarefaction technique. With the "expected number" of taxa independent of the number of counted pollen grains, the comparison between levels of a set of samples is meaningful. For the first time, rarefaction analysis was performed on a such great number of western French Holocene pollen sequences. Additionally an analysis was made on the development of a selection of vegetation groups represented in Armorican pollen records during the period under study. During the Holocene time span, the plant diversity and more generally the landscape underwent a set of major changes linked to far-reaching socio-economic transformations. The taxonomic richness increases steadily. Some spatio-temporal differences are observed. The increasing richness values correspond with the growing impact of human activities. At the same pace the number of vegetation groups at a regional scale provides insights on the level of landscape heterogeneity and the character of the landscape mosaic. The highest diversity is reached in the later Middle Ages. Most pollen records demonstrate a decrease in floristic richness since the 18th/19th century AD, due to agricultural intensification.

*Speaker

Unprecedented changes in lake functioning in the Anthropocene: assessment of lake ecological trajectories over the last millennium

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This study is based on a synthesis of research carried out on lacustrine archives by a multidisciplinary team since ten years. The 20th century was characterized by unprecedented changes in lake functioning due to local human impacts as outlined by two case study (Lake Igaliku in South-Western Greenland and Lake Remoray in the French Jura) and by a synthesis derived from the an extended dataset of 22 lacustrine records. A paleolimnological approach combining aquatic and terrestrial proxies evidenced the accelerated eutrophication of Lake Igaliku and Remoray consecutively to local agricultural intensification over the last century. In Lake Remoray, a critical threshold was crossed in 1975. The deep zone has since become " a dead zone " with a strong loss in biodiversity. In the extended dataset, the major changes in lake functioning were identified from the main shifts in chironomid communities. The probability distributions for the age of these shifts were derived from depth-age models and cumulated over the last 1300 years. This cumulative frequency curve combined to the individual ecological trajectory of lakes indicate that a strong shift occurred at the end of the 19th century. Before this turning point, ecological changes are asynchronous and mainly controlled by climate, whose impacts may be modulated by lake specific sensitivity and local human activities. The 20th century is characterized by a very high frequency of ecological changes and by the strength of the associated shifts in lake functioning. Local human impact (mainly eutrophication) is identified as the key driver of this unprecedented situation. Finally, this study shows that the Anthropocene corresponds to a paradigm shift in lake functioning (from climate to human control) and is marked by heavy loss in ecosystem goods and services.

Combining multi-variate palaeoecological indicators and mining closed gradual patterns for refining past lake dynamics and the induced ecological legacies

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The overloading of water bodies with nutrients is a widespread ecological alteration. A recent synthesis (CNRS, IFREMER, INRA, IRSTEA) shows that lake ecosystems are particularly concerned by the eutrophication process which results in: (1) ecological disturbances (e.g. invasive species, loss of biodiversity, algal and cyanobacterial blooms), and (2) public health problems (e.g. water quality degradation due to cyanotoxin production). This makes the restoration of eutrophic freshwaters an environmental top-priority and a key-issue for scientific research. Accurate assessments of the present-day lake ecosystems state are thus needed. Moreover, long-term retrospective models of lake dynamics must be developed concomitantly to the analysis of natural and anthropogenic modifications of the catchment, which enhance the external input of sediment and nutrients. Palaeoecological researches are therefore required because they characterize through time the lake's responses to cumulative changes caused by natural (e.g. climate) and anthropogenic impacts (e.g. vegetation clearance, agriculture). They furnish thus fresh insights into a good understanding of the ecological legacies which also determine current lake structure and function, and which must be considered for sustainable lake management. A palaeoecological research was conducted in the hyper-eutrophic Lake Aydat (837 m a.s.l.), located in the Chaîne des Puys (French Massif Central). The high resolution and multi-proxy analysis (pollen, non-pollen palynomorphs, diatoms, sedimentology) was combined to an approach of data mining (extraction of frequent (closed) gradual patterns of multi-variate indicators under temporal constraint) and allow to address the:

- (1) reference conditions of the lake (prior to extensive human impact) and its natural variability;
- (2) aquatic changes phases: timing, intensity, frequency, delay;
- (3)reversibility or directions in which the lake is driven by the long-term cumulative impact (e.g. loss of resilience, ratchet effect);
- (4) potential drivers: climate *vs* the diverse range of land uses;
- (5) degree of resistance/sensitivity and vulnerability of present-day lake ecosystems.

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Woodland management, biodiversity and tree rings: the view backwards forwards

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Looking on biodiversity and how it is affected by land use on a long-term, (pre-) historical scale is done by several proxies in the field of palaeoecology (pollen, plant carpological and animal remains, wood, charcoal etc.). Floral, faunal, community, and landscape diversity is shaped considerably by human action, for good or for bad, enriching or depriving. However, to understand today's and future biodiversity a long-term perspective is needed, which includes changes of diversity caused by land-using humans. One aspect in this discussion is the way woodland management has affected landscapes and species richness, past and present, including onsets, intensities and types of wood sourcing. A standard-with-coppice management was very common in central European landscapes since at least medieval times. Such stands are managed in a ca. 30 year clearing cycle, coppicing the smaller trees, and let grow some, commonly oaks, until 90 or 120 or more years old. The yield is both small diameter material for fire wood or charcoal, and construction wood for houses or ships, on the same sites. Today, rarely existing, its high structural diversity supports endangered species like the butterflies *Euphydryas maturna*, or *Eriogaster catax*, or the bat *Myotis bechsteinii*. Dendrochronology can help find out the onset and intensity of this cyclic woodland usage with these positive effects on biodiversity in European history. For this, we started to build a reference data set of samples from standard-with-coppice trees still managed actively. In a first step, a characteristic growth pattern was identified and compared to archaeological material. The talk will give examples of archaeological sites from different periods (Medieval, Iron Age, Neolithic) where the ring patterns of some woods hint to a comparable woodland management, creating richly structured semi-open woodland which enhanced biodiversity. Data will be discussed in the context of other palaeoecological proxies.

*Speaker

Tracing back bio-cultural evolution using ancient DNA

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In the context of the Anthropocene, marked by extreme global changes, living organisms are undergoing consequential damages. Crucial knowledge is though expected to understand how climatic and anthropic forcing interact in disorganizing and re-organizing living communities and affecting long term biodiversity. The Neolithic transition constitutes a unique case allowing us to analyze the impact of a major societal and cultural transformation (transition to farming) on local biodiversities at multi-regional scale. This anthropic "revolution" changed the place of humans in the ecosystem with a greater impact of their imprint through the introduction from the Near-East of domestic taxa and synanthropic species, triggered and facilitated by the development of agriculture and the general anthropization of landscapes. Pluridisciplinary studies, including paleogenomics, can provide informations on the response of living organisms to anthropogenic pressures. This is what we will illustrate with two examples. First we will focus on dog domestication and trace back their common history with humans through space and time. We will show how human cultural evolution and history strongly influenced dog evolution, dispersion and metabolism. In a second part influence of Neolithic transition on diachronic changes of past living communities will be investigated through past environmental genomic approaches in combination with archeology, geomorphology and bioinformatics.

*Speaker

Soil charcoal analysis of a Mediterranean old-growth forest: historical relict or anomaly?

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In the Mediterranean area, old-growth forests are "anomalies" subsisting in the degraded landscapes made of semi-open to open ecological systems. The history of these forests remains poorly documented so far. Indeed, most of these forests are small in size and therefore need to be investigated at local scale. This is a challenge in the Mediterranean context where suitable archives for the recording and the preservation of paleo-indicators are rare. Thus, aiming to document with suitable paleo-signals the origin and the history of old-growth forest in Mediterranean context we have done soil charcoal analysis in the Sainte Baume old-growth forest (southeast France). This forest is a remarkable forest presenting nowadays many temperate species (eg, *Fagus sylvatica*, *Taxus baccata*, etc.). Soil charcoal analyses combined with geomorphological assessment have been carried out. 17 soil profiles have been open and sampled within the forest and 5 nearby the forest. Macroscopic charcoal assemblages have been extracted. Their taxonomical spectrums show a clear distinction between the samples from the forest and from the surrounding. The charcoal assemblages from the forest are clearly dominated by temperate tree species such as *Fagus* and deciduous *Quercus*, while those from the surroundings are dominated by evergreen vegetation, with only few deciduous *Quercus*. Radiocarbon dating from selected charcoal pieces proves the ancient presence of the temperate forest, as an island in a semi-open landscape. Also, the presence of the forest is attested before becoming a holly place and being protected by the establishment of a monastery during the Middle-Age. Thus it is postulate that this forest is the subsistence of a former larger forest, which was degraded in some places, and remains at the Sainte Baume place due to specific physical condition and also thanks to its holly statute.

*Speaker

Did Inuit influence the evolution of the Labrador landscape? Palaeoecological evidence from Nain region

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Arctic and subarctic environments are usually considered to be pristine natural environments lacking anthropogenic disturbances. In Labrador, recent studies have shown that major changes of the landscape have occurred over the last centuries. Most of them have been related to climate changes; one of the primary driver of vegetation change in northern area. However, various indigenous populations have called Labrador home during the last 7000 years such as Maritime Archaic, Paleo-Eskimo, and Neo-Eskimo. The Nain region of central Labrador is the traditional territory of the Inuit. For them, natural resources like wood has always been an essential material used in their day life activities. However, the idea that pre-settlement forests represent initial environmental conditions suppose that Inuit did not play a role in shaping landscapes. In fact, very few research has been done about anthropogenic impacts on subarctic and arctic ecosystems. Given the long history of Inuit natural resource harvesting in Labrador, it is necessary to identify the source of disturbances on vegetation in order to raise the question if did Inuit influence the evolution of the Labrador landscape? The study aim to document the role of the anthropogenic impact on ecosystem using palaeoenvironmental investigations in the Nain region. According to our data, vegetation changes linked to human occupation took place since the late 17th century at local scale in the Nain region. Also, two periods of intensive vegetation changes in the forest dynamic have been identified at the late of 18th century and in the 20th century linked to anthropogenic disturbance following wood harvesting. This study provides a useful example of the dynamics of present-day landscape and the importance of knowing past events, patterns and processes that shaped current vegetation dynamics in contexts where humans have long histories of occupation.

*Speaker

Pedoanthracology, a relevant tool for past ecosystems and landscapes reconstruction

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Origin of present day vegetation is closely related with anthropic activities. Therefore historical and palaeoecological data should be more considered when facing environmental management, especially in context of socio-economic mutations. Since more than 30 years, pedoanthracology allows the investigation of past occurrences of fire events and the taxonomic identification of the correlated burnt woody vegetation by anatomical analysis and absolute dating of charcoal fragments which are present in soils and soil sediment sequences. This original approach contributes in a better understanding of past ecosystems and lanscapes structures related to anthropic activities (origin of alpine meadows and mediterranean grasslands, holocene forests composition, naturalness). This communication provides a brief overview of the recent developments in pedoanthracology, focusing on why this discipline would be very helpful for the current ecological studies.

*Speaker

Inferring changes in agricultural soil amendments, from the late Bronze Age until Late Antiquity, in northern France, by investigating the weed flora composition

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We investigate the weed flora composition of 372 archaeological occupations, dated from the Late Bronze Age (1350 BP) to Late Antiquity (500 AD), in order to gain better insight into the evolution of agricultural soil amendments in northern France. The settlements under review are located in Brittany, Pays-de-la-Loire, Normandy, Haut-de-France, Ile-de-France, Centre-Val de Loire and Grand Est regions. For each site, topographical location, geological and pedological contexts were listed. 250 taxa of arable weeds, ruderals and grassland species were indexed for the entire data set. Life traits of the species (physiological, phenological traits, ...) are analysed according to functional ecology principles as defined in the FIBS (Functional Interpretation of Botanical Surveys) approach developed by Charles *et al.* 1997. Fertility management by soil enrichment with organic matter (meaning the role of manure) and carbonate rocks (that is potential role of marling and liming) were explored. We used the composition of weed assemblages, in order to trace (archaeo-) agronomic soil chemistry manipulations in relation with such agricultural practices. Archaeobotanical indicators under examination are "nitrogen demand of arable weeds" and "sensitivity of arable weeds to soil pH" on 3 types of pedological context (calcareous soils, silicic soils with underlying limestones, silicic soils with underlying acidic rocks).

Charles M, Jones G, Hodgson JG (1997) FIBS in Archaeobotany: functional interpretation of weed floras in relation to husbandry practices. *J Archaeol Sci* 24:1151-61

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Participative Sciences in Ecology

How to go beyond the collection of data in citizen science projects? Opening the field of analysis and interpretation to citizens

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Over the last decade, citizen science has experienced an unprecedented expansion into a large number of disciplines, due to increased public participation, the development of a variety of digital applications, and the creation of new and innovative interactions between science and society. In the fields of biodiversity and the environment, the role of citizens is often limited to data collection. The objective of this study was to investigate existing programs employing recent innovations that involve members of the public in the analysis, interpretation and formulation of new questions using collected data in order to draw lessons for the future. In the analysis, 30 case studies were examined, 10 of which were particularly detailed, to determine the different types of citizen involvement, the factors that contributed to this involvement, and the types of tools used. This resulted in a typology of citizen science projects categorized by their ability to involve participants in data analysis and interpretation. The study concludes with recommendations for coordinators and project managers of citizen science programs.

*Speaker

Citizen scientists of a national garden butterfly survey shift to biodiversity-friendly garden practices with multi-annual participation

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By monitoring their local environment through citizen science (CS) programs, participants increase their knowledge and awareness of the surrounding biodiversity. However, whether improved knowledge and/or such type of experience of nature may lead to environmentally-friendly behaviors is still intensely debated.

Here, we explored whether short- to long-term participation to the French Garden Butterfly Observatory is associated to changes in gardening practices. Specifically, using annual information provided by participants (> 2 350, from 2006 to 2013), we quantified gardening practices through three different index: 1) garden nectar resources, 2) garden naturality, and 3) use of pesticides.

We found quantitative evidence, at a national scale, that gardening practices shifted with participation, with garden nectar offer and naturality increasing and the use of pesticides decreasing. Other covariables (e.g. garden area and urban context) not only affected gardening practices but also mediated the effects of participation on practices. This confirms the relevance of other factors as co-determinants of participants' behaviors.

This study reveals that from participation to a biodiversity-focus CS program can emerge biodiversity-friendly behaviors, and highlights CS not only as a way to collect ecologically sound data on unprecedented scales but also as a direct tool to locally improve the environment for biodiversity. Further research is still needed to understand and enhance the potential of CS for promoting biodiversity-significant behaviors.

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When citizens and scientists work together: a French collaborative science network on earthworms communities distribution

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Scientists have become more and more interested in earthworms because of their impact on soil functioning and their importance in provision of many ecosystem services. In order to improve the knowledge on soil biodiversity and integrate earthworms in soil quality diagnostics, the University of Rennes 1 has been developing since 2011 a collaborative science project called "Observatoire Participatif des Vers de Terre" (participative earthworm observatory). It has several purposes: i) to offer, through earthworm assessment, a simple tool for soil biodiversity evaluation, ii) to offer training courses to farmers, territory managers, gardeners, iii) to build a databank on earthworms and iv) to propose a website (https://ecobiosoil.univ-rennes1.fr/OPVT_accueil.php) providing for example general scientific background (earthworm ecology and impacts of soil management), sampling protocols and online visualisation of results (data processing and earthworms mapping).

Different sampling protocols are proposed: Mustard, Spade test, Mustard + Spade test according to the objectives and available facilities of the participants. Participants can then count and classify the individuals collected according to their ecological category (epigeic, epianecic, strict anecic and endogeic). Some participants can also send the earthworms collected in 96% ethanol pill boxes to our laboratory of the University of Rennes 1 in order to obtain a precise analysis (species level, individual weight ...).

Up to now, more than 5000 plots have been prospected since the opening of the project in 2011. Citizen science approaches allow us to increase the number of observed taxa extant in some habitats: with 70 taxa sampled, 12 were found only with collaborative sampling. The first results confirm that earthworms' abundance and functional structure are influenced by land cover (gardens, grassland, crops, ...) and land management (tillage, fertilization, ...). Details of this collaborative project will be presented, i.e. the adaptation of the sampling protocols, tools for training, results and returns from end-users.

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Monitoring, understanding and accompanying the impact of global changes on shorelines thanks to citizen monitoring programs of strand lines

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Monitoring, understanding and accompanying the impact of global changes on shorelines are crucial for biodiversity conservation. Coastal sand dune ecosystems that have high conservation and functional roles (trophic, erosion mitigation) are often dependent from seaweed and marine debris deposition. Those are expected to change in quantity and composition under global warming and eutrophication. We hypothesized that surveying strand line could i) inform on marine ecosystem changes (seaweed biomass and community composition) and ii) allow to better understand the impact of global changes on (socio)-ecosystem relationships (sand beaches). Citizen monitoring, in addition to provide data at large spatial and temporal scales, could facilitate the appropriation of conservation issues in management of shoreline ecosystems. We develop a citizen shoreline monitoring program "Plages vivantes" focusing on strand lines (seaweed biomass, composition, flora, associated fauna). The program is addressed to different volunteers. That raised the questions of the adaptation of protocols to scientific aims and to public motivations and constraints. We co-constructed the protocols with volunteers (NGO, scholar, outdoor sports, natural areas managers...) and tested their relevance to detect the effects of environmental changes. The study was conducted on 150 sampled sites along France Channel-Atlantic coastline in 2017-2018. First results on seaweed composition of the strand line highlighted the potentiality of such citizen monitoring programs to assess coastal biodiversity states and changes and to contribute to the connexion of volunteers with conservation issues in such ecosystems.

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Cognitive mapping as a relevant tool to capture small-scale fishers' perceptions on fish resources and Upper Maroni River environment (Amazonian French Guiana)

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When we have too little information on small-scale subsistence fishing within remote areas, it seems now relevant to incorporate traditional knowledge into our scope before contributing to environmental management. Embedded in a participatory science approach, our project aims at using cognitive mapping to consider the state of ecological status of Upper Maroni River (French Guiana) from 45 semi-directed interviews of small-scale fishers who belong to various ethnic communities (Amerindians & Alukus). This methodology allows to capture how fishers perceive their environment and resources they depend on. In addition, this is the only way to get a timeline basis to address the evolution issue of the river without any previous recorded knowledge. The obtained mental maps translate the dynamics of their social ecosystem. By comparing these maps, we found that all fishers share the same view despite their different ethnic group or way of life: (i) the environment is getting worse mainly due to illegal gold panning that changes the aquatic environment and fish viability; (ii) the fishing effort has increased with a change of fishing gear by using more and more cheap gillnets, which probably leads to lower fish daily diets per capita; (iii) a higher availability of technologies within remote villages are being changing their relationships with the river and the fish status. These results should contribute to a co-management of the fisheries.

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Using citizen data to assess ecological continuities

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Habitat fragmentation is one of the major causes of biodiversity loss. To combat the negative effects of habitat fragmentation, France has a policy to implement ecological networks at different scales in land planning documents. So far, these ecological networks have mainly been defined using land cover data as data on actual movement of species or even on species presence are scarce. Data collected by local naturalists could be a mean to inform the design of these networks. The aim of this study is to exploit data from a citizen science program to improve knowledge of the influence of landscape structure on amphibian distribution and assess amphibians as suitable indicators of ecological quality in mosaic farming landscapes and ecological continuities. Amphibians are multi-habitat species with restricted dispersal ability with, nevertheless, a life cycle involving annual migrations to and from aquatic habitats such as ponds and wooded habitats.

Six hundred ninety aquatic sites spread across the Pays-de-la-Loire region were monitored at least one year between 2013 and 2018. Our analysis is based upon 230 ponds sampled twice a year and where no fish were caught. This data set was completed in 2018 by adding 45 new ponds selected along gradients of hedgerow and ponds density. The results show that despite many classical biases related to data from citizen sciences, these data are nonetheless informative when sorted according to relevance and completed by strategic additional sampling.

*Speaker

Transdisciplinary Bioblitz project at the Biological Field Station of Paimpont opens new research opportunities

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The Biological Field Station of Paimpont (Station Biologique de Paimpont, SBP), owned by the University of Rennes and located in the Brocéliande Forest of Brittany (France) has been hosting student scientific research and field trips during the past 60 years. Historical surveys in the study area of the SBP focused on butterflies and birds, however some of the records lack exact occurrence information and metadata.

With this study, we aimed at increasing the range of taxa observations, observing changes in species composition and landscape, and providing a basis for interdisciplinary research perspectives.

We gathered historical data, implemented all taxon biodiversity inventory (ATBI) in different habitats of the SBP study area, measured abiotic factors in the air, water and soil and started a photographic landscape observation during the BioBlitz held in July 2017.

During the 24h BioBlitz organized at the SBP, different habitats were individually sampled. Seventy-five experts accompanied by 120 citizens and 12 European volunteers observed, identified and databased over 700 species and over 1600 occurrences. Historical data collection resulted in about 700 species in time series. We also recorded climatic, soil and water parameters. Habitat cartography was further detailed by new biotic and abiotic observations. Socio-ecological landscape changes were assessed with a comparative approach using 32 historical photographs and historical maps.

The coupling of historical biodiversity data with new biotic and abiotic data and a photographic comparative approach allows an integrative understanding for how the SBP changed from agriculturally-used land into managed natural area within the last 60 years. Hence, this BioBlitz represents an important holistic sampling of biodiversity for studies on trophic webs or on trophic interactions, or on very diverse but connected habitats. The integration of social, biotic and abiotic data opens innovative research opportunities on the evolution of socio-ecosystems and landscapes.

*Speaker

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Biodiversity monitoring in farmland by farmers: lessons from the first seven years of the French Farmland Biodiversity Observatory

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Agriculture and agricultural intensification are considered major drivers of biodiversity loss in agroecosystems, yet few long-term studies actually correlate temporal trends in biodiversity with agricultural practices or landscape characteristics. As a result, the identification of mechanisms responsible for temporal changes in biodiversity relies mostly on spatial comparison, via a space for time substitution that is questionable. To fill in the lack of long-term monitoring of biodiversity in farmland, the French ministry of agriculture initiated in 2011 a citizen science monitoring scheme, where volunteer farmers document the diversity and abundance of wild bees, butterflies, earthworms and aboveground invertebrates in their field, using simplified but highly standardized protocols. They also provide detailed information on their practices. Here we report the results of the first seven years of the program, with above 2000 fields surveyed. We first test whether the spatial approach yields patterns that are consistent with ecological studies based on more thorough biodiversity data. Our results show that the well-known positive effects of organic farming or a diverse landscape are detected by the citizen science programme, with the possibility to isolate specific correlates of biodiversity: for example, hedges are associated with higher wild bee abundance only if they are old enough; no-till farming is associated with a higher proportion of phytophagous invertebrates in the fields; or the presence of cover crops greatly increase earthworm abundance. We then examine whether the data can be used to detect temporal trends in abundance or diversity and pinpoint some possible environmental drivers. In the long term, this observatory can be useful to track the effects of changing practices on biodiversity in farmland, and a powerful communication tool for farmers, to discuss changes in biodiversity, their causes and their consequences.

*Speaker

Voluntary and professional contributions to knowledge of the Paris Basin flora

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The French National Botanical Conservatories (<http://www.fcbn.fr>) are involved in citizen science. They manage a collaborative database and they motivate a network of volunteers and professional botanists to contribute to knowledge of flora. Using the National Botanical Conservatory of the Paris Basin (hereafter CBNBP) as a case-study we examined the composition of three datasets – from CBNBP staff, from other professionals and from volunteers – with respect to recorder contribution and spatial and taxonomic biases, *i.e.* how, when, where and what observers record.

The external botanist network contributed 30% of the contemporary data, with 20% from volunteers. In both professional and volunteer networks, only a few observers contributed many records while many observers contributed few records; moreover a high temporal turnover in the participation of observers was noted. For the three datasets, the timing of data collection is greatly determined by floristic atlas projects. Spatial coverage of the external botanist networks was very incomplete and heterogeneous among and within administrative entities because of interest for species rich hotspots, home patch effects and heterogeneous organization of botanical events. Volunteers focused on rare species and professionals on forest species.

An increased understanding of volunteer behaviour gained from analyzing the composition of records could thus enhance the fit between volunteers' interests and the needs of scientific projects. Moreover, data collection by CBNBP staff appeared highly necessary to prevent spatial and taxonomic biases in order to build robust indicators.

*Speaker

Population and Community Ecology, From
Micro- to Macroorganisms

Field and theoretical study of the role of biotic interactions on community assemblage in nettle-feeding butterflies

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Biotic interactions structure communities and determine species co-occurrence patterns. However, because they often operate in complex networks, biotic interactions are difficult to study and it remains unclear how they will interfere with species response to environmental changes. The analysis of occurrence data of two nettle-feeding butterflies (*Aglais urticae*, *Aglais io*) has shown the potential effect of a third species (*Araschnia levana*) that has expanded its range across southern Sweden. Throughout the establishment of *A. levana*, we observed directional changes in the distribution of the two resident species. Based on our knowledge of this system and the lack of direct competition between the species, we suggested that these changes in realized niches are likely to be triggered by modifications in parasitoid pressure in relation to the arrival of *A. levana*, increasing apparent competition where species co-occur. To test our hypothesis, we started collecting field data (2017-2018), fortnightly throughout the reproductive period of the species and 19 sites spread across a latitudinal gradient (where *A. levana* is present or absent). The results from our first field season already suggest that the population dynamics of our three study species are partly regulated by parasitoids. This regulation process is likely to be cumulative and shared across species as they were infected by the same parasitoids. In parallel to our field study, we developed an R program to run spatial explicit simulations and test hypotheses related to apparent competition in hosts-parasitoids systems. With this tool, we started investigating the role of niche breadth, dispersal, and reproduction, on the population dynamics and spatial distribution of the hosts. We also explored the combined effect of the spatial structure of the environment on niche partitioning. Together with our empirical data, these models can be useful to understand the role of biotic interactions on community assemblage in a changing environment.

*Speaker

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Mechanisms behind population responses to variable thermal environments: experiments and model-based analyses of the role of intraspecific phenotypic variation

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Foliar pathogens inhabit environments exhibiting drastic thermal changes and a high degree of patchiness. Although temperature strongly affects individual growth and ecological processes that drive disease development, the mechanisms that underpin population dynamics in response to thermal variations are not fully understood due to a lack of knowledge of inter-individual variations in thermal responses, phenotypic plasticity and the thermal environment actually perceived by each individual. To explore consequences of inter-individual variations and thermal patchy structure on the adaptive responses of populations, we developed a spatially explicit individual-based model addressing these problems. In our model, we simulate temporal changes in the phenotypic composition of a population in response to thermal variations occurring in a patchy environment. We have performed numerical simulations tailored to field and greenhouse selection experiments all specifically focusing on the wheat pathogen *Zymoseptoria tritici* and its foliar environment. Three general and complementary results from our simulation outputs of population dynamics and ecological processes will be presented: (i) quantitative impacts of three oversimplifications regarding phenotypic diversity, plasticity and environmental characterisation currently adopted in disease prediction models; (ii) the role of inter-individual variation on the dynamics and the adaptive potential of populations and (iii) the influence of spatio-temporal thermal heterogeneity on maintenance of phenotypic diversity. This flexible modelling framework operates based on individual reaction norms and as such can be easily applied to other biological systems. It establishes a quantitative framework for increasing our understanding of how environmental signals, inter-individual phenotypic variations and ecological processes interact and influence both population and evolutionary dynamics.

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Quantifying the relative contribution of breeding vs. non-breeding environmental conditions to survival variations in a trans-Saharan migratory bird of prey

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Migratory species are subject to environmental variability occurring on both breeding and non-breeding grounds. As a result, conditions experienced sequentially can affect the ability of individuals to survive over the whole year. Estimating the relative contribution of environmental factors experienced at different periods of the life cycle, and their potential interaction, to the variation in survival is of paramount importance to predict population dynamics.

Here we investigated how much environmental variability affects age-specific survival rates of the Montagu's harrier *Circus pygargus*, a trans-Saharan migratory raptor. We studied two distinct areas in western France, based on the monitoring of marked chicks and adults from 1988 to 2005 in RO and adults only in ML between 1999 and 2017. We tested for correlations between age-specific survival and different proxies for food availability available in breeding and non-breeding grounds.

Adult survival in RO was lower and more variable compared to ML, a result consistent with the fact that environmental conditions were harsher and more variable during the former period. Indeed adult survival in RO was positively related to the amount of rainfall, but not NDVI, during the wet season in Sahel and, to a lesser extent, to annual mean breeding success. By contrast, survival in ML was not affected by any proxy. First-year survival in RO was similarly affected by rainfall in Sahel. However age-specific survival rates varied asynchronously as first-year survival was lower in years with higher annual mean breeding success, suggesting competition occurred between chicks during their first months of life. Overall, our results indicate that Montagu's harriers are primarily sensitive to environmental conditions experienced on wintering grounds, and particularly when such conditions are below a given threshold, with no evidence for an interaction between summer and winter conditions.

Factors explaining the densities of European wild rabbits (*Oryctolagus cuniculus*) in central-southern Iberia

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Several studies have investigated the causes determining population densities of rabbits (*Oryctolagus cuniculus*) in Iberian Mediterranean habitats, where the species plays key ecological roles. However, population effects of widespread predators like red foxes (*Vulpes vulpes*) on rabbits remain poorly known. Here we extend on the research of factors explaining rabbit population dynamics in central-southern Spain, focusing on fox predation and rabbit density- dependence.

We estimated fox diet by scat analyses, and fox abundance and rabbit density by spotlight counts in eight localities during two years. We run a multi-model selection procedure with mixed models to explain rabbit densities. The candidate models included all possible combinations of the following individual variables: fox predation index (i.e. fox kilometric abundance index multiplied by percentage of rabbits in fox diet), rabbit density in the previous semester, and predator control (yes/no) by hunters to benefit game species. The models always included year and season effects as fixed factors, and locality as random factor.

The most parsimonious model included only the previous rabbit density (negative effect), besides year, season and locality. According to this model, 12% of variation in rabbit population density was explained by fixed factors, and 97% of variation when considering both fixed and random factors. Hence, the locality showed the greatest effect, though past rabbit densities and year significantly explained rabbit densities.

Results suggest current rabbit densities may determine future dynamics, as higher densities will be followed by lower growth rates and vice versa. Moreover, local conditions (e.g. soil softness, availability of food, water and shelter, etc.) might explain why rabbit density varied considerably between sites. Though fox predation might locally deepen rabbit population declines, we did not find such effects at regional scale. In conclusion, rabbit densities depend on many factors (some not studied here, e.g. diseases, hunting pressure, etc.) characterizing each locality.

Manipulating organism-environment feedback strength affects nonlinearity and hysteresis in a microbial predator-prey system

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Organism-environment feedbacks have shown their importance in the context of global change mostly in theoretical ecology. These theoretical studies suggest that increasing the strength of feedback will 1) increase the likelihood of observing alternate stable states; 2) cause greater nonlinearity between an environmental change and ecosystem state; and 3) will increase the likelihood of hysteresis in response to an environmental change.

In an empirical test of the importance of organisms-environment feedback, we manipulated the metabolism-dissolve oxygen concentration feedback strength in an aquatic heterotrophic tritrophic community in microcosms. The manipulation consisted of five levels, from low to high feedback strength: free gas exchange between the microcosm atmosphere and external air (metabolism not strongly affecting environmental oxygen), regular addition of 200, 100, or 50mL of air and no gas exchange. Additionally, to test for nonlinearity and hysteresis in response to environmental change, all microcosms experienced gradual temperature change from 15°C to 25°C, and then back to 15°C. We measured regularly the oxygen concentration in both head and liquid phases, the densities of the predator *Spathidium* sp., the prey (*Colpidium striatum* and *Dexiostoma campylum*) and the bacteria (initially *Serratia fonticola* and *Bacillus subtilis*).

Composition and dynamics of the communities showed evidence of multiple clusters (potentially alternate states), though the likelihood of residing in one or multiple of these clusters did not depend on the feedback strength treatment. In contrast, there was evidence of greater nonlinearity and greater hysteresis of the response to temperature change in treatments with stronger environment-organism feedbacks. These empirical results are in broad agreement with the theory that stronger feedbacks increase nonlinearity and hysteresis, and represent one of the first direct empirical tests of the importance of feedback in such theory.

*Speaker

A comprehensive examination of the network position hypothesis across multiple river metacommunities

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The hierarchical branching nature of river networks can have a strong influence on the assembly of freshwater communities. This unique structure has spurred the development of the network position hypothesis (NPH), which states that the strength of different assembly processes depends on the community position in the river network. Specifically, it predicts that (1) headwater communities should be exclusively controlled by the local environment given that they are more isolated and environmentally heterogeneous relative to downstream reaches. In contrast, (2) downstream communities should be regulated by both environmental and dispersal processes due to increased connectivity given their central position in the riverscape. Although intuitive, the NPH has only been evaluated on a few catchments and it is not yet clear whether its predictions are generalizable. To fill this gap, we tested the NPH on river dwelling fishes using an extensive dataset from 28 French catchments. Stream and climatic variables were assembled to characterize environmental conditions and graph theory was applied on river networks to create spatial variables. We tested both predictions using variation partitioning analyses separately for headwater and downstream sites in each catchment. Only 10 catchments supported both predictions, 11 failed to support at least one of them while in 7 the NPH was partially supported given that spatial variables were also significant for headwater communities. We then assembled a dataset at the catchment scale (e.g. topography, environmental heterogeneity, network connectivity) and applied a classification tree analysis (CTA) to determine which regional property could explain these results. The CTA showed that the NPH was not supported in catchments with high heterogeneity in connectivity among sites. In more homogeneously connected catchments, the NPH was only supported when headwaters were more environmentally heterogeneous than downstream sites. We conclude that the NPH is context dependent even for taxa dispersing exclusively within streams.

*Speaker

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Resilience of the biomass pyramid to increasing disturbance regimes

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Ecological pyramids, which represent the distribution of abundance and biomass among body sizes or trophic levels, depict one of the most striking similarities among the world's ecosystems. As a general rule, larger organisms, higher in the food chain, are less abundant than smaller ones lower in the food chain. The metabolic theory of ecology provides theoretical baselines regarding the shape of such ecological pyramids in undisturbed environments. However, while climate change is expected to increase the frequency and intensity of disturbances such as storms, fires or drought, it remains unclear how growing disturbance regimes may affect ecosystem structure and dynamics. We experimentally investigated the response of ecological pyramids to varying disturbance regimes using protist communities that cover a wide range of body sizes, feeding types and have populations with densities varying over orders of magnitudes. We disentangled the links between disturbance regime, organism growth rates and community resilience to build a size-based theory that predicts the level of disturbance an ecological pyramid can recover from.

*Speaker

Understanding an un-described symbiosis; implications for resilience, evolution and conservation of *Oxalis* in the Cape flora biodiversity hotspot

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The unique biogeographic region located at the southwestern tip of the African continent, the Cape Floristic Region (Cape), is globally renowned for its extremely species-rich and diverse flora. Current models of climate change predict shorter, drier winters for the Cape, which may directly affect the future success of many species. Research on the important role of endophytic microbes in generating and maintaining plant species diversity has largely been neglected in this hyper-diverse region and to date there is very little known about micro-organismal community composition within and between Cape plant species, and we risk losing complex interactions before they have been documented.

Our research is focused on the indigenous plant genus *Oxalis*, which is the largest eudicot geophytic lineage in the Cape (ca. 230 species). Our work has revealed that *Oxalis* species possess an extraordinary diversity of endophytic associations with fungi and bacteria (119 bacterial morphotypes and 29 fungal genotypes isolated from only five plants each of six *Oxalis* species; metabarcoding results pending) distributed across different storage, vegetative and reproductive plant organs.

Thus far we have identified an average of 20 bacterial and 7 fungal endophytes per plant, which is an order of magnitude higher than the number commonly encountered in angiosperms. Interestingly, 11 of these endophytic species occur in the seeds, which suggest that the endophytes are vertically transmitted from one generation to the next. More than 80% of the endophytes found in *Oxalis* seeds are microbes with known beneficial effects for plant hosts, for example microbes capable of nitrogen fixation and phosphate solubilisation. *Oxalis* appears to host a rich and diverse endobiota, which may play critical roles in plant germination, survival and evolutionary success that allows this genus (and possibly other plant lineages) to tolerate, persist and thrive in such a wide range of environments across the Cape.

*Speaker

Distribution of the genus *Boeckella* (Copepoda: Centropagidae) at high latitudes in South America and the main Antarctic biogeographic regions

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Copepods are present in almost all aquatic environments, playing a key role in food webs, and are thought to be useful indicators of environmental change. *Boeckella* is a calanoid copepod genus distributed mainly in the Southern Hemisphere, with 14 species reported exclusively from higher southern latitudes. We present an updated database of these 14 species of *Boeckella* generated from a combination of three sources: 1) new field sampling data, 2) published records, and 3) Global Biodiversity Information Facility (GBIF), to provide a comprehensive description of the geographic distribution of the genus south of latitude 40°S in southern South America and the three-main terrestrial biogeographic regions of Antarctica. The database includes 380 records, 62 from field sampling, 278 from the literature and 40 from GBIF records. Southern South America, including Falkland/Malvinas Islands, had the highest richness and records (14 and 297), followed by the sub-Antarctic islands with 34 records and five species, South Orkney Islands (15 and 2), South Shetland Islands (23 and 1) and finally a single species (*B. poppei*) recorded from the Antarctic Peninsula south to Alexander Island and continental Antarctica. This latter species is the only representative of the genus, and more widely the only terrestrial/freshwater invertebrate, currently reported from all three main biogeographic regions in Antarctica (sub-, maritime and continental Antarctic). Future development of molecular systematic studies in this group should contribute to assess the correspondence between morpho- logical taxonomy and molecular evolutionary radiation.

Keywords: Antarctica, Calanoida, freshwater ecosystems, sub-Antarctic islands, Patagonia

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Multi-scale study of the potential of phototrophic biofilms as functional indicators of small streams ecological state in agricultural areas: from watershed to micro-habitat

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Headwaters account for nearly 80% of the total river system. However, their functioning remains largely under-studied in comparison with large rivers, the latter being regularly monitored under the Water Framework Directive.

In small streams, phototrophic biofilms provide essential ecological functions and appear as relevant indicators of the ecological health of these aquatic ecosystems. The AQUAFUN project proposes to understand the role of biofilms as a functional indicator by combining three complementary approaches allowing a spatial scaling up from the biofilm micro-habitat to the watershed.

Firstly, a GIS approach will be used to characterize on a regional scale (Lorraine) anthropogenic pressures (land use and hydromorphology) on a large number of small watersheds (< 50 km²). A second stream-scale approach will compare inter- and intra-site variability of the biofilm response as a functional indicator of these small streams. Finally, a high spatial resolution imaging approach (CLSM, AFM) will be conducted at the scale of the biofilm in order to characterize the link between its functioning and its microscale physical structure.

*Speaker

Plant traits as drivers of habitat selection and community composition in North American forest birds

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Forests are constantly altered by human activities. The recent development of broad-scale, remote-sensing methods has allowed the quantification of changes in forest composition with an increasing accuracy and scale. However, the implications for advances in remote sensing for capturing species-habitat associations and associated changes on avian biodiversity remain poorly understood. Here, we investigated whether functional and structural plant traits, as captured by advanced remote sensing, are influencing habitat selection in forest birds of Wisconsin. We asked (1) Are specific forest bird species responding to variability in plant traits? (2) Do these differences in species-habitat associations influence the diversity and composition of forest bird communities? We studied 26 forest sites covering the full-range of stand densities and tree species composition present in Northern United States (Wisconsin). Plant traits were measured and point counts carried out over two field seasons. Bird abundances and several metrics characterizing bird communities, such as species and functional richness or community trophic index, were correlated to spatial variation in structural and functional plant traits. We found that the abundance of individual forest birds varied strongly along plant-related environmental gradients, with specific nesting requirements making it difficult to predict the bird responses based on their functional traits alone. At the community level, however, plant traits appeared to be clearly driving diversity metrics such as species richness, functional richness, functional divergence or several trait-related indices. Our results suggest that (1) bird species are highly responsive to the functional properties of forests, with a wide variety of species-specific responses, (2) functional and structural plant traits are two independent variables influencing different properties of birds communities, and (3) remote sensing methods can be used as an alternative to time-intensive ground-based methods to monitor forest avian biodiversity and potentially predict changes in community diversity.

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Interactions between green and brown food webs in aquatic ecosystems

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Food webs can be split into two paths: the green food web relying on primary production and the brown food web relying on the decomposition of dead organic matter. These two food webs are connected through nutrient cycling (bottom-up coupling) and through generalist consumers (top-down coupling). Thus, perturbations in one food web can have cascading effects on the other and then deeply change community composition and ecosystem functioning. We investigated these interactions by an experiment in aquatic mesocosms performed in the Experimental Lake Platform of the CEREEP Ecotron Ile De France. We crossed three treatment in 5 m³ mesocosms: daylight shading to specifically affect the green food web, organic carbon addition to specifically affect the brown food web and fishes addition as generalist top predators. We quantified abiotic compartments (dissolved carbon, sediments, mineral nutrients...) and biotic pelagic compartments from bacteria and phytoplankton density and composition to fish growth rate. We found that fishes affect phytoplankton, not through cascading effects mediated by zooplankton consumption, but probably by modifying the quality and the quantity of sediments and of dissolved organic carbon decomposed by bacteria that recycle nutrient limiting primary production. This effect of fish on the brown food web also increased phytoplankton density when light is depleted probably by compensating the decreased exudation of phytoplankton that stimulates nutrient recycling by bacteria. The organic carbon treatment weakly affected the ecosystem because of the weak degradation of some of the added compounds by bacteria. Our results emphasise that top consumers can deeply change the community not only through top-down control but also through bottom-up control by modifying the quantity and the quality of basal resources.

*Speaker

Upscaling the ecology of Andean Grasslands

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This is a study on the effect of environmental change on the ecosystem functioning and ecosystem stability of Tropical Andes grasslands, which hold one of the highest variety of fauna and flora species and its natural and semi-natural ecosystems deliver key ecosystem services to more than 50 million people living in the Andean mountain chain. Latest climate models predict a reduction up to -30% in the precipitation in the Central Andes for the coming decades with an increase in the occurrence of extreme events. These events are main drivers of ecosystem functioning, having also an effect in the management strategies, which are implemented to safeguard the economy while adapting to changes in the environment. Studies in the Andes showed that above and below-ground grasslands' productivity is dominated by a marked seasonal shift in carbon allocation. However, to date, the impact of environmental change on the Andean grassland's stability has not been evaluated. The aim of this study is to evaluate the changes in the ecosystem's functioning and land use management of grassland ecosystems at the Central Andes in Bolivia. I will conduct a local assessment of the vegetation dynamics and soil conditions along a gradient of grazing intensity. The results will be upscale to the landscape scale, to evaluate the stability of the ecosystems' productivity and to provide guidelines for future land use management in face of current changes in the climate. I hypothesise that grasslands at different grazing pressures will show changes in the ecosystem functioning. Next to that I hypothesise that higher biodiversity and functional biodiversity are important factors for stabilizing the studied ecosystems at a spatial landscape scale, which is relevant for future management of grasslands in the region and for the application of new policies that will improved the sustainable management of the Andean Grasslands.

*Speaker

Pollen dynamics sets the tempo of fruiting pulses in oak tree populations

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In many perennial wind-pollinated plants, the dynamics of seed production, commonly known to be highly fluctuating from year to year and synchronized among individuals within populations, dramatically impacts forest regeneration and biodiversity. However, the proximate causes of such seeding dynamics, called masting, are still poorly understood, making any accurate forecasting virtually impossible. Combining long-term surveys of airborne pollen amount and acorn production over large-scale field networks and a mechanistic modeling approach, we investigated the role of pollen dynamics and limitation on the acorn production of temperate oak trees that are widespread and abundant in Northern hemisphere forests. From this novel approach, we found that pollen dynamics displays masting-like pattern reflecting resource depletion and limited pollen production the year following large pollen release, yet with dampened inter-annual pollen fluctuations compared to those of acorns. Both the airborne pollen amount and acorn production are positively related, according to a logistic function, to increasing temperature and decreasing rainfall in spring. By coupling field and simulated data, we found that the dynamics and limitation of pollen are key drivers of oak masting. Mechanisms at play involved both synchronized internal resource dynamics and depletion among trees, limiting pollen production at the population scale, and spring weather conditions that affect pollen aerial diffusion. The sensitivity of airborne pollen amount (then acorn production) to spring weather should make oak

masting highly sensitive to climate change. Thus, with the ongoing warming climate, we predict

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that the fruiting dynamics, initially unpredictable, should keep highly fluctuating (because of resource depletion mechanisms) yet with much more deterministic variation, which should markedly affect the whole forest biodiversity through cascade effects.

Variations in immune response and immune genes in an insectivorous bird facing agricultural intensification in Canada

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The immune system plays an important role in survival of organisms. Despite an increasing complexity in its evolution, we still see individual variability in sensitivity to diseases. Life-history theory states that maintaining the immune system and producing an immune response is costly, leading to trade-offs with other life-history traits such as growth and reproduction. In environments with few resources, those trade-offs should be exacerbated. We aimed to understand how variations of individual phenotype such as immune responses are shaped by environmental and genetic factors. In a context of increasing human activities, such as agricultural intensification, how immunity could be affected in a population of Tree swallows (*Tachycineta bicolor*)? Moreover, are there genetic markers that could characterise immunity to detangle the causes of variations in immune responses at the individual level? Contrary to what we expected, individuals in intensive breeding habitats (monocultures on large surfaces) had a higher constitutive immune response than those breeding in non-intensive farmlands. Moreover, we noticed a temporal decline in immune response at the population and individual levels. Finally, when looking at specific immune genes (β defensin), the genetic variations we detected was not linked to the constitutive immune response, suggesting that this immune response was mainly affected by environmental factors.

*Speaker

How similar islands and continents are? A phylogenetic approach in plant communities

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Although most of insular lineages have a continental origin, communities in islands and in continents may highly differ. Compared to the mainland, islands harbor high rates of endemism and are also noted by disharmonies in their community composition. Speciation and extinction rates, geological history, in addition to dispersal events blur the frontier between insular and continental communities. However, how similar islands and continents are is still unclear. Here, we used for the first time a phylogenetic approach to estimate divergence between plant communities in islands and in continents. We focused on monocotyledons in 4,600 islands and 610 continental areas, and used two well-known measures of phylogenetic beta diversity: beta Mean Pairwise Distance (MPD β) and beta Mean Nearest Taxon Distance (MNTD β). We first explored the role of spatial and environmental distance on the phylogenetic divergence between each island and the surrounding continental areas. Then we determined spatial patterns of continental-island divergence across world islands. We looked for geographic, climatic, historic factors, as well as community structure factors, that may explain why some islands are more divergent than others. All analyses were performed thanks to Boosted regression trees and Generalized Linear Models. We showed that spatial distance and difference in solar radiation may be the main factors of phylogenetic divergence between a given island and the surrounding continental areas. Abiotic and community structure features of highly divergent islands varied with the measure of beta phylogenetic diversity used. MPD β and MNTD β were thus complementary to shed light on geographic, historic and climatic processes at the origin of divergence between continents and islands. Here we showed how rarely employed phylogenetic approaches may give new insights in the continental origin of plant diversity in islands and may explain how divergence, or similarity may have arisen.

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Soil Ecology

Grazing on mycorrhizae by the rhizosphere food web regulates seedling survival

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We selected the eastern white pine (*Pinus strobus*) germinated in soil microcosms, in a full factorial design with 5 treatments each randomly replicated in ten trays (n=10, 50 seedlings) in a controlled-environment greenhouse. The pine is an obligate mycorrhizal species, and the five treatments provided more or less fungivory on the mycorrhizal association during the first 120 days of growth. Treatments were a) no ectomycorrhizae; b) 3 species of ectomycorrhizae (EM); c) EM and enriched with fungivorous nematode culture (Nf); d) EM, Nf, and enriched with microarthropods (MA); e) EM and MA. Seedlings were destructively sampled at four months or at seedling death (< 4 months). Data were analysed with ANOVA and multivariate procedures and results were compared across treatments for seedling survival rate, age at death, growth, mycorrhization and animal abundance and composition. Canonical scores plot in discriminant analysis clearly separated treatments by mean (%) root tip colonization. We observed trophic cascades during mycorrhization by varying community structure, and fungivory decreases mycorrhization levels, affecting both seedling survival and growth. Next we used stable isotopes tracer studies to measure the rate of fungivory by three microarthropods and their predator, for nutrient transfer through trophic levels. Excretion rates were also determined as well as moulting rate for the collembolan *Lepidocyrtus*, and food processing efficiency for the mite (Astigmata) *Tyrophagus*, the mites (Oribatida) *Oribatula* sp, *Hypoaspis* sp and the predatory mite (Mesostigmata) *Lepidocyrtus* sp. Our results show that we can measure stable isotope enrichment for single microarthropods using our modified mass spectrometry technique, that fungivory rates can be measured, and confirm our microcosm results, that grazing pressure on early stages of mycorrhization reduces seedling growth and can lead to seedling mortality.

*Speaker

Trait patterns of soil decomposers under climate manipulation field experiment: Collembola communities in the CLIMAITE study

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Soil ecosystems and the fauna they host, are known to provide many services. Soil Collembola can therefore be used as bioindicators of soils functionality. In a global and climate change context, they are expected to be threatened. Thus, previous studies showed that European Collembola communities structure can be shaped by long-term adaptations to climate. Then, temperature plays a major role in the variation of species traits, especially in open habitats. We aim here to evaluate how trait patterns, at a community level, are impacted by an experimental climate manipulation design. The present study allows us to qualify the impacts of the upcoming climate changes during 21st century. In addition to a taxonomic approach, the functional approach allows us to detect changes in a complementary facet of soil biodiversity.

The CLIMAITE study was carried out in Denmark and aimed to simulate the predicted climate for year 2075. The study site consisted in an unmanaged heath/grassland ecosystem. The climate manipulation experiment included the following treatments: elevated CO₂ concentration, elevated temperature, induced drought and control plots. The treatments were combined in all combinations for a total of 48 plots (Mikkelsen et al. 2008). Collembola were sampled in 10 cm depth soil cores, in 2007 and 2013, after 2 and 8 years of climate manipulation, respectively.

In a taxonomic approach, Collembola communities were impacted by elevated CO₂ through increased C:N ratio, after 2 years (Holmstrup et al. 2017). This effect was not observed after 8 years, suggesting resilience within the soil biota in the long term. In a trait-based approach, most up-to-date Collembola trait databases versions of the BETSI.cesab.org (France) and SoilBioStore.au.dk (Denmark) projects were compiled. These latest results will focus on characterizing the functional diversity of communities, and will aim to study the functional trajectory of communities along the different climatic factors combinations.

Vertical soil evolution of microbial biomass over a deforestation & culture chronosequence

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Luvisols are part of the world most productive soils and are widely used for intensive farming, like in North-West Europe. The wideness of deforestation over those lands emphasizes the necessity to study soil evolution triggered by those land use changes. Recent works on loessic luvisols revealed deep alkalization dynamics through decennial to secular scale following soil liming. Therefore, soil land use changes strongly influenced soil physico-chemical characteristics (notably pH). However, soils host a)H) belowground biodiversity, which is implied in numerous ecosystem services and related to soil properties. This aspect is still debated and poorly studied at the long term (century) scale and in the deep soil horizons.

Through a synchronic approach the geohistorical analysis brought the deep time perspective with a deforestation and culture chronosequence on loessic luvisols located in North France. Five plots were studied; an ancient forest (about 1500 years), an ancient field (at least medieval) and 3 ancient forests plots deforested and cultivated since 5, 30, 170 years. We do characterize soils physico-chemical (granulometry, pH, organic carbon, major and trace nutrients, CEC, Base-cation Saturation ratio) and biological properties (bacterial and fungal abundance and biomass).

Multivariate and mixed-effect model analysis revealed the predominant role of depth (and O₂ availability), deforestation and pH over soil microbial biomass distribution. Total soil carbon was more correlated to bacterial than fungal biomass, as expected both biomasses are strongly decreasing between topsoil and 50cm depth.

The fungic biomass and Fungi/Bacteria ratio strikingly increase from 50 to 200cm depth in the ancient forest soil but not in the cultivated soils. This study outlines a rapid collapse of deep fungal biomass in the first 5 years following deforestation. We thus infer that deep soil microbial ecosystems, especially their fungic part are very poorly resistant to land use changes such as deforestation and culture.

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Soil and phyllosphere microorganisms with potential impact on natural emissions of ozone-depleting chloromethane

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Natural chloromethane (CH₃Cl) sources, mostly from vegetation, are responsible for 16% of the chlorine-dependent fraction of stratospheric ozone destruction with the phasing out of its anthropogenic emissions since the application of the Montreal Protocol in 1987. Atmospheric CH₃Cl emissions can be modulated by plant-associated microbial communities [1]. However, the taxonomical and metabolic diversity of the biotic CH₃Cl sink remains largely uncharacterized. Under laboratory conditions, CH₃Cl-degrading bacteria isolated from leaves and soils harbour the *cmu* pathway for chloromethane utilization [2]. Bacteria associated with CH₃Cl degradation in soils and plant leaves were identified by stable isotope probing [3] following incubation with ¹³C-labelled CH₃Cl. High through put sequencing of the heavy DNA targeted taxonomical and *cmu* genes as well as metagenomes.

In most experiments, detected taxa did not correspond to known *cmu*-containing bacteria [4],[5],[6]. In forest soil, taxa closely related to *Methylovirgula* and *Actinobacteria* were suggested to be associated with CH₃Cl degradation. Ongoing work on ¹³C-labeled metagenomes of CH₃Cl-degrading ferns and soils are expected to provide further information on one-carbon metabolism of the biological CH₃Cl sink in the phyllosphere and soil.

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*Speaker

Impact of fine plant genetic variations on plant-soil-feedback using a model hybrid system

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Plants can alter the soil biotic and abiotic characteristics, these modifications can in turn, affect positively or negatively the local plant community. It is important to know better about the mechanisms responsible for plant-soil-feedbacks (PSFs) to explain invasive plant species success, plant population dynamics and diversification. Several studies have been done on PSFs at the interspecific or at the plant functional-group level, but less is known considering fine genetic variations. Here, we study the effect of small plant genetic variations on PSFs. To do so, a model hybrid system from the crossing between *Jacobaea vulgaris* and *Jacobaea aquatica* was used. The F2-hybrids obtained from this crossing have distinct genotypes. We study how these genotypes respond to soil conditioning by their parental species: Using the ~400 SNPs of the Ragwort cross genetic map, a gradient of F2-hybrids was chosen. A PSFs experiment was performed, with first, a soil conditioning phase by the parental plant species, and then, a feedback phase where F2-hybrids were grown in the soil previously conditioned by the parental plants. This will allow to test the following hypotheses:

- F2-hybrid genotypes would express different phenotypes depending on the plant conditioning the soils. As the *Jacobaea* genus is known to have a strong negative conspecific PSF, the more similar the genotype between the parental species and the F2-hybrid is, the more negative will be the PSF.
- The plants conditioning the soil would act like a first selective filter for the rhizosphere and root microbial community, the F2-hybrid genotype will act like a second filter. This would lead to particular communities of microorganisms colonizing the F2-hybrid rhizospheres and roots. This project will open the door to other studies linking genotypes and PSFs to plant competition and resistance to herbivory, and allow us to explore co-evolutionary relationships between plants and soil microorganisms.

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Impact of logging residue management and wood ash fertilization on forest soil-plant interface biology: a microcosm study

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In the context of energetic transition, an increase in woody biomass export is one of the investigated solutions for Bioenergy. Among solutions, export of logging residue with a diameter smaller than 7 cm, currently discarded on the forest floor, was investigated. To compensate organic matter losses due to harvesting, mineral fertilization by wood ash was proposed. Nevertheless, impacts of increased organic matter export and/or fertilization by wood ash in temperate forest are still scarcely studied. Our study in forest-soil microcosms investigated the response of soil communities to an export of organic matter and ash compensation on two soil types (acidic soil and basic soil). Four soil-interface biological groups were studied: Lumbricidae, collembola, vesiculo-arbuscular mycorrhizal fungal community, and grass species. In each microcosm, five experimental amendments were set up following a gradient of organic matter content: i) control (100Residue), ii) 70% of logging Residue and 30% of Ash (70R30A) iii) 30% of logging Residue and 70% of Ash (30R70A), iv) 100% of Ash (100A) and v) no amendment (R-). Each group was surveyed at three time points after the setting up of experiment (at one, four and twenty weeks). There were significant responses after twenty weeks. Earthworms biomass only increased in 100A amendment regardless of soil fertility. In basic soil, collembola abundance did not show any variation between 100R, 100A and R- but a decrease of 50% was observed for 70R30A and 30R70A mixed amendments. For acidic soil, collembola abundance was higher in 100R than in other amendments. Vesiculo-arbuscular mycorrhizal fungal community and grass epigeic growth exhibited the same pattern of response than collembola abundance. These various responses by soil types can be explained by pH modification due to ash application that are more important in acidic than in basic soil. Mineral fertilizations need to be modulated by soil characteristics.

individuals' biomass was significantly more important in the cultivated alleys and control plots than in the tree rows for epigeic, epi-aneic and endogeic earthworms. Mean SOC stocks in 0-30 cm were significantly higher in both tree rows and agroforestry alleys than agricultural control system (treeless) across the sites. Within agroforestry plots, SOC stocks in the tree rows were significantly higher than in the alleys.

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Earthworms' distribution could be linked to an absence of soil perturbation in the tree rows, but also to an enhanced resource availability, as shown by the higher SOC stocks. We also hypothesized that the lowest individual biomass of adult earthworms in the tree rows could be due to competition within earthworm communities.

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Response of soil microbial enzymatic activity to earthworm species (epi-anecic vs strict-anecic)

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Earthworms are qualified as soil engineers and play a key role in the degradation of soil organic matter (SOM). Their contribution to this function is either direct, by consuming dead organic matter, or indirect by influencing microbial communities and activities in the soil. Most of the studies evaluating their contribution to this function were conducted at the level of four ecological categories (epigeic, epi-anecic, strict anecic and endogeic).

The aims of this study were to determine and compare the contribution of (1) three separate epi-anecic species, (2) three separate strict anecic species and (3) the mixing effects between these different species (by pairs of two species), on litter mass loss and soil enzymatic activities in their middens (surface casts) and burrows. Enzyme activities measured were FDA, Beta-Glucosidase, Cellulase, Leucine Amino Peptidase and Phosphatase involved in C, N and P cycles.

After 30 days of the experiment, Beta-Glucosidase was significantly higher in middens than in burrows for both epi-anecic and strict anecic species whereas no differences were observed on the others enzymatic activities between middens and burrows. In monoculture, and compared to the control condition (without earthworms), we observed that litter mass loss and enzymatic activities were significantly higher in presence of epi-anecic compared to strict-anecic species. These differences are more pronounced with FDA, Leucine Amino Peptidase and Beta-Glucosidase enzyme activities than with Cellulase and Phosphatase (respectively, +34, +57, +78 and +14, +8 %). Still, in monoculture, no difference was found between species of the same ecological category. Interactions between earthworm species (intra- or inter-ecological category) on litter mass loss and enzyme activity were mainly additive indicating functional redundancy. These initial results on microbial activities confirm the grouping of earthworms species into ecological categories initially based on morphological, physiological and ecological criteria.

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How much or how often? Rainfall quantity controls microbial decomposer activity, but rainfall frequency controls that of macrofaunal decomposers

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Understanding the consequences of ongoing climate change on litter decomposition is fundamental to predicting feedbacks on atmospheric CO₂ concentrations and consequent climate change. Yet, although the increase in precipitation variability is one of the main climate changes expected, its effect on litter decomposition have received considerably less attention than the effect of changes in the mean state of climate. To date, the rare studies that focused on precipitation variability effect on decomposition considered the microbial response, leaving the responses of other groups of decomposers such as litter-feeding detritivores largely unknown. To fill this gap of knowledge, we used a full-factorial experiment to disentangle the effects of cumulated precipitation and precipitation frequency over microbial-driven decomposition, and macrofaunal-driven decomposition, using the common pill woodlouse (*Armadillidium vulgare*). After a six-weeks incubation under controlled-conditions, we found that while precipitation quantity was the only significant factor driving microbial-driven decomposition, litter consumption by isopods did not respond to precipitation quantity, but peaked when precipitation pulses were delivered at low frequency. This shows that different groups of decomposers respond differently to altered precipitation regimes, and that large soil animals may be more resistant to infrequent precipitation than microorganisms. Collectively, this suggests that under alter precipitation regimes, the relative contribution of different groups of decomposers to carbon cycling may be reshuffled.

*Speaker

Mediterranean coastal print and litter type drive litter microbial responses to drought stress

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Warming and disturbance of precipitation dynamics are expected in the Mediterranean basin, resulting in longer, more intense drought and heat waves. Here we investigated how litter microbial functioning and responses to stress may be shaped by the particular conditions of coastal environments, and whether this depends on litter species identity (*Pinus halepensis* and *Pistacia lentiscus*) and on whether litters are mixed or not. Mesocosms of monospecific and mixed litters collected from both inland and coastal areas were subjected to either control (25°C, 60 % WHC) or stress conditions (5 drying-rewetting (D/rW) cycles: 1 week of drying at 35°C, 1 week at 25°C, 60 % WHC). Litters were characterized using chemical (C/N ratio and solid-state NMR13C) and microbial markers (lignocellulolytic activities, basal respiration (BR), microbial active biomass, fungal and bacterial catabolic profiles). The 'coastal print' depended on litter type for certain microbial markers (cellulases, BR and catabolic profiles), showing the importance of litter chemical signature on microbial functioning. Fungal and bacterial catabolic profiles were mainly shaped by the coastal print and litter type respectively, with fungi more sensitive to coast-specific conditions and bacteria to their immediate surroundings, i.e. chemical signature. After stress, the litter admixture showed a weaker microbial biomass with higher tyrosinase activities, suggesting a shift in microbial balance which favored fungal communities. Catabolic profiles revealed a more pronounced stress effect on inland microbial communities. Our findings show stress legacy and litter chemical signature to be major factors structuring microbial responses to drought stress.

*Speaker

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Influence of physical heterogeneity of flow on microbial horizontal gene transfer in subsurface ecosystems

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Microbial life in the subsurface environment face changes stemming from human activities such as the use of antibiotics and pesticides, or industrial contamination. There, the physical structure changes across distances of a few micrometers creating a multitude of microenvironments where abundant bacterial species thrive under fluctuating conditions. Porous media such as soils consist in a distribution of pores fulfilled by fluids such as gases or liquids characterised by flow dynamics. This physical system is coupled with the microbial life. For example, fluid flows transport resources creating gradients affecting spatial distribution of bacteria which in turn through planktonic biomass growth or the development of a biofilm can modify the dynamics of fluid flow. Bacteria demonstrated adaptability through rapid evolution processes. Competent bacteria have the ability to uptake free DNA from their environment and to express it, a mechanism of gene transfer known as natural transformation. Here we investigate the influence of fluid flow on transformation as water is a critical component for most of the soils and may contribute to the dispersion of free DNA. We combined microfluidics methods with fluorescent optical microscopy in order to have a dynamic visualization of bacteria expressing fluorescence from free plasmids. Microfluidics chips were used to allow the control of hydrodynamic parameters in small confined environment. Then numerical treatment of images was applied to render the efficiency of the transformation under different flow conditions. This method is very promising to study this critical process source of biodiversity with naturally competent bacteria species involved in soil key processes.

^{*}Speaker

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Assessing the impact of lumbricid earthworms (keystone species) on greenhouse gasses and ecosystem multifunctionality

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One of the aims of the Paris Climate Agreement is to reduce the emissions of greenhouse gases (GHG) in a manner that does not threaten the food production. In an agricultural context, lumbricid earthworms (family Lumbricidae) have always been considered indicators of soil fertility and productivity. In contrast to this view, a couple of recent meta-analyses suggested that earthworms enhance the emissions of soil GHG (CO₂ and N₂O) and can reduce soil carbon storage. However, there is accumulating evidence that the difficulty of setting up realistic experiments manipulating earthworm treatments is responsible for numerous idiosyncratic findings in natural and agro-ecosystems. Also, there is increasing realization that there is an urgent need of earthworm studies assessing simultaneously the multitude of ecosystem functions present in nature - ecosystem multifunctionality – such as primary productivity, nutrient cycling and carbon storage and water fluxes.

To address these knowledge gaps we started a large experiment using the 12 Macrocosms with lysimeters (5m², 1.5 m deep and weighting 13 tonnes each) of the CNRS Ecotron facility (www.ecotron.cnrs.fr), and established treatments with and without different earthworm functional groups (none, anecic and endogeic). Our overarching hypotheses are that: i) in contrast to the methodologically biased meta-analyses using predominantly data from unrealistic microcosm experiments, in realistic field conditions including plants, earthworms reduce greenhouse gas emissions and increase soil carbon stabilization and sequestration and ii) in a multifunctional context earthworms will have an overwhelming positive effect on multiple ecosystem functions. In this presentation we will discuss the experimental design, hypotheses, preliminary results and opportunities for collaborations.

*Speaker

UV and blue light enhance tree litter decomposition in a temperate forest by accelerating the decomposition rate

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Sunlight, alongside warm temperatures and high humidity, can accelerate litter decomposition by direct breakdown of organic matter through photodegradation. This process is mainly driven by radiation at the high-energy short-wavelength end of the solar spectrum: UV radiation and blue light. Although this process is widely studied in arid environments, few studies have been done in temperate forests.

This study aims to test how sunlight, and particularly UV-B, UV-A, and blue light, affects litter decomposition of different tree species under a temperate forest canopy. Litter mass loss and C:N ratio of: European ash (*Fraxinus excelsior*), European beech (*Fagus sylvatica*) and pedunculate oak (*Quercus robur*), differing in their leaf traits and consequently decomposition rate, were analysed over 7-10 months in litterbags made using filters attenuating different regions of the solar spectrum. We expected less mass loss and higher C content when UV and blue light were excluded, due to the lower photodegradation.

Over the entire period, mass loss was smallest in the absence of UV and blue light and this litter had the lowest C:N ratio. The filter treatment had a greater effect on decomposition than the biotic community composition as controlled through mesh size. The three litter type responded differently to the filter treatments, suggesting the magnitude of photodegradation to be dependent on litter quality and especially on the initial C:N, known to affect decomposition rate.

This study shows that even under the reduced irradiance found in the understorey of a temperate forest UV radiation remains important in accelerating decomposition, increasing mass loss and thus C released into the atmosphere. Blue light was also revealed to make an important contribution to these decomposition processes. Knowing the role of UV and blue light in decomposition is crucial to estimate the contribution of temperate forests to carbon cycling under a scenario of climate.

*Speaker

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Spatio-temporal Dynamics of Ecosystems

Post-dispersal diaspore fate in degraded and pristine areas in a tropical grassland

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Granivore invertebrates and vertebrates have important effects on seed fate. The removal or predation of diaspores during the post-dispersal (natural or seed sowing) phase can affect plant community dynamics and regeneration processes. The campo rupestre vegetation (mosaic of tropical grasslands and rocky outcrops) presents little natural resilience to soil disturbances. The aim of this study was to test the hypothesis that seed predation could be an important factor limiting natural plant recolonization in campo rupestre. We performed a factorial experiment involving the assessment of diaspores removal in four paired disturbed and pristine sites, and in vertebrate-excluded and control paired stations. We used two native seeds, three native fruits and made artificial diaspores containing sugar and fat, with attractive aroma and color. In each area, we placed six stations with vertebrate's exclusion cages and six control stations open structures with diaspores that were evaluated for removal after 24 and 48 hours of exposure. Additionally, for the three natural diaspores that presented the most significant removal rates we performed direct observations totaling 20 hours for each diaspore type distributed equally between the sites. Our results suggest that invertebrates comprised the group that contributed most to seed removal. Removal by vertebrates was not affected much in disturbed sites, whereas invertebrate activity seemed to be significantly reduced. Contrary to our expectations, we found that diaspore removal can be reduced by more than two fold in disturbed sites compared to pristine sites. Post-dispersal removal can vary remarkably between diaspore types. To conclude, seed removal and predation, still occurs and even at low rate could negatively affect vegetation regeneration, especially if seed rain in disturbed patches is limited.

*Speaker

Rainfall and functional traits shape restoration success in dry forest of Reunion island

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Tropical dry forests belong to the most endangered habitats worldwide, due to habitat degradation. In the Mascarenes islands, however human settlement is relatively recent (\simeq less than 400 y. o.), native dry forests only remain as fragments among the three islands of the archipelago. On Reunion island, only a percent of the original surface still remains in remote locations. Since 2009, the National Park of Reunion has started restoration works in the north of the island. Around 400 000 seedlings of 45 dry-forest species were planted and their survival and growth have been followed from 2012 to 2018. Environmental parameters as shadowing and rainfall were registered respectively at the start and from 2012 to 2018. In 2018, we sampled and complete a database with functional foliar traits for each species on the field.

Our results show that environmental changes during the plantation had an impact on the survival of seedlings and on their relative growth. In particular, amounts of rainfall during the dry seasons might act as a major determinant of survival through years. Globally survival and growth were higher for some species according to their succession group. However some species categorized as slow-growers and shadow-tolerant were surprisingly similar to "pioneers" species. Functional traits as SLA and LDMC content explain a large part of survival and growth observed.

Those results highlight the use of studying functional traits in restorative works and in restoration ecology. Selecting species based on their succession group is limited, because these groups are mainly made on experts opinions. Functional traits offer an easy and objective way to guide restoration nowadays and should be the first exploratory step of any restorative program. At local and regional scale, this study gave tools for dry forest restoration in particular but also for any restorative program of native habitats.

*Speaker

Forget returning to lost ecological paradises or how ecosystems respond to various pressures and follow unexpected ways (Saga of Willapa bay, NW, USA)

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The purpose of this research is to illustrate the panarchic structure & dynamics of ecosystems to understand its evolution over time towards a novel "eco social system" by highlighting its biocomplexity, which involves the on-going multiplicity of interrelated relationships and levels. The framework includes the three dimensions of complexity (spatial, temporal and organizational) in order to increase the exploratory analysis power of the case study. The method wants to be as simple as possible and reproducible to other cases.

Our case study concerns Willapa Bay (NW, USA) and its watershed that was not really populated until early 1800s. We built a huge multidisciplinary database to document the "natural" and human stories on this territory for a progressive exploitation of its terrestrial and aquatic biodiversity. Examining three groups of living resources (forests, salmon and oysters) as integrators of the evolution of the ecosystem, we sought the interactions among non-human (climate, weather, major events such as earthquakes, tsunamis, wildfires) and human (exploitations, institutions, various level regulations, economic crises, wars, markets and technological innovations).

This reconstruction describes this multiscale dynamics through adaptive cycles associating the elements of "natural", economic, social and political systems without forgetting management agencies and users.

These dynamics are always shaped by uncertainties that arise not only from ecological and natural variability, but also mostly from economic disruptions, political changes, and changes in societal perceptions (Hanna, 1998). In many cases, the revelation of changes in the past lead to awareness and the need to change the *statusquo* between stakeholders.

Therefore, it seems essential to knowing the environmental and social theatre where the episodes and events have taken place and are still taking place to admit the endless change of novel ecosystems that never will go back to their initial status.

*Speaker

A multi-treatment experiment for floodplain grassland restoration in Bordeaux: hypotheses and preliminary results

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All over the world and especially in floodplains, there is a growing concern about the necessity to restore grasslands that have been converted to cultures for long. The early stages of restoration are known to be of great importance at least for the short-term dynamics of the restored grassland. In particular, the modification of soil properties and the complexity of the biological input are likely to influence the establishment of the desired community. In order to test the combined effect of soil treatment and biological input complexity on restoration dynamics, we set up, in 2017, a field experiment on a former crop culture. We combined two modalities of soil treatment (no treatment and 40 cm-deep ploughing) with five modalities of biological input (common grassland species seeds, specific grassland seeds, hay transfer, soil blocks and control) tested on 100 plots of 16 m². On the one hand, we assume that soil treatment will reduce the soil seed bank, thereby decreasing interspecific competition by undesirable species, and diluting the trophic levels inherited from fertilizers input during the agricultural period. On the other hand, by introducing a more complete species pool and even associated micro-organisms, we assume that more complex biological inputs will accelerate the initiation of the ecological restoration. The effect of the interaction between soil treatments and biological input complexity will be evaluated by the means of floristic monitoring during spring 2018. We expect a greater change in plant species composition and richness along the gradient of biological input complexity and especially for ploughed plots. This first monitoring will enable us to identify the processes involved in the very first stages of the dynamic of alluvial wetlands.

*Speaker

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Early successional vegetation patterns of alluvial deposits following dam removal: a functional approach

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The early successional vegetation stage is crucial for ecosystem development. A good understanding of this stage is especially important in restoration projects. Fluvial systems, heavily human-modified are now subject to increasing restoration efforts such as dam removal, are notably concerned. This study aims to describe the fine-scale spatial and temporal patterns of the initial phase of colonization in a dam removal context using a functional approach. The study was conducted on the Sélune River (Normandy, France), where two dams, 32 and 16 m high, respectively, are in the process of being removed. We recorded vegetation cover and composition changes during the 2015 growing season on dewatered alluvial deposits at two scales and three dates (March, May and July at site scale, March, June and September at impoundment scale). Grime Strategies and functional traits related to sediment stabilization and colonization capacity were recorded for each species according to databases. Physical drivers were estimated using spatial proxies: the distance to and the relative elevation from the channel, the longitudinal distance of the sampling station to upstream. Results showed at the two scales a rapid terrestrialization of the formerly submerged area. The colonization patterns of plant communities during the growing season exhibit an increase in species richness, a shift from ruderal to competitor species and a sediment stabilization potential notably by herbaceous species. Interestingly, we observed meaningful cover of species with hemirosettes all over the vegetation season. Moreover, pollination was mostly operated by abiotic factors in early season, and by biotic factors in late season. Woody species (*Salix atrocinerea* Brot and *Alnus glutinosa* (L.) Gaertn) regeneration was registered in the late growing season. Vegetation patterns were more influenced by abiotic factors in the early growing season than in the late growing season. These results highlight the passive restoration potential of vegetation colonization.

*Speaker

Spatio-temporal Dynamics of Ecosystems

*Speaker

Network analysis provide new perspectives to identify plant bioregions: a case study in the Mediterranean region of France

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The delimitation of bioregions helps understand historical and ecological drivers of species distribution. The Mediterranean basin offers a rich mosaic of plant distribution patterns, whose description constitutes a great challenge toward a global understanding of the flora. In particular, transition areas between biomes have raised difficulties to set comprehensive limit between bioregions.

We performed a network analysis of plants distribution in south of France (Languedoc-Roussillon and Provence-Alpes-Côte d'Azur) to analyze the biogeographical structure of the French Mediterranean flora. We analyzed a large database containing 2.5 millions of geolocalized plant records, corresponding to more than 3,500 plant species. This method allowed us to identify biogeographical regions under the form of spatial network communities, and analyze their interactions based on the relative contribution of plant species to each bioregion.

First, we identified 2 sub-networks that distinguish mediterranean and temperate-mountainous biota. Then, we separated eight statistically significant bioregions that present a complex spatial structure. Some of them are spatially well delimited, and match with particular geological entities. On the other hand fuzzy transitions arise between adjacent bioregions that share a common geological setting, but are spread along a climatic gradient. This is exemplified by the identification of the cluster "Mediterranean border", that constitutes a transition entity between the two biomes.

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The proposed network approach illustrates the biogeographical structure of the flora and provides precise insights into the relationships among bioregions. It gives analytic clues to spatially identify the Mediterranean bioregion, whose delimitation has been long debated among biogeographers. This approach demonstrates how climatic gradients and geological substrate shapes biodiversity patterns in the Mediterranean, and exemplifies why fragmented distributions are common in the Mediterranean region, isolating groups of species that share a similar evolutionary history.

*Speaker

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Which aspects are usually assessed by studies on ecological restoration of cultural landscapes?

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Ecological restoration has been experiencing a progressive integration of various disciplines (e.g. social, cultural and political) other than the initial ecological focus. This is likely due to the notion of how important other contexts are for the long-term effectiveness of restoration projects. Nevertheless, a new paradigm is necessary, especially in order to comply with recent ambitious targets promoted by international agreements on ecological restoration. When restoring cultural landscapes (i.e. landscapes shaped by long-term human activity and its relationship with the environment), several aspects could be involved and therefore assessed. Here, we performed a literature survey on studies linking cultural landscapes and ecological restoration and evaluated the number and type of aspects assessed in studies involving data collection (primary or secondary data). Two study types were considered: baseline studies (i.e. research on baseline for planned restoration) and studies evaluating previous restoration actions. We found 60 studies that fitted our criteria, ranging from 1995-2017. We categorized assessed aspects into ecological, landscape and people perceptions/cultural. Although ecological aspects are more commonly studied (e.g. vegetation/soil dynamics, biodiversity changes; 40 studies), aspects related to landscapes (e.g. landscape scenarios and connectivity, and land-use history) and people perceptions (e.g. general perceptions and preferences about ER) were significantly represented, with 32 and 17 studies, respectively. Only three studies involved aspects belonging to all three categories, and 23 involved aspects belonging to two categories. Studies were mostly on baseline for restoration (48). We suspect that restoration linked with a cultural landscape approach is not reaching the scientific arena, although it is most probably happening "on the ground". Hence, we now have undergoing research aimed at finding out if cultural landscapes are being considered by restoration practitioners in France and to what extent other aspects have been considered when developing restoration projects.

*Speaker

Adaptive and neutral differentiation in the Mediterranean grass species *Brachypodium retusum* populations: consequences for ecological restoration

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The ecological restoration of Mediterranean *Thero-Brachypodietea* steppes is a slow process because dominant perennial grass species are poor colonizers. In Spanish and Southern French steppes, *Brachypodium retusum* (Pers.) P.Beauv. is a key species but its seedling recruitment is often very low. To evaluate the importance of plant origin in reintroduction approaches and the mechanisms driving genetic structuring, neutral and adaptive differentiation were tested using AFLP markers and morphological traits. Plant material from seventeen populations was collected in France (14 populations), Spain (2 populations) and Italy (1 population) for a total of 322 individuals genotyped with 330 AFLP markers. A subset of thirteen French populations was grown for two years in a common garden experiment to measure vegetative growth and reproduction. Based on AFLP marker analysis, diversity indices and their relations to climate and soil conditions were calculated. Population differentiation in neutral AFLP markers was estimated using pairwise *theta*ST. First axis PCA scores of quantitative traits were fitted to determine PST values (adaptive differentiation), and PST were compared to *theta*ST. Populations collected from habitats with high grazing pressure showed higher clonal reproduction. Clonality was negatively correlated with average annual precipitation and temperature. Global dataset *theta*ST (0.102 ± 0.02) indicates significant differentiation between populations. PST (0.66 ± 0.12) was higher than *theta*ST suggesting that phenotypic population differentiation is driven by directional selection leading to adaptive differentiation. This adaptive differentiation at a regional scale (Southern France) advocates a careful choice of plant origin in ecological restoration.

*Speaker

The Role of Aquatic Macrophytes in the Functioning of Freshwater Ecosystems

Effects of a large irrigation dam on aquatic and riparian plants: a history of survival and loss

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Dammed rivers have unnatural streamflows, disrupted sediment dynamics and rearranged geomorphologic settings. Fluvial landscapes of regulated rivers are also altered in land-use and land cover (LULC) and in human infrastructures. Consequently, fluvial biota experiences disturbed functioning on the novel aquatic and riparian ecosystems, and alter their abundance, composition, and functions. Usually, ecological studies on effects of damming on flora and vegetation are traditionally focused on downstream sections. Here, we studied: i) the backwater effect of dammed flows upstream ii) the dramatic change of a river to a lentic waterbody in the reservoir area and iii) the effect of reduced flows downstream. The case study is the Alqueva dam, a large irrigation dam in Guadiana river, Southeast Iberia. We analyzed airborne imagery before and after the commissioning year (1990, 2013, respectively), and floristic data in comparable dates (1987-1999 and 2017, respectively). We positioned 45 circular sampling units in the three sections of the river. We collected information on LULC, aquatic and riparian cover and geomorphology using high resolution airborne images in both periods. We used floristic data (aquatic and riparian) and classified the recorded species into functional groups related to species origin, plant growth-forms, or resources. We performed non-metric multidimensional scaling to assess the pairwise dissimilarity between sections and periods. Regulation of Guadiana river by Alqueva dam resulted in a novel landscape with an increase of irrigation crops in detriment of oak woodlands, and in dramatic declines in plant abundance and biodiversity values in all river sections. Loss of native and endemic species (e.g. *Salix salviifolia*, *Flueggea tinctoria*, *Nerium oleander*, *Marsilea batardae*) and gains on alien plants were observed. However, we found some ‘relic habitats’ in adjacent wetlands nearby the reservoir holding species-rich communities of riparian herbs. Hard bedrock substrates halt partially biodiversity losses in the downstream section.

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Merging studies in allelopathy, phenology and community transfer to enhance community biotic resistance: plant engineering as a control method of invasive plants

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Aquatic invasive plants are now identified as a main problem in many European rivers. Unfortunately, this phenomenon became particularly critical in floodplains where many restoration, conservation and ecological management programs aimed to set 'blue corridors' and create the ecological continuity required to restore biodiversity. Moreover, these zones are now often concerned by recent civil engineering works to recover more natural fluvial dynamics but that consequently create a large amount of bare soil surfaces highly favorable to the invasive colonization.

In order to avoid massive colonization of these floodplains by invasive plants, stakeholders should thus develop new ecological control methods of invasive plants. We here explore some control methods aiming to enhance biotic resistance of native communities and therefore prevent invasions.

We here present both experimental results exhibiting the negative allelopathic effects of a local macrophyte species, *Potamogeton lucens* (and hybrids) on invasive species and some field study cases on the Upper Rhine Floodplain, using this allelopathic effect. Community biotic resistance was enhanced in these study cases through several methods: (i) **Macrophytes transfer**; (ii) **Soil propagule bank transfert**, both methods as a way to enable a quick local species colonization and/or limit the invasions, through the settlement of biotic interactions (allelopathy, competition); and (iii) a **temporary disconnection** to connect restored sites with potential invasive plants' sources when these plants invasiveness is lower due to their **phenology**. Several restoration types were studied: creation of shallow water zones in a former gravel pit and channels recreation within the Rhine floodplain.

Our results suggest that the transfer of a local macrophyte species (or one of these hybrids) that may develop negative allelopathic effects on invasive species together with a timing of restoration in accordance with the species (local and invasive) phenology could efficiently be used as control method of the invasive *Elodea nuttallii*.

*Speaker

Landscapes of facilitation: bio-physical self-organization of aquatic plants promotes diversity in streams

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Spatial heterogeneity plays a crucial role in species coexistence. Despite the importance of self-organization in creating environmental heterogeneity in otherwise uniform landscapes, little is known about the effects of self-organized pattern formation on species coexistence and facilitation. We investigated the effects of large-scale pattern formation on species interactions using the aquatic macrophyte *Callitriche platycarpa* in streams as a model system. Specifically, we focused on the effects of *Callitriche* on other macrophyte species through flow velocity modification and turbulence generation. Our theoretical model predicted that feedback interactions between plant growth and water flow could promote species coexistence by creating spatial heterogeneities in hydrodynamic conditions. Field observations and transplantation experiments in naturally vegetated rivers supported this hypothesis: we found a significant spatial aggregation of two macrophyte species around *C. platycarpa* and a facilitative effect on their growth through hydrodynamic stress reduction. Next to flow velocity modification, we explored the effects of turbulence generation by macrophytes on species interactions. Flume experiments showed that the dense patches of *Callitriche* had a strong hydrodynamic effect, creating high-turbulence regions that facilitated nutrient uptake by a sparser species with weaker hydrodynamic effects. Our results emphasize the importance of self-organized patchiness in promoting landscape-scale species coexistence and influencing ecosystem functioning. Understanding the link between spatial pattern formation and facilitation is therefore essential for successful management of ecosystems.

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Bringing image-based methods into the assessment of riparian ecosystems health

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Riparian vegetation drives flow regime, water quality, habitat and biota in freshwater ecosystems. In this presentation, we summarize ten years of research on image-based methods to characterize riparian ecosystems health, in Mediterranean areas, from spatial, temporal and spectral perspectives. Structural and compositional indicators of riparian vegetation, such as the lateral and longitudinal continuity, diversity and naturalness of vegetation were assessed using a combination of remote sensing techniques, GIS, landscapes metrics and historical cartography. Results showed that spatial resolution and especially high-scale resolution (< 2m pixel size) is mandatory to achieve accurate classifications due to the small width of Mediterranean riparian zones and high spatial complexity of riparian communities. In addition, the linear nature of these ecosystems constrains remote sampling procedures and restrains the selection of classification methodologies, such as object-based approaches. Nevertheless, riparian vegetation show peculiar phenological, structural and physiological traits, at species and community level, with clear implications in the spectral behaviour, that can be used to improve the remote detection of these communities. Particularly, spectral separability analysis, using aircraft or satellite multispectral data, are able to distinguish between riparian species, namely alder, willow and oleander based solely on their optical traits. However, to distinguish similar native and alien invasive stands, hyperspectral data and complementary phenological information are required. For instance, the spectral distinction of the invasive alien species *Arundo donax*, from the alike native species *Phragmites australis* can only be obtained in a reduce number of wavelengths located in near infrared region. Likewise, image-based methods, combined with the application of landscape metrics, to actual and historical cartography allowed the remote characterization of near-natural and impaired riparian areas using solely structural parameters. Well-preserved riparian woodlands are characterized by large and highly complex vegetation patches while riparian zones invaded by alien species usually showed monospecific and elongated stands.

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Does plasticity of the aquatic invasive plant, *L. grandiflora*, to terrestrial environment involve an epigenetic component?

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Ongoing global changes and human activities impact ecosystems and open new opportunities for biological invasion (Early et al. 2016). Moreover, the ability of invasive species to adapt rapidly to new environments using phenotypic plasticity represents a relevant model to study short-term adapting mechanisms.

In this context, the aquatic invasive plant, *Ludwigia grandiflora*, is recognized as harmful in rivers and its recent dispersion in wet meadow in France results in the depreciation of their fodder values and losses of financial aids for farmers. Haury et al. (2013) distinguished two morphotypes, one living in submerged environment, the aquatic morphotype, while the other undergoing a seasonality of water level, the terrestrial morphotype. Billet et al. (2018) have shown that both morphotypes responded differentially at morphologic and metabolomic levels to submerged and emerged environments. In addition, this invasive plant mainly exhibiting clonal propagation was shown to adapt rapidly from the aquatic morphotype to the terrestrial one in less than five years. We propose to test the possibility that epigenetics known as a source of flexibility will be involved in the case of *Ludwigia grandiflora* fast adaptation (Richards et al., 2017).

To test the epigenetic hypothesis, we evaluate the variations of global methylation between both morphotypes in both submerged and emerged environments. And we use the DNA hypomethylating agent zebularine, to evaluate the impact of variations of methylation on both morphotypes in submerged and emerged environments by analysing their morphology, phytohormones and metabolites profiles. Our first results suggest that DNA methylation variations may play a role in the plasticity processes in *Ludwigia grandiflora*. Altogether our data encourage now realizing a genomic investigation using transcriptomics (RNA-Seq) and methylome analysis using an original approach focused on the gene-rich open chromatin fraction (Lafon- Placette et al., 2013).

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Role of Aquatic Macrophytes in freshwater Ecosystems

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First study on the occurrence of the invasive Water hyacinth (*Eichhornia crassipes*) in Al Kabir Al Janoubi River, Lebanon

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Eichhornia crassipes is a hydrophyte considered as the most dangerous invasive plant throughout the world as cited by the European and Mediterranean Plant Protection Organization, "EPPO". It causes ecological and economic problems affecting fishing, navigation and biodiversity. Since 2006, *Eichhornia crassipes* was detected in Al Kabir Al Janoubi River, which constitutes the natural Northern border between Lebanon and Syria.

As a first study on water hyacinth in Lebanon, we focused on the characterization of its monthly growth (size, mass and morphology) on two different sites. We have also analyzed its growth variation as a function of abiotic factors (TDS, conductivity, salinity, pH and temperature), and experimented its tolerance to gradients of salinity in and ex-situ studies. Moreover, the ecological relationships of water hyacinth with aquatic and amphibious plant communities was studied.

This study showed a rapid monthly growth of the Water hyacinth with increasing size and biomass of plants between June and November, as well as morphological changes of petioles and laminae. Delayed growth and proliferation of Water hyacinth was detected between the two sites, mainly due to salinity, which was confirmed experimentally in the laboratory: Water hyacinth is sensitive to salt concentration more than 5 per thousand. In addition, Water hyacinth coexisted in the river with other aquatic and amphibious plants such as *Myriophyllum spicatum* and *Ludwigia stolonifera* (native macrophytes), *Paspalum distichum* and *Alternanthera sessilis* (invasive macrophytes).

These biological and ecological results, together with future detailed and continuous analysis of the distribution and cover changes of *Eichhornia crassipes* can help in the understanding of its dynamics and therefore its management.

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Effects of aquatic vegetation on hydrodynamics and biogeochemical processes: from ecosystem engineering to feedbacks for plants

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Submerged aquatic plants are ecosystem engineers that are able to modify their habitat. In streams, patches of aquatic plants are porous objects through which flow can partly pass, but with a reduced velocity, shear stress and turbulence. As a result, the potential of resuspension and erosion is reduced within plant patches, where fine sediment tends to accumulate, whereas flow acceleration next to the patch contributes to particle resuspension and erosion. Our objectives were to investigate the effects of patch size on plant-flow-sediment interactions in lotic ecosystems and the possible feedbacks for the plant themselves resulting from these modifications of the habitat. We performed in situ measurements of hydrodynamics, sediment characteristics, nutrient concentrations in interstitial water and plant growth along natural plant patches. Our results demonstrate that a minimum patch size was needed to induce in-patch streamwise velocity reduction and the accumulation of fine sediment. Streamwise velocity and the sediment grain size decreased with patch length, following a linear and exponential relationship, respectively. Our results also demonstrate an increased organic matter content of the in-patch sediment as well as increased concentrations of orthophosphate and ammonium and a reduced nitrate concentration in interstitial water in patches compared to bare sediment. All these changes in biogeochemical characteristics were dependent both on patch length and on position within patches and resulted in feedbacks for plant growth that may determine vegetation dynamics in flowing ecosystems. The modification of some important physical characteristics of the habitat (flow, sediment deposition...) induced by plants may play an important role in ecosystem functioning through the changes in the nutrient cycling of nutrients occurring within plant patches.

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Influence of temperature and water flow on the annual abundance of macrophyte communities in the Rhône and Garonne Rivers

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In large rivers, temporal evolution of macrophyte communities is directly under the influence of the environmental parameter annual cycle (temperature, water flow, nutrients, etc.). Yet, the specific interactions between abiotic factors and macrophyte abundance and diversity are still overlooked. Floristic and environmental monitoring were performed on several stations and years on the Rhône (i.e., 2010-2017) and Garonne (i.e., 2012-2017) rivers to determine the key environmental factors triggering the annual growth, abundance and diversity of the macrophyte community. The results showed that higher water temperature and lower flow conditions during the earlier growing season in the spring were the best environmental metrics inducing the highest abundance of macrophytes during the summer. In contrast, lower temperature and high flow conditions in the spring would limit the maximum growth of macrophyte during the summer. For instance, accumulated water temperature over 15°C in the spring in the Rhône River was the best metric correlated with the maximum annual abundance of macrophytes in the summer and especially that of invasive alien species. For example, *Elodea nuttallii* was always collected on lower flow stations but also on the warmest years. Water flow was also an important factor, as flood events in the spring were able to limit and partially prevent the growth of macrophytes in the summer. However, discharges are often artificialized in large rivers, then the impact on vegetation is quite biased. On all studied stations, the macrophytes species occurrence drops in 2013, which has been demonstrated as the coldest and wettest year over the studied period. This study demonstrates the influence of some environmental parameters on the macrophyte abundance but also highlights the need for long-term monitoring data to determine the spatial and temporal evolution of macrophyte communities related to environmental changes.

*Speaker

Theoretical Ecology

Consequences of migration pulsedness on genetic divergence

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Spatial isolation between sub-populations of the same species is one of the principal sources of genetic differentiation and a possible cause of speciation. When such sub-populations remain partially connected, the resulting gene flow acts as a force opposing divergence and tending to homogenize the two gene pools. Existing theory mostly consider migration as a constant exchange rate between populations. However, the isolation degree between sub-population is often governed by non constant phenomena such as climatic fluctuations, or accidental long-distance transportation of individuals by sea or wind. Such processes can be periodic or completely stochastic, and therefore gene flow is likely to be highly temporally variable. Some theoretical arguments have suggested that the more variable the migration rate, the higher the expected genetic divergence, but few studies have addressed this question, and they restricted themselves to neutral genetic variation. In this work we study the consequences of a pulsed gene flow pattern for the genetic divergence of two partially connected sub-populations. We model pulsed migration (episodic events of genetic exchange) between two population, and how it interacts with genetic drift, mutation and potentially selection to determine the genetic divergence rate. Four genetic scenarios are considered: (i) neutral divergence ; (ii) divergent selection where populations specialize on each habitat and migrants are mal-adapted (local adaptation) ; (iii) accumulation of deleterious recessive mutations (buildup of inbreeding depression) ; and (iv) hybrid incompatibility (accumulation of incompatible mutations). We study analytically a simplified mathematical model and validate predictions by confronting it with stochastic Monte-Carlo simulations. By quantifying the probability of genetic identity between the two populations, we find that depending on the genetic scenario and other parameters, genetic divergence may be higher or lower with pulsed migration than with continuous migration.

Keywords: pulsed migration, selection, mutation, genetic divergence, FST, Monte-Carlo simulation, Moran model, population genetics

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When ecosystems do reproduce

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The analogy between communities and organisms proposed by Clements (1916) has long been criticized, but is nevertheless at the origin of the still lively concept of ecosystem (Tansley, 1935). A major debate on this subject opposed Lovelock, the father of the Gaïa hypothesis, to evolutionary biologists such as Dawkins. Dawkins pointed out that our planet cannot undergo natural selection since there is not "a set of rival Gaïas, presumably on different planets" and "some kind of reproduction whereby successful planets spawned copies of their life form on new planets" (Dawkins 1982, p236). Similar arguments regarding the absence of ecosystem's populations and reproduction are often opposed to the idea that ecosystems could evolve by natural selection. The main idea of this paper is that ecosystems **do** reproduce. To begin, I propose an overarching definition of reproduction, which encompasses both sexual and asexual reproduction as a cycle of increase and decrease in genetic information. This definition applies to both organisms and ecosystems and allows identifying situations in which ecosystem **do** reproduce. A first one is experiments of ecosystem artificial selection (Swenson et al., 2000a & b; Blouin et al., 2015). I will present the main results obtained on microbial ecosystems as well as conditions responsible for variation and those required for heritability. Second, I will introduce the recent concept of coalescence of microbial communities (Rillig et al. 2015), an enlargement of the meta-community concept to the dispersal of a set of species transmitted together with abiotic components. Ecosystems that undergo coalescence in the wild **do** reproduce in some specific cases. In these two situations, the three conditions required for selection to occur (Lewontin, 1970) are fulfilled: there is variance in properties among the different ecosystems experiencing selection, this variance is heritable and differences in ecosystem properties are linked with different fitness values.

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The selection ratio as the unifying metric of habitat selection analyses

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In the last decades, the study of habitat selection by animals has shifted towards more complex analyses, integrating more variables, often both categorical and continuous. This has led the field to shift from the use of selection ratios – which were once the standard metrics of selection strength – to the use of resource selection functions (RSF). However, the use and interpretation of RSF analyses is deceptively simple. The concept of relative probability of selection is not always understood, sometimes leading to misinterpretations and inconsistent reporting of RSF results, and statisticians still debate what functions can actually be used as RSF. These issues have been known for some time (e.g. Lele et al. 2013 *J. Anim. Ecol.* 82:1183-1191), but haven't yet found obvious solutions. In the hope of solving some of these issues, I will present an updated, yet simple, framework for the analysis of habitat selection, based on the reformulation of selection ratios, thereby facilitating the interpretation of habitat selection analyses. I will demonstrate the strength of this framework using simulations, and its application to real-world data by analyzing the habitat selection of Plains zebras in an African protected area.

*Speaker

Warming effects on predator-prey interactions – a resource-based approach and a theoretical synthesis

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Processes such as metabolism, growth and feeding typically speed up with warming over the so-called ‘biologically relevant’ temperature range. This view has been widely incorporated into models of consumer-resource interactions that describe warming effects on food webs. Despite a striking structural similarity of these models, their predictions can differ widely, and no single model can accommodate the full range of observations from warming experiments in consumer-resource systems. We explored the temperature dependence of predator-prey interactions with a dynamical model that makes broader assumptions than most previous work. (1) Temperature dependence of the prey’s carrying capacity is not assumed a priori but emerges from the interaction of the prey with its own resources. (2) The entire physiologically tolerable temperature range is considered over which several rate parameters show hump-shaped relationships to temperature. (3) The predator’s functional response can be of type II or type III. Depending on the mode of resource supply, prey carrying capacity can be near-independent, monotonically declining or strongly hump-shaped in temperature. Yet, the influences of temperature and resource enrichment on predator-prey dynamics are qualitative the same in all of these cases. When plotted against temperature and enrichment, predator persistence and stability boundaries are U-shaped functions of temperature when the predator has a type II response; i.e. predators persist - but also oscillate - at lower enrichment levels when temperatures are intermediate. If the functional response is of type III, the persistence boundary is also U-shaped but a large region of stability opens up at intermediate temperatures. Warming can thus predictably increase or decrease stability and predator persistence, depending on current temperature, enrichment and the predator’s functional response. The results of most previous modeling studies can be mapped onto the U-shaped persistence and stability boundaries, suggesting that previous, contrasting predictions are special cases of the more general model.

*Speaker

How complex is the stability of complex trophic communities?

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Measuring the stability of complex ecological networks is a matter of increasing importance, yet it has proven to be a hard task, oftentimes leading to conflicting results. Recently, the fact that the concept of stability itself was not clearly defined has attracted the attention of the scientific community. More precisely, the existence of many different aspects of community responses that can be assessed to evaluate “stability” has been drawn to focus. This, together with the fact that most scientific studies focus only on one of those aspects, holds to the key to understanding the reasons for some of the conflicting results that still remain present, e.g. regarding the stability of complex trophic communities. To study the multidimensionality of the stability of complex ecological communities we propose a unifying approach, measuring at the same time a wide variety of quantities frequently used in scientific literature to assess the stability of ecological networks. Our approach is based on dynamical simulations of realistic trophic networks submitted to different perturbation scenarios (pulse and press). Working with many different metrics simultaneously we shed some light on how these different aspects of stability relate to each other, what they entail for community survival, and provide an estimate of the minimum information that should be taken into account when studying the response of these communities.

*Speaker

General Laws of Ecology: Thermodynamics and the ten-percent rule

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Ecology is a relatively young science compared to other traditional subjects such as physics, chemistry, biology, geology, even botany, zoology, ornithology, e.g., and other "ologies" in the biological sciences pre-date it. One criticism of the field is that it lacks fundamental theory and is largely a science of contingencies. Relatedly, it builds on theory and laws in physics and chemistry, particularly thermodynamics and stoichiometry, but it is more than simply an extension or new application of those fields. It clearly has something unique to offer that is not housed in those other disciplines, which has to do with the self-organization and maintenance of complex adaptive systems. Shortly after Sir Arthur Tansley coined the term ecosystem, whole ecosystem studies were conducted using Lindeman's trophic-dynamic concepts. The idea being that general patterns of ecosystems emerge along this standardized approach. One such outcome was the so-called ten-percent rule of trophic transfer efficiency. However ingrained this rule is in the field of ecology today and introductory biology textbooks, there is not a clear understanding of where this number originated. In this presentation, I review the historical and empirical evidence that led to this rule and put it in context of other current thermodynamic principles. Notably, the ten-percent rule stemmed from early work by Patten and Slobodkin in the late 1950s and early 1960s. Remarkably, in spite of the paucity of evidence that spawned this numeraire, it probably is a reasonably correct value for many ecological conditions.

*Speaker

Ecosystems are developing! Qualitative modeling of complex interaction networks

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Several concepts have been proposed to understand ecosystem dynamics over the long term. Among them, basins of attraction capturing the system resilience and tipping points capturing sharp changes in the ecosystem dynamics are everyday more used in ecology (Scheffer et al. 2001, Brook et al. 2013). Yet, to identify and to quantify such behaviours remain a challenge, whatever the ecosystem types and dynamics.

In this study, I propose a family of models aiming at exhaustively characterizing ecosystem dynamics, once the ecosystem functioning has been clearly defined. Such models are based on discrete systems borrowed to theoretical computer sciences and are already applied in biology (Pommereau 2010, Reisig 2013), but not yet in ecology. Hence, we have developed a qualitative model based on Petri nets representing a complex interaction network, then rigorously handled through its long term changes.

Conversely to traditional (equation based-) models, the functional rules used in our qualitative model strongly modify the network structure (i.e. the ecosystem components and processes present). I illustrate this model in a theoretical ecosystem chosen as an insect (termite) colony as well as in more realistic ecosystems (Gauchere and Pommereau 2017, Gauchere et al. 2017). Every ecosystem modeled here combines trophic, non-trophic, abiotic and anthropogenic processes (and components), and allows exhaustively exploring its trajectories.

Some specific "ecosystem developments" (more or less stable dynamic types) are easily detected and quantified, such as some stable behaviours (i.e. strongly connected states), tipping points (critical processes along trajectories), and various kinds of collapses (functioning system, yet with a frozen structure). Some of these qualitative developments have been validated on observed trajectories. In addition to theoretical abilities, qualitative Petri nets already proved useful to capture ecosystem developments in long time and to recommend some sustainable trajectories to stakeholders.

*Speaker

Warming food webs: response of marine intertidal communities to temperature increases across a global gradient

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Global warming is a major threat for ecosystems, but how it will affect species coexistence in complex food webs, and how this response is modified by preadaptation of communities to local temperature conditions is still unknown. Using 124 marine rocky pool food webs sampled across a global gradient spanning four continents and representing different local temperature conditions, we explored with a dynamical model how warming affects species persistence depending on local temperature conditions. Surprisingly, we found similar empirical food-web structures and body-mass distributions across the gradient, leading to a general humped-shaped relationship between simulated species persistence and temperature. In consequence, our results show that communities from warmer regions, close to the hump, might be more sensitive to warming. Our findings do not match predictions of generic network simulations, which stresses the importance of considering the specificities of natural food webs for predicting community response to environmental changes.

*Speaker

Pinus kesiya spread on the endemic Tapia forest: ecological characteristic analysis approach

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Biological invasion of alien species is the second major threat to the sustainability of biodiversity within natural forest ecosystems. In Madagascar, the forest vestige of the highlands, Tapia forest which is source of more than 7% of income of the local population, is subject to such invasion. Pinus sp are invading more and more this ecosystem. In relation to this phenomenon, two great theories can be raised to explain the installation of species within a community. In order to understand the method of installation of Pinus species inside the Tapia forest, this study has tried to understand if there are parameters that influence this phenomenon. From a forest inventory on a total area of 3.75 ha, or 0.7% of the total Tapia forest at Arivonimamo II, we collected all ecological data concerning the biophysical, dendrometric and topographic characteristics of the stand. Statistical analyzes such as multi-component analysis and comparison analysis of the environment (invaded and non-invaded) yielded the abundance of Uapaca bojeri (a dominant species in the forest) but also the specific diversity within the stand negatively affects the existence of Pinus. This means that the smaller the number of individuals and fewer species, the easier Pinus is to install. As a result, we concluded that the environmental characteristics influence the distribution of exotic species such as Pinus sp within a forest ecosystem such as the Tapia forest.

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Animal home ranges: where are we at?

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In a context of increasing abundance of movement data and diversification of statistical methods, it seems timely to pause and reflect once again on the concept of home range and the implication of a choice of a strategy for home range estimation. I review the different operational definitions of the home range, both in terms of the factors that drive home range formation and the spatio-temporal scale at which the term is defined. I insist that often-used kernel density estimation methods include many alternative realizations of the movement process, that the animal did not actually follow, into the home range; and this may not be what the end users intended. By contrast, the standard definition of the home range sensu Burt (1943) calls for interpolation methods like the Brownian bridge. In addition to the distinction between interpolations and extrapolations, home range studies can be categorized into mechanistic, parametric approaches (mechanisms » home range) and observational, non-parametric approaches (home range » mechanisms). In between, I propose a new type of semi-parametric home range extrapolator. I also emphasize the notion of home range scale, as opposed to home range area. Simple metrics based on asymptotic semi-variance or asymptotic net squared displacement perform well at measuring the home range scale. This may be sufficient in many situations. I illustrate this review with the analysis of an example dataset from a plains zebra (*Equus quagga*) moving in a mosaic of vegetation types and interacting with a permeable barrier. Home range size and composition estimates varied about 10-fold depending on the choice of estimation strategy. I conclude with a summary of best practices and recommendations for applications to the study of home range size, home range borders, and home range composition.

*Speaker

From winter to summer and back: linking seasonal food web models to community dynamics

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Although effects of seasonality are increasingly well understood at the population level and for small communities, little is known on how seasonality affects large food webs. Theoretical perspectives put forth that some level of temporal niche partitioning could promote community persistence and stability. In particular, a recent theoretical study based on the empirical food web of Bialowieza forest in Poland proposes that the interaction turnover due to seasonality is such as to limit the risk of species extinction. Yet, theory on small systems suggests that seasonality can induce rich dynamics, including cycles of varied periods and chaos, which are prone to species extinctions. These contrasted results invite to further explore the consequences of interaction seasonality on community stability, from both structural and dynamical viewpoints. To that effect, we model the dynamics of the prey-predator community of Bialowieza forest by means of a Lotka-Volterra model with seasonal forcing on prey growth and predators' attack rates. With this model, we investigate on how climate change leading to more or less interaction turnover can affect community dynamics. We specifically explore the ability of the prey-predator community to persist over time, the community-wide synchrony of species abundances, and their temporal variability. To contribute to bridging the gap between the study of small systems and large communities, we extend the module-based approach previously developed for non-seasonal food webs, and explore how the seasonal dynamics of a large community relates to those of small communities.

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Communications Orales

Trait-based Approaches in Ecology

Functional and phylogenetic diversity of copepod communities among Mediterranean ecoregions

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The diversity of natural communities is classically estimated through species identification (taxonomic diversity) but can also be estimated from the ecological functions performed by the species (functional diversity), or from the phylogenetic relationships among them (phylogenetic diversity). Estimating functional diversity requires the definition of specific functional traits, i.e., phenotypic characteristics that impact individual fitness and are relevant to ecosystem functioning, such as size or trophic regime. Estimating phylogenetic diversity requires the description of phylogenetic relationships using molecular tools. In the pelagic environment, the distribution of plankton diversity is driven by complex interactions between environmental factors, ecological interactions, and dispersal constraints. However, the distribution of the different facets of plankton diversity and its interplay with ocean dynamics and biogeochemical provinces is poorly documented.

In the present study, we aimed to compare functional and phylogenetic diversity of copepod communities among different ecoregions. Ecoregions are defined as geographical entities with relatively homogeneous hydrodynamical and biogeochemical characteristics. Since the boundaries between ecoregions mainly result from oceanographic constraints, how could they influence the distribution of plankton diversity? To address this question, we compiled an unprecedented dataset of copepod abundances recorded at the species level over the entire Mediterranean Sea. We computed the taxonomic, functional, and phylogenetic diversity of copepod surface communities within each of the recently defined consensus ecoregions of the Mediterranean Sea. Functional diversity was estimated using a specific trait database for the most commonly-sampled and abundant copepod species of the Mediterranean Sea. It included four traits encompassing diverse ecological functions. Secondly, we reconstructed a phylogenetic tree using the

available sequences of 18S rRNA. Our tree included 154 of the analyzed Mediterranean copepod species. Comparing the different facets of copepod diversity among ecoregions allows to relate oceanographic features to the distribution of plankton diversity at a regional scale.

Abundance vs biomass: effects of the traits weighting on the measure of functional diversity

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While coastal ecosystems experience increasing pressures due to human activities and climate change, measurement of functional diversity based on the biological traits analysis (BTA) is increasingly used as a tool to assess ecosystem functioning and its responses to disturbance. A review of more than 80 papers published since 2003 highlights large differences in the methodology used to measure functional diversity, for instance in terms of the number of traits used, ranging from 3 to 25, the identity of the traits, the nature of the raw data (abundance vs. biomass). Using two different datasets on benthic macrofauna in the English Channel (i.e. a time-series of samples collected yearly from 1977 to 2016, and a spatial survey of 72 stations sampled once in 2016), we analysed how some methodological choices affect the measures of functional diversity, its spatial or temporal changes. The local diversity was calculated from different diversity indices while multivariate methods were applied to describe \tilde{A} diversity. A peculiar attention is given on the effects of one methodological choice: the selection of biomass data rather than more commonly used abundance data.

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Using species functional traits to explore the potential impacts of climate change on plankton functional diversity. The case of planktonic copepods in the Mediterranean Sea

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In this presentation, we show how to use quantitative and qualitative species-level functional traits to define functional groups and estimate functional diversity (FD). FD has emerged as an estimate that better quantifies the impacts of changes in species composition and richness on ecosystem functioning. It has therefore gained substantial attention over the last decade.

The functional traits and the geographic distributions of 106 copepod species were used to estimate the zooplankton FD of Mediterranean assemblages for the 1965-1994 and 2069-2098 periods. Multiple environmental niche models were trained at the global scale to project the species habitat suitability in the future Mediterranean Sea and assess their sensitivity to climate change. Simultaneously, the species traits were used to compute a functional dendrogram from which functional groups were defined and FD was estimated through the Faith index. Null models were implemented to test if changes FD were significantly different from change in species richness alone.

All but three of the 106 species presented range contractions of varying intensity. A relatively low decrease of species richness (-7.42 on average) is predicted for 97% of the basin, with higher losses in the eastern regions. Changes in FD follow the same pattern and are often not different from those that can be expected from changes in richness. Relative sensitivity to climate change is not clustered in functional space and does not significantly vary across the seven copepod functional groups we defined. Consequently, the most and the least sensitive copepod species are functionally redundant. Such redundancy should buffer the loss of ecosystem functions in Mediterranean zooplankton assemblages induced by climate change. However the most negatively-impacted species are affiliated to temperate regimes and share Atlantic biogeographic origins, so our results are in line with the hypothesis of the "tropicalization" of Mediterranean biological communities.

*Speaker

From genomic dark matter to functional traits: an innovative bioinformatic strategy to investigate their genomic bases within non-model organisms transcriptomes

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The advent of high-throughput sequencing approaches has unveiled the extent of Earth biodiversity and revealed our ignorance with respect to the role of this diversity in ecosystems' functioning. The fundamental molecular mechanisms associated to the functional traits of organisms are poorly known, and often restricted to model organisms. For instance, symbiotic relationships are widespread and are critically important for the functioning of ecosystems but the genomic bases of the establishment and the maintenance of these associations remain largely unknown. The study of holobiont transcriptomes involving non-model lineages represents bioinformatic challenges in order to circumvent the production of chimera or to distinguish the taxonomic origins of the assembled sequences. In addition, the vast majority of the sequences obtained remain functionally unknown, limiting the analyses to a subpart of the genomic data newly produced. Here we present an innovative bioinformatic approach and applied it to marine holobionts, in order to investigate the genomic basis of some of their traits. Using a k-mer based similarity method, holobiont reads were sorted out and independent assemblies were performed for each partners, leading to a significant diminution of de novo assembled chimeras compared to classical assembly methods. Thereafter, sequence similarity network analyses were used to perform comparative studies including the functionally unknown sequences. Following this strategy, candidate protein domains associated to symbiosis were identified. These genomic markers characterizing functional traits constitute working hypotheses to be further confirmed by targeted molecular studies. To conclude, our efficient and innovative analysis strategy allows to study the genomic of non-model organisms and their dark matter on a massive scale, and represents one of the very few studies available to date to expand our genomic knowledge about functional traits.

*Speaker

Morphological diversity increases with oligotrophy along a zooplankton time series

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Biological diversity encompasses all the variations of life, from genes to ecosystems, and is typically described from a taxonomic, genetic, phylogenetic, or functional point of view. Here we describe the changes in morphological diversity of zooplankton along a coastal time series. Morphology is of course characteristic of taxa but also has functional consequences; size, for example, is often considered as a dominant functional trait for zooplankton.

Using high-throughput imaging of weekly plankton samples, collected from 2009 to 2017 in the Mediterranean Sea, we automatically measured ~40 morphological traits on ~542,000 individuals. A reduced morphological space was defined through Principal Component Analysis and individuals were regrouped in 200 "morphs" through clustering in that space. In this morphological space, time series of indices of morphological richness, divergence, and evenness were computed using the same metrics as the ones usually defined for functional diversity.

Size, circularity, and opacity were the characteristics of the organisms that varied the most along the series. The morphs were homogeneous in appearance and recognisable, but often comprised more than one taxon. All morphological diversity indices were lower in the spring. This seemed related to the dominance of copepods during this season, which are quite homogeneous in appearance. But this could also be caused by selective disadvantages of extreme (and specialised) morphological types in this relatively eutrophic time of the year. Over the nine years, morphological divergence increased significantly while overall plankton concentrations decreased; since 2001, surface waters became significantly warmer and more oligotrophic. Overall, this fits the theory that oligotrophy leads to niche specialisation which, here, translates into morphological divergence.

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Effects of indirect facilitation on functional diversity, dominance and niche differentiation in tropical alpine communities

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Positive interactions between plants are common and their effects on community richness via environment improvement are well known. However, the effects of indirect facilitation by a nurse through protection against grazing on its associated plant community have attracted less attention, in particular regarding functional traits. As the characteristics of trait distribution can reveal selective pressure, they offer valuable information for the study of grazing pressure. We tested to what extent indirect facilitation affects the amount of trait combinations (H1), the trait dominance (H2) and the niche differentiation (H3) of associated communities.

We set up a grazing exclusion experiment over two nurse cushion species: one providing indirect facilitation through grazing to its associated community and the other not. We measured on the associated communities three functional traits, which are known to vary according to grazing: LDMC, leaf thickness and maximum height. We assessed the amount of distinct trait combinations by computing the volume of the phenotypic space (H1). The variation in trait dominance was quantified with the kurtosis and skewness of the trait distributions (H2). The variation in niche differentiation was evaluated by using the community-wide overlap of intraspecific trait variation (H3).

We did not find a significant effect of grazing or indirect facilitation on the volume of the phenotypic space. However, our study revealed a significant effect of indirect facilitation on dominance in the associated community by maintaining the evenness of the trait distributions (H2) and on niche differentiation by maintaining trait overlaps between species in grazed compared to ungrazed contexts (H3). The effects of indirect facilitation were however found to depend on the trait considered. Our results highlight that indirect facilitation

*Speaker

promotes evenness of trait distributions and niche differentiation between species, suggesting that it buffers the selective pressures of grazing on plant communities.

*Speaker

Stoichiometric Traits: a relevant approach for relating nutrient availabilities to community structures and ecosystem functioning?

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To investigate the relationships between community structures and ecosystem functioning in response to environmental changes, the use of functional traits has often been proposed as a pertinent approach. While often successfully predicting some general ecosystem processes, trait-based approaches often lack accuracy for precisely relating communities and biogeochemical cycles.

Ecological stoichiometry (ES), a conceptual framework focusing on how proportions of elements in resources and consumers (mainly C, N, and P) affect organisms and ecosystems, might represent a complementary approach for answering these questions. In particular, elemental imbalances between resources elemental content and consumers' requirements will ultimately impact consumers' life history traits (e.g. reduced growth rates and survival) and affect consumer-driven nutrient recycling in a predictable way. While commonly applied to single organisms or species, ES has rarely been studied at the community scale. The integration of stoichiometric traits (e.g. organisms' C:P or N:P ratios) in the general framework of trait-based community ecology might represent a promising way for enlarging ES results from organisms' physiology and individual-based approaches to communities and ecosystem functioning.

In this presentation, the main principles of ES will be briefly summarized. Then, I will present what biological parameters could be proposed as pertinent stoichiometric traits, discussing their main advantages and drawbacks. Finally, first results aimed at testing the influence of headwater stream nutrient (mainly N and P) availability on the community structure of macroinvertebrates will then be briefly shown, before presenting a non-exhaustive list of research perspectives using the stoichiometric traits approach.

*Speaker

Deciphering selection process using Trait-Environment relationships

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One of the major goals of community ecology is to understand how selection acts at ecological scales to shape community structure. Functional traits, as continuous measures of individual's characteristics determining their fitness in a given environment, are used as a powerful tool to understand the mechanism of selection. By understanding how traits vary along environmental gradients, one can understand how environmental conditions favor or discard different strategies and trade-offs in resource allocation. However, a lot of challenges remain, as the role of biotic filtering, the inclusion of phenotypic diversity and the necessity appropriate scale to look at. We propose here a structure approach decoupling biotic and abiotic conditions, based on crossed gradients of fertility and species diversity, with a focus on individuals. We used Bayesian distributional regressions to disentangle the consequences of selection both on community trait distributions and on the variation of dominant species niches. By a rigorous selection of models predicting the distributions of a set of seven traits related to different strategic axis, we were able to show that the displacement of mean of community trait distribution were coordinated with varying constraints on trait diversity along an abiotic gradient. Moreover, our principal results clearly states that the realized niche of dominant species of an ecosystems depends upon the number of species with which they grow. Our results highlight the need to include population levels considerations to understand community assemblage.

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Which functional diversity measures for systemic conservation planning?

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Human activities are changing climate and habitats worldwide, leading to a significant increase in extinction rates. Consequences of extinctions are not restricted to the loss of species per se but also it result in a loss of functional traits and thus the erosion of functional diversity which in turn negatively affects ecosystem functioning and services. Thus, several studies emphasized the importance of incorporating functional diversity in systematic conservation planning. Numerous measures of functional diversity have been proposed, however, so far no consensus has been reached on which better discriminate the processes shaping the functional structure of communities. Despite a multiplicity of indices, conservation planning applications for functional diversity are limited to dendrogram-based metrics. Dendrogram-based metrics have shown strong limitations in representing the functional distances between species, and their relevance for conservation planning is thus questionable. In this study, we propose an alternative conservation planning approach based on functional attribute diversity (FAD) that optimize the sum of the distances between species in multidimensional trait space. In order to determine which functional diversity measure performs better for conservation purposes, we compare two optimization methods based on FD and FAD measures. As a case study, we used distribution and traits data for coastal Mediterranean fish assemblages. We calculated functional dissimilarity using a generalization of the Gower's distance. Then, using integer linear programming to optimize an objective function integrating FD or FAD, we established corresponding conservation area networks. We examined and compared the conservation effectiveness of FD and FAD networks and report the respective advantages and drawbacks of this two approaches.

*Speaker

Biogeography of mixotrophy in the global ocean: an ubiquitous traits sustained by a high diversity of differently distributed mixotrophic protists

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Mixotrophy, or the ability to acquire resources from both auto- and heterotrophy, is an ecological trait that has been shown to be widespread in marine protists. In the last decade, the historic dichotomy between phyto- and zooplankton disappeared to give way to a new vision of continuity between a state of full heterotrophy and one of full autotrophy. Hence, mixotrophic organisms should always be considered when it comes to estimating primary production in the ocean, and their population dynamics should be included in marine ecosystems models. For that, we need to study the different types of mixotrophs to identify the biotic and abiotic factors that shape their distributions. Here, using a metabarcoding dataset of marine plankton from the global ocean, we identified a set of 140 taxonomic lineages classified into four mixotrophic functional types: constitutive mixotrophs, generalist non-constitutive mixotrophs, endo-symbiotic specialist non-constitutive mixotrophs, and plastidic specialist non-constitutive mixotrophs. We confirmed that mixotrophy is ubiquitous and we showed that constitutive and non-constitutive mixotrophs share similar global distributions, even though not always dominating in the same environmental conditions. Several lineages were evenly found in the samples. Yet, some of them displayed strongly opposed distributions, between mixotrophic types but also within types. Particularly, very divergent biogeographies were found within endo-symbiotic non-constitutive mixotrophs. We propose that the ability to form colonies, as well as the mode of symbiosis are traits playing an important role on the distribution of these mixotrophic organisms. We shown how metabarcoding can be used in a complementary way with morphological observations to study the biogeography of protists and to identify key drivers of their biogeography. This way, our study will facilitate the integration of under regarded groups and functional traits

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into ecological modeling studies.

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”Resistance is futile!” - or is it? A study on natural colonisation resistance and colonisation success in experimental plant communities along functional and phylogenetic diversity gradients

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Community resistance to colonizers remain a central question in ecology. While functional and phylogenetic diversity (FD and PD respectively) of the resident community are expected to exert a role in community resistance, very few studies have assessed this experimentally or evaluated their interactive effects. We used a diversity experiment to disentangle the role of FD and PD by sowing monocultures and mixture of 6 species, drawn from a pool of 19 species naturally coexisting in Czech mesic meadows. The mixtures were designed to cover four independent combinations of high and low FD and PD. Species covers were estimated in spring and late summer over 3 seasons. We then assessed the resistance of the resident (sown) communities to natural colonizers, and characterized the success of colonizers in relation to their functional and phylogenetic distance from the resident communities.

Results generally indicated that FD decreased community resistance to natural colonisation. However, PD tempered this effect: with high PD, FD was not significant, suggesting over-

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lapping information between these components of biodiversity. Decomposing the community structure in trait means and diversity values, we were able to identify key features of dominant species promoting colonisation resistance. From the colonizers perspective, greater difference in functional traits from the resident community tended to improve colonisation success. However, the effect was subtle and significant only for a reduced proportion of colonizers (14%). Phylogenetic distance had no detectable effect.

Our results confirm a certain interplay between FD and PD in their support of ecosystem functioning, namely resistance to colonizers, suggesting that they only partially overlap in their information about community structure. The widespread hypothesis that higher FD increases resistance by a more complete use of resources was challenged, suggesting rather that greater FD could provide an unsaturated functional trait space allowing functionally unique species to occupy it.

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Disentangling the effects of tree diversity and identity on soil invertebrates in four different European forests

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Soil macroinvertebrates is a highly diversified group of organisms that play important roles in many ecosystem processes, from decomposition to primary productivity. Besides of the effects of climatic and edaphic factors, their diversity, abundance and activity also respond to aboveground vegetation properties such as species richness or functional diversity. However, relationships between plant diversity and soil animals are not yet well understood and have been mainly studied in grasslands, but much less in forests, which limits our ability to predict soil fauna community patterns and their effects on the functioning of these ecosystems.

We investigated the taxonomic and functional responses of three groups of soil macroarthropods (carabids, isopods and diplopods) in 64 forest stands either composed of single tree species or mixtures of three species in a total of four major European forest types. We used two different sampling methods, hand sorting of excavated soil blocks and pitfall traps. We used redundancy analyses and structural equation modelling to disentangle the effects of climate, edaphic factors, tree identity and diversity and resource availability (leaf litter or prey) on soil fauna communities.

Soil macroarthropod abundance, richness and functional diversity did not differ between single tree species stands and mixtures of three species regardless of forest type, but was affected by the proportion of evergreen tree species in the canopy. We also showed that tree identity was an important determinant of soil fauna community composition. These identity effects were driven by canopy cover and leaf litterfall or indirect effects on soil pH and understory cover.

Our study describes some of the complex interactions between biotic and abiotic factors shaping soil fauna communities, and highlight the predictive power of the functional traits approach.

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Co-activity networks reveal the structure of planktonic symbioses in the global ocean

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Microbes interact both with the environment and their siblings, sometimes forming highly connected networks of metabolic interactions. These communities play crucial ecological roles on our planet, sustaining Earth's biogeochemical cycles in the ocean, or impacting host nutrition, immunity, and development in our intestinal tract. Limited by the fact that most microbes can hardly be isolated and cultivated in lab-controlled environments, we are just starting to grasp the complexity and diversity of such interactions. Even when successful, laboratory experiments inherently lose valuable information about the richness and diversity of community functioning and interactions in situ. Today, large scale environmental surveys of microbial communities across Earth's ecosystems (e.g. Tara Oceans expeditions, Human Microbiome Project) gathered large volumes of meta-omic and contextual data that are enabling the reconstruction of genomes of uncultivated microbial species (Metagenome-Assembled Genomes – MAGs). While classical co-occurrence analyses enable to predict interactions between newly identified microbes, these approaches are inherently limited since true biotic interactions can hardly be disentangle from abiotic (environmental) effects. Here, we propose a trait-based approach to enrich co-occurring information and uncover putative biotic interactions among MAGs. Genomic and growth traits can directly be inferred from MAGs and meta-omics data. Notably, co-growth signals across samples and ecosystems can be used to reveal positive or negative interactions between co-occurring microbes. In addition, the functional content of MAGs can be used to predict microorganisms appearing to depend on others, in particular if they deviate from general scaling laws governing the functional content of microbial genomes. Inferring and combining (meta-)genomic traits in a global approach can help to identify consortia of microbes and pave the way towards the functional understanding and the metabolic modeling of their interactions.

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Linking functional diversity of floral traits with land-use intensification to study pollination function in permanent grasslands

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Permanent grasslands cover one third of the total utilised agricultural area in Europe. They play a major role in livestock feeding and ecosystem service supply. European grasslands are submitted to agricultural practices with different levels of intensity defining land-use intensification. Land-use intensification impacts indirectly pollinator communities due to change in flower traits. These modifications of the plant-pollinator interactions and pollinator communities can impact pollination function in grasslands. However, little is known about the mechanisms explaining the modification of pollinator communities and pollination function due to change in flower traits with land-use intensification. Furthermore, no study establishes these links with a set of quantitative flower traits giving a holistic view of flower. Hence, we will answer to the following questions: (1) what are the impacts of contrasting land-use intensification levels on functional diversity of flower traits of grasslands? (2) What are the consequences of these impacts on plant-pollinator interaction frequencies, which are proxies of pollination function? We selected 16 grassland plots with a contrasting level of intensification in the North East of France (Moselle). 2800 pollinators belonging mainly to three Orders (Hymenoptera, Diptera, Lepidoptera) were captured in interaction with flowers on transects five times from May to August 2017 on each plot. Flower areas were measured on 47 grassland plant species. Using linear mixed models, our first results indicate a negative relationship between the land-use intensification and the community weighted mean of flower area. We also found a positive relationship between the flower area (community weighted mean and functional diversity) and plant-pollinator interaction frequencies. These results suggest an impact of land-use intensification on diversity of floral traits and change in plant-pollinator interactions. Our future measurements of other flower and pollinator traits will allow us to better understand the relationships between level of land-use intensification and pollination function in European grasslands.

*Speaker

A plant trait-based response-and-effect framework to assess vineyard inter-row soil management

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Biodiversity impacts ecosystem properties and the ecosystem services provided by those ecosystems. As a result, promoting plant diversity in agricultural systems has been a key issue in agriculture over recent years. In this context, weeds have an important role in maintaining field biodiversity, when it is balanced with their potential negative impact on crop production. Functional trait diversity, rather than the diversity of species per se, is a facet of biodiversity most directly related to species and community responses to management practices, with subsequent consequences for ecosystem services. Trait-based approaches, originally developed in the field of comparative ecology, allowed the description of weed species responses to management practices in annual crop systems. Here, we aimed to extend the trait-based approach to the spontaneous vegetation of vineyards. First, we propose a brief summary of current knowledge about weed communities in vineyards. Then we show how the relationships between management practices, weeds and grape vines can be translated into a response–effect framework: soil management practices (tillage, cover crops, spontaneous vegetation) can be considered as environmental filters that determine the composition and structure of vegetation, which, in turn, modify grapevine growth conditions in the vineyard. Finally, we tested this framework in a Mediterranean vineyard where, for 3 years, we characterized the responses of different components of weed communities (taxonomic and functional composition) in three inter-row management practices.

*Speaker

Does demographic performance predict species distribution? A trait-based analysis on European tree species.

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In the face of climate change, there are increasing concerns about the future redistribution of species ranges. Species ranges are thought to reflect demographic trends, which are governed by vital rates (e.g. survival, growth, reproduction). However, we have a poor understanding of how demography drives species distributions. This issue is particularly complex for large and long-lived organisms such as trees, for which populations' dynamics are strongly dependent on their size structure. Integral projection models (IPMs) have been proposed as a powerful tool to predict the fate of such size-structured populations due to their flexibility, robustness to low sample size, and ability to explicitly include a/biotic factors such as density dependence and climate. Here, we used forest inventory data from over 90,000 plots and 27 tree species, containing over one million adult trees across Spain, France, Germany, Sweden, and Finland to parameterise IPMs. These models include the effect of both climate and local competition. To describe each species' niche, we estimated species probability of presence with ensemble species distribution models (SDMs) fitted on 250,000 plots across Europe. Next, we compared key demographic metrics of the population dynamics derived with these IPMs such as life expectancy or passage time against the species probability of presence to test whether climatic-dependent IPMs capture the demographic signature of the species ranges. Specifically, we evaluated whether the level of local competition modifies the links between demography and species ranges. Finally, we explored whether species' functional traits such as wood density or specific leaf area help to explain why for some species there is a strong match between demographic performance and range, whereas for other species demography seems disconnected from their distribution.

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Defining ecological and morphological traits of zooplankton based on imaging technology

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Historically, communities have been described using a taxonomic classification, based on phylogenetic relationships, and the diversity defined by a number of species in an ecosystem. To better understand the function of organisms within their communities, the trait-based approach takes into account morphological, physiological, behavioral and life history characteristics. However, in marine, (mainly pelagic) environment, a strong limitation to this approach is the requirement of in situ data related to feeding, growth and reproduction or survival. The development of novel imaging technology such as Remotely Underwater Vehicles (ROV), Underwater Vision Profiler (UVP) or cytometry, allows automatic, non-intrusive and quantitative observations of phytoplankton and zooplankton within a wide range of sizes. The acquisition of such a huge amount of information is an opportunity to increase our knowledge on understudied traits, such as morphological ones (bioluminescence, transparency, size) both at individual and communities levels. In this work, we will focus on those understudied morphological traits, based on samples from the circumpolar Tara Expeditions. Images of the planktonic samples can be described into a defined number of quantitative descriptors related to grey levels and shape of each individual. We will show how the trait-based perspective highlighted patterns over environmental gradients. Moreover, we will propose some new methodological tools to cross informations from imaging, omics and environmental datasets.

*Speaker

Soil fertility and photosynthesis strategy

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In photosynthesis production, climate plays a decisive role in the diffusion of CO₂ inside the leaf to the chloroplast (Ball et al., 1987). The theory of lower cost of photosynthesis (Wright et al 2000) proposes that this process be optimized to minimize the total unit costs of transpiration (water requirement) and carboxylation (enzyme requirement and nutrient extension) according to climatic conditions of plant habitat. This theory explains about 40% of photosynthetic variations. We propose to increase the precision of this prediction by better identifying the role of the soil in the modulation of the CO₂ diffusion process towards the chloroplast but also by including it in the theory. To this end, we use and complete two international geo-referenced databases of photosynthetic features (Globamax: instantaneous photosynthesis measurements, Glob13C: integrated photosynthesis measurements, including 1015 and 3642 site-species combinations respectively) that we couple to basic climatic and edaphic data (WorldClim and soilgrids, respective resolution of 1km and 25 0m). Preliminary results show that soil pH and silt content strongly modulate the co-variation between the water requirement and the nutrient requirement, direct parameters of photosynthesis. Considering only the soil variables, we explain 38% of the photosynthetic variations. When soil variables are coupled with climatic variables, we observe an interaction showing a stronger influence of the soil when the climate is arid or the altitude is high, two conditions that increase the cost of water use according to the theory the least cost. We seek to understand the ecophysiological mechanisms behind the role of the soil and its interaction with the climate in order to integrate this interactive role in global vegetation models.

*Speaker

Litter decomposition is predicted by community-weighted mean trait while non additive effect are driven by functional diversity of the species mixture

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The role of functional traits of plant assemblages in ecological processes has been often hypothesized while the underlying mechanisms remain unclear. The Biomass-Ratio Hypothesis assumes that the community-weighted mean trait value (CWM) drives the community's effect while the Diversity Hypothesis assumes that functional diversity (FD) plays a significant role. As the CWM and FD values are two related variables in natural communities, an experimental design is required to disentangle their respective effects. This study quantified the independent effect of the CWM and FD value for the decomposition process of plant assemblages, considering the Leaf Dry Matter Content (LDMC) in particular. We tested whether the importance of the non-additive effects increases with increasing FD values. The experimental design consists of six groups of three-species combinations from a pool of 18 grassland species, combining CWM (high, low) and FD (high, medium, low) values. After six months of incubation in controlled conditions, the mass loss rate of the litter mixtures varied from 65% to 75%. The mass loss was overall higher for low CWMLDMC values. Non-additive positive effects occurred for five litter mixture groups out of the six CWM x FD modalities. The effect of FD on the importance of the non-additive effects was dependent on the CWM value, as it led to higher non-additive effects for mixtures with a high CWMLDMC only. Our results suggest that functional diversity constitutes a significant driver of decomposition but that its effect must be assessed while taking the role of dominant traits into account.

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Leaf nutrients and macroinvertebrates control litter mixing effects on decomposition in temperate streams

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Plant litter decomposition is an essential ecosystem function that contributes to carbon and nutrient cycling in streams. The composition of both plant and decomposer communities are major determinants of the decomposition rates and the interactions (synergistic *vs.* antagonistic) occurring in litter mixtures. However, the extent to which such litter mixture interactions are affected by combined shifts in litter traits and decomposer community are not well understood. We used leaf litter from 10 European tree species in order to evaluate how litter mixture effects occurring in two-species litter mixtures are affected by litter nutrients in a temperate forested stream of northwestern France. The study distinguished between (i) decomposition involving microorganisms alone or microorganisms together with invertebrates, and (ii) decomposition involving litter mixtures of similar litter quality (two nutrient-poor or nutrient-rich litters) or of dissimilar litter quality (one nutrient-poor and one nutrient-rich litter). The highest litter mixture effects occurred in mixture containing two nutrient-rich litters, rather than in the mixture of dissimilar litter quality. Moreover, the synergistic effects of litter mixing were found to occur only in macroinvertebrate presence. Both the community weighted mean traits (TraitCWM) and the functional dissimilarity of litter traits (TraitFD), as metrics of the mass-ratio and niche complementarity mechanisms, respectively, contributed to explain litter mixture effects. TraitCWM was found to be a better predictor than TraitFD. No evidence was found of the TraitFD effect in the presence of macroinvertebrates, while both TraitCWM and TraitFD contributed to litter mixture effects driven by microorganisms alone. Finally, when evaluated separately the individual contributions of litter nutrients, calcium and magnesium appeared as important drivers of litter mixture effects. As litter decomposition is mainly controlled by macroinvertebrates in temperate streams, our findings suggest that the mass-ratio hypothesis overrules the niche complementarity hypothesis as a driver of litter diversity effects.

*Speaker

Integrating reproductive phenology in the description of plant phenotype

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In the last 30 years, there has been a renewed interest in a detailed description of the phenotype using a trait based approach, with an aim of improving our understanding and prediction of plant, community and ecosystem functioning. Despite its recognized importance for plant survival and reproduction, phenology has been largely understudied in trait based approaches to describe plant functioning. How reproductive events relate to other plant functional dimensions and integrate into the whole phenotype therefore remains to be established.

The aim of this study is to explore how events of reproductive phenology combine in the phenotypic space derived from several traits commonly used in comparative ecology. Relationships between phenological traits and traits contributing to the Leaf-Height-Seed scheme proposed by Westoby (1998: *Plant and Soil*, 199: 213-227) are tested using data collected for 117 species growing in the Mediterranean region of southern France and belonging to three growth forms (annuals, herbaceous perennials and woody perennials of low stature).

Phenological traits were related both to plant height and seed size in annuals. They were related only to plant height in herbaceous perennials, while no correlation was found for woody species. Whether reproductive phenology can be considered as an independent axis of functional variation in plants therefore seems to depend on the species group considered. This study confirms the value of using phenological traits as a functional dimension in comparative approaches. It brings new insights into the links between phenology and other dimensions of plant functioning, putting back phenology into the broader context of plant ecological strategies.

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The effects of sublethal doses of pollutants on crop pest, *Spodoptera littoralis*

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Pesticides have long been used as the main solution to limit agricultural pests but their widespread use resulted in chronic or diffuse environmental pollutions, development of insect resistances and biodiversity reduction. The effects of low residual doses of these chemical products on organisms that affect both targeted species (crop pests) but also beneficial insects became a major concern, particularly because low doses of pesticides can induce various effects. In addition to the negative effects, some studies highlighted unexpected positive - also called hormetic - effects on insects, leading to surges in pest population growth at greater rate than what would have been observed without pesticide application. The present study aimed to examine the effects of sublethal doses of various representative products of large pesticide families used against a major pest insect, the cotton leafworm *Spodoptera littoralis*, and known to present a residual activity and persistence in the environment. Using an integrated approach from genes to behavior, we studied the impact on the peripheral olfactory system and the sexual or feeding behavior of our crop pest model following application of sublethal doses of deltamethrin, methomyl and chlorpyrifos. Whereas sublethal doses of methomyl appeared to disrupt the feeding behavior of larvae, we demonstrated a hormetic response of males to sublethal dose of deltamethrin. We completed our study by molecular (qPCR), biochemical (proteomic, AChE activity and metabolic) and electrophysiological approaches in order to decrypt the involved mechanism in pesticide response as well as in the behavioral disruption.

*Speaker

Morphological diversity of the world freshwater fishes is driven by both taxonomy and biogeography

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More than 13000 freshwater fish species are distributed throughout the World Rivers, with strong differences in species composition between realms, but how such taxonomic turnover translates into morphological differences remains unanswered. Here we use a global database of freshwater fishes to test the variability of the morphological traits among biogeographic realms. We measured ten morphological traits on 9150 species, i.e. 75% of the described freshwater fish species to test if these traits are homogeneously distributed among the fish faunas of the six terrestrial biogeographic realms. We then analysed the contribution of order membership and within order morphological variability to the morphological differences between realms, and determined to which extent the realm distributions of morphological traits were supported by extreme morphologies (i.e. species belonging to the 2.5% tails of the trait distributions). We report a strong morphological variability among freshwater fishes of the world, with significant morphological differences among realm fish faunas, caused by an interplay between taxonomic composition of the realm faunas and morphological differences within orders among the realms. Morphologically extreme species accounted for a large percentage of the trait range and distribute throughout the world. Moreover, the Neotropical realm hosts a disproportionate proportion of extreme morphologies. Our results indicate that fish morphology, which differs among realms, is largely supported by a few species with extreme morphologies, encouraging therefore forthcoming studies to focus on the functional role played by those extreme species. To this aim, our results will serve as a benchmark for future regional and local assessments of morphological diversity.

*Speaker

Characterizing oxygen consumption and its relation to other functional traits: a case of *Tetrahymena ciliates*

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The mechanisms underlying the relationship between biodiversity and ecosystem functioning are still poorly understood. Although species richness is commonly used as a biodiversity measure, recent studies showed that functional diversity, i.e. the diversity of functional traits, is a better proxy for biodiversity when studying the ecosystem functioning. Functional traits are defined as the components of an organism’s phenotype that determine its niche, its response to environmental factors, and its influence on ecosystem functions. Nevertheless, the use of functional traits to quantify biodiversity is associated with several challenges. For example, which traits should be considered as functional, and why? Do we need to measure the whole set of phenotypical traits? Here we investigate these questions using an actively dispersing protist, *Tetrahymena thermophila*, as a study species. We focus on the oxygen consumption, which is considered a highly structuring trait among natural protist communities, thus matching the definition of a functional trait. We selected 42 genotypes (clonal strains) of *T. thermophila*, which represent variation in phenotypical traits and thermal niches of this species. Firstly, we quantified the variation in oxygen consumption between those genotypes. Secondly, we estimated the correlation between oxygen consumption and other phenotypical traits (e.g. morphology and motility traits). We evidenced large differences between genotypes in the oxygen consumption rates, with some strains consuming four times more oxygen than others. Our results also highlight strong correlations between oxygen consumption rates and other traits that could be considered as functional in *T. thermophila*, e.g. a positive one with cell movement speed, or a negative one with cell size. This suggests that functional diversity of this species could be efficiently assessed by measuring a limited number of traits.

*Speaker

Assessing anthropogenic pressures on stream communities: new modelling approaches based on traits of macroinvertebrates, diatoms and fishes

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Identifying the anthropogenic pressures impairing ecosystems is a challenging task, especially in streams that integrate multiple pressures (related to water quality, land use and hydromorphology) from their catchment. The impacts of those pressures can be assessed investigating the communities inhabiting the systems. However, traditional biomonitoring methods such as biological indices mainly aim at assessing the impairment magnitude of pressures, and not at estimating the respective importance of the involved pressure categories.

In streams, assemblages of macroinvertebrates, benthic diatoms and fishes are characterized by different combinations of attributes related to life history, dispersal, resistance and resilience strategies. They integrate variations in environmental conditions over various time-scales (from weeks to years) and space scales (from microhabitat to watershed). Such differences may result in contrasted – and potentially complementary - responses to different categories of pressures. Moreover, habitats act as a templet on which characteristic combinations of species attributes are selected. In this context, examining combinations of trait-based metrics can help to assess the ecological impact of specific anthropogenic pressure categories on ecosystems.

Using the random forest algorithms, we have built models exclusively (invertebrates) or predominantly (diatoms and fishes) based on trait descriptors of communities. Most of these models have demonstrated a good efficiency for identifying specific pressures related to water quality degradation (e.g. nutrient, pesticide or metal contamination) and/or hydromorphological alteration (e.g. degradation of riverine vegetation, hydrological instability, clogging risk) even under multi-stress scenario. These complementary tools represent a further step in stream ecological diagnostic and can support stakeholders in decision-making processes.

*Speaker

Predator and prey traits interactively determine the strength of trophic cascades

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The strength of ecological interactions is classically considered as driven by the densities of interacting species, a dogma dubbed "law of mass action". However, recent studies showed that inter- and intraspecific trait variation may also play an important role in driving the strength of ecological interactions. Here, we experimentally show in fish-zooplankton-phytoplankton lake enclosures that the strength of predator-prey interactions may depend interactively on the hunting mode of fish predators and the mobility-dependent predator avoidance ability of zooplankton prey. Compared to filter-feeding roach, visual-feeding perch reduced more severely both the abundances and body sizes of fast-swimming and large-sized zooplankters, which are also the most efficient phytoplankton grazers. In contrast, roach and perch had equal predation efficiencies on slow-swimming, small-sized zooplankters. The overall stronger effect of perch on the herbivorous zooplankton community resulted in higher phytoplankton concentrations and in lower abundances of epibiotic primary producers (essentially fixed on herbivorous planktonic microcrustaceans) in perch enclosures compared to roach enclosures. Specifically, the effect sizes

of perch relative to roach on the concentrations of planktonic and fixed microscopic primary producers were of the same magnitude as the effects of roach relative to fishless controls. Our results demonstrate that the law of mass action is not sufficient to predict the strength of ecological interactions. Accounting for the potentially complex interplay between predator and prey behavioral and morphological traits is also necessary to accurately predict community dynamics.

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Communications Orales

Tropical Ecology

Functional diversity increases aboveground biomass via increasing tree crown complementarity in tropical forests of Hainan Island, Southern China

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The niche complementarity and mass ratio or selection hypotheses are well-accepted and widely applied in contemporary ecology. Yet, few studies have provided a multivariate test for the tree crown complementarity mechanism in natural tropical forests. Here, we hypothesized that crown complementarity is a potential ecological mechanism for linking positive functional diversity and aboveground biomass while considering for the positive direct and indirect effects of climatic water availability and soil fertility in natural tropical forests. To test this hypothesis, we used structural equation models on biophysical data from 187,748 trees across 712 plots in tropical forests in Hainan Island of Southern China. The results showed that aboveground biomass increased directly with increasing functional diversity ($\beta = 0.24$, $P < 0.001$), individual tree crown variation ($\beta = 0.18$, $P < 0.001$) and climatic water availability ($\beta = 0.17$, $P < 0.001$). As such, functional diversity enhanced individual tree crown variation ($\beta = 0.26$, $P < 0.001$) and hence increased aboveground biomass indirectly via individual tree crown variation ($\beta = 0.05$, $P < 0.001$). Additional positive effects of climatic water availability and soil fertility on aboveground biomass were accounted indirectly via increasing individual tree crown variation and/ or functional diversity. This study shows that individual tree crown variation is a potential ecological mechanism for the positive effect of functional diversity on aboveground biomass, and as a mechanism for species coexistence through maintenance of functional diversity in natural forests. This study suggests that a multilayered stand structure, having a species mixture of both shade tolerant and intolerant with contrasting functional strategies, can increase species coexistence and aboveground biomass in natural forests. We, therefore, suggest that proper silvicultural operations would be helpful to further improve the light partitioning for biodiversity conservation and high forest functioning in the studied forests, and other natural forests in general.

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Optimizing environmental DNA sampling effort for fish assessment in tropical streams and rivers

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Since Earth experiences a notable decline of biodiversity and considering the services that it provides to humanity, there is an urgent need to develop accurate and efficient methods to measure species diversity. The environmental DNA (eDNA) metabarcoding is a promising tool to measure aquatic biodiversity. It is based on the capture of DNA from a water sample, but the water volume sampled (*i.e.* sampling effort) displays a high variability among studies. We determined the optimal sampling effort to detect fish assemblages in tropical streams and rivers. We collected eDNA replicates in Guianese sites (streams and rivers). We show that a single eDNA replicate of 34 litres of filtered water detected more than 64% of the expected fish fauna, with little variation between replicates. The number of detected species per site saturated after 2 replicates, with a detection rate higher than 71%. Considering fish assemblages, we reveal a strong consistency between replicates that permitted to distinguish the fauna between sites and between ecosystem types (stream *versus* rivers) using a single eDNA replicate. These results testify that filtering eDNA from few litres of water is sufficient to achieve relevant inventories of local species assemblages and to distinguish sites according to their fauna. Therefore, this method deserves to be used in the assessment of human impacts such as gold mining, logging and intensive agriculture in highly diverse and threatened ecosystems such as Amazonian rivers.

*Speaker

A multi-faceted view of biodiversity to disentangle the assembly rules of Guianese freshwater fish assemblages

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Both evolutionary and ecological processes affect the assemblage composition and spatial structure. To disentangle their relative strength, community ecologists have shifted from the use of taxonomic based information (species identity and richness) towards a more extended view of biodiversity that also encompasses the species role in the ecosystem (functional diversity) and their evolutive history (phylogenetic diversity). Combining taxonomic, functional and phylogenetic information and looking at the relationships between those facets can help to better understand assembly rules. We here used this framework to unravel the local and regional processes that structure Guianese freshwater fish assemblages, in both small streams and larger rivers.

We showed that, locally, neither environmental filtering nor limiting similarity dominates within-assemblage diversity, both for river and stream assemblages. The explanation to this neutral assembly process might lie on the fact that fish diversity is mainly driven by the size of the stream in French Guiana, leading to a high heterogeneity of habitats that blurs environment and competition effects. At the regional scale, dispersal limitation was the main driver of fish assemblage spatial structure, but the causes of this limitation differed between streams and rivers. Indeed, between streams assemblages, rivers constitute the main barriers to dispersal for stream fish, whereas the marine environment is a barrier to fish inhabiting rivers.

This work will constitute a basis to evaluate the future impact of anthropogenic disturbances on freshwater fish assemblages, as we can expect that, with the strong changes induced in local environmental conditions, the processes structuring both local assemblages and their structures will also change.

*Speaker

How important are microhabitats, litter traits and decomposer communities for stream and soil litter decomposition in a tropical rainforest

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Plant leaf-litter decomposition is a major determinant of energy and nutrient sources in forested terrestrial and aquatic ecosystems. Despite known similarities of biochemical processes (C and nutrient cycling), both ecosystems exhibit functional singularities and only few studies compare decomposition across both ecosystems. Also, decomposition is driven by a vast diversity of organisms among which invertebrates communities are supposed to play a key role. However, in the tropical rainforests, their influence in the decomposition process and the ecosystem functioning remains poorly understood and it is even truer across both ecosystems. In order to understand of how invertebrate communities of both microhabitats control leaf-litter decomposition we first described particularities of terrestrial (soil) and aquatic (streams) communities associated to leaf-litter and then we conducted a 100 days decomposition aquatic and terrestrial field study with 17 leaf-litter tree species in a tropical forest of Yasuní National Park, Ecuador. Invertebrate communities showed deep spatial and structural differences across both ecosystems. Soil communities were 5 times richer in morphospecies and were more heterogeneously distributed in space than aquatic ones. In contrast, biovolume and abundance between morphospecies were largely more heterogeneous in streams. Our experiment revealed global equal leaf-litter decay rates in soil and streams, but with significant differences between species. Results also underlined the consistent importance of litter traits for decomposition processes across ecosystems. Among these traits, micronutrients concentrations (mainly Mn and Cu) appeared to significantly control litter decay. We also identified high variability of decomposition in both ecosystems with a larger one in streams. In the soil, variability was mainly related to site location, i.e. to local-scale microhabitat particularities such as the associated decomposer community. In streams, variability was more stochastic and related to large key species presence (*Machrobrachium sp.*) in litter bags consuming at "micro-scale" a great quantity of litter.

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The role of fire in tropical dry forest regeneration

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In fire-influenced ecosystems some plant species have the ability to recover, germinate and establish after a fire; however, their proportion and dominance varies between sites. Currently, there is a debate on the influence of fire in Colombian tropical dry forests and if the vegetation has the capacity to regenerate after fire. In that way, in a tropical dry forest of the Upper Magdalena River Valley in Colombia, we characterized natural regeneration following a fire as well as we evaluated the effect of heat shock on seed germination of five dominant legume species. All seedlings and saplings of woody species were recorded 1.5 years after a fire in 75 2x2m plots installed in burned and unburned sites. Additionally, we exposed 810 seeds per species to nine experimental heat shock treatments (*i.e.* 80 °C, 100 °C and 140 °C for 1, 3 and 5 minutes) and then, seeds were incubated in an acclimatized germination chamber.

Regarding natural regeneration following fire, species richness was lower in burned sites, but the number of individual per species was higher than in unburned areas. *Machaerium capote*, *Cordia alliodora* and *Casearia corymbosa* were highly abundant in the burned plots, while poorly represented or absent in the unburned ones. On the other hand, germination of legume species was stimulated by heat; however, germination percentages of *Albizia niopoides*, *Pseudosamanea guachapele* and *Piptadenia* sp were higher under less-intense heat treatments. In contrast, *Enterolobium cyclocarpum* and *Chloroleucon manguense* exhibited a better germination response under high temperatures (100 and 140 °C for 3 and 5 minutes). Our findings indicate that some tropical dry forest species might have fire-tolerant traits that should be considered in restoration programs in light of future and more frequent forest fires due to climate change.

*Speaker

Cricket communities monitoring as an innovative approach to evaluate tropical island biodiversity. Insights from the New Caledonian biodiversity hotspot

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In insular tropical ecosystems, crickets (Grylloidea) are among the most diverse and abundant insects in forests, from ground to canopy levels. Crickets contribute to various ecosystems processes, representing a significant part of the food resources in the food web. Most of cricket species are soniferous and can be monitored using acoustic sensors. These properties appear to be highly relevant to foster research on proxy of ecosystem state of tropical islands, which are facing high rate of habitat destruction and invasive species spread. To improve biodiversity monitoring and habitat assessment, we propose an innovative approach based on cricket communities monitoring in the New Caledonian biodiversity hotspot. In the context of a rich and highly endemic cricket fauna (> 190 taxa, > 90% endemism), we characterized cricket communities through a standardized taxonomic and acoustic census effort. We considered an ecological gradient including shrubland, pre-forest, and forest, in the context of the spread of a major invasive ant (*Wasmannia auropunctata*). We monitored 24 sites (4800 m²) representative of the three gradient stages (shrubland, pre-forest, forest) and the two invasion modality (invaded and non-invaded). Results show a clear signature in term of cricket community for each stage, with a complete species turnover from shrubland to forest. Cricket communities also respond to the invasive ant spread showing a significant decrease in species number, abundance and acoustic activity. Furthermore, passive recording at night showed a high contribution of crickets to the ambient sound, and these changes in cricket acoustic communities revealed underlying community changes in response to habitat gradient and invasion status. These results highlight a promising field of research based on non-invasive, innovative and fast monitoring of specific, abundant and rich insect fauna. As crickets are present in virtually every island ecosystem, they could be widely assessed as indicator to improve management of tropical island ecosystems.

*Speaker

Nitrogen partitioning and tree grass coexistence in savannas

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Coexistence between trees and grasses in savannas is generally assumed to be due to a combination of partial niche separation for water acquisition and disturbances impacting the demography of trees and grasses. We propose a mechanism of coexistence solely based on the partitioning of the two dominant forms of mineral nitrogen (N), ammonium (NH₄⁺) and nitrate (NO₃⁻). We built a mean-field model taking into account the capacity of grasses and trees to alter nitrification fluxes as well as their relative preferences for NH₄⁺ versus NO₃⁻. Two models were studied and parameterized for the Lamto savanna (Côte d'Ivoire): a first where nitrification only depends on the quantity of available NH₄⁺ and a second where nitrification rate is also controlled by tree and grass biomass. Consistently with coexistence theories, our results show that taking these two forms of mineral N into account may allow coexistence when trees and grasses have contrasted preferences for NH₄⁺ and NO₃⁻. Moreover, coexistence is more likely to occur for intermediate nitrification rates. Assuming that grasses are able to inhibit nitrification while trees can stimulate it, as observed in the Lamto savanna, the most realistic case of coexistence would be when grasses prefer NH₄⁺ while trees prefer NO₃⁻. Mineral N partitioning is thus a stabilizing coexistence mechanism that would act in interaction with already described mechanisms based on disturbances by fire and herbivores. This mechanism virtually applies to all African savannas where grasses have nitrification inhibition abilities but should be thoroughly tested through empirical studies and new models taking into account spatial heterogeneity in nitrification rates.

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Environment, but not phylogeny, drives herbivory and leaf attributes in trees from two contrasting forest formations of the Brazilian Atlantic Forest

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Phylogeny, as well as the environment and leaf quality, can influence herbivory in plants. Plants with nutrient and water-rich leaves are generally more attacked by herbivores, and phylogenetically related plants tend to display similar leaf attributes. The aims of this study were to (1) compare the herbivory and leaf attributes of shrub-tree species from a rain forest (RF) and a coastal forest (*Restinga* Forest, REST); (2) verify possible relationships between herbivory and leaf attributes; and (3) determine whether environmental factors or phylogeny explain differences in herbivory and leaf attributes. The study was carried out in an Atlantic rain forest fragment (RF) and in a Restinga forest (REST) in Rio de Janeiro, Brazil. Herbivory and leaf attribute analyses were carried out on ten congeneric plant pairs from both studied areas. Mean foliar herbivory was significantly higher at RF ($7.2 \pm 0.24\%$) compared to REST ($3.2\% \pm 0.9$). Among leaf attributes, the C/N ratio was negatively correlated with herbivory, while N was positively correlated. A principal component analysis revealed that the co-occurring congeneric pairs from both areas formed two distinct groups, with RF species presenting mainly higher N concentrations and water content, while REST species presented mainly higher total phenol and C concentrations, as well as dry mass per foliar unit area (LMA). The variances observed among the congeneric pairs for eight of the eleven attributes evaluated herein were explained by the environment, while only four of the eight also had their variances explained by phylogeny. Phylogeny alone explained the observed variance for only one attribute (Mg concentrations). Thus, the results suggest that environment has a significantly higher influence on the herbivory and leaf attribute patterns of the studied areas compared to phylogeny.

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Drivers of spider assemblages in Hawaiian forest fragments (kipuka)

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Kipuka are small Hawaiian tropical forest fragments surrounded by recent lava flows. Many of these kipuka are rich ecosystems that have been previously investigated for their importance for native passerine birds, plants (trees and ferns) and picture-winged flies (e.g. Muir & Price 2008 // *Molecular Phylogenetics and Evolution* 47: 1173-1180). However, these kipuka are threatened by several factors, including invasions by rats. Here, we assessed how assemblages of spiders, a taxon of generalist predators ecologically dominant in a large variety of habitats, were structured over space (sampling outside and inside kipuka of different sizes) and time (comparison with a similar study from 1998: Vandergast & Gillespie 2004 // *Environmental Entomology* 33: 1296-1305). Fieldwork (standardized hand-collection by night) was carried out near the Mauna Loa volcano (at an altitude of 1500m asl) on the Big Island of Hawaii, the youngest and largest island of the Hawaiian Archipelago, in April 2016. A total of 702 spiders was collected, representing 6 families and 26 (morpho-)species. We found that the number of individuals was linearly correlated with the area of sampled forests, suggesting that kipuka act, at least partly, as separate islands for these arthropods. Species richness and abundance of endemic spiders both dramatically decreased as the distance to the kipuka increased, with no more influence of the kipuka after 20m (result from 1998). Surprisingly, the number of non-native spider species substantially increased over the last 20 years, possibly due to an enhanced road traffic along the renovated highway (Saddle Road) that may have increased the spread of introduced species. The impact of these new generalist predators on the structure and functioning of kipuka is currently investigated using NGS techniques.

*Speaker

First quantification of the difference in spider diversity between tropical vs. temperate forests

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High diversity in tropical compared to temperate regions has long intrigued ecologists. Terrestrial arthropods are among the most speciose orders in tropical rainforests. Previous studies show that arthropod herbivores account for much tropical diversity, yet differences in diversity of arthropod predators between tropical and temperate systems have not been quantified. Here, we present the first standardized tropical-temperate forest comparison of species richness and evenness for understory spiders, a dominant and mega-diverse taxa of generalist predators. Species richness was 13-82 times higher in tropical vs. temperate forests. Evenness was also higher with tropical assemblages having 12-55 times more common and 10-40 times more dominant species. By contrast, proportion of rare species were only up to two times greater than that of temperate measurements. These differences in diversity far surpass previous estimates, and exceed tropical-temperate difference for herbivorous taxa. Thus, the extreme diversity of arthropod predators is associated not only with the higher diversity of prey in tropical vs. temperate ecosystems, but probably also with increased diet breadth of understory spiders in the tropics. This work contradicts the widely accepted hypothesis that tropical diversity is associated with more specialization of predators.

^{*}Speaker

Trophic ecology of eighty freshwater fish from French Guiana, South America, and their response to stream habitat alteration by gold mining

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The Guiana Shield is a hotspot of freshwater fish diversity in South America. Scientific knowledge on the ecology of most of the species is limited, however, preempting efficient management policies for conservation. The trophic ecology of 80 fish species commonly met in small streams of French Guiana was studied by means of stable C and N isotope analyses on muscle samples. When available, connections were made with published information on their diet, allowing to depict major trophic groups with unambiguous isotopic values. Based on the spread of isotopic values, trophic niche breadths, trophic positions (from primary consumer to predator) and energetic pathways (aquatic primary producers vs. terrestrial plant and detritus) were estimated for each species. We observed that 75% of the species had a mean trophic position of 2.6-3.6, and that carbon in their tissue mostly originated (95%) from terrestrial sources, suggesting a high competition for food within communities. Phylogenetic analyses of feeding strategies (trophic position and energy pathway) showed that a strong heterogeneity prevailed between and within families, preventing extrapolation of the results to other related species. Finally, values of biomass per species indicated that trophic position might be relevant for detecting functional changes in fish communities when streams are subjected to habitat alteration by gold mining.

*Speaker

Habitat loss and frugivores defaunation in Réunion island (Indian Ocean)

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Whereas human settlement on Mascarene islands occurred only recently during the 17th century, the native insular biota experienced a drastic extinction of the vertebrate fauna mainly explained by rapid habitat transformation. At archipelago scale, La Réunion is the last of the Mascarene islands with large areas of untransformed habitats still covering 40% of the island area (2512 km²). Conversely, Mauritius native forests covers less than 1% of the initial area (1872 km²) but still retain several native frugivore species that went extinct in La Réunion during early human settlement (fruit bats, skinks, pigeons). In order to explain these patterns, we compare habitat transformation history between both islands using past and present vegetation maps, subfossil archives and reports of early travellers. We also question the consequences of native frugivores extinction at island scale. Preliminary results of forest dynamics studies confirm the lack of recovery of native plant communities after natural disturbance that can be explained by dispersal limitation of most native trees, new plant invasions and drastic changes in frugivores community composition.

*Speaker

Influence of fragmentation and climate on biomass dynamics of seasonally dry tropical Atlantic forests in Brazil

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The stability of tropical forest biomass is critical for the maintenance of carbon stocks and for the preservation of carbon fluxes near steady-state. However, changes in climate patterns and human-induced disturbances are capable of transforming these forests from a carbon sink to source. This study evaluated changes in aboveground biomass (AGB) and demography of the highly fragmented secondary seasonally dry tropical (SDTF) Atlantic forest, affected by a severe drought. We hypothesized that forest fragments would experience changes in AGB, carbon stocks and tree density depending upon fragment size and climate. We expected that: (1) smaller fragments would have less biomass stock and carbon gain than larger fragments; (2) the persistence of severe droughts would decrease AGB through time due to an exacerbation of tree mortality, especially in the small fragments. Trees (> 10cm dbh) were measured in 6 fragments (5 plots, 20x20m) from 13ha to 1190ha of SDTF in 2007/2010 and 2016, in a 9-year period during which a drought was reported. The rates of AGB loss and gain, tree recruitment and mortality, did not change among fragments. As a consequence, neither the AGB (Mgha⁻¹, census1=139-246; census2=137-196) nor the stem density (Individuals ha⁻¹, census1=1410-1820; census2=1345-1880), varied significantly with time or with fragment size. Carbon stocks ranged from 60 to 116 Mgha⁻¹. AGB was concentrated in the largest (38% > 25cm dbh), late secondary trees and in some species, such as *Metrodorea nigra*, *Pseudopiptadenia contorta* and *Astronium concinnum*. The intense degradation of those SDTF in the past can influence the change in biomass, hiding the edge effect of the fragments and the possible differences that may have occurred among the fragments of distinct sizes. The low rainfall may have affected tree growth, causing stagnation in AGB increment of the forests, independent of the fragment size.

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Communications Orales

Urban Ecology

Ecological and sociological perception of urban green spaces

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Facing urbanization, urban green spaces are now important landscape elements for sociological and ecological concerns. Although in the past, stakeholders considered mainly the aesthetics of these elements, users are now demanding for diversified urban green spaces. The current challenge for stakeholders is thus to transform urban green spaces to be both ecologically diverse and aesthetically pleasing to fulfill current social and ecological purposes. Using an eye-tracking participative experiment, we thus tested if ecological management of woodland edges by stakeholders in urban green spaces in Rennes city was in accordance with user's perception and aesthetic preferences. The experiment revealed that ecological management and aesthetic preferences of woodland edges managed by stakeholders did not entirely fulfill these two objectives.

*Speaker

Allergens in the City: Effects of novel plant communities on seasonal pollen allergies in urban areas

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Pollen allergies are a leading cause of chronic disease affecting over 20% of adults in Europe. Allergy prevalence have been on the rise in the past decades, particularly in cities. This increase seems largely driven by global changes: air pollution increase human sensitivity to allergens; warmer temperatures and increased atmospheric CO₂ increase yearly pollen production; and the introduction of plant species outside their native range spreads novel allergens – i.e. allergens previously absent from the resident flora. In this context, urbanization – where warmer temperatures, pollution and thriving neophyte invasions shape novel urban ecosystems– is a rapidly changing terrain of allergenic potential.

We investigated how allergenic properties of grasslands change with urbanization in Berlin, Germany. We expected the more urban and neophyte-invaded grasslands to exhibit the highest allergy risk. In 2017, we recorded plant species abundance in 56 plots of grasslands covering a double gradient of urbanization and neophyte invasion. We collected publicly available data on flowering phenology and allergenic properties of 234 plant species, including specific allergenic pollen molecules. Borrowing from trait-based community ecology, we developed new methods to characterize the mean allergenic potential, diversity and seasonal spectrum for each community along the urban-rural gradient.

Urban grasslands of Berlin were not more allergenic than rural ones. Neophytes and Natives were as frequently allergenic (35%). However, neophyte-rich urban grasslands produced a higher diversity of allergenic molecules. Both natives and neophytes contributed to a wider spectrum of molecules in the city, possibly affecting a wider range of people. Increasing human population densities in cities imply that novel allergens may cause more harm in urban than rural conditions. Cities may yet remain a relative haven for people suffering from hay fever, but efforts to identify novel risks and control them early should be a priority in urban nature management.

*Speaker

”A walk on the wild side”: Designing streets to enhance biodiversity and nature experience in cities

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In the current context of urban sprawl, it becomes urgent for researchers and designers to propose urban approaches that synergistically promote ecological functions and people-nature relationships. Streets, that are often only viewed as corridors for pedestrians and vehicles, can represent strong opportunities to promote biodiversity in the whole urban matrix and facilitate daily nature experience. We conducted ecological and psychological studies to assess the role of streets in promoting nature in cities.

Based on a plant survey along 48 km of street pavements in Blois (France), we firstly examined the relative importance of multi-scale factors on spontaneous plant assemblages of pavements. Secondly, we combined online and field surveys conducted at the French scale to assess people preferences for various management and design practices promoting pavement herbaceous vegetation.

More than 300 plant species (1/5 of the regional species pool) were recorded on the pavements of Blois. Pavement type was the strongest determinant of plant assemblages, plant cover and species richness being strongly higher on permeable sandy than on asphalt pavements. The effects of weeding frequency and the presence of green space around pavements were marginally important.

Contrary to conveyed ideas, social surveys showed that extensively weeded pavements with spontaneous vegetation were in average as much valued by people as intensively managed pavements without vegetation and a mineral aspect. Vegetation integrated in small pavement designs (flower or grassland strips) was the most appreciated, showing that people acceptance for vegetation can highly increase with visible signs of human actions.

These results support the fact that streets can become biodiversity-friendly urban greenspaces appreciated by urban dwellers. In already built-up areas, we suggest to reduce the pressure of weeding allowing the appearance of spontaneous vegetation. In future constructions, we suggest that civil engineers and architects integrate vegetation on pavements through innovative designs.

*Speaker

Intraspecific trait variation in grassland plant communities along urban-rural gradients

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Trait-based approaches have been successfully used to demonstrate how the modified ecological conditions within urban areas filter plant species within plant communities. These approaches use functional trait databases, often based on trait measurements made outside urban areas and which therefore may not be relevant for urban studies. Over the past decade, there is growing evidence that trait measurement *in situ* may improve knowledge of the ecological mechanisms underlying such filtering processes. Taking into account intraspecific variability has improved research in natural or semi-natural contexts but has not been tried in urban environments. This study aimed to determine the relative contribution of inter- and intra-specific trait variations in explaining the influence of urban-rural gradients on grassland plant communities. Twenty-one stations were sampled along an urban-rural gradient in two French cities. Three functional traits (Specific Leaf Area, maximum height and phenology), chosen to represent general adaptive strategies of plants, were measured on the 26 most abundant grassland plant species. By decomposing the community-level variance of these traits into species turnover, intraspecific trait variability and covariation, we showed how important it may be to take field measurements into account when studying trait distributions in urban ecology. High intraspecific variability may reinforce trait selection effects, for example by favoring both taller species and populations of taller individuals in urban areas in comparison with rural contexts. Advanced phenology at community-level was influenced by early flowering for almost all urban populations of each species while Specific Leaf Area responses were inconsistent. Because trait distributions and ecosystem functions are closely linked, we suggest that it is now important to develop trait-based approaches at community-level, including both intra- and inter-specific trait variability, in order to improve our knowledge of ecological processes operating in urban areas.

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Spatial scaling of urbanization impacts on species distribution within the ant genus *Tetramorium*

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Urbanization is a global change of high magnitude and speed, which deeply impacts biodiversity. Weakly mobile species (e.g. insects or small mammals) should respond to urbanization patterns at finer spatial scales than larger species and could benefit from man-made structures which could provide them with alternative nesting or sheltering sites in urban environments. All studies about impacts of urbanization on ant communities show strong differences in species composition in urban habitats compared to nearby natural areas, suggesting that urbanization, through factors such as temperature or land-use changes, significantly alters ant species distributions. Within the ant genus *Tetramorium* the scales at which urbanization shapes species spatial distribution have never been investigated. The present study focuses on *Tetramorium* species at four spatial scales, from urban microhabitats (one meter around the nest) to urban landscapes (500 meters around the nest). We investigated how urbanization structures the distribution of *Tetramorium* species at these different spatial scales, and which scale is the more impactful for each of the studied species. We sampled ca.1400 colonies belonging to four common species (*Tetramorium immigrans*, *T. semilaeve*, *T. moravicum* and *T. caespitum*) along 19 urban gradients in South-eastern France. Microhabitats were characterized in the field and landscape data were obtained from semi-automated interpretation of high-resolution (one meter) aerial imagery. Combining similarity analyzes (anosim, simper) with model selection procedures and model averaging, we show that species distributions are affected by urbanization differentially at different scales. We discuss how at these different scales, urbanization leads to environmental filters favoring some species while hindering others. This study highlights the importance of considering several nested scales when investigating species distribution patterns. **Keywords** : Landscape, Microhabitat, Spatial scaling, *Tetramorium* species, Urbanization

*Speaker

Phenological shifts of flowering plants and their pollinators along an urbanisation gradient

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Urbanisation is one of the main drivers of landscape modification, as vegetation and open lands are replaced by paved surfaces, roads and buildings. These changes imply the phenomenon of urban heat islands – urban and suburban areas show increased temperatures compared to their rural surroundings. However, its influences on flowering period and pollinator activity remains poorly investigated.

We surveyed 12 meadows managed by local practitioners with standardised native seed mixes in the Métropole Européenne de Lille (northern France). Sites were selected according to an urban gradient (three urbanisation levels, based on the proportion of impervious areas within a 500m radius), and were visited bi-weekly from April 4th to June 29th 2017. We estimated the flowering abundance at all sites at any given observation period. At the same time, we sampled pollinators (bees and hoverflies) using pan traps and hand net. We estimated the effects of sampling day and urbanisation level on flower cover and pollinator activity using GLMMs.

Urbanisation had a strong effect on average flowering phenology of the whole plant community. In medium and high urbanisation sites, flowering peak occurred respectively 7 and 30 days earlier, compared to rural areas. Similar patterns were found for the most common flowering species. Our results also suggest that flowering duration has increased in urban areas. We observed phenological shifts of pollinators as urbanisation increased. Bumblebees experienced a similar advance of activity in moderately and highly urbanised sites, compared to rural sites. Likewise, we observed an advancement of the activity of some solitary bees (Halictidae) in urban areas. We are currently analysing data regarding the other bee and hoverfly taxa found during the study. We will discuss the possible effects of phenology shifts on plants and pollinators, and their consequences in relation to temporal mismatches among species.

*Speaker

The Urban Heat Island effect on carabid beetles phenology: a case study of Rennes, France

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The Urban Heat Island (UHI) is a local climate phenomenon due to urbanization. It raises temperatures in cities at night that could lead to discomfort and over-mortality during heat waves. However, the UHI has a spatial variability as urban parks and green places form cool islands in comparison with surrounding built environment (Oke 1987). The UHI phenomenon is known to influence the phenology of several plants (Chmielewski and Rotzer 2001; Sparks *et al.* 2001; Mimet *et al.* 2009). The highest urban temperatures make earlier step of growth development. Impacts of the UHI on animals have been less investigated (Baur and Baur 1993; Parris and Hazell 2005; Youngsteadt *et al.* 2015; Youngsteadt *et al.* 2017) and there is no study on the effect of the UHI on carabid beetles to our knowledge. Those insects have a larval development in the soil and their activity is sensitive to temperature (Saska and Honek, 2003; Tuf *et al.* 2012). In this study, we evaluate the influence of the UHI on the emergence and activity of carabids beetles along urban and rural areas. In spring 2013, we investigated the composition of species carabids beetle and the temperature for 19 woodlots. The carabids activity was estimated with pitfall traps and the emergence were assessed by adding arenas to the pitfall traps. In addition, thermal sensors were placed in each site to measure air and soil temperature. Based on previous studies on the UHI in Rennes (Foissard *et al.* 2015, 2018), we investigate connections between the UHI, landscape metrics and the carabids community or phenology (for 2 species). We lead a spatial analysis with evaluating the influence of landscape and temperature on carabid communities according the woodlot context. The temporal variability is studied with the effect of temperature on potential carabids lagged phenology.

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Role of species' originality in plant community assembly along an urban gradient in Ile-de-France region

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Urbanization is one of the most intensive, rapid human-driven factors that influence ecosystem dynamics. Many previous studies analysed the effect of urbanization on the spatial distribution of species number and abundance. Yet, little is known about the role of species' originality in community assembly along an urbanization gradient. In a species assemblage, a given species is said original (or inversely redundant) if it shares few (or many) trait values with other species (functional originality/redundancy) in the assemblage and/or if it is distantly (or closely) related with the other species (phylogenetic originality/redundancy).

There are more and more evidence that urban filters could be drivers of species coexistence through a trait-based selection of species. In this study, we explored how urban filters could explain species community assembly in terms of functional and phylogenetic originality versus redundancy. We investigated two main questions: are species from urbanized areas more original/redundant in their traits and phylogenetic positions, compared to surrounding suburban, and rural areas? and what are the ecological and evolutionary processes of community assembly linked to urbanization?

The data we analysed were extracted from a French national citizen-science survey of angiosperm species, named "VigieFlore". We analysed data from 2008 to 2017 in the Ile-de-France region, which includes many towns with Paris as the biggest one and suburban and rural areas. We used Land Use Pattern data to define an urbanization gradient. The composition of each geo-

*Speaker

referenced plot (1 plot = 10 quadrats of 1m²) was considered as a community. We analysed the distribution of species originality across the urbanization gradient, by comparing observed patterns with those expected by chance using a null models where species are randomly assembled. A non-random distribution of species originalities indicates that assembly rules linked to the degree of urbanization shape the functional and phylogenetic composition of communities.

*Speaker

Domestic gardens as locally selected habitats in favorable landscapes for pollinators

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Urban expansion is correlated to negative biodiversity trends. The amount of impervious surfaces, associated with urban areas is a determinant of pollinator species assemblages. While the increase in urbanization and impervious surfaces negatively impacts pollinators, cities also encompass urban green spaces, which have a significant capacity to support biodiversity. Among them, domestic gardens that represent a non-negligible fraction of green spaces have been shown to benefit pollinators. Domestic gardens may form patches in residential areas, although their value at a landscape scale is still unknown. Here we investigate the combined effects of impervious surfaces and domestic garden areas on pollinator richness. Due to the difficulty of accessing privately owned domestic gardens we chose to use citizen science data from a well-established French citizen science program known as the SPIPOLL. Using regression tree analysis on buffers located from 50m to 1000m around the data points, we show the importance of pollinators being in close proximity to domestic gardens as locally selected habitats that are embedded within a landscape scale, in which impervious surfaces represent unfavorable areas. We highlight the inter-connection between local and landscape scales, the potential for patches of domestic gardens in residential areas, and the need to consider gardeners' taxon-dependent management decisions within a landscape context.

*Speaker

Bird feeder attendance during winter in the face of urbanization and weather, questioned thanks to an original citizen science scheme (BirdLab)

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Supplementary feeding of birds during the winter is a widespread phenomenon in temperate countries. While such practice can boost individuals' winter survival, species don't use bird feeders in the same way. We were particularly interested in examining if feeder use by birds is impacted by urban landscape and weather.

Since 2014, the French MNHN started an ambitious citizen science schemes named BirdLab to observe the bird communities and the intra- and inter-specific interactions by asking participants to reproduce the movements (arrival, feeder switch, leaving) of each bird on two identical bird-feeders, on their smartphone or tablet by drag-and-drop small characters representing species, for a protocol of exactly 5 minutes. Four seasons after, this with more than 27000 samples that observe more than 530000 birds of 27 easily recognisable species among the most common species that used the birdfeeders in France.

We use this well-standardised dataset to examine whether the weather conditions and the proportions of the artificial, agricultural, and semi-natural areas around the feeders affect the avian diversity.

As expected, the diversity of species is a function of the harshness of the weather conditions and of the presence of natural elements in the gardens but also impacted by the urbanisation intensity. Nevertheless, our results point to a clear synergy between agricultural territories and urban areas around the gardens, with diversity increasing in urban areas adjacent to agricultural territories.

Our result supports the hypothesis that private gardens may participate in the conservation of declining farmland species by providing an alternative source of seeds, particularly in an intensive landscape which does not provide food for animals during the whole winter.

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Urban Ecology Needs to Move Beyond the Low Hanging Research Fruits

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As cities around the globe continue to grow in both size and population there is an unprecedented call for information about urban ecosystems. Scientists, as well as many urban professionals, are now focused on addressing issues related to the conservation of natural resources and the development of resilient planning and building practices, while also providing a safe and healthy environment for humans. Historically urban ecosystems have not been the object of study by ecologists and thus there is a crucial lack of knowledge regarding the structure and dynamics of these human-dominated systems. In this presentation, I will argue that in order to effectively elucidate the multiple dimensions of urban ecosystems and create sustainable and resilient cities in the future, urban ecologists need to develop comprehensive ecological and sociological knowledge bases for cities with a range of sizes, developmental histories and at local, regional and global scales. Such knowledge bases expand our research questions beyond the scope of an individual city and begin to ask whether specific ecological patterns and processes are common to cities in general. When there are exceptions, a comparative approach also allows us to investigate what social, biophysical or climatic factors are moderating the observed responses. Finally, I will describe the need to collect and use more explicit question-driven measures of the urban condition in order to improve our understanding of urban ecological drivers (predictors), and record more detailed ecological responses to provide insights into the ecological mechanisms underlying our observed responses.

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Analysis of the relationship between structural landscape heterogeneity of urban green spaces and the psychological well-being of their users

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In this era of global urbanization, there is a growing number of studies showing that biodiversity within urban green spaces (UGS) can provide psychological well-being values to their users. Most of these studies have focused on biodiversity in terms of species diversity. However, studies also showed that the majority of the UGS users are not able to perceive the full diversity of species present in an environment. Recent studies suggest that they perceive biological diversity on a more structural level. Thus, the indirect correlation between species diversity within UGS and the psychological well-being of the users has not yet fully been explained.

We tested in 13 UGS in Rennes (France) the hypothesis that ; (1) a correlation between the psychological well-being experienced by the users and effective measures of landscape structural heterogeneity, (2) a correlation between landscape structural heterogeneity as objectified by landscape ecology and landscape structural heterogeneity as perceived by the users, and (3) a correlation between the subjective perception of landscape structural heterogeneity and the psychological well-being experienced by the users can be expected.

Following landscape ecology theory, structural heterogeneity was based on configurational and compositional landscape metrics. The perception of landscape structural heterogeneity and the well-being of the 13 UGS users were measured by surveys. First results showed a significant correlation between the subjective perception of landscape structural heterogeneity and the psychological well-being experienced by the respondents. We also found a correlation between the landscape structural heterogeneity measures and the subjective perceptions of landscape structural heterogeneity, and finally a correlation between the psychological well-being experienced by the respondents and the measure of configurational heterogeneity. These results confirm the paradigm that urban dwellers perceive the biological diversity of UGS on a structural level.

*Speaker

Seasonal Morphometric Variation in Field Collected Populations of *Culex pipiens* complex

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The establishment of industrial sites is known to induce biodiversity loss through habitat destruction, fragmentation and pollution. However, because these sites harbor specific architectural structures and green spaces, they can be used by some species to nest, forage and reproduce. More specifically, the way in which they are designed, and how their green spaces are managed, may have an impact on the biodiversity they can host.

The purpose of our study was to understand the influence of the design and management of industrial gas well platforms, on species richness and abundance of Flora, Lepidoptera and Avifauna, in order to give the best advice for biodiversity preservation.

We chose to survey plants, butterflies and birds because they constitute the largest part of the species present in the platforms and are representative of different trophic levels. We particularly would like to know if the same practices could be beneficial for all these taxa.

During spring and summer 2017, we monitored 51 gas well platforms with various designs and management practices in three French sites. Among them, 22 were only covered by gravel. The 29 others were also designed with grassy strips. Hedgerows surrounded the platforms. They were managed with or without herbicides on the gravel surface and with different cutting methods on the grassy strips (i.e. mowing and rotary cutting).

Obviously, the diversity of plants depended on the surface of the grassy strips and the non utilization of herbicides. Results also showed that the presence of grassy strips and mowing instead of rotary cutting increased significantly butterfly diversity. Concerning birds, only the length of the hedgerows had a significant positive effect.

This work will allow to give indications to managers on how to favor biodiversity in their sites.

*Speaker

Posters

Posters Agroecology and Ecology of Agroecosystems

Diversification of crop and non-crop vegetation in agricultural landscapes: a benefit for the diversity of pollinator communities?

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Vegetation diversification is considered a promising management strategy to promote biodiversity, improve the functioning of agro-ecosystems and increase crop yields in various farming systems. Vegetation diversification can be set up at different spatial scales – field, field border, landscape - and targets both crop and non-crop vegetation. Management strategies based upon the diversification of crop vegetation rely on the combination of different varieties or crop species and on their organization in space and time. Conversely, strategies based upon the diversification of non-crop vegetation rely on the maintenance of semi-natural elements, such grassy field margins, hedgerows, or the introduction of new landscape elements such as flower strips.

Previous works have investigated the effects non-crop vegetation diversification. They have shown that non-crop elements fulfill resources (nectar, pollen) and shelters for pollinators, and that increasing the diversity of non-crop vegetation at field borders increases the diversity and abundance of pollinators in crops. At the landscape scale, the diversity, extent and spatial arrangement of crops and non-crop elements, i.e. landscape heterogeneity, play an important role for pollinators and pollination. However, the relative influence of crop and non-crop vegetation diversity in the field and its adjacent border on pollinator communities and pollination in different landscape contexts still remain unknown. It is thus unclear whether crop and non-crop vegetation diversity can have synergistic or antagonistic effects on pollinator communities and pollination.

Here, we aim at i) disentangle the effects of crop and non-crop vegetation diversity on pollinators in crop fields and field borders, and ii) evaluate whether these relationships are mitigated by the diversification of crop and non-crop vegetation at the landscape scale. Pollinator surveys were carried out in 10 pairs of monoculture and mixed-crop fields along a gradient of landscape heterogeneity, in the Zone Atelier Armorique, France.

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^{*}Speaker

Disentangling the relative effects of semi-natural elements and organic farming practices to enhance biodiversity in agricultural landscapes

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In a context of strong biodiversity decline in agricultural landscapes, it becomes urgent to find agronomic and landscape levers capable of mitigating this trend. The establishment of semi-natural elements and limitation of pesticide uses have been recommended for promoting agricultural biodiversity. However, under real conditions the amount of semi-natural elements is often highly spatially correlated with organic production systems, making it difficult to understand their respective influences on species assemblages.

Thanks to the establishment of a semi-experimental protocol in the Zone Atelier "Plaine & Val de Sèvre", we assessed the responses of three taxa assemblages (earthworms, carabid beetles and small mammals) to three decorrelated landscape gradients: surfaces of grasslands, organic fields and hedgerows. We also measured the amount of pesticides in soils of the sampling habitat (hedgerow).

We expect to have contrasted responses between taxa depending on their dispersal abilities. In particular, earthworm assemblages are expected to more be driven by local parameters than carabid beetles and small mammals. We also assume that in landscapes with a high proportion of semi-natural elements, animals of highest mobility would be less sensitive to disturbances related to pesticide use in the landscape (due to refuge areas, recolonisation).

These results will help to better understand assemblage rules of several taxa in agricultural landscapes and to prioritize recommendations for promoting biodiversity.

*Speaker

Effects of the energy crop *Miscanthus x giganteus* on soil quality across a pollution gradient

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Miscanthus is a perennial rhizomatous grass native to Southeast Asia. The ability of *Miscanthus* to grow on polluted sites and to phytostabilize trace elements allows its use in a phytoremediation context. Once planted, the rhizome system allows continuous biomass production for up to 20 years with low tillage and nutrient inputs and without crop rotation. Previous work has shown that low tillage increases invertebrate diversity, the number of birds and the presence of small mammals [1, 2]. Moreover, the cultivation of *Miscanthus* offers the possibility of economically developing marginal lands through biomass production.

The work presented here is part of a broader project that seeks to evaluate the entire *Miscanthus* thermal chain from cultivation, through energy production, to the production and reclamation of ash as a fertilizer or in aided phytostabilization of contaminated sites. The objective of this first step is to study the impact of *Miscanthus* crops (*Miscanthus x giganteus*) on soil quality in polluted and unpolluted sites through multi-criteria soil quality analysis. For this purpose, soil samples were collected from three sites with varying levels of soil pollution. Soil and earth-worm samples were taken from the *Miscanthus* plots and nearby grasslands to allow the study of biological, chemical and physical parameters. Analysis of results will allow for inter-site and *Miscanthus*-grassland comparisons through the implementation of a soil quality index and results will be presented during the conference.

Keywords : *Miscanthus giganteus*, Soil quality, Pollution, Energy crop,

References:

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*Speaker

Biodiversity conservation in agricultural land: statistical analysis method to understand media representation of policies and species

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The complexity of the relationship between agriculture and biodiversity can be an obstacle to the implementation of conservation measures. Media, selecting information, are a key player in the political agenda setting of a public problem (Mac Combs and Shaw, 1972). To improve biodiversity conservation in agricultural land, we need to understand better media representation of policies and species. We analyze newspaper coverage of seven French national daily newspapers between 1999 and 2017 (*Le Monde*, *Libération*, *La Croix*, *Les Echos*, *Le Figaro*, *L'Express*, *La Tribune*; $N = 2\,547$). We make text analysis with open source software IRaMuTeQ (Ratinaud and Déjean, 2009) and ALCESTE method which consists of providing clusters of similarity. A decreasing hierarchical classification (DHC) is used to identify articles' classes. We can analyze temporal evolution with year as a covariate.

Bee (*apis mellifera*), wolf (*canis lupus*) and bear (*ursus arctos*) are the majority species used to talk about agriculture and biodiversity. Bee is associated with ecosystem services while wolf and bear are endangered and pests. Biodiversity policies are in conflict with agriculture (national park, Natura 2000 network) or in synergy (regional nature park). Agriculture and biodiversity belong to the most global environmental issues including world's food and climate change. At the beginning of 21st century, articles are ecocentrist with an international scale and become anthropocentrist with a national and local scale after 2008.

Take media representation into account allows to understand the evolution of relationship between agriculture and biodiversity and can help to improve conservation measures in agricultural land.

Keywords: biodiversity, agriculture, national media, lexicometry, statistical analysis.

Mac Combs, M., Shaw, D.L., 1972. The agenda-setting function of mass media. *Public Opin. Q.* 36, 176–187.

Ratinaud, P., Déjean, S., 2009. IRaMuTeQ: implémentation de la méthode ALCESTE d'analyse de texte dans un logiciel libre.

*Speaker

Agroecology, Research, and the place of ecology and biodiversity: A review

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Agroecological practices represent a promising alternative to mitigate negative consequences of industrial farming practices, as they rely on ecological services rather than on the intensive use of chemical inputs. Their use aim at improving the overall quality and sustainability of cropping systems. Despite a growing interest for ecology within the field of Research in Agroecology, socio-economic studies seem to represent a large part of the literature. It also seemed to focus on productivity rather than on the functioning of agroecosystems, and on cereal crops and large-scale farms rather than on vegetables and micro-farms. The aim of this study is to quantify the previous observations, as well as to review the knowledge on the impact of six commonly used agroecological practices on biodiversity. We performed a bibliometric analysis of the scientific literature (Web of Knowledge Core Collection; 1900-2017) to identify the major fields and ecoregions where research in agroecology were performed. We then focused on literature dealing with agroecological practices to investigate to what extent each practice is studied. Finally, we linked previous terms with biodiversity and ecological terms to highlight any underestimated link between agroecological practices and ecological process. Our results show an upsurge of agroecological studies since 1990, with the USA, France and India as leading countries. Studies focusing on Agronomy represent more than 20% of agroecological studies, while Ecology represent less than 10%. Very little attention is given to vegetable farming with only 4% of agroecological studies. Finally, small-farm studies do not excess 10% of agroecological studies, with only 10% of those studies related to the impact of agroecological practices on ecology. In view of these results and because of increasing development of those exploitations, we suggest to carry out researches on small farms in vegetable production, with special interest on how biodiversity is impacted by agroecological practices.

*Speaker

Certified and peasant seeds: which network for millet seed supply?

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In West Africa, alliance built between researchers, policy makers and foundation aspire to enhance agricultural productivity, food security and rural well-being of 33 million smallholder farming households. In order to, they bred and released quality-improved certified seed through a network of agro-dealers and regulatory frameworks. Supported at the expense of peasant seed used and shared for ages by farmers, this process is likely to impact agroecosystem's resilience and crop diversity. For now, certified and peasant seed coexist within farmer's field. However, coexistence modalities between certified and peasant seeds in farmer seed network are still un- appreciated. By combining quantitative and qualitative analysis, we present a study of millet seed circulation according to their certified or peasant origin. The aim is to identify the coexistence modalities in seed exchange between farmers. From surveys of 79 people in the Koungheul region of Senegal, we identified several levels of coexistence, both in the perceptions of varieties by farmers and in networks mobilized for seed supply. Based on our comparative analysis, our results suggest that origin of seed shapes farmer seed networks. The acquisition of certified seeds from agro-dealer also modifies the context and modalities of exchange by inducing their social isolation and limiting self-production. Nonetheless, after the harvest, certified and peasant seed are commingled and embedded into an open and complex social network involving multiples actors. Our results provide a better understanding of seed exchange networks between farmers, by characterizing the structure, the scope and modalities of exchange of certified seed. This study highlights a gap between agricultural policies and local seed management by farmers, results that could feed into

*Speaker

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the reflections on the governance of plant genetic resources.

Is the perception of urban biodiversity related to ecosystem services?

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With increasing global urbanization, it becomes important to reconnect humans with nature in cities. In this context, ecosystem services can be a good way for this reconnection. In this study, we tested how knowledge of the ecosystem services provided by undesirable urban fauna might influence citizens' perceptions of this wildlife. To do so, we first tested the fertilizing effect of pigeons' guano as a potential ecosystem service. Then, we examined how this ecosystem service changed the citizen perception toward pigeon.

Guano's effects were tested on cherry tomato plants. Pigeons' guano was applied on 29 plants on early June 2017 and the production estimators were compared to control 29 plants (without guano). Meanwhile, 200 people were asked with a questionnaire to know what they think about pigeons. This year, 200 additional respondents will be sampled with the same questionnaire, but people will be informed on the fertilizing effects of pigeons' guano before answering and we will examine if the perception of the respondents will change.

First results show that cherry tomato plants with guano have more flowers and are taller than those without guano. We also found that plants with guano gave more mature fruits than those without guano. For questionnaires, we therefore predicted that respondents will perceive pigeons more positively when they are aware of the service provided by them.

Our results support the first prediction of our hypothesis: pigeons' guano can be used by humans as a local fertilizer for urban agriculture and constitute thus an ecosystem service. We are still running the study to validate the second prediction on the human perception. Our study underlines the importance of knowledge on services provided by undesirable animals in cities that may favour a better cohabitation between humans and urban wildlife.

*Speaker

Multiple ecosystem services valuation with theoretical bio-economic modeling in intensive agricultural-landscape

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Global change is a significant contributor to biodiversity loss and hence affects ecosystem services delivery. Ecosystem services are sustained by complex ecological processes or functions that are emergent properties of the natural system. The social or monetary value of ecosystem services depend on the ways that particular services are used by different stakeholders. Therefore, to assess ecosystem services delivery and the inherent trade-offs among them, it is essential to separate the valuation (monetary or not) of individual services from the ecological patterns and processes that deliver the former. Understanding how changes in biodiversity affects trade-offs among ecosystem services requires to include querying stakeholders and components of well-being from their perspective.

Here, we explored scenarios of public policies to determine the landscape composition that best supports sustainable and multifunctional agricultural landscapes. We develop a bio-economic model to analyse the dynamics of ecosystem services in an intensive-agricultural landscape. We consider four ecosystem services among which crop pollination service, which is key by linking the ecological and the economic models. We also consider two stakeholders: farmers and beekeepers with different demand in ecosystem services delivery. The analysis of scenarios of public policies focussed on beekeeping support reveals a perverse effect of this policy on biodiversity conservation, because of an existing substitution between wild and domestic pollinators. Furthermore, a structural antagonism between ecological and economic good state exists but can be reduced by supporting both farmers and beekeepers. In this way, our model highlights the importance to have a wide overview in public policy planning and show that various levers to promote multifunctional and resilient agricultural landscapes.

*Speaker

Impact of intercropping cultures on truffle production and soil microbial communities in Mediterranean oak orchards

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Truffle orchards are agroecosystems that play an economic, cultural and structural role in Mediterranean landscapes. In Southern France, some truffle growers associate secondary production in truffle orchards, such as the intercropping of aromatic and medicinal plants (AMP). Recent works described AMPs as acting positively on soil microbial activity. We hypothesized that this beneficial impact of AMPs may also improve truffle production through direct and indirect mechanisms involving biotic and abiotic soil parameters. The survey, conducted among truffle growers, indicates that AMP intercropping was mainly limited to lavender (*Lavandula hybrida*) production, and occasionally to rosemary (*Rosmarinus officinalis*) and thyme (*Thymus vulgaris*). According to one-third of the truffle growers, the production of truffles was improved and for 40% this intercropping allowed a contribution of organic matter and a protection against the drought. The study aimed at better testing this reported effect and exploring the mechanisms underlying this pattern by characterizing soil physicochemical and microbial community changes induced by AMP culture. A multidisciplinary approach associating microbiology and molecular ecology has been conducted in truffle orchards with a historical practice of AMP intercropping culture. We report a positive effect of AMP culture on *Tuber* populations, with no major change on soil microbial community diversity. Nevertheless, we identify microbial taxa indicators associated with truffle production and/or plant types. The investigation of a wider range of truffle-based agroecosystems may provide important guidelines for the development of intercropping culture to improve the productivity and sustainability of truffle orchards.

*Speaker

Flower strips increase natural enemies abundances: experimental evidence across French agricultural fields.

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Conservation biological control aimed to provide resources that attract natural enemies of crop pests. The sowing of flower strips near agricultural fields is one of the options considered as alternative to pesticide use. However, the relationship between the diversity of these habitats and the presence of beneficial insects in the crops and their impact on pest control is still under discussion. The French CASDAR project MUSCARI aimed to assess the effect of four different types of flower strips (noted "A" to "D") on the abundance and the diversity of beneficial arthropods as well as the abundance of pest species, aphids and leafhoppers, and compared to a grassy strip ("E" with one or two gramineous species). These four mixtures contained from one ("B": vetch) to 20 species ("A": commercial mixture) and two mixtures were designed to maximise the functional diversity supposed favourable to natural enemies ("C" and "D" mixtures with 6 and 15 different species, respectively). These surveys were performed in 12 different sites with different adjacent crops (arable crops, legumes, vine and orchards), and plant and beneficial arthropod surveys were performed in 2016 and 2017 from April to August in the different sites. We first found that the vegetation diversity originating from seed bank and surrounding habitats was greater than the sown species in several sites. Nevertheless, the mixtures C and D showed higher species diversity and turnover of flowering individuals. Within beneficial arthropods, we mostly collected Hymenopteran parasitoid species, ladybirds and hoverflies. Mixture D attracted the highest abundance of beneficial species whatever the site, the year and the trapping period. Even if the abundances of parasitoid and predatory species were high within the flower strips, we did not show any effect on the regulation of pest abundances in the adjacent crops.

*Speaker

Insecticidal activities of essential oil from *Piper borbonense*(Miq.) C. DC., an endemic Piperaceae from Reunion island

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The future of agriculture and its economic, sanitary and ecological sustainability depend on a significant and expected evolution of crop protection practices, which today are too dependent on the use of synthetic pesticides. It is within this framework that biocontrol tools based on the use of plants or plant extracts are developed. Reunion's chemiodiversity presents a great wealth and promising prospects in this context. The challenge of the BIOPIPER project was the sustainable production of the natural extracts of two Piperaceae, with the prospect of their use within the framework of the agroecological protection of crops against pests. Within this framework, the aims of the study presented here were to i/assess the biocidal properties of the essential oils obtained from different ecotypes of *Piper borbonense* against pests of economic importance worldwide, ii/ compare the sensitivity of some of these pests and their natural enemies towards these essential oils and iii/ identify the potential toxic compounds involved and assess whether or not their proportions and presence are modified in wild *vs* cultivated plants. Contact tests on filter papers impregnated with essential oils showed that they were highly toxic to a large range of pest insects (LD50 ranged between 36 and 183 mg/cm²). Comparison of toxicity of essential oils on some pests and their natural enemies indicated that the later were less sensitive but still affected by these oils. Five phenylpropanoids dominated the composition of active essential oils: asaricin, safrole, elemicin, dillapiole and myristicin. Although some variations were observed depending on ecotypes, the presence and proportion of these compounds were comparable whether the plants were harvested in nature or cultivated. Suitable and selective modes of application of the biocidal essential oils identified remain to be studied.

*Speaker

Documenting crop diversity management practices in West-Africa: raising perspectives for improving governance frameworks

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Crop diversity is pivotal for the 33 millions of small farms that produce most of Africa's food, being the main option for smallholders to deal with limited resources and to cope with a changing environment. Small farms access to crop diversity relies on complex seed supply networks involving multiples actors and sources of diversity, such as other farmers, local markets, NGOs, farmers' organizations, research institutes, or private companies. Regulatory frameworks for access, use and conservation of both seed and plant genetic resources do not recognize the complexity of these seed supply networks, which affects farmers' ability to mobilize crop diversity needed for production and innovation. This opposition between the formal market-oriented seed system and the informal farmer-oriented system is largely documented, while the interaction and intertwining between the different components of seed supply networks and their consequences on crop diversity on-farm have attracted much less attention. This study conducted in the context of CoEx project thus aims at documenting crop diversity management practices in West-African agricultures. It combines large-scale analysis in four west-african countries to get a picture of the state of crop diversity management at the regional scale, with in-depth analysis at the local scale in four sites in Senegal and Burkina-Faso to get insights into the mechanisms involved. This study focuses on the interplay between: i. diversity in crop species and varieties cultivated on-farm, ii. their functions in farmers' livelihoods, and iii. the diversity in seed sourcing and actors involved. Recent statistical network analysis methods will be used to disentangle the relations between these components. Through an interdisciplinary approach at the interface between agroecology and social sciences, this study ambitions to document the gap between the diversity of farmers' crop diversity management practices and regulatory frameworks and policies, and to propose innovative governance mechanisms that better account for that diversity.

*Speaker

Soil legacy effects of climatic stress, management and plant functional composition on microbial communities influence the response of *Lolium perenne* to a new drought event

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Drought events, agricultural practices and plant communities influence microbial and soil abiotic parameters which can feedback to fodder production. This study aimed to determine which soil legacies influence plant biomass production and nutritional quality, and its resistance and recovery to extreme weather events. In a greenhouse experiment, soil legacy effects on *Lolium perenne* were examined, first under optimal conditions, and subsequently during and after drought. We used subalpine grassland soils previously cultivated for two years with grass communities of distinct functional composition, and subjected to combinations of climatic stress and simulated management. The soil legacy of climatic stress increased biomass production of *Lolium perenne* and its resistance and recovery to a new drought. This beneficial effect resulted from higher nutrient availability in soils previously exposed to climatic stresses due to lower competitive abilities and resistance of microbial communities to a new drought. This negative effect on microbial communities was strongest in soils from previously cut and fertilized grasslands or dominated by conservative grasses. In subalpine grasslands more frequent climatic stresses could benefit fodder production in the short term, but threaten ecosystem functioning

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and the maintenance of traditional agricultural practices in the long term.

*Speaker

Rubber tree plantations in Northern Thailand: challenging the positive impact of "afforestation" on soil degradation

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South-East Asia is among the regions most threatened by water erosion, due to extreme climatic conditions and rapid land use changes. In the past decades, due to strong economic and political incentives, farmers in marginal regions converted large areas under annual crops to rubber tree plantations. While afforestation is usually considered favourable to soil protection, the impacts of rubber trees are not consensual. In this study, we compared surface runoff and soil detachment under maize, young rubber tree plantations with intercrop and mature rubber tree plantations. Using 1m² erosion microplots over 2 years in mountainous northern Thailand, we showed that mature plantations caused soil detachment approximately 10 times higher than maize or young plantations, reaching 8kg/m²/year in some areas. This was concomitant to intense soil surface degradation and was due to concentrated flows from the canopy and to very low soil cover, especially at the end of the monsoon when rains were very erosive. These findings challenge the common belief that tree cover is always more environment-friendly than annual crops and call for urgent action in order to improve management practices in rubber tree plantations on steep slopes.

*Speaker

SEGAE: A Serious Game for Agroecology learning

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European agriculture is facing many challenges, among which producing food and nonfood products in sufficient quantity and quality and generating added value for farmers and food chain actors, while reducing agricultural impacts on the environment. Agroecology is seen as a very pertinent option to reorient European agriculture in order to answer these major challenges.

However, higher education in European Universities is not yet fully adapted to train the present and future agricultural professionals on agroecology. In particular, multidisciplinary approaches are not very developed. Moreover, current pedagogical methods often lack interactivity. Innovative learning tools are thus urgently needed.

The SEGAE project (SERious Game in AgroEcology) aims at facilitating a multidisciplinary and systemic understanding of agroecology for higher education students as well as agricultural professionals through the development of a digital training tool. This tool will take the form of a serious game, i.e. a computer simulation game that will help students and agricultural professionals understand concretely how to implement agroecological practices on a virtual farm, and evaluate the impacts of their choices on the economic, social and environmental dimensions of the farm.

Several game modes will be accessible to answer different learning outcomes and to reach different publics. The game will include learning tools, factsheets and other information to help learners taking decisions on their virtual farm. A tutorial, pedagogical guide and online course will also be developed to help teachers integrate the game in their lessons. The game, tutorial and pedagogical tools will be freely accessible online at the end of the project and proposed in five languages.

This poster presentation will be a unique opportunity to discuss about the learning outcomes of the tool, the technical details of the conceptual model, and the needs and expectations of potential users before implementing the software.

Impact and bioecology of *Tuta absoluta* (Meyrick, 1917) on three greenhouse tomato varieties (Tavira, Kawa and Barbarina).

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Impact and bioecology of *Tuta absoluta* (Meyrick, 1917) on three greenhouse tomato varieties (Tavira, Kawa and Barbarina)

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The tomato (*Lycopersicon esculentum* Mill.) Of the Solanaceae family is an annual plant native to the Andes and America, very cultivated for its fruit consumed fresh or processed (Chaux and Foury, 1994). Today, the tomato is facing a new pest, the leafminer tomato "*Tuta absoluta* Meyrick". This species of endophytic micro-lepidopter considered in its native range, South America, as the most formidable pest on tomato because it can cause economic losses of up to 100% (Moreira, 2005; Niedmann et al., 2006).

Our recent study was conducted in the spring of 2017 in the region of Emir Abdelkader (Jijel) on the bioecology of *Tuta absoluta* at three greenhouse tomato varieties (Tavira, Kawa and Barbarina) and revealed that the the highest rate of leaves and seedlings is noted at the end of the crop cycle, the maximum recorded is 75% on Kawa plants and 64% on Barbarina leaves, the damage recorded on them is more in the basal part of the plants than on the middle and upper levels. This work has shown that the tomato plant hosts the different larval stages throughout its vegetative cycle with variable numbers, namely that the L3 stage is more important than that of stages L1, L2 and L4.

Key words: Bioecology, tomato (Tavira, Kawa and Barbarina), *Tuta absoluta*.

The effect of agroecological practices (reduced tillage, pasture-crop rotation, organic farming) on soil biodiversity and ecosystem services: SoilMan project

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Soil biodiversity is pivotal for delivering food, fibre, biofuels, clean air, drinking water and carbon storage to society. However, as stated by the European Commission Soil Thematic Strategy, our understanding of how soil biodiversity is linked to soil functions and ecosystem services is still very limited. The European project SoilMan, involving Germany, France, Spain, Estonia, Sweden and Romania, is determined to work on a deeper understanding on the interrelationship between soil management i.e. agricultural practices (e.g. reduced tillage, crop-pasture rotation, organic farming), soil biodiversity (microorganisms, collembola, mites, earthworms, gastropods), and ecosystem services (e.g. soil structure maintenance, aggregate stability, water infiltration, disease repression, yield). The first year, data were obtained at Long Term Observatory scale (e.g. SOERE-PROs EFELE, SOERE-ACBB Lusignan); the second year, data were obtained from farm networks in Sweden, Romania and France. Results presented in this study will focus on Brittany farms. By developing a pluri-criteria analysis, this study will help the evaluation of the environmental, economic and social sustainability of these practices.

Eukaryotic communities characterized using airborne DNA from poultry buildings: first insights towards pest control improvement in layer henhouses

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Dermanyssus gallinae is a haematophagous pest of economic importance in poultry farms where improving environmentally friendly control strategies is a major challenge. In layer farms, this mite is a perfect target to biological control as it spends life at a distance of the host, in hen-house's microhabitats possibly shared by natural enemies. A diversity of predatory arthropods were previously shown naturally occurring in manure of some barn laying henhouses. To be able to encourage natural processes of pest regulation, a better understanding of biotic interactions that occur naturally in such farm buildings is required.

Here we hypothesized that direct (e.g. predation) and indirect (antagonistic to or facilitating natural enemies) biotic interactions are important drivers of the abundance of *D. gallinae* in hen-houses. The overall objective of this study was to evaluate the extent to which some eukaryotic communities as a whole can contribute to regulate pest populations. Eucaryotic communities from 20 barn henhouses were described using metabarcoding of airborne DNA (18S) coupled with visual inventories of manure-dwelling arthropod morphospecies.

Consistent information on the abundance of arthropod taxa was obtained from paired airborne metabarcoding and visual inventories data, including *D. gallinae*, with richer communities from air samples (representative of the whole building) than from the manure compartment. Interestingly some strong negative and positive correlations were reported between *D. gallinae* and several fungal operational taxonomic units (OTU) belonging to the Pezizomycetes class, suggesting that indirect interactions exist between the pest mite and some farm-dwelling fungi. Present results pave the way for further investigation of pan-Eukaryote trophic networks involving the pest mite *D. gallinae* and thus help progress biocontrol in poultry. Besides, eDNA analysis of airborne particles sampled from livestock buildings reveal to be an interesting tool to monitor populations of arthropod pests or biological control agents.

Effect of polycultural systems on the abundance of arthropods and crop yield

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Multiple studies have stressed the positive impact of both local- and landscape-scale plant biodiversity on sustainable biological control of agricultural pests; however the actual impact of crop richness itself on biological control has been sparsely documented. We carried out a three- year study at Langfang Experimental station (CAAS) to evaluate the effect of mono- vs. multi- cropping systems on key pests and associated natural enemies. At the three cropping periods considered i.e. early, mid and low in the season, increasing crop richness impacted arthropod populations in two different ways; most polyphageous herbivores showed higher abundance, whereas it decreased in case of monophageous ones. Natural enemies usually highly dependent on their main prey (e.g. ladybirds) or hosts (e.g. aphid parasitoids) showed less straight- forward relationships with the crop richness throughout the cropping season. Predatory ground beetles, lacewings and parasitism rate were positively correlated to crop richness. Aside these effects on arthropod populations, the multi-cropping system also enabled increasing the yield in tomato plots (two-fold increase between mono- vs. multi-cropping systems). The diversity and abundance of crop plant species selected in agricultural schemes could play a key role in modulating the abundance of pests and their natural enemies according to the resource concentration hypotheses.

*Speaker

Securisation of the production of Gwell, a fermented milk specialty from Bretagne

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Gwell is a type of "gros-lait", a fermented milk traditional in Bretagne, produced with milk from Bretonne Pie Noir cows. It is produced through a back-slopping process, meaning that some of a previous production is inoculated in milk as a ferment in order to get a new batch of Gwell. This process doesn't work sometimes and the Gwell is "lost". The only way to make Gwell is to get a new ferment from another producer. The Union Bretonne Pie Noir, who owns the brand "Gwell" has collaborated with the CIRM-BIA to work on the securisation of the production. The project originally consisted in lyophilising strains isolated from Gwell, so as to use them as a ferment to make a new Gwell in case it was lost. The farmers finally considered this option incompatible with their values and their vision of the product, and they decided to secure the production by conserving the whole ferment so as not to standardize it. I established a protocol with the farmers to study the effect of different methods of congelation and lyophilisation on the microbial ecosystem and on the product. I visited the farmers to see how the Gwell is produced and to perform interviews. I could propose conservation methods adapted to the context of production of the Gwell: collective preservation by creating a bank where ferments would be conserved at -80° C, or individual preservation at -20° C in the farms. Other complementary methods are available. The farmers can keep on sharing the ferments following a plan to prevent a loss of global diversity. A work on the production process can also be conducted in order to prevent losing the Gwell. I produced preliminary results that let think that back-slopping the Gwell every day could lead to the loss of the ferment.

*Speaker

Multi-scale analysis of the trade-off between ecosystem services provided by arable weeds community

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Arable weeds are managed because they compete the crop for resources and can thus cause yield loss in case of high infestation. However, weeds are also the cornerstone of food webs, because they provide food and shelter for many organisms inhabiting the agroecosystem. Current weeding strategies thus need to consider the trade-off between services and disservices provided by weeds communities. The objective of this PhD project is to identify farming strategies that maximise potential ecosystem services while minimising negative impacts of weeds on crop production, at different spatial and temporal scales. This analysis will be based on data collected on the Fenay landscape platform, a 1000ha area of arable farming located near Dijon (Eastern France). Across the Fenay landscape, information on detailed farming practices implemented by farmers and the composition of the weed flora of crop edges and field cores have been surveyed annually. This unique landscape scale long-term dataset will be used to analyse the impact of pluri-annual farming strategies on the taxonomic and functional composition of the weed communities across the landscape. We will estimate services (pollination, food supply to insects and birds) and disservices (competition with crop) provided by each sampled weed community using existing trait-based indicators. This analysis will enable us to assess the spatial and temporal variations in the provision of weed services and disservices across the landscape. We will notably assess the specific role of crop edges in the provision of ecosystem services across the landscape. The role of combinations of farming practices or of specific management, strategies on the stability of ecosystem provision but also on potential synergies and trade-off between ecosystem services will be analysed.

*Speaker

Posters

Behavioural and Dispersal Ecology

Hatching event influences long-term decisions of pied avocets (*Recurvirostra avosetta*)

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Spatial location of birds throughout life-cycle stages may lead to strong consequences at both individual and population levels. The study of the correlates of lifetime inter-individual variations in wintering and breeding grounds selection constitutes a fieldwork challenge. Based on a 10-year ringing study, we investigated long-term distribution patterns in winter and breeding seasons in a shorebird species, the pied avocet (*Recurvirostra avosetta*). Birds were ringed among five of the major breeding colonies of the French Atlantic coast, then re-sighted across Western Europe. Firstly, our analyses highlighted a facultative partial migration pattern involving the coexistence of three wintering tactics: wintering in the natal colony site (strictly resident), in a neighbouring site located along the French Atlantic coast (locally resident), or in farther quarters (migrant). We showed that hatching date within the season and hatching colony particularly influenced the choice of the wintering tactic. Furthermore, we showed that birds were highly faithful to their first wintering tactic in subsequent winters. Then, we showed that birds preferentially bred in their hatching colony. In addition, we found an effect of the wintering location on site fidelity between consecutive breeding seasons. We also showed that survival between years was very high since the first winter (> 90%), and independent from the wintering and breeding grounds. Overall, these results highlight the influence of hatching features such as location and date on the spatio-temporal dynamics of the targeted subpopulation. More specifically, our results advocate for a conditional control of partial migration, then for the good quality of the sites used in both winter and breeding periods by French pied avocets. Finally, most of the birds being faithful to a resident tactic and to their hatching colony for breeding, our works contribute to explain the growth of the French subpopulation in winter and breeding seasons.

*Speaker

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The genomic response to male courtship and kin avoidance during mate choice in the parasitoid wasp *Venturia canescens*

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Many animals use cues produced by conspecifics to distinguish between kin and non kin. While at the core of social behavior, little is known on the molecular mechanisms involved in kin recognition. Here we analyzed the transcriptomic changes accompanying i) courtship and ii) kin avoidance during mate choice in the head of the parasitoid wasp *Venturia canescens*. We sequenced female head transcriptomes after exposition to two stimulus: courtship by unrelated male or courtship by brother, while transcriptome of female alone was used as control. First, comparison of control and female courted by unrelated shows a consistent pattern of change in gene expression, representing 16.5% of the transcriptome, mainly involving post-transcriptional modifications, signal transduction, transcription factors, sensory genes, neuropeptides and neu- rotransmitters. Secondly, we showed that the relatedness of the courting male has a major influence on female head transcriptome; courtship by brother forming a consistent outgroup compared to the control and courtship by unrelated males group. Indeed, the comparison of transcriptome after courtship by unrelated male and brother reveals important transcriptomic shift, with 11.8% of the transcriptome differentially expressed, including numerous transcrip- tion factors and 3 homologs to Protein Yellow/Major Royal Jelly Protein. Network analysis performed on the global differentially expressed genes set identify no common pattern in gene expression associated to courtship by unrelated males and brothers, indicating that very specific molecular pathways are activated according to the relatedness of the courting male, which are likely to be at the origin of inbreeding avoidance in this wasp.

*Speaker

Impacts of light pollution on energy reserves and state-dependent decision-making in a parasitic wasp

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Artificial Light At Night (ALAN) is a worldwide phenomenon and represents a growing threat for biodiversity. Well-studied in Vertebrates, effects of light pollution on Invertebrates, and more particularly insects, have been less investigated. It is however a particular concern because many insect species are involved in ecosystemic services, such as pollination and biological control.

We aimed to determine the effects of ALAN on the behaviour of a diurnal parasitoid wasp, *Venturia canescens*. At night, the insects were submitted to one of three light intensities: 0 lux (dark control), 0.7 lux (low pollution) and 17 lux (high pollution), during two nights or eight nights. First, on three batches of insects, we compared according to light pollution treatment:

i) the decision whether to search for hosts (immediate gain of fitness) or food (delayed fitness gain), ii) the feeding behaviour of the insects and iii) the energetic budget of the insects. Second, we investigated possible trans-generational effects of light pollution by looking at dynamic of emergence, feeding behaviour and energetic reserves of the offspring of wasps submitted to the three treatments of artificial light at night.

We discussed the results of these experiments in terms of the impacts of light pollution on the efficiency of parasitoids to parasitize their hosts.

*Speaker

Common drivers of seasonal movements on the migration – residency behavior continuum in a red deer

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This study aimed to (1) identify the scale of environmental drivers of seasonal movements on the migration – residency behavior continuum in a large herbivore species and to (2) test the hypothesis that the same environmental drivers and spatio-temporal scaling should influence spatial processes in both migrants (long distance migration) and residents (short distance range shifts). We performed a comparative analysis of the influence of plant phenology and snow cover duration on seasonal movements of five partially migrating red deer populations with contrasting environmental conditions, at the seasonal range scale and the study area scale. The five populations presented varying proportions of migrants, large gradients of migration distances and seasonal range shifts. The probability for a red deer to migrate was strongly influenced by large-scale environmental conditions, consistent with the resource heterogeneity hypothesis (high spatio-temporal scaling favor migration). Distances moved by both migrants and residents were both strongly related to large-scale environmental conditions as well. We showed that similar proximal causes influenced these seasonal movements reinforcing the idea of a continuum from migration to residency in response to seasonal environmental changes. Together, our findings suggest that global warming, by homogenizing large-scale environmental conditions may thus decrease migratory tactics.

*Speaker

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Posters Biological Invasions

Restricted gene flow and strong genetic drift in an invasive species

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Studying the spread of invasive species provides a tremendous opportunity for understanding the mechanisms behind the colonization of new environments. This issue is important for predicting both the spread of invasive species and the consequences of global change on the distribution of native biodiversity. Theoretical and experimental models of species spreading generally give a prominent role to dispersal evolution at leading edges, suggesting that dispersal overcomes the effects of genetic drift during the spread phase.

We examined the interplay between dispersal and genetic drift in 36 populations of the red swamp crayfish, in a relatively recently invaded wetland area (30 years, Brière, northwestern France). Despite the small spatial scale of our study (15 km²), population genetic analyses surprisingly revealed very low gene flow, and thus, restricted dispersal. The populations (ponds and marshes) were highly structured according to the strong barrier of land surfaces, and waterways were clearly identified as dispersal pathways. These populations also exhibited very small effective population sizes, suggesting that genetic drift dominated in the evolution of these populations. Indeed, we observed a significant decrease in genetic diversity and an increase in genetic structure over only two years, and this effect was the strongest in isolated populations. Such changes in small and isolated populations likely prevent local adaptation and evoke an extinction vortex, a concept developed to describe the processes triggering extinctions in declining species.

Our results emphasized the role of genetic drift in addition to dispersal in the fate of this invasive species. Some of its populations may even locally disappear as a result of demographic and genetic effects linked to isolation. Looking forward, these unseen findings could have a significant impact on management issues of this species.

Biological Invasions

below the carrying capacity. We also found that *Corbicula* exhibited a density-independent population growth, which suggest that density of this invasive species is mainly regulated by abiotic factors rather than biotic ones. Populations with a reduced *per capita* rate of increase were composed by clams with faster growth which, in turn, reach breeding size earlier (*i. e.*, at a younger age) compared to those from higher populations growth rate. Together, these results support theoretical predictions that front-edge populations experience strong r -selection, favoring early reproduction as an effective mechanism to increase population growth rate, prevent stochastic extinction, and accelerate range expansion.

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†Speaker

Contribution to the study of Phlebotomine (Diptera: Psycodidae) in the region of Tizi Ouzou

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Sandflies are dipterans widely responded to Tizi-Ouzou, are known for their role in the transmission of several diseases and pose real public health problems. In order to better know the sandflies in the Illoula-Ummalou region and the Beni-Zmenzer region, an entomological inventory was carried out from April to August 2016 (5 months) in 12 stations. Phlebotomus specimens were captured using two types of traps: oiled papers, of which 1868 were collected at Illoula-Oumalou and 236 individuals in the Beni-Zmenzer area, for bright CDC traps. was placed in Illoula-Oumalou where 340 specimens were captured. Thus, six species have been identified, namely Phlebotomus perniciosus, Phlebotomus longicuspis, Phlebotomus perfiliewi, Phlebotomus papatasi, Phlebotomus sergenti and Sergentomya minuta parroti. The use of ecological indices has indicated that in the Illoula-Ummalou region, Phlebotomus perniciosus predominates with 1008 individuals (54%) and in the Beni-Zmenzer region the same species predominates with a population of 163 individuals (69%). Phlebotomus perniciosus is constant in most stations. Two techniques have been adopted in the laboratory: on the one hand, the ELISA blood meal which revealed about 40 tested females that 60% of the latter took their meals on cows.

Key words : Phlebotomes; Inventory; Ecological index; ELISA test; Region of Illoula Oumalou; Region of Beni Zmenzer

Empirical evidence that *P. antipodarum* is a low quality food for fishes

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Potamopyrgus antipodarum – one of the most widespread invasive species worldwide. Previous study indicated, the tench (*Tinca tinca*) to be most effective predator of this snail (able to crush the shell) under laboratory experiments. The same tendency was expected in natural ecosystems keeping in mind that native snail *B. tentaculata* is visually similar and common object in tench diet. Though field studies indicated that *P. antipodarum* is not incorporated in its diet. It raised the question, how the abundant invader escapes one of its effective predators - tench. Enemy avoidance mechanism, such as small hard shell with an operculum, is often attributed for *P. antipodarum*. To test the assumption, shell crushing resistance for the first time was estimated empirically. It should be indicated is that the size of studied molluscs is naturally different – the individuals of *P. antipodarum* are smaller than individuals of *B. tentaculata*. The average shell length of studied snails was respectively 4.2 mm for *P. antipodarum* and 8.8 mm for *B. tentaculata*. Despite the different shell length of studied snails, there were no significant differences (Kruskal-Wallis test, $p > 0.05$) in shell crushing resistance of *B. tentaculata* and *P. antipodarum*. Additionally, it was estimated that dry weight of soft tissues constitute respectively 9-20 % of total *B. tentaculata* and 5 – 13 % of total *P. antipodarum* dry weight. In general, the obtained results confirm the assumption, that *P. antipodarum* is poor food object for fishes. Particularly high shell resistance to crushing, small individual size and together low amount of digestible soft tissues and large brood pouch consisting mostly of shelled embryos, allows the invader to escape the predators.

To control or not to control: when the ecological costs of management-driven phenotypic changes counterbalance the benefits of invasive species removal

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Biological invasions are a key component of the current biodiversity crisis and affect all levels of biological organization. Across the globe, large-scale eradication programs aiming at controlling invasive species are implemented. Interestingly, such programs represent a unique opportunity to assess the effects of harvest-driven trait changes on ecosystem functioning. Indeed, intraspecific variability is now widely recognised as a key driver of ecological dynamics and a well-known potential driver of intraspecific variability is harvest-driven trait changes occurring in exploited populations. Virtually all control programs induce a non-random removal of individuals from targeted populations and therefore control efforts do have the risk to modify trait distribution in managed populations and ecosystem functioning. Additionally, when complete eradication is not achieved, re-established populations may contain individuals with potentially contrasting traits compared to the pre-control period. Harvest-driven trait changes in invasive species might induce unexpected and potentially counterproductive results that are not explicitly considered by scientists and managers and that remain to be quantified. Using invasive freshwater fish and crayfish as model organisms, the present study aimed at assessing the efficiency of control programs by i) quantifying managed-induced phenotypic trait changes in invasive species along a gradient of management practices (biomanipulation and trapping) and comparing the benefits of population size reduction versus the risks of harvest-driven trait changes. Although some differences across invasive species were observed, our observational approach in the field first revealed the existence of significant changes in a suite of phenotypic traits of functional importance between populations with different levels of management. We then demonstrated using experimental mesocosms that the ecological (recovery of some ecological functions) achieved by removal (i.e. reduction in invasive species density) could be substantially reduced by management-induced phenotypic changes in invasive species. We then quantify how it modifies the resilience trajectory of invaded and managed ecosystems.

Global economic costs of invasive species

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As a pervasive component of global change, biological invasions are responsible for substantial damages throughout the world such as species extinction, spread of diseases or devastation of crops. Quantifying the economic costs related to invasive species is crucial to raise awareness and improve the multi-criteria assessment encouraging preventive measures or changes of practices at relevant scales. Until now, the few studies attempting to provide a global overview of these economic costs suffered from inherent flaws and questionable methodologies. Therefore, a reliable global cost synthesis remains a major challenge in the assessment of invasive species. We aimed to provide the most comprehensive and robust global-scale data compilation of the monetary costs associated with invasive species. We developed a standardised method to collect information from both peer-reviewed and unpublished literature, while avoiding possible publication bias and minimizing the probability of missed material. To maximize the reliability of the data we collected, we double-checked all sources, and included qualitative and quantitative details of each source we retrieved. We found that the minimum economic costs associated directly and indirectly (including control and research costs) with invasive species are expansive (in the order of hundreds of billions of dollars annually worldwide). Moreover, these costs are grossly underestimated, emphasizing crucial gaps such as the scarcity of cost estimates (compared to the large number of invasive species), a biased research effort towards particular areas and/or taxa, and many unreliable estimates (i.e., not based on available and repeatable methodologies or traceable original references). We discuss the mismatch between the huge economic cost of invasive species and the disproportionately lower concern expressed by management authorities and the general public. By providing the first rigorous global summary of accessible monetized costs of invasive species, we provide an essential basis for national and international policies in the management of invasive species

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Behavioural responses to control practices: lessons from common mynas

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Throughout their history, humans have harvested wildlife from their surroundings. There is strong evidence that, like natural predators, humans can shape the evolution and behaviour of the species they target. Yet the fact that species behaviour is likely to adjust to anthropic risk is seldom taken into account in the context of control of invasive and pest species.

The common myna, *Acridotheres tristis*, is a highly successful worldwide invader. It was introduced in Australia in the 19th century and is now the target of increasing control efforts. Following evidence that in areas with high levels of management, trapping success has decreased beyond what might be expected from the number of birds culled, we investigated potential compensatory responses to this anthropic predation pressure. Our results revealed a number of behavioural differences between areas of high and low trapping pressure. Where the risk was higher, mynas were overall more risk-averse and less conspicuous. This suggests that common mynas adjust their behaviour to the level of anthropic risk in the environment.

We highlight the importance of considering behavioural changes in the context of control programs. These changes have the potential to modify the ecological impact of the target species, to hinder the sustainability of control practices, and to interfere with the assessment of program effectiveness.

Cold acclimation triggers major transcriptional changes in *Drosophila suzukii*

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Insect life is directly depending on environment temperature. Low temperatures can alter cellular homeostasis resulting in chill damages and in most extreme cases, lethality. To counter-act these deleterious effects, insects can use acclimation-related physiological adjustments. The spotted wing drosophila (SWD) *Drosophila suzukii* is an invasive pest of red berries. SWD is known to be chill susceptible, succumbing to cold exposures way above 0 °C. Yet, it overwinters in harsh European winter conditions, which might be partly due to its highly plastic cold tolerance. However, little is known about underlying mechanisms of cold acclimation in SWD. Here, we promoted SWD cold tolerance through increasing acclimation periods (i.e. from 2 h to 9 days) and selected the most extreme phenotype to characterize transcriptional changes by RNAseq. Significant changes were noticed in SWD cold tolerance after acclimation: the longest the acclimation period, the highest the cold tolerance. Flies acclimated for 9 days were selected for sequencing. RNAseq revealed up to 2200 significantly differentially expressed genes (1200 up- and 1000 down-regulated) compared to non-acclimated flies. Functional annotations on the up-regulated set revealed many enriched GO-terms among which transport of ions across membranes and signaling were highly represented. We also noticed upregulations of several genes involved in thermal stress resistance, like heat shock proteins and Starvin. Involvements of a cluster of genes related to ion transport in cold-hardy flies is sensible, considering that loss of ion homeostasis is the major mechanism responsible for chill-injuries. Functional annotations on the down-regulated set revealed many GO-terms related to oogenesis. This likely reflects reduced reproductive process of acclimated females. Data were validated with rt-qPCR on selected genes. Overall, these results participate to our understanding of SWD low temperature biology, a knowledge of importance for better prediction of SWD population dynamics in temperate areas.

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Bee hotels as a tool to monitor the expansion of the exotic bee *Megachile sculpturalis*

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Megachile sculpturalis (Hymenoptera, Apoidea, Megachilidae, Smith, 1853) is an exotic bee species first recorded in Europe in Allauch near Marseille in 2008. Ten years after its first mention, *M. sculpturalis* now occupies the whole South-Est of the French territory. However, little is still known about the ecology of this species since its arrival in France. The few evidences we do have indicate a preference toward exotic or ornamental flowering species for pollen collection and a good ability to nest in manmade insect hotels. Furthermore, we also recorded several events of aggressive eviction of *Osmia* spp. and *Xylocopa* spp. individuals from their nest by which could be worrying for the local bee fauna. To better understand the ecology of *M. sculpturalis*, we launched two years ago a field campaign to monitor this species. We installed insect hotels in twelve parks of Marseille (8 hotels/parks) composed of logs and stems. Each year we collected each stems or logs occupied by bees. These substrates were then placed in a room at 20°C until the emergence of bees. Each bee emerging from these substrate were collected, pinned, identified and measured. Their size was then linked to the diameter of the stem or logs from which they emerged. Finally, stems and logs were opened to collect pollen residuals in order to identify the diet behavior of each individual. Our results indicate that insect hotels are a perfect tool to monitor *M. sculpturalis*. Indeed, after two year, *M. sculpturalis* was the dominant species of insect hotels representing more than 50% of emergences. We present here our results together with new insights on the ecology of this exotic species.

Challenges and Difficulties of sharing data on biological invasions management

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Since 2002, a working group on invasive alien species management is active in the French Loire watershed. Initiated by the Water Agency, its coordination was taken up by the Nature Conservancies Federation in 2007. The dynamic of the group relies on a structured, active and informed network of practitioners, exchanging information on management techniques and territorial coordinations. Gathering shared and comparable data on localisation and costs has been a target as well as a challenge during this period. In 2018 a new survey to detail the management costs was submitted to the working group and the practitioners' network. It revealed that if more and more species are managed and fought against on a regular basis, it is still very difficult to get any feedback on the elemental data of the projects as well as on the efficiency of the methods used on the site, except in "pilot" projects. The Nature Conservancies Federation proposes in response to these results the definition of a core of informations to gather, accompanied by a users guide for the motivation and voluntary use by the practitioners. It completes a range of tools developed by practitioners for practitioners, with the help of researchers and scientists : a management strategy at the Loire watershed level, an identification guidebook, another on management guidelines e.g. To perfect these useful and widespread tools, it will be proposed to the stakeholders financing the management projects to send the grid of minimal information and the users guide to the supported project holders, to maximize the return of information.

Life at the expanding front: Freshwater invasive clams reproduce earlier in populations with reduced per capita rate of increase

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In newly invaded habitats, individuals are forced to rapidly respond to novel stressful conditions at the expanding front of their distribution, where differing selective pressures favor the evolution of life-history traits that increase the rate of population growth. Freshwater clams of the genus *Corbicula* are successful global invaders, but the ecological and evolutionary factors that drive their range expansion remain poorly understood. We conducted an exhaustive search for peer-reviewed articles providing enough information on *Corbicula* to estimate population density, population growth rate (per capita rate of increase), individual growth rate, age at first reproduction, and time since population foundation. We retained 16 out of 223 studies, covering 19 invasive populations of *Corbicula* from different ecosystems worldwide. We tested whether (i) recently established populations (assumed to represent the invasion front) occur at lower densities than older populations, (ii) populations' growth rates are higher at initial low densities and decrease as densities build up, and (iii) populations with reduced per capita rate of increase are constituted by clams exhibiting faster growth, as predicted by theory. We found that newly established populations showed lower abundance compared to long establish ones. This is consistent with front-edge populations occurring at low conspecific densities below

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†Speaker

Biological Invasions

the carrying capacity. We also found that *Corbicula* exhibited a density-independent population growth, which suggest that density of this invasive species is mainly regulated by abiotic factors rather than biotic ones. Populations with a reduced *per capita* rate of increase were composed by clams with faster growth which, in turn, reach breeding size earlier (*i. e.*, at a younger age) compared to those from higher populations growth rate. Together, these results support theoretical predictions that front-edge populations experience strong *r*-selection, favoring early reproduction as an effective mechanism to increase population growth rate, prevent stochastic extinction, and accelerate range expansion.

Do native birds drive away invasive birds from urbanised Australia?

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The noisy miner is a highly aggressive native Australian bird whose density is negatively associated with avian abundance and richness. Noisy miners are endemic to eastern and south-eastern Australia in rural and urban habitats. Miners have been shown to be highly aggressive both within the species and towards other bird species. They seem to be particularly aggressive in urban areas where introduced birds such as common mynas, occur. The common (Indian) myna (*Acridotheres tristis*) was introduced to Australia in the 19th century and is expanding its range. Here, we aimed to determine how behavioural interactions between the native noisy miner and the introduced common myna impact the invasive common myna's range expansion. We experimentally studied noisy miner responses to territorial intrusions by common mynas and compared them with the responses of noisy miners to conspecific and novel bird species intrusions in both urban and rural environments. We also compared noisy miner response to intrusions in areas with both long-established (> 40 years) and recently-established (< 10 years) common myna populations to investigate whether the response could vary as a function of the period of time both species overlap. We discovered that urban noisy miners displayed higher levels of aggression towards the common myna compared to a conspecific and the level of aggressiveness was the same in both long-established and more recently-established myna locations. In an experimental setting using bird mounts and playbacks, noisy miners did not respond to a novel bird, nor to common mynas and conspecific mounts in rural habitats. By displaying a high level of aggression towards the species with which they already coexist in urban areas and presumably, based on their lack of response to a novel bird, ignoring them when they first encounter them, the noisy miners might contribute to the spread of mynas in new areas.

*Speaker

Water primrose, an evolutionary success?

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Biological invasion are considered as the 3rd cause of biodiversity loss in the world. Understand the adaptation and dispersal mechanisms of these species are a major challenge in ecology. In France, two species, *Ludwigia grandiflora* (LG) and *Ludwigia peploides* (LP) colonized since 1826 aquatic environments and more recently wet meadows. These 2 species are an ideal model to understand the processes of adaptation to a new environment (new ecosystem, adaptation to the terrestrial environment). Their characteristics are a mixed reproductive system (clonal and sexual), different levels of ploidy (LG = 10x, LP = 2x), two types of pollination (allogamous (LG) and autogamous (LP)). However, to study population genetics of polyploid organisms with mixed reproductive mode, the tools available are little or not suitable for allelic assignment and dosage, which represents an important lever for our study. The Loire river in France presents contrasted climatic variations and large hydrological network which could contribute to the dispersal of the water primrose. It is for these reasons that we have chosen this area as zone of study.

The main hypothesis of this work is that sexual reproduction participates in the water primrose adaptive potential and represents a risk in the dispersion of both *Ludwigia* sp in France. To test this hypothesis, we will answer three questions:

- (i) Is there genetic diversity in the populations of the Loire and how is it spread over the Loire?
- (ii) What is the share of sexual reproduction in the dispersion of the water primrose?
- (iii) Do plants resulting from sexual reproduction present a more important potential than those resulting from vegetative propagation for adaptation to the terrestrial environment?

The expected results could bring knowledge to understand the success of colonization and the adaptation of water primrose and to give recommendations for population management in French aquatic ecosystems.

*Speaker

Native versus invasive strains of *Drosophila suzukii* : changes in life history traits

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Drosophila suzukii of Asian origin has been an invasive species in Europe since 2008. This fruit fly also became a major pest of many cultivated red berries and other fruits.

The question we are asking in this study is pretty straightforward: besides taking advantage of new - and potentially free - ecological niches, what changes in their life history traits make invading populations so successful on their route of invasion?

The object of this study was to compare life history traits (females' preferred substrate for egg laying, duration and success of development, adult size) of two strains – a French one and a Japanese one – of *Drosophila suzukii*, when raised on either a host plant of Japan origin *Aucuba japonica*, or a European one *Viscum album* subsp. *album*. All tests were conducted in standard conditions in the laboratory.

Results show that females of both French and Japanese *D. suzukii* strains preferred to lay eggs on *Aucuba japonica*. However, both French and Japanese *D. suzukii* strains show better success of development and also give rise to bigger adults when developed on *Viscum album* than on *Aucuba japonica*. In addition, the French *D. suzukii* strain develops faster and gives bigger adults than the Japanese strain on both plant hosts.

Our results demonstrate that *Viscum album* is more favorable to the development of *D. suzukii* compared to *Aucuba japonica*. However, female flies of any geographical origin prefer to lay eggs on *A. japonica*, possibly because *D. suzukii* has shared a longer evolutionary history with this host plant. All together, the invasive French *D. suzukii* strain performs better on any tested host plant than the Japanese strain, thus suggesting a rapid evolution of life history traits during the invasion process.

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Invasion success of Black cherry (*Prunus serotina*) in Europe: importance of root traits and associated mycorrhizae

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Native of North America, Black cherry (*Prunus serotina*) is one of the most invasive tree species in European temperate forests. Although the abilities of *P. serotina* for light competition are well documented, we know little about competition for belowground resources (water, nutrients). Our study aimed to better understand the incidence of belowground processes in the invasion abilities of *P. serotina*. We thus compared the root functional traits and the mycorrhizal colonisation rates between *P. serotina* and two European native species (European beech and Scots pine), in pure and mixed-species stands.

To analyse the effects of competition, we focused on (i) fine roots of beech and pine, in pure stand and in mixture with *P. serotina*, and (ii) on fine roots of *Prunus serotina*, in pure stand and in mixture with the beech or the pine. In each case, we measured the mean root diameter, the branching intensity, the specific root length (SRL) and the abundance of arbuscular and ectomycorrhizae. Our results show that, although *P. serotina* seemed disadvantaged by its root morphology (lower branching intensity than pine and beech), its ability to host both arbuscular and ectomycorrhizae could confer an advantage. Finally, we did not find any global negative effect of *P. serotina* presence on the native species root traits, whereas pine reduced the mycorrhizal colonisation rate of *P. serotina*.

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Morphological variations of *Myriophyllum heterophyllum*, a new invader in French freshwaters

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Since the 2 August 2017, the European legislature banned the sale, purchase, cultivation, distribution and transplantation of *Myriophyllum heterophyllum* because this aquatic grows in thick, dense mats and outcompetes native vegetation and while it can restrict water movement, particularly when decomposing, that reduce water quality and available oxygen. This plant reproduces both sexually and vegetatively, however, vegetative regeneration is a dominant mode of reproduction. *Myriophyllum heterophyllum* is released to aquatic ecosystems by dumping of aquaria in the wild or cleaning of ponds, and also by boats. It is a brittle plant and fragments are easily broken off by wave action as well as boating.

The first observation of dense mats of *M. heterophyllum* in France was noticed in 2011 in a private pond in Saint-Sylvestre (Nouvelle-Aquitaine region), whereas few individuals detected in 2010 were present in a pond at Villeurbanne (Auvergne-Rhône-Alpes region). Oldest cited locations from Adour river (Nouvelle-Aquitaine region) ZHU H U H P e r m a n e n t and then not studied. More recently a new site was found at Contre (Hauts-de-France region).

We study the morphology of these populations established in three different ponds throughout the phenological cycle using traits approach. We also characterized its habitat. Our results showed that the plant grows from acidic (Saint-Sylvestre site) to alkaline waters (Contre and Villeurbanne) and can tolerate a wide range of mineral content. *Myriophyllum heterophyllum* grows on fine textured sediments such as silt, sand and gravel and prefers high ammonium nitrogen levels (sites Contre and Saint-Sylvestre). In spring emergent whorls were observed at Saint-Sylvestre *M. heterophyllum* produce aerial leaves during the summer months. The regeneration ability (number and length of lateral shoots) of *M. heterophyllum* was the lowest at the site of Villeurbanne, whereas the colonization ability (number and length of the roots) didn't differ between sites.

*Speaker

Posters Chemical Ecology

Cleome Arabica L. (capparidaceae) a spontaneous plant of South-Algerian proposed as a remedy for Alzheimer's disease

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Plants have always been part of the daily life of man, through ages, man has been able to rely on nature to provide for his basic needs: food, shelters, clothing. The world of plants is full of resources and virtues from which man draws not only his food but also active substances that often provide a benefit to his body sometimes affected by insidious disorders. The therapeutic use of the extraordinary virtues of plants for the all diseases treatment of man is very old and evolves with the history of humanity.

Medicinal plants are still the first reservoir of new drugs, they are considered as a source of essential raw material for the new molecules discovery needed for the future drugs development. This plant material contains a large number of molecules that have multiple interests sed in the food industry, cosmetology and pharmacy; Among these compounds include flavonoids.

From biological activities of medicinal plants, in recent years the focus has been on antioxidant activity because of the role it plays in disease prevention. Attenuation oxidative stress by the anti oxidant molecules is proposed as a potential treatment therapeutic in Alzheimer disease.

This disease is characterized by the presence of β -amyloid deposits in the cerebral blood vessels. The flavonoids can be as good β -secretase inhibitors.

Cleome arabica L. (Capparaceae) is a medicinal and desert plant widely distributed in the northern part of Africa and is very rich in its composition of flavonoids.

Our item consists to study the inhibition of the β -secretase, enzyme implied in the Alzheimer's disease with a *Cleome Arabica* L. The purpose of this study is to decrease the formation of β -Amyloid and consequently to delay its progression.

*Speaker

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Overcoming specialized metabolites by gaining essential nutrients: a lichen/snail case study

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Specialized metabolites often rule predator/prey relationships. As lichens are slow-growing symbiotic organisms, they must defend strongly against lichen-feeding invertebrates, including gastropods. In Sub-Antarctic islands, the fruticulous chlorolichen *Usnea taylorii* is characterized by its erect, corticated and extensively pigmented thallus. Abundant on rocks in the windy fell-fields, this lichen is eaten by the only gastropod widespread on Possession Island, *Notodiscus hookeri*.

To explore thoroughly the lichen palatability, spatial mapping of the specialized metabolites was investigated using Imaging Mass Spectrometry (Imaging-LDI-MS). To assess the possible phagostimulant or phagodeterrent effect of lichen metabolites on the snail feeding decision, no-choice experiments were realized by incorporating the metabolites in waxy starch supports.

Cortical consumption of *U. taylorii* by the snail appeared to be in line with the localization of usnic acid, the main specialized metabolite strictly confined to the cortical layer of the lichen. However, no consumption of the gel enriched in usnic acid (4 mg.g⁻¹ dry mass (DM)) was observed, suggesting that phagostimulant compounds in thalli reduced its deterrence. Among sugars and polyols known for their attractive properties, D-arabitol occurred in *U. taylorii* thalli at high concentration, around 100 mg.g⁻¹ DM. Waxy gels incorporating arabitol were tested with and without usnic acid at the same concentrations than those quantified in the lichen. The mixture usnic acid-arabitol led to increasing snail feeding, while waxy gels enriched in arabitol alone were by two fold more consumed. By using Imaging Mass Spectrometry (Imaging-MALDI-MS), the co-location of arabitol with usnic acid was confirmed.

These results underline the crucial role of primary metabolites in overcoming the deterrent effect of specialized metabolites. The "generalist" trophic status of *N. hookeri* combined with its ability to cope with potentially toxic metabolites might explain how successful was this species in the near totality of Possession Island.

Speaker

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The quality of saffron: *Crocus Stavum* in western Algeria

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The present work describes the study of the chemical composition and biological activity of saffron extracts from *Crocus Stavum* flowers.

The quantitative analysis of the extracts shows the richness of saffron in phenolic compounds. The antioxidant activity of the extracts was studied using two different tests and then compared with vitamin C.

The results obtained reveal that the aqueous extract has a large capacity for scavenging the radical DPPH with IC₅₀ of the order of (0.45 µg / ml). HPLC chemical analysis results indicate the presence of picrocrocin, hydroxy-trimethylcarboxaldehyde-cyclohexene (HTCC), kaempferol, safranal and crocus.

Posters Conservation Biology

Increasing disturbance: the challenge of conserving the last subpopulations of endangered megafauna in the southeast of Nicaragua.

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Nicaragua is in the core of the Mesoamerican Biological corridor, meaning an important country to connect biodiversity between South and North America. However, even though the East Coast of the country represents most of the national part of the corridor, this region highlights as one of the most deforested area of Latin America. This forest loss, within and outside protected areas is driven mainly by cattle farming and a series of socio-political reasons such as lack of governance. In addition, the national government of Nicaragua has open new roads to the most remote and forested areas of the east coast and even signed a concession for an Interoceanic Canal. All those new infrastructure projects represent a perpendicular barrier that might interrupt the north-south corridor. We conducted camera trapping and poaching surveys to understand how those disturbance is affecting the national red listed Jaguars (*Panthera onca*) and Tapirs (*Tapirus bairdii*) occupancy as umbrella species and to understand the dimensions of those threats. We determine that Forest loss has increase since 2000's, and consequently the poaching events has increase for both species and mainly conducted by non-indigenous cattle ranchers since 2000 as well. We mapped the occupancy of Jaguars and Tapirs and determined that the current species distribution has limited to a stripe along sea shore where mostly Palm swamps forest remain, and that Indio Maiz Biological Reserve represents a stronghold for the conservation of a stable subpopulations for both species. We hypothesis that without effective conservation actions this stronghold and remaining corridors might disappear within a decade. Main actions must include the withdraws of thousands of cattle ranchers that invade communal indigenous lands and PA's, strengthen environmental legislation and stop poaching, restore degraded habitat along corridors, mitigation actions of infrastructure projects, increase awareness and update/apply protected areas management plans.

*Speaker

Phytoecological study of *Rhus pentaphylla* (Anacardiaceae) groups in north-western Algeria.

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The present work deals with the phytoecological study of *Rhus pentaphylla* groups in north-western Algeria. It will be interesting to know the characteristics of *Rhus pentaphylla* and its behavior for better adapted in this region. *Rhus pentaphylla* belongs to the family Anacardiaceae, one of the listed families of medicinal interest. This contribution to be reinforced by a pedological and bioclimatic study of the region, we pointed out that the study stations are in the center of semi-arid climate with temperate winter. The study of biological diversity, allowed us to know the biological, morphological and biogeographical characteristics of this Anacardiaceae. The calculation of the index of environmental disturbance shows us that the stations are dominant by the Therophytes which explains a strong disturbance. Keyword: Phytoecology, Anacardiaceae, *Rhus pentaphylla*, northwest, Algeria.

Density-dependent detectability of a vulnerable beetle species in hollow trees

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Conservation of threatened species living in fragmented habitats crucially relies on evaluating their occupancy and their ability to colonize and persist in habitat patches. Fitting stochastic patch occupancy models (SPOMs) to occupancy data can help assessing these features. However it is critical to account for the limited detectability of target species in this type of analysis to avoid severe biases in estimation. Detectability of a population in a habitat patch often tightly depends on the local density of individuals. This connection between density and detectability has rarely been used in SPOM analysis, even when abundance data are available. The two quantities are often considered independent and estimated separately. Here, we propose a framework for using density-dependent detectability in the analysis of a SPOM. We illustrate our approach with the example of *T. opacus*, a beetle inhabiting hollows in old trees. We use a 6-year survey of adults abundances in an woodland pasture area harbouring a high density of old oaks, in Östergötland, south-east Sweden. *T. opacus* is classified as "vulnerable" on the Swedish red list. We modeled abundance data in occupied trees as a function of tree and environmental features. We used this model to predict density-dependent estimates of detectability in all the trees of our study site. Importantly, we could explore how the environmental features affect carrying capacity and detectability of trees, with the latter aspect being rarely explored in metapopulation studies. Our study thus shows that density-dependent framework allows for a simple integration of limited detectability into metapopulations studies, based on a more thorough use of abundance data than classic approaches. In particular, it may be applied even with no or a limited number of repeated surveys, although further statistical analyzes would be necessary to assess this point.

*Speaker

An individual based model to optimize population introductions. Applications to conservation biology and biological control.

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Conservation biology and biological control both involve the introduction of populations in the environment to reinforce or reintroduce a species for patrimonial or ecological reasons, or to combat pest infestations with their natural enemies. General predictions about population introductions indicate that increasing the number of individuals introduced at each introduction or increasing the number of introductions itself, favors the success of the introduction programme, because both increase the rate of introduction of individuals. At a given rate of introduction, hybrid mathematical population dynamics models show that the aggregation pattern of introduction in time also has an influence when the dynamics of the introduced population are affected by density dependence. To evaluate these theoretical predictions in a more realistic, stochastic and spatially explicit setting, a stochastic individual based model has been built on the multi-agent programmable modeling environment Netlogo. Extensive simulatory experiments were performed to assess the effects of density dependent processes on the success of the introduction programme in a reintroduction scenario in which the population experiences positive density dependence dynamics as well as in an augmentative biological control scenario in which the natural enemy population suffers from interference competition (negative density dependence). Some theoretical predictions were confirmed, but only in some regions of the parameter space. In addition to being used to test hypotheses on population introductions, the model has also been designed to ease the communication with a non-specialist audience regarding the effects of complex population dynamics processes on the efficacy of population introduction strategies.

*Speaker

Climate sentinels research program : the effects of climate change on biodiversity in the region of New Aquitaine (South-West, France)

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Understanding local effects of climate change on biodiversity are essential for environmental policy orientation. Lacks of knowledge at regional level have led to the development of a research program: "Climate sentinels" (www.sentinelles-climat.org). A research hypothesis is that the effects can be studied from indicators of species that have weak displacement. These "sentinel" species will be the first to respond to local climatic variations by adaptation or local extinction. In France, New Aquitaine region is a relevant research laboratory. It offers both sensitivity to climate change and a variety of natural ecosystems. The approach to understanding the response of these indicators to climate change is based on: observations in a whole region, standardized protocols in relationship with models using mainly abundance data, validated data linked to associated sufficient coverage, scalable campaigns based on these data, and relevant observations in connection with time and space scales. In the presentation of research in progress, we will present 4 points characterizing this project: 1) the research-action approach of the program brings together different types of actors (decision makers, naturalists, managers, researchers and the public), within an independent organisation and catalyst "Cistude Nature", 2) the method of establishing a list of development indicators called "Climate sentinels", 3) the protocols and data analysis of multi-ecosystems, multi-species at different scales that are used to support projections of climate change impacts on biodiversity, 4) the presentation of the exploratory results of an example of sentinels species : lepidoptera of "calcicolous grasslands". The aim is to share feedback on this topic concerning on how the program was identified and structured at the interface between science and society.

*Speaker

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Macroinfauna diversity associated to seagrass meadows on the northeast of Cancún, Quintana Roo, México

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Seagrasses are a group of marine vascular plants that produce flowers. This ecosystem harbors a high diversity of species that includes almost all known phyla in the sea due to trophic and non-trophic interactions that develop at different scales of time and space. Despite its importance, seagrass meadows have deteriorated and have had reductions in their coverage, due to the increase in anthropogenic activities along the coastal areas of the Caribbean, which is why it is necessary to conduct a study of the benthic communities that this ecosystem can harbor. The study of benthic communities is important, because it allows the development of strategies for monitoring and evaluating the quality of the ecological status of marine and coastal ecosystems. Also, the relationship between the macroinfauna and the sediments, as well as its limited mobility, facilitates the use of these organisms to detect environmental disturbances, which can not be detected in the water column as they respond quickly to stressors in the environment. Given the high natural and anthropogenic disturbance to seagrass meadows in the region and their importance, it is necessary to know the diversity they harbor, since the health status of the ecosystem as a whole depends on it.

The present work aims to contribute to the knowledge of the diversity of the macrofauna associated with seagrass meadows in the Mexican Caribbean. based on this, the intention is to understand the impact on the macroinfauna being this a potential key factor in decision making about the management and use of these ecosystems and thus be able to propose future conservation and restoration strategies in these ecosystems.

*Speaker

Integrating niche models into demographic studies: a step forward to reconcile conservation and niche models

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Species Distribution Models or niche models are widely used to model environmental suitability and predict current or potential future species distributions. They have been advocated to inform conservation planning or translocations programs. However, most of the modelling approaches do not account for demographic processes that are relevant for conservation planning because directly linked with population dynamics and extinction (e.g. reproduction success or survival), making difficult to assess the contribution of SDMs to some conservation actions.

We developed a conceptual framework integrating niche models to demographic studies to enhance our understanding of the ecological processes influencing population dynamics along environmental suitability. We applied this framework in the translocation programme of the North African Houbara bustard (*Chlamydotis undulata undulata*). Using the long-term monitoring of Houbara populations in Morocco, we studied the relationship between environmental suitability and two major demographic parameters: survival and reproduction success. We also studied how the temporal variation in population abundances influences its relationship with environmental suitability.

We found a positive relationship between survival rates and environmental suitability and highlighted some density-dependence effects in high-quality sites. We showed how biotic interactions can influence the relationship between reproduction success and suitability along the breeding season through the study of its intra-annual variation. We also described a triangular relationship between abundances and suitability and further explored how source-sink dynamics and biotic interactions can lead to deviations from expectation over time. Overall, these empirical approaches help us to explicitly measure the adequacy between niche models and demographic parameters. We discuss how the results can inform our understanding of SDMs and population dynamics in the context of species translocations.

*Speaker

Semantic management and valorisation of data from biodiversity and ecosystem studies within the AnaEE-France research infrastructure

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As the national Research Infrastructure devoted to the study of continental ecosystems and biodiversity, AnaEE-France (Analyses et Expérimentations sur les Écosystèmes) provides facilities for experimentation in controlled (ecotrons), semi-controlled or in natura environments. It also offers analytical and modeling platforms as well as Information Systems (IS) for FAIR data management. Most AnaEE-France platforms also contribute to AnaEE(-EU) Europe.

AnaEE adding value relies on the possibility of linking environmental pressures or factors with the characteristics or the trajectories of the studied ecosystems (grassland, forest or freshwater). Indeed environmental data are jointly collected with the data produced by the experiments.

The consistent management and exploitation of the data is a real challenge due to their great heterogeneity of origin and nature. With the overall objective of ensuring accessibility, use and re-use of the resources, a distributed IS is developed based on the semantic interoperability of its components and the use of common vocabularies (AnaeeThes thesaurus and an OBOE-based ontology). Discovery and access portals are fed by the information produced by the semantic annotation of AnaEE distributed resources: relational databases and modeling platforms.

Pipelines are developed for the automation of the data semantic treatments. A first pipeline is devoted to annotation and production of the semantic data that may represent a huge conceptual and practical work. A second pipeline is devoted to the exploitation of these semantic data through the generation i) of standardised ISO and GeoDCAT metadata records and ii) of data files (NetCDF) from selected perimeters (experimental sites, years, experimental factors, measured variables...). Tool genericity should ensure re-usability in different contexts of ontologies and databases. These pipelines are developed within the ENVRIplus context (Cluster of the European environmental RI, including AnaEE) and contribute to its service portfolio.

*Speaker

Population dynamics of the highly endangered *Eryngium viviparum* within its last French locality.

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Eryngium viviparum (Apiaceae) is an endemic plant of the Atlantic region of Europe, growing in seasonally flooded sites. The species is characterized by a highly disjunct distribution. Indeed, it occurs only in a few sites in the North-West part of the Iberian Peninsula and in a single locality in France. Theoretically, the strong isolated context of this population could have negative consequences for the species conservation in France. In order to evaluate its vulnerability, ecological survey, genetic analyses and demographic survey were performed to answer the following questions : (1) Which ecological variables affect the demographic modalities of the species ? (2) Is there any evidence of loss of viability of this population ? (3) How did the geographical isolation acts on the genetic diversity and the demographic behaviour ? (4) Can the population persist over the long term ? As expected, the French population of *Eryngium viviparum* has a very low genetic diversity consequent to a recent bottleneck and strong geographical isolation. The population seems stable, but very vulnerable to the variation among ecological modalities. These worrying results imply new questions on the conservation of *Eryngium viviparum* in France, but provide new indications to improve the persistence of these last population.

*Speaker

Posters Dealing with heterogenous data

Synthesis and collaborative science in ecology

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There is an increasing interest and investment in transdisciplinary and collaborative science in ecology. While unprecedented data availability opens new possibilities to address challenging questions in ecology and environmental sciences, this endeavor requires more integrated and interdisciplinary approaches to provide new perspectives and develop methods and frameworks capable of addressing the complexity of the challenges. As a result, collaborative projects are becoming more the rule than the exception in ecology. Collaborative research and synthesis science not only requires accessing and manipulating complex data sets, but also depends strongly on sharing knowledge, skills and expertise, and often on reconciling alternative perspectives. This implies important paradigm shifts in the way we collect, use and share data, but also in how we work

*Speaker

Dealing with heterogenous data

and communicate among science areas, venturing beyond our silos and inviting genuine and more open dialog across fields. While ecologists are generally eager to collaborate and adopt new methods within and beyond their field of expertise, effective transdisciplinary collaboration requires a realistic awareness of the aspects of such collaborations. Team science is known to be labour intensive and requires proper preparation, real leadership and genuine trust among participants. Here we provide our perspective as current and former post-docs involved in synthesis centres, highlighting the challenges and key elements to consider when working on team science projects. We discuss solutions to challenges and suggest approaches that can help build capacity and leverage the full benefits of team science and transdisciplinarity. This should facilitate positive outcomes such as integrated knowledge and novel perspectives and discovery in ecology and environmental science.

Semantic management and valorisation of data from biodiversity and ecosystem studies within the AnaEE-France research infrastructure

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Posters Eco-evolutionary dynamics

Rapid evolution of an annual plant species uncovers coexistence mechanisms

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Using a mechanistic trait-based neighborhood-model, we quantified the impact of spontaneous mutations on intraspecific genetic variation governing plant coexistence. We quantified the effects of mutation on neighbor responses on plant fitness in a field experiment, using 100 replicated *Arabidopsis thaliana* twenty-fifth generation mutation accumulation (MA) lines derived from a single Columbia accession founder. We constructed individual-based maps and calculated matrices of neighboring plants (10,560 individuals) to quantify the mutational effects of intra- (same MA-line) and inter-genotypic (different MA-line) variation on plant fitness. At small scales we found neighboring plants of different genotypes to have stronger competitive effects on plant fitness than plants of the same genotypes. However, at larger scales, the effect of inter-genotype neighbors becomes positive, i.e. facilitation, and intra-genotype neighbors have no or negative effects. Spontaneous mutations may allow plants to expand their niches and become more competitive at smaller scales but at larger scales mutations contribute to coexistence.

*Speaker

Erosion of phylogenetic signal of niches through eco-macroevolutionary feedback

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Phylogenetically closely related species often occupy more similar niches than distantly related species, but the strength of this phylogenetic signal is mostly only moderate. We suggest that strong phylogenetic signal in niches negatively feeds back on itself: Strong phylogenetic signal both increases the chance of a given focal species to coexist with closely related neighbors due to shared niche preferences, and is responsible for the fact that a large number of patches is dominated by distantly related neighbors. Ecological interactions with such distantly related neighborhoods might affect microevolution of the focal species by (i) increasing fitness due to decreased competition or enemy pressure, or (ii) selecting for different traits than do closely related neighborhoods. Both microevolutionary processes would erode the focal species' preference for its ancestral niche and eventually the phylogenetic signal of niches across species. We experimentally tested both microevolutionary effects using oaks as focal species and manipulating pressure by specialist and generalist enemies. We confirmed selection for different traits in closely and distantly related neighborhoods. We then used individual-based modeling to test how a strong phylogenetic signal in niches or in interaction-related traits modulates neighborhoods and microevolutionary responses to neighborhoods, and how this eventually feeds back on phylogenetic signal. We found, again, selection for different traits in distantly related and closely related neighborhoods but only if competition acts hierarchically and enemies are specialists. Strong phylogenetic signal controlled ecological coexistence among species, and particular types of ecological interactions among coexisting species then trigger microevolutionary responses that erode phylogenetic signal of niches. An eco-macroevolutionary feedback. Prinzing

*Speaker

Posters

Ecological Interactions

The breeding system of *Watsonia knysnana* (Iridaceae): an assessment of pollinator effectiveness

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The ongoing debate about specialisation vs generalisation in plant-pollinators interactions has led to criticism about the reliability of the pollination syndrome traits to predict the main pollinator of a species. The South-African plant species *Watsonia knysnana* is a good example to illustrate this debate as its tubular corolla fits with the ornithophilous floral traits to attract Sunbirds (specialist nectarivore passerines) but the range of colour exhibited is more likely to attract Insects. From exclusion experiments we identified Sunbirds as most effective pollinators of *W. Knysnana* with Honeybees playing a minor role, if any. In addition, the nectar properties (concentration and volume) conform to plants mainly pollinated by specialist nectarivorous birds.

Study of the trophic ecology Fennec in the area of Ouargla

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Abstract

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The aim of this study is to know the diet of Fennec *Fennecus Zerda*, in the region of Ouar- gla (31°58' N, 5°19' E) and specifically at two stations Oued N'sa. The study area belongs to the bioclimatic floor Saharan mild winter. It was based on the analysis of droppings to this review. 1537 individuals are consumed Insecta which ranks first with 1288 individuals (83,82%), followed by 69 Mammalia(4,49%), Crustacea by 58 individuals, fragments Plantae (2,67%) and 41 individuals Aves 11 individuals (0,72%), Reptilia 8 individuals (0,52%) in terms of biomass, Mammalia occupy the first rank with a rate of 81,58% followed by Insecta with 5,72% and 3,66%. Aves. . Based on these findings are the dominant vertebrate in terms of biomass, we can say that the Fennec adopt a carnivorous diet.

Keywords : *Fennecus zerda*, Diet, Oued N'sa, Ouargla

*Speaker

Inventaire comparatif des tiques de la région de Bouzeguène et la détection moléculaire des *Rickettsia*.

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Inventaire comparatif des tiques de la région de Bouzeguène et la détection moléculaire des
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Summary

The inventory of ticks in the area led to Bouzeguène bioclimatic per-humid and cold winter. A sampling technique is used for this inventory is live capture by hand. This technique has revealed the existence of 7 species distributed in order Ixodida and family Ixodidae. The use of ecological indices compositions was used to estimate the relative abundance, total and average wealth of species studied. The parasite rates tell us about the infestation rate and parasite loads of species. The results of molecular diagnostics using PCR demonstrates and confirms the existence of pathogenic germs in the reckettsiales Bouzeguène region.

Mots clés: Inventaire; Tiques; Bovins; Indices parasitaires; Agent pathogène; *Rickettsia* sp.; Région de Bouzeguene.

*Speaker

Intraspecific interference does not reduce weed seed consumption in two carabid species.

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In arable systems, weeds remain one of the most challenging management issues. The depletion of weed seeds by seed consumers could impact the dynamics of weeds. Carabid beetles are the most important seed consumers in temperate regions, but predicting weed seed depletion rates in field conditions remains difficult as carabid trophic interactions are still not clearly understood. The role of competition between conspecific carabids on weed seed predation, in particular, is poorly documented.

In this study, we tested for potential effects of intraspecific interference competition on seed consumption for two carabid species *Poecilus cupreus* and *Harpalus affinis* and weed species, *Taraxacum officinale* and *Viola arvensis*. For each pair of carabid and weed species, we assessed total and per capita seed consumption in laboratory microcosms, in four experimental combinations of low and high densities of carabids and weed seeds.

The objectives of the study were to test: i) whether seed predation by carabids was affected by the density of conspecifics; ii) whether seed availability affected seed consumption; and, iii) the effect of any interaction between seed and carabid density on seed predation.

Our results show that the co-occurrence of conspecifics has an impact on total seed consumption, but no effect on per capita consumption. Positive density-dependent effects on the consumption of preferred seeds, which are observed without competition, disappear when interference between conspecifics occurs. This might suggest that, under field conditions of high conspecific interference, total weed seed consumption is generally additive with increasing conspecific number.

Keywords: Predation, Weed control, density dependence, intraspecific interference competition, *Poecilus cupreus*, *Harpalus affinis*, *Viola arvensis*; *Taraxacum officinale*

*Speaker

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An empirical Niche model-based approach to identify the structure of complex foodwebs and assess species invasiveness

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In lakes, the benthic foodweb is expected to exhibit a more complex topology than the pelagic one leading to a structural asymmetry supposed to enhance dynamic stability in non-equilibrium context. Characterizing trophic interactions is notoriously challenging due to practical constraints and limited taxonomic resolution often dampening our ability to fully appreciate foodweb complexity. The consideration of body size as predictor of trophic interaction is the basis of the Niche model and can help to circumvent field limitations to estimate predator-prey interactions. I compiled exhaustive species inventories in two large French lakes (Lakes Bourget and Annecy) and fitted empirical Niche models using species body size. Several refinements such as weighting of trophic links and the consideration of a vulnerability trait allowed establishing realistic foodwebs comprising 474 and 388 species and 28016 and 24215 trophic links for Lake Bourget and Annecy respectively. For the two lakes, directed connectance and linkage density were higher for the benthic than for the pelagic subfoodwebs supporting structural asymmetry. The empirical calibration of the Niche model further allows predictions of benthic and pelagic vulnerability to invasive species. These results highlight the fruitful convergence between field and theoretical approaches to embrace lake ecological complexity and develop methodological frameworks to support their conservation.

*Speaker

fluxweb: a package to easily estimate energy fluxes in food webs

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We present the R package 'fluxweb', allowing to easily calculate trophic fluxes in food webs. By integrating the metabolic theory (Brown et al. 2004) with the food webs energetics approach (Hunt et al. 1987), fluxes can now be estimated using widely available information such as population biomass, individual body mass and network topology. We will illustrate the method with a step by step example, starting from data collection and ending with a quantitative network of interspecific energy fluxes. Thereafter, we will show how these fluxes can be used to estimate ecosystem functions and to assess mechanisms of biodiversity - ecosystem functioning relationships in multitrophic communities.

*Speaker

From coexistence to water competition between two native species in an environment of high rainfall: a study case on Trindade Island.

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Habitats are spatially and temporally heterogeneous in respect to resources available for plants. And species differ in their responses to this heterogeneity. In periods or areas of resource scarcity, more tolerant species may become more abundant, suppressing and/or excluding others with which they previously coexisted. Volcanic islands, for example, frequently consist of several habitats within a small area, an opportunity to verify the interaction between species under different microclimatic regimes. On Trindade Island, a Brazilian volcanic island subjected to a tropical oceanic climate, differences in the interactions between two native species, *Guilandina bonduc* and *Cyperus atlanticus*, were observed. In some, apparently wet areas the species coexist and in others, drier areas *G. bonduc* suppresses *C. atlanticus*. So, the aim of this study was to analyze factors that may influence the interaction between these two species in different areas of the island. Water potential, temperature and nutrients of the soil, leaf water potential, specific leaf area and root distribution of both species, and recolonization potential of *C. atlanticus* were investigated. We found that in areas with greater water availability and milder temperatures the two species coexist, but in areas subjected to more intense water deficit *G. bonduc* suppressed and displaced *C. atlanticus*. All the analyzed sites have large amounts of macro and micro nutrients. The presence of *G. bonduc* decreases the leaf water potential of *C. atlanticus*. The experimental removal of *G. bonduc* stands allowed the Cyperaceae to recolonize, even under the most restrictive conditions. Thus, in environments with favorable conditions, especially with respect to water availability, the two species coexist. As resources become more limiting the interaction becomes competitive, *G. bonduc* suppresses populations of *C. atlanticus*. Trindade Island is a small scale experimental model for the study of species interactions than can be widely studied in response to resource levels.

*Speaker

Pine seedling survival results from direct and indirect biotic interactions mediated by shrubs.

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Mortality in early stages of seedling establishment is crucial for natural regeneration of forest and can be influenced by many biotic and abiotic factors, which can vary from year to year.

In this study, we investigated the impact of drought and plant-plant-herbivore interactions on maritime pine seedlings survival in coastal dune forests over 2 cohorts and 2 years.

We established a trial where we transplanted seedlings two successive years (288 in April 2015 and 288 in April 2016) according to three nested factors: topography (bottom, mid and top position), herbivory (fenced/not fenced areas) and shrub (with or without, *Arbutus unedo*). Seedling survival and causes of mortality were monitored monthly for two years until April 2017.

Overall, we found that shrubs were the main factor influencing seedling survival, while topography had no effect. In detail, high year-to-year variation in both number and causes of death was observed the year after planting: 50% of seedlings planted in 2015 died from 3 different causes (respectively 22%, 18% and 10% of seedlings died because of drought, rodents and large mammals herbivory), whereas 90% of the seedlings planted in 2016 died, only from drought. Predation by rodents increased when seedlings were associated to shrubs, while the opposite pattern was observed for predation by large mammals (only in not fenced areas). Shrubs facilitated seedling resistance to drought in the early summer for both years, but this effect collapses or reverses when drought continues.

These results show that the intensity of summer drought and both direct (facilitation and competition) and indirect (associational susceptibility or resistance) biotic interactions with shrubs strongly impacted pine seedling survival. This illustrates the complexity of interactions influencing early survival, with contrasting effects varying within one year and from one year to the next.

*Speaker

Arbuscular mycorrhizal fungi cooperator behavior generates plastic responses on *G. hederacea* functional traits

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Due to their sessile lifestyle, plants have to efficiently face and buffer environmental changes to survive and reproduce. Phenotypic plasticity promotes rapid adjustment to biotic and abiotic conditions. Indeed, plant can plastically adjust their phenotype to promote resource foraging. It has recently been shown that symbiotic microorganisms can modify their host-plant phenotypes. Among the plant symbiotic microorganisms, Arbuscular Mycorrhizal Fungi (AMF) are known to play a major role in the plant mineral nutrition (i.e. P, N and trace elements exchanged for photosynthesized C). Depending on their evolutionary trajectory and evolutionary constraints, AMF can be either mutualists (i.e. good cooperators) and bad cooperators. Depending on the cooperation behavior of AMF, we thus hypothesized changes in the plant phenotype and fitness. We grown *Glechoma hederacea* in controlled conditions, inoculated with 9 different isolates (i.e. 10 treatments) and used 10 individuals (5 genotypes x 2 replicates) per treatment. The experiment was done in controlled conditions during fifty days.

We demonstrated contrasted effects of AMF isolates on plant performance and functional traits, compared to control plants. The *Rhizophagus invermaium* isolate promoted the highest performance through a higher biomass and ramet number whereas *R. irregulare* and *Diversispora celata* isolates lead to the lowest one. AMF isolates did not impact architectural traits whereas it did on allocation traits. *R. invermaium* generated the highest allocation to dispersal unit (biomass of stolon / total biomass). In addition, *R. irregulare* promoted the highest phosphorus quantity captive in plant roots, which limit the phosphorus plant nutrition.

This work confirmed that AMF are not necessarily mutualists but evolved in a continuum from mutualism to parasitism. Their interactions with plants impacted *G. hederacea* clonal strategy, acting on space colonization and their fitness. One major perspective of this work is to analyze whether these impacts can be modulated by their transmission along the clonal network.

*Speaker

Differential phenotypic selection on floral odours in three orchid taxa growing in distinct environments

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How variations in the selection exerted by pollinators on floral traits can contribute to taxonomic and floral diversification is an important question in evolutionary biology. Variations in floral traits between conspecific populations are often interpreted as local adaptations to geographically structured pollinator communities, but only a handful of studies have pointed out the very process that may have generated such a pattern, by quantifying the selection exerted on these traits in the field. In addition, few of these studies have focused on floral odours, despite the well-known implication of olfactory signals in pollinator attraction. Pollinators could select for the most scented individuals, but they could also drive chemical divergence between conspecific populations, as different insect guilds may select for distinct blends of floral compounds. In this study, we focused on three closely related orchid taxa, *Anacamptis coriophora*, *A. fragrans* and *A. coriophora* var. *martrinii*, which grow in different environments and are pollinated by distinct insect guilds. We first investigated differentiation in terms of floral odours between these three taxa, and we then quantified the selection exerted on these odours in seven populations. We found that the three studied taxa were characterized by distinct floral scents, with two dominant compounds per taxon, one common to these three taxa and one taxon-specific. In addition, we found a significant selection on relative amounts of 1,4-Dimethoxybenzene in two *A. coriophora* populations and of p-Anisaldehyde in one *A. fragrans* population. Our study is one of the first to document variations in the selection exerted on floral odours between closely related orchid taxa. Our results suggest that pollinator-mediated selection may have contributed to chemical divergence between *A. coriophora* and *A. fragrans*.

*Speaker

*Speaker

Importance of mating system and pollinator activity in the conservation of an endangered plant species (*Astragalus tragacantha*, Fabaceae)

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The increase of habitat fragmentation impacts plant-pollinator interactions threatening the sustainability of many plant species. *Astragalus tragacantha* (Fabaceae) is an endangered plant species present along fragmented coastal habitats mostly in the Calanques National Park (Marseille, France). Populations of *A. tragacantha* face a regressive demographic dynamic. To explore the causes of this regression we realized here controlled pollination treatments, observation of pollinator activity and pollinator captures in six populations of *A. tragacantha* to study (1) the existence of an inbreeding and/or outbreeding depression, (2) its different pollination strategies and, (3) the role of pollinators in its reproductive success.

We showed that *A. tragacantha* is not self-spontaneous but completely reliant on pollinators for its reproduction. Pollinator abundance (but not the richness) positively influenced the seed production. Three populations were currently mostly linked to a single pollinating species i.e., *Bombus terrestris*, *Eucera caspica*, and *Anthophora plumipes* respectively. This triggered differences in reproductive strategy (outcrossing vs. selfing) due to the different foraging behavior of pollinators. Particularly, *Bombus terrestris* practiced a dominant facilitated-selfing behavior leading to an increased inbreeding depression. Furthermore, nearly all populations showed a better performance for between-population crossings comparatively to within-population crossings i.e., outbreeding depression. All these processes illustrate an increased population isolation of *A. tragacantha* along its fragmented coastal habitats. This could accentuate their regressive demographic dynamic and more and more reduce their sustainability.

This raises the question of the management of its populations for the actual restoration procedures in the Calanques National Park. It notably implies that the contrasted plant-pollinator interactions and mating systems have to be taken into account to enhance the reproductive success and the sustainability of *A. tragacantha* populations.

*Speaker

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**PARASITIC STUDY OF THE CATTLE
EGRET *Bubulcus ibis* (Linnaeus, 1758),
(CICONIIFORMES: ARDEIDAE) IN
NORTHEASTERN ALGERIA**

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This work was carried out for the first time in Algeria to make an inventory and a monitoring of the parasites found in *Bubulcus ibis* (Linnaeus, 1758), bird belonging to the Ardeidae family. It was conducted during the year 2015- 2016, in the wetland complex of the National Park of El Kala (PNEK 36 ° 51 'N-8 ° 30' E). The study area is one of the richest and most diverse wetlands in Algeria. We were interested to study the endoparasites and also ectoparasites communities of this specimen. We have resulted in the identification of a very wide range of endoparasites with the most abundant were coccidia followed by nematodes and trematodes. All individuals were infested with a large number of parasites. However the collection of ectoparasites allowed us to identify some mites and lice found on the bodies of our studied subject. This study provided us with important data that can be used for the implementation of action plans aimed at the safeguarding, protection and conservation of this species of bird not only in the El Kala region but also in north Africa. Key words: Ardeidae, *Bubulcus ibis*, endoparasites, ectoparasites, PNEK.

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Is the mycorrhizal fungi distribution limiting the orchid establishment in restored meadows?

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In the Czech Republic, vast areas of former species-rich grasslands converted into arable land are undergoing restoration using seeding of regional plant species and regular mowing. Recovery of species with complicated life cycles, such as orchids, is particularly slow though the seed source populations grow in close vicinity. Orchids are obligately mycorrhizal plants which need mycorrhizal fungi (mainly saprotrophic fungi from Tulasnellaceae, Ceratobasidiaceae or Serendipitaceae) for germination. We focused on seven both rare and common orchid species and investigated (i) in situ germination and (ii) in vitro germination and specificity. Only two rather common orchid species (*Neottia ovata* and *Gymnadenia conopsea*) germinated in the restored grasslands while others germinated only in undisturbed natural grasslands with established orchid populations. *Gymnadenia conopsea* showed also lowest specificity to mycorrhizal fungi during in vitro germination. Thus, diversity of orchid mycorrhizal fungi in restored habitats may be one of the factors limiting the establishment of some orchid species. The slow restoration of orchid species due to absence of appropriate fungi could be potentially overwhelmed by targeted introduction of fungi and substrate amelioration of restored sites.

*Speaker

Modelling and predicting the dynamics of trophic networks; peri-urban agroecosystems as a case study

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The main objectives of this project are (i) to model predator-prey relationships in peri-urban agroecosystems containing two predators and four prey compartments and to evaluate their consequences on the dynamics of the different trophic network compartments, and (ii) to predict the possible trajectories of the system in response to anthropogenic perturbations.

We aim at developing deterministic and stochastic trophic network models, fitting its parameters and initial data with our field data (prey and predator densities, predation rates), and global databases (intrinsic parameters).

First, we constructed a deterministic model, inspired by a predation competition Lotka-Volterra model, composed of discrete time equations to account for species biological cycles, seasonal variations of prey and predator densities and their trophic relationships. This model includes an intra-population term, describing the dynamics of the studied populations, and an inter-population term, describing the gain or loss of biomass of each population due to their trophic interactions.

Second, we introduced intrinsic and/or extrinsic sources of stochasticity to the system, such as demographic hazards (intra-population term), changes in predation rates or prey preferences (inter-population term) or environmental changes (external factors), that directly affect predator and prey population dynamics. It will allow us to estimate the relative impacts of each source of stochasticity on the network structure and targeted population dynamics.

Finally, we will make the structure of the model more sophisticated to account for possible inter-individual trophic differences in predator populations (sub-populations of generalist and specialised individuals). Our ultimate goal is to construct and validate the most pertinent models to (i) better understand and predict the trajectories of the studied system (e.g. predators' impact on prey dynamics, cascading effects), (ii) predict the possible outcomes of different anthropic pressure scenarii (e.g. human practices influencing predator population dynamics) and (iii) provide guidelines to stakeholders to maintain peri-urban biodiversity and ecosystem services.

Ecophysiology

Comparative study of the resilience capacity of different populations of *Alphitobius diaperinus* exposed to different durations of thermal stress

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As extreme temperature events are expected to occur more frequently in the future, knowing more about insects' ability to cope with - and recover from - exposures to such conditions is important for improving our understanding of the effects of these environmental changes on insects. Insect pests, including the tenebrionid beetle *Alphitobius diaperinus* can cause sanitary and economic issues. Because pesticide treatments are frequently sprayed in areas where *A. diaperinus* pullulates, pesticide resistant populations have been reported. The periodic treatments also means that the quantity of insecticides in their habitats vary over time. By using three populations sampled from different localities (two were sampled from poultry houses, and one obtained from a mass-rearing under control conditions), we compared the recovery time after the beetles were exposed to extreme temperatures. We were interested in determining if the recovery time could vary according to the sampling origin of the insects, i.e. we hypothesised that insects from the poultry houses would have better abilities to cope with environmental stressors as compared with those from the mass-rearing maintained in constant optimal conditions. The insects were exposed to either 0.25, 0.5, 1, 2, 3 or 4 hours of extreme cold conditions (-6 °C) or 0.25, 0.5, 1, 2, 3 or 4 hours of extreme heat conditions (42.5 and 43 °C). Then, the time to recovery (full movements restored) of each individual was measured over 2 hours after the thermal treatment was stopped. This analysis can provide an insight into insects' ability to cope with extreme temperature events, and how the responses of the insects could vary if they are thriving in constantly optimal habitats as compared with more variable ones.

*Speaker

Belowground interaction between plants does include exchange of nutrients

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Two distinct mechanisms of plants competition have been classically distinguished, competition due to exploitation, and competition due to interference. However recent literature suggests that interactions between plants are much more complex and include exchange of information, molecule and resources, through the mechanism of rhizodeposition.

We tested the hypothesis that competition between oak seedlings (*Quercus petraea*) and a common grass (*Molinia caerulea*) during forest natural regeneration does include a competition by exploitation of nitrogen (N) resources but also exchange of N between both species to the benefit of the grass.

Both species were cultivated together in pots, either directly in contact or separated by a membrane with different pore sizes, so that roots of both species can cross the membrane, or only hyphae of mycorrhiza, or only molecules. Oak seedlings were on a drip with a ¹⁵N enriched solution of urea (cotton-wick technique) at the beginning of the growing season. Oak, grass, and soil were harvested 2, 4, 6, and 10 months after start of labelling. Samples were analysed for N content and ¹⁵N excess.

The presence of grass reduced oak growth and the presence of oak favoured the grass growth. ¹⁵N was found in all oak organs, but also in the soil and grass organs. ¹⁵N was found in all grasses, meaning that ¹⁵N circulated in both sides of the membrane without any root contact, yet chemical forms of N has not been identified.

Those results suggest that beyond the exploitation of N by the grass to the detriment of oak, grass also benefited from a release of N by oak. The underlying mechanisms are not fully understood but they emphasize the important role of rhizodeposition, mycorrhizas, and microorganisms. They also suggest that exchange of nutrients, other molecules and information are much more common than suspected in belowground plant interactions.

*Speaker

What determines the interannual variability of fecundity in holm oak (*Quercus ilex*L.)?

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The physiological mechanisms that determine the reproductive success in forest trees -in particular in mast seeding species- and how they are regulated by environmental conditions remain poorly understood. Despite the many correlative studies that investigated the link between masting and meteorological conditions, no environmental factor has been clearly identified so far as a reliable predictor of massive fruit production, both across and within species. In oaks as in other genera, three steps of the reproduction seem particularly key for determining the number of mature acorns produced at the end of the season depending on studies: the number of female flowers, the initial fruit set (number of acorn initiated after pollination among female flowers), and acorn development. We expect that these two steps might be affected differently by the environmental conditions between temperate and Mediterranean oaks, with summer water deficit affecting more strongly fruit growth and ripening in Mediterranean oaks and temperature affecting more strongly flowering and fruit set in temperate oaks. In this poster, we present the results of a study, which aimed at investigating the relationships between environmental factors, growth, and fecundity in *Quercus ilex*, a very widespread Mediterranean tree. We used the data collected in the long-term experimental site of Puéchabon (Hérault, France), where a rainfall exclusion experiment combined with a thinning experiment generates four levels of water stress since 2003. Acorn biomass has been related to male flowers biomass, temperature, water availability, leaf water potential, flowering date, primary and secondary growth, and net primary production.

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Respirometry of ground beetles according to increasing weights

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Functional connectivity within agricultural landscapes can be evaluated directly by measuring the movement of model species, associated for instance with their functional traits, habitat preferences, etc. These data can be used to assess the quality of different habitats, as well as their resistance or permeability to movement, which can be represented on a landscape map. It can constitute important decision-making tools for conservation or restoration of ecological continuities. Research on monitoring the movement of insects in the field is booming since the miniaturization of active tracking systems. Numerous insects can now be investigated including ground beetles (Coleoptera: Carabidae), important biocontrol agents in agroecosystems. However, the weight of transmitters is still high compared to that of studied insects and can in some cases represent up to 100% of their weight, while it is considered that it should not exceed 10% of the weight of vertebrates (Kissling, 2014). The cost of such excessive weight on the metabolism of insects is largely unknown, and may induce bias in monitoring insect movements by means of active tracking systems (Kissling, 2014). In order to evaluate this impact, we studied respiration, as a proxy of their metabolism, and survival of ground beetles depending on the load carried by individuals. Our aim is to compare the impact of a range of weights, from no load to a load of 200% of individual's weight on two ground beetle species of small and medium size (*Anchomenus dorsalis* and *Poecilus cupreus*, respectively). The respiration experiment (instantaneous CO₂ production, frequency and duration of respiration phases) was done with a LI-COR 6400. In parallel, we monitored activity and survival over 10 days of individuals.

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Changes in accumulation of essential macronutrients during vegetative growth of rapeseed exposed to NaCl

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Stress caused by increased salt concentrations affects plant metabolism and the final outcome of plant production in many ways. The excess of salts has an osmotic effect, thus reducing the amount of water which plants can take up by their root system. Increased salt concentrations may lead to disorders in the mineral nutrition of plants.

To assess the extent to which the steady presence of sodium chloride in relatively low concentrations (0.1- 1.2 g NaCl L⁻¹) affects plants, an experiment was set with rapeseed (*Brassica napus* L, Brassicaceae), in semi-controlled conditions of a greenhouse. Plants were grown in water cultures, on strength Hoagland nutrient solution, to which NaCl was added 2 weeks after planting. Plant growth and accumulation of N, P, K, Ca and Na and their distribution between leaves, stems and roots were analyzed 1 and 2 months following the beginning of the treatment. Concentration of Na increased in all plant organs over the time, and it was related to its concentration in the nutrient solution. Potassium concentration declined in stems and roots after one months; this decrease was more pronounced over time and with the increase in NaCl concentration in the nutrient solution. Concentration of P declined significantly in roots in the presence of

1.2 g NaCl L⁻¹. Calcium concentration declined in the presence of NaCl over time in all tissues. Concentration of N slightly increased in leaves during the first month, but its concentration declined in all tissues after two months, with respect to the control. Overall, NaCl affected to a higher extent concentrations of K and Ca than N and P. Even though applied concentrations of NaCl were relative low, they induced significant changes in accumulation and distribution of examined elements.

*Speaker

Morphological responses of the invasive species *Elodea canadensis* and *Elodea nuttallii* under salt pulses.

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Salinization of freshwaters is of great ecological concerns, which is further intensified by changing climatic conditions and anthropogenic activities. In general, freshwater biota do not extend into saline or slightly saline water and most freshwater plants do not tolerate increasing salt concentration. The success of the invasion in inland waters will depend on the functional traits of the invasive macrophyte species (i.e. tolerance vs resistance to salt) and the habitat characteristics (salt level). Fluctuations in salt concentrations may affect the aquatic organisms in addition to high concentration because of difficulties in regulation of osmotic balance. Here, we determined the response (mortality rate, apical and lateral growth, production of roots) and the level of tolerance of two invasive macrophytes (*Elodea canadensis* and *Elodea nuttallii*) to salt pulses in spring via a laboratory experiment and their transplantation in a naturally salty river. Our main results showed that plant tolerance was higher when the plant was exposed to three salt pulses than one concentration and depended on species identity. In laboratory, we showed after a salt pulse exposure, a root inhibition (number and length) for *E. canadensis* at the salt concentration of 5 g.L⁻¹, whereas at a salt concentration of 1 g.L⁻¹ the number of roots of *E. nuttallii* increased and its root length was stimulated. In the field experiment, a higher mortality rate of the shoots was observed at 1 g.L⁻¹ than at 3 g.L⁻¹ of salt, as well as a root production inhibition. The influence of several abiotic factors (e.g. water temperature, velocity, and nutrient content) could explain the lowest performance of *E. canadensis* and of *E. nuttallii* in the field transplantation. It is difficult to determine the exact salt concentration that is toxic to a plant, due to the interactive effect of all of these environmental factors with salt pulses.

*Speaker

Posters

Ecotoxicology and Environmental
Pollution

Can SSD models help assessing interspecific competition impact on organisms' tolerance against chemical stress?

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Organisms are not alone in the environment. They interact with other individuals of same or other species in different ways. Interspecific competition is an important interaction for herbaceous plants in grass strips. Such vegetated areas generally act as buffer strips against pollutant flows and are thus submitted to various chemical exposures. However, competition is rarely considered in environmental risk assessment. To address this point, we tested whether competition modifies the way plants respond to herbicide (isoproturon) toxicity in an attempt to link individual tolerance of organisms and community dynamic. Then we investigated the impact of competition on species sensitivity distribution (SSD), a widely used community-level risk assessment tool that usually considers monospecific bioassays only.

To do so, we exposed during 25 days 6 herbaceous species (representing varied isoproturon tolerance and competition ability) to 6 isoproturon concentrations (0 to 1.75 μ M) in presence and absence of a selected competitor, *Bromus erectus* (choice based on its high resistance to isoproturon and its high competitiveness). For each condition, 8 replicates were realized. After exposures, 10 different traits corresponding to morphological, biomass and physiological responses, representing respectively soft (easy to acquire) traits. The consequent dataset generated was used to model plant responses depending on isoproturon concentration and competitor presence/absence.

Dose-responses curves were built for each species, in presence and absence of competitor for each endpoint to define (1) their sensitivity, (2) their relevance to assess toxicity, (3) how competition modify points (1) and (2). This was done with the use of a workflow created to handle high-throughput dose-response datasets from omics experiments. We then calculated toxicity values and built SSDs with and without competitor presence in an attempt to quantify competition effects compared to competitor-free ecotoxicological data.

*Speaker

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USE OF MACROPHYTES IN THE ASSESSMENT OF LITTORAL WATER POLLUTION BY HEAVY METALS AND HYDROCARBONS - CASE OF THE GREAT BEACH

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The Mediterranean is the most polluted sea in the world by its exposure to the maritime traffic and the rejections of the various activities of the man; In Algeria the telluric contributions of pollutants are important. The coastline of Skikda is highly industrialized and receives domestic and industrial wastewater by emissaries without prior treatment.

The choice of stations is based on the proximity of potential pollution sources to allow an effective assessment of the contamination of hydrocarbons and heavy metals. The sampling of water and algae took place over a period of three months in March, April and May, 2017.

The heavy metals assay in both matrices was performed using the ICP-OES Inductively Coupled Plasma-Optical Emission Spectrometry at the THLMM laboratory. the determination of the content of hydrocarbons was made using the OCMA-350 which is based on infrared analysis.

The study of the evolution of the Ni, Zn, Cu, Pb, Cd and chromium concentrations in the water of the site helps to highlight their variability according to climatic data; Unlike Nickel, Lead, Cadmium and Chromium which have concentrations below the limit of detection over the three months of monitoring. The concentrations of Zinc and Copper are quite significant with maximum values of 4.55 µg / L (May), 1.37 µg / L (April), for algae. The highest concentrations of Zn were recorded during the month. May at *Derbesia tenuissima* with 232.6 µg / g followed by Cd with 82.68 µg / g and Cu with 31.24 µg / g, however the Ni remains below the limit of detection; The concentration of Zinc and Copper are higher than the limit concentration required by the IAEA (169µg / g for Zn and 11.1 µg / g for Cu).

Embryotoxic effects of an anxiolytic drug to a freshwater gastropod: coupling of macroscopic, transcriptomic and proteogenomic approaches

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French psychotropic drugs consumption is one of the most important in Europe. These molecules are a significant part of emerging contaminants in aquatic ecosystems. Indeed, derived from both hospital and domestic effluents, some psychotropic drugs are barely eliminated by wastewater treatment plants and can be found at significant concentrations in freshwater. Among these contaminants, oxazepam, which belongs to the benzodiazepine family molecules, acts as an inhibitor of the central nervous system by interacting with the GABA receptors. Despite its prevalence in the freshwater, the toxicity of oxazepam on aquatic organisms remains little investigated. The aim of our study is to assess the toxicity of oxazepam at environmental concentrations on the European freshwater gastropod, *Radix balthica*. We will focus on the embryogenesis, which is known to be the most sensitive stage at the environmental contamination. Therefore, we will conduct our toxicity assessment to the first stages of development of *R. balthica* at macroscopic, proteomic and transcriptomic levels on physiological key parameters. During the trochophore stage (3 days post fertilization), we will focus on embryo rotation through ciliary beating measurement, in association with gene expression study of cilia development and nervous regulation. At the hippo stage (6 dpf), shell malformations will be observed and the cardiac function will be evaluated by heart rate quantification. Simultaneously, we will analyze the expression of genes involved in nervous regulation and in heart and shell development. Finally, at the post hatching stage (8-15 dpf), developmental abnormalities, developmental delay and hatching rate will be investigated, as well as expression of genes involved in displacement, nervous system and detoxification mechanisms. Our preliminary macroscopic results tend to show that the embryonic rotation decreased while the heart rate increased when embryos were exposed to oxazepam. Previous study also revealed a decrease of hatching success on embryos exposed to oxazepam.

*Speaker

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The effect of various doses of Cd on productive features and quality of wheat

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Similarly to the other heavy metals, cadmium (Cd) is in higher concentrations toxic to all living organisms, including plants. The main path by which Cd enters food chain is by the food of plant origin. Therefore, we set experiments to examine to which extent Cd to which wheat grain was exposed during imbibition, can affect later plant growth and Cd content in harvested grain. Winter wheat grains, cultivar Pobeda, were soaked in the following concentrations of CdCl₂, dissolved in deionized water: 0 (control), 10⁻⁵, 10⁻⁴, 10⁻³ and 10⁻² M Cd, for 24 h. Thereafter, grains were briefly rinsed with deionized water and the excess of water removed by filter paper. One portion of seeds was used to assess concentration of Cd. With the increase in Cd concentration on the imbibition solution, the concentration of Cd in grains significantly increased. The other portion of imbibed grains were sown in the field on soil classified as a calcareous, gleyic chernozem in which concentration of Cd in the soil was significantly lower than the maximally allowed (2 mg kg⁻¹). The plants were grown to maturity and analysed at harvest. Plant height, number of spikes per m² and grain yield significantly declined with the increase in Cd concentration in the solution in which grains were imbibed prior to sowing. Concentration of Cd in harvested grains increased up to 40%. Concomitantly, length of spikes, number of spikelets per spike, mass of grains per spike, harvest index and mass of 1000 grains changed to a much lesser extent.

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Seasonal Morphometric Variation in Field Collected Populations of *Culex pipiens* complex

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Abstract

Species in the *Culex pipiens* complex are considered as important vectors of a number of arboviruses including Rift Valley, St. Louis Encephalitis and West Nile viruses. To reduce the impact of associated vector borne diseases, insecticides have been widely used worldwide against vector organisms. Prior studies have noted that asymmetry is predicted to increase with the levels of insecticide resistance and the rate of insecticide use. In this study our aim was to compare the levels of variation of 15 wing characters in field populations of the *Cx. pipiens* complex. For this purpose, the samples were collected at three different seasons; first before the application of insecticides in spring 2012, second after the final application of insecticides in fall of 2012 and finally in the spring of 2013 before the application of insecticides. The samples were collected from six provinces in Aegean region of Turkey which is characterized by high insecticide usage for agro-industry, public health, and the personal protection. Based on the studied wing characters our results showed the presence of variations in *Cx pipiens* complex samples at three different collection seasons which indicate that insecticide usage might have important effect on morphological variation of this complex members.

Key words: *Culex pipiens* complex, Insecticides, Ecotoxicology, Morphometry, Turkey

Acknowledgement

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Effects of Titanium Dioxide Nanoparticles on the Antioxidant System of *Galleria mellonella*

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The nanoparticles which rapidly release to the environment could cause adverse effects on living organisms. Titanium dioxide nanoparticles (TiO₂-NPs) are extensively used in a wide range of products. The physiological effects of TiO₂-NPs are still not completely understood. Hence, the influence of TiO₂-NPs should be investigated by establishing experimental model organisms. For this aim, we examined the effects of different doses of TiO₂-NPs ((100, 500, 1000, 3000 and 5000 ppm) on total protein amount, antioxidant enzyme activities and malondialdehyde (MDA) amounts in the hemolymph of the greater wax moth, *Galleria mellonella* (L.) (Lepidoptera: Pyralidae). Exposure with dietary TiO₂ NPs caused a significant increase in the total protein amount and content of MDA and glutathione S-transferase activity in the hemolymph at 100, 500 and 1000 ppm compared with control and other doses of TiO₂ NPs. While the activity of catalase increased by 1000, 3000, and 5000 ppm and superoxide dismutase activity increased at all doses of TiO₂ NPs when compared with control. Our results indicated that TiO₂ NPs have dose-dependent toxic effects on the *G. mellonella* larvae and can enhance the stress resistant capacity of insects at low concentrations.

Key words: Antioxidant enzymes, *Galleria mellonella* Model insect, Nanotoxicology, Titanium dioxide nanoparticles

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Responses of wild fish populations to multiple stressors, a multilevel approach to assess the combined effects of temperature and immune challenge

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In the context of climate change, aquatic ecosystems are exposed to multiple stressors, which can interact and have unexpected negative effects on aquatic organisms. In this study, we investigated the combined effects of temperature increase and parasitism, a biotic stress factor that has rarely been considered in previous work. Because immunity is costly, immune activation caused by parasites might affect fish physiology and interact with stress responses caused by temperature increase. Using wild gudgeon fish from contrasted sites, we tested the crossed effects of temperature and immune challenge on fish physiology and performance across levels of biological organization (e.g. cell, tissue, whole individual). We also took into account the interindividual variation of sensitivity across populations. Results show that single stressors (temperature or injection alone) had limited effects across biological levels except on activity. Interestingly, combined stressors (temperature increase and injection) increased oxidative damages, and decreased energy consumption and feeding motivation. This suggests that it is essential to take into account biotic stressors such as parasites and that multiple stressors have consistent effects on energy allocation across levels of biological organization. In addition, the two studied populations exhibited contrasted responses to stressors, suggesting that it is important to take into account interpopulation variability in sensitivity to better predict the responses of aquatic wildlife to current and future stressors.

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Modeling the direct and indirect effects of copper on phytoplankton-zooplankton interactions

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Predicting the effects of pollution on community is difficult because of the complex impacts of ecosystem dynamics. To predict the effects of copper on plant-herbivore interaction in a fresh-water ecosystem, we built a model that focuses on the interaction between an alga, *Scenedesmus* sp., and a herbivore, *Daphnia* sp. Internal copper concentrations in *Scenedesmus* and *Daphnia* are calculated using a biodynamic model. We include two types of direct effects of copper on *Scenedesmus* and *Daphnia* that results from hormesis: a deficiency effect and a toxic effect. We perform a numerical analysis to predict the combined effects of copper and nutrient enrichment on the *Scenedesmus*-*Daphnia* interaction. Results show three types of outcomes depending on copper concentration. First, Copper may lead (1) to the extinction of all populations, (2) to only the extinction of consumer population, and (3) to the survival of the two populations. Second, copper has a stabilizing effect by reducing or suppressing oscillations. Third copper opposes the destabilizing effect of nutrient enrichment. Our model shows that (1) *Daphnia* is more sensitive to copper when community interactions are taken into account than when analyzed alone and (2) counterintuitive effects may arise from the interaction between copper pollution and nutrient enrichment. Our model also suggests that single-value parameters such as NOEC and LOEC, which do not take community interactions into account to characterize pollutants effects, are unable to determine pollutant effects in complex ecosystems. More generally, our model underscores the importance of ecosystem-scale studies to predict the effects of pollutants.

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Developmental and reproductive responses of two bio-indicator freshwater species to pharmaceutical drug exposure: setting the stage for evaluating aquatic micro-pollutant environmental impact

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Face with population growth and climate change, the reduction of our accessible water resources and their quality is a considerable challenge. Despite undeniable progress over recent decades, a large number of micro-pollutants (including drugs) are ubiquitous in water at concentrations below $\mu\text{g/L}$ and may constitute a risk for water quality and aquatic environments. There are overwhelming evidences that aquatic environment is continuously the discharge of wastewater effluents where pharmaceuticals are increasingly found due to the non-specific methods of degradation at sewage treatment plant level. In this context, it is of prime interest to evaluate the eco-toxicological impact of drugs on the aquatic ecosystems. For this purpose, we analysed the presence of various drugs within representative waters of both treatment effluents of psychiatric hospital (Montpon-M'énestrol, Dordogne, France) and urban wastewaters (Albi, Tarn, France). Two points were sampled per site, at the direct station exit and in the receiving waterway rejection. Based on the quantification of these four natural wastewaters, an anti-epileptic drug (carbamazepine) and two other major pharmaceuticals were chosen. Toxic effects of each drug and their synergic effects in association with carbamazepine were tested at three different concentrations on two non-models species commonly found in French rivers: the flatworm *Schmidtea polychroa* and the freshwater gastropod *Radix balthica*. Toxicological impacts of these pharmaceuticals have been performed on exposed adult flatworms (fertility and fecundity) and embryos offspring snails (malformation and delayed hatching). Previous studies conducted in the lab on the psychotropic drug carbamazepine have already highlighted a developmental delay in *R. balthica* (> 8 days). Contrastingly, while the cocoon production by planarian (fecundity) significantly decreased, the number of juveniles per cocoons (fertility) remained stable. This present work will help further investigations and provide a better understanding to the toxic effect of pharmaceuticals on aquatic environment.

Posters

Environmental Genomics

Evolutionary dynamics of repeated sequences in polyploid *Spartina* species

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Activity of repeated sequences and whole genome duplication (polyploidy) are two main processes involved in eukaryote genome dynamics. Transposable element bursts or loss and polyploidy (whole genome duplication) have resulted in a large genome size range across species (e.g. from 60Mb to 152.000Mb in Angiosperms). The *Spartina* genus (Poaceae, Chloridoideae) is known for its well-documented events of reticulate evolution (resulting from interspecific hybridization) and recurrent polyploidy. This genus evolved through two main lineages, a tetraploid clade ($2n=4x=40$; $1C=1.8-2.2Gb$) and a hexaploid clade ($2n=6x=60,62$; $1C=0.71-0.98Gb$) which diverged 6-10my ago. More recent hybridization and polyploidization events within and between these lineages led to additional ploidy levels (7x, 8x, 9x, 12x). The aim of our work is to explore the *Spartina* repeated compartment in the context of polyploid diversification, using multiple genomic and transcriptomic datasets from various tetraploid and hexaploid species. Diversity of repeats were in silico analyzed by detecting repeated sequences from Illumina reads (using a graph-based clustering method) and by annotating the assembled sequences produced by clustering. The study of particular Copia and Gypsy retrotransposons (major proportion of the repetitive component in *Spartina* genome (75%)) showed an accumulation or loss of copies which could explain the size variation among species of same ploidy level (i.e. within the tetraploid and the hexaploid clades respectively). Interestingly, the expansion of a particular satellite repeat (on telomeric chromosomal positions as evidenced by FISH) appears to have accompanied divergence between two sister hexaploid species, *S. alterniflora* (where it represents up to 6.5% of the genome) and *S. maritima* (0,14 % of the genome) that differentiated 2-4 my ago on the European and American Atlantic coasts respectively. The identified TEs are used for small-RNA annotations and to analyze siRNA expression in the context of recent hybridization and allopolyploid speciation events.

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Differential gene expression revealed with RNA-Seq and parallel genotype selection of the Ornithine Decarboxylase gene in fish inhabiting polluted areas

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How organisms adapt to unfavorable environmental conditions by means of plasticity or selection of favorable genetic variants is a central issue in evolutionary biology. In the Maipo River basin the fish *Basilichthys microlepidotus* inhabits polluted and non-polluted areas. Previous studies suggested that directional selection drives genomic divergence between these areas in 4% of Amplified Fragment Length Polymorphism (AFLP) loci, but the underlying genes and functions remain unknown. We hypothesized that *B. microlepidotus* in this basin has plastic and/or genetic responses to these conditions. Using RNA-Seq, we identify genes with differential expression for individuals from two polluted sites compared with fish inhabiting non-polluted sites. In one polluted site, the main upregulated genes were related to cellular proliferation, suppression and progression of tumors, while biological processes and molecular functions involved in apoptotic processes were overrepresented in the upregulated genes of the second polluted site. The ornithine decarboxylase gene (related to tumor promotion and progression) was sequenced and a parallel pattern of heterozygote deficit and an increase of the same homozygote genotype in both polluted sites compared with fish inhabiting the non-polluted sites was detected. These results suggested both plastic response in gene expression and an interplay of phenotypic change and genotypic selection in face of anthropogenic pollution.

*Speaker

Environmental Health

The Anacardiaceae family medicinal interest theoretical study

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Traditionally, medicinal plants have been used to prevent or cure various diseases, and most of the current medicines have a natural origin.

Research on natural substances has been a buoyant theme for a number of years and pharmaceutical laboratories, always in search of new active compounds, are turning more and more towards the molecules identification and characterization from natural matrices, and inspire their molecular structure to develop new drugs.

The medicinal plant actives principles are the components naturally present in this plant; they give it its therapeutic activity.

The Mediterranean basin, have significant natural wealth with a proven floristic diversity. The Tlemcen vegetation is a good example of the study vegetal diversity and especially an interesting synthesis of the ecosystems natural dynamics, from the littoral to the steppes.

The *Anacardiaceae* family has about 800 tropical and subtropical species, with some representatives the around Mediterranean.

Most plants in this family are safe (non-toxic plant). They even have many interesting medicinal properties.

Our work consists to the *Anacardiaceae* family medicinal interest study by molecular modeling methods.

Keywords: *Anacardiaceae*, Molecular modeling, medicinal interest.

*Speaker

Study of *Vibrio tapetis*' type IV secretion system by mutagenesis approach: the case of Brown Ring Disease (BRD) affecting the Manila Clam *Ruditapes philippinarum*

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Type IV secretion systems (T4SS) have first been describe in the plant pathogen *Agrobacterium tumefaciens*. They are well known to be responsible of pathogenicity in multiple infections as Brucellosis (*Brucella spp.*) or Legionnaires' disease (*Legionella pneumophila*). T4SS can deliver proteins directly into host cells to cause infection. In the case of BRD, Dias et al. (2018) recently highlighted that the gramm negative bacteria *Vibrio tapetis* play an essential role in aquisition of pathogenic power of this bacteria throught evolution. We choose to focus on the T4SS' protein VirB4 by an approach of gene deletion to confirm the role of this protein in pathogenicity of *Vibrio tapetis*.

We succeed to construct a *Vibrio tapetis* lacking protein VirB4 and have shown that VirB4 mutant displays an important loss of cytotoxic activity *in vitro* and then that T4SS plays an essential role in pathogenic power of the bacteria.

Dias, Graciela M., Adeline Bidault, Patrick Le Chevalier, Gwenaëlle Choquet, Clio Der Sarkissian, Ludovic Orlando, Claudine Medigue, Valerie Barbe, Sophie Mangenot, and Cristiane C. Thompson. 2018. *Vibrio tapetis* Displays an Original Type IV Secretion System in Strains Pathogenic to Manila Clam. *Frontiers in Microbiology* 9: 227.

Posters

Epigenetics, Phenotypic Plasticity and Physiological Ecology

Cardiac activity, filtration and respiration rates as non-invasive physiological indicators of the oyster (*Crassostrea gigas*) susceptibility during a disease event

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Recent studies on mortality outbreaks of juvenile oysters (< 1-yr old) *Crassostrea gigas* have focused on the causative agents (and on their pathogenicity), *i.e.* the herpes virus OsHV-1 μ Var and *Vibrio* spp., as well as on the factors that influence the disease transmission. But physiological changes of the host during infection remain poorly documented. Here we propose to study the eco-physiology of *C. gigas* during a dual laboratory and field infection method in order to provide non-invasive indicators of the health status of oysters.

Filtration, respiration, and cardiac activity of oyster juveniles were monitored at the individual scale over three successive phases, *i.e.* before (6 days), during (8 days) and after (13 days) a disease event. Cardiac activity, filtration and respiration were found to be affected by the disease transmission. The cardiac activity and filtration of oysters appeared to be relevant clinical signs of the host susceptibility to disease agents. Before infection, cardiac activity differed among individuals that later died compared individuals that survived. During infection, oysters stopped to feed for 40 hours at least. After infection, filtration and respiration of the survivors were back to values that did not differ than before infection, suggesting that the animals had likely recovered. But their cardiac activity was still lower than before infection, indicating that the full recovery of survivors was not reached.

Monitoring cardiac and filtration activities on sentinel animals (in the lab and field) could provide precursory information on disease events and may be very helpful to better understand the interactions between the host and its pathogens.

*Speaker

Comparative study of the resilience capacity of different populations of *Alphitobius diaperinus* exposed to different durations of thermal stress

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As extreme temperature events are expected to occur more frequently in the future, knowing more about insects' ability to cope with - and recover from - exposures to such conditions is important for improving our understanding of the effects of these environmental changes on insects. Insect pests, including the tenebrionid beetle *Alphitobius diaperinus*, can cause sanitary and economic issues. Because pesticide treatments are frequently sprayed in areas where *A. diaperinus* pullulates, pesticide resistant populations have been reported. The periodic treatments also means that the quantity of insecticides in their habitats vary over time. By using three populations sampled from different localities (two were sampled from poultry houses, and one obtained from a mass-rearing under control conditions), we compared the recovery time after the beetles were exposed to extreme temperatures. We were interested in determining if the recovery time could vary according to the sampling origin of the insects, i.e. we hypothesised that insects from the poultry houses would have better abilities to cope with environmental stressors as compared with those from the mass-rearing maintained in constant optimal conditions. The insects were exposed to either 0.25, 0.5, 1, 2, 3 or 4 hours of extreme cold conditions (-6 C) or 0.25, 0.5, 1, 2, 3 or 4 hours of extreme heat conditions (42.5 and 43 C). Then, the time to recovery (full movements restored) of each individual was measured over 2 hours after the thermal treatment was stopped. This analysis can provide an insight into insects' ability to cope with extreme temperature events, and how the responses of the insects could vary if they are thriving in constantly optimal habitats as compared with more variable ones.

*Speaker

How migration ecology may influence hormonal status in birds ?

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Fusani and Gwinner (2005) reviewed a serie of experiments, attesting a lower nocturnal melatonin concentration in migrating warblers, diurnal birds which show a reversal in activity pattern, and thus migrate during nighttime. A possible explanation for these lower melatonin levels would be a permissive effect to increase restlessness over night. Indeed, a recently discovered neurosteroid, called 7alpha-hydroxypregnenolone, was found to increase activity rate as well as being regulated with melatonin levels. It is currently assumed that 7alpha-hydroxypregnenolone synthesis is inhibited with melatonin in diurnal animals – leading to low activity during the night

–, whereas it is stimulated with melatonin in nocturnal ones. If this model actually fits with observations in diurnal birds migrating nocturnally, this could not explain the case of strictly nocturnal migrating birds. We investigated cerebral melatonin and 7alpha-hydroxypregnenolone concentrations in two nocturnal duck species through winter : the Eurasian teal (*Anas crecca*) and the mallard (*Anas platyrhynchos*), which migrates over respectively long and short distances. We attested a decrease in melatonin concentration, associated with higher levels in neurosteroid in teals during migration, whereas no significant evolution is observed in mallards. These observations may help to better understand the hormonal control of migration, and the evolution in melatonin and 7alpha-hydroxypregnenolone interaction.

*Speaker

What determines the interannual variability of fecundity in holm oak (*Quercus ilex* L.)?

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The physiological mechanisms that determine the reproductive success in forest trees -in particular in mast seeding species- and how they are regulated by environmental conditions remain poorly understood. Despite the many correlative studies that investigated the link between mast seeding and meteorological conditions, no environmental factor has been clearly identified so far as a reliable predictor of massive fruit production, both across and within species. In oaks as in other genera, three steps of the reproduction seem particularly key for determining the number of mature acorns produced at the end of the season depending on studies: the number of female flowers, the initial fruit set (number of acorn initiated after pollination among female flowers), and acorn development. We expect that these two steps might be affected differently by the environmental conditions between temperate and Mediterranean oaks, with summer water deficit affecting more strongly fruit growth and ripening in Mediterranean oaks and temperature affecting more strongly flowering and fruit set in temperate oaks. In this poster, we present the results of a study, which aimed at investigating the relationships between environmental factors, growth, and fecundity in *Quercus ilex* a very widespread Mediterranean tree. We used the data collected in the longterm experimental site of Puéchabon (Hérault, France), where a rainfall exclusion experiment combined with a thinning experiment generates four levels of water stress since 2003. Acorn biomass has been related to male flowers biomass, temperature, water availability, leaf water potential, flowering date, primary and secondary growth, and net primary production.

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Speaker

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*Speaker

Respirometry of ground beetles according to increasing weights

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Functional connectivity within agricultural landscapes can be evaluated directly by measuring the movement of model species, associated for instance with their functional traits, habitat preferences, etc. These data can be used to assess the quality of different habitats, as well as their resistance or permeability to movement, which can be represented on a landscape map. It can constitute important decision-making tools for conservation or restoration of ecological continuities. Research on monitoring the movement of insects in the field is booming since the miniaturization of active tracking systems. Numerous insects can now be investigated including ground beetles (Coleoptera: Carabidae), important biocontrol agents in agroecosystems. However, the weight of transmitters is still high compared to that of studied insects and can in some cases represent up to 100% of their weight, while it is considered that it should not exceed 10% of the weight of vertebrates (Kissling, 2014). The cost of such excessive weight on the metabolism of insects is largely unknown, and may induce bias in monitoring insect movements by means of active tracking systems (Kissling, 2014). In order to evaluate this impact, we studied respiration, as a proxy of their metabolism, and survival of ground beetles depending on the load carried by individuals. Our aim is to compare the impact of a range of weights, from no load to a load of 200% of individual's weight on two ground beetle species of small and medium size (*Anchomenus dorsalis* and *Poecilus cupreus* respectively). The respiration experiment (instantaneous CO₂ production, frequency and duration of respiration phases) was done with a LI-COR 6400. In parallel, we monitored activity and survival over 10 days of individuals.

References :

Kissling, W.D., Pattemore, D.E. & Hagen, M. (2014) Challenges and prospects in the telemetry of insects. *Biological Reviews* 89 : 511-530.

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Speaker

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*Speaker

The tolerance to low temperature of tropical cockroach *Gromphadorhina coquereliana*

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Most species of insects are characterized by the highest activity at moderate temperature, however, some show full activity at temperatures close to 0 °C, while others in turn are able to survive at extremely high temperatures. Through evolution, cold-exposed insects have developed adaptations that enable them to survive in adverse thermal conditions. An example of such adaptations may be the synthesis of cryoprotectants (polyols or trehalose), the synthesis of anti-freezing proteins (AFPs) and ice nucleating agents (INAs). Other adaptations may be changes in the activity of individual metabolic pathways and differences in the level of expression of heat shock proteins or aquaporins.

However, the question arises whether organisms that are not exposed to stress associated with low temperature in the natural environment also possess such protective mechanisms? To answer this question and learn about the mechanisms associated with the metabolic response to cold stress, we decided to carry out research on Madagascar hissing cockroach (*Gromphadorhina coquereliana*), which naturally occurs in the equatorial climate areas. We examined the effect of cold on mitochondrial activity and the level of heat shock proteins (HSPs), and aquaporins (AQP) in leg muscle and fat body, physiological analogue of mammalian liver and cytological counterpart of brown fat, as well as changes occurring in lipid levels, glycogen and the soluble fraction of proteins of these tissues. Moreover we observed the cold-induced changes in uncoupling protein (UCP) activity. This may suggest that UCPs may play role in thermogenesis in fat body in insect upon cold exposure.

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*Speaker

Changes in accumulation of essential macronutrients during vegetative growth of rapeseed exposed to NaCl

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Stress caused by increased salt concentrations affects plant metabolism and the final outcome of plant production in many ways. The excess of salts has an osmotic effect, thus reducing the amount of water which plants can take up by their root system. Increased salt concentrations may lead to disorders in the mineral nutrition of plants.

To assess the extent to which the steady presence of sodium chloride in relatively low concentrations (0.1- 1.2 g NaCl L⁻¹) affects plants, an experiment was set with rapeseed (*Brassica napus* L., Brassicaceae), in semi-controlled conditions of a greenhouse. Plants were grown in water cultures, on strength Hoagland nutrient solution, to which NaCl was added 2 weeks after planting. Plant growth and accumulation of N, P, K, Ca and Na and their distribution between leaves, stems and roots were analyzed 1 and 2 months following the beginning of the treatment.

Concentration of Na increased in all plant organs over the time, and it was related to its concentration in the nutrient solution. Potassium concentration declined in stems and roots after one months; this decrease was more pronounced over time and with the increase in NaCl concentration in the nutrient solution. Concentration of P declined significantly in roots in the presence of 1.2 g NaCl L⁻¹. Calcium concentration declined in the presence of NaCl over time in all tissues. Concentration of N slightly increased in leaves during the first month, but its concentration declined in all tissues after two months, with respect to the control. Overall, NaCl affected to a higher extent concentrations of K and Ca than N and P. Even though applied concentrations of NaCl were relative low, they induced significant changes in accumulation and distribution of examined elements.

*Speaker

Microcalorimetry: a powerful tool to investigate stoichiometric constraints on small ectotherms

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Environmental conditions constraint populations and ecosystem dynamics through their direct effect on individual metabolism. However, besides temperature, individual metabolic responses to environmental factors remain unclear. As an example, if dietary stoichiometric constraints are well known to reduce individual growth rate, their direct consequences on metabolic rate still require clarifications. It is commonly assumed that dietary stoichiometric constraint increases metabolic rate of small ectotherms but experimental support remains scarce. Here, using a microcalorimetric approach, we determine the standard metabolic rate (SMR) of *Daphnia magna*, fed with a stoichiometric balanced diet (C/P: 160) versus imbalanced diet (C/P: 1440). Regardless of dietary treatment, daphnids presented the same somatic C/P ratio demonstrating their strict homeostatic regulation. However, daphnids fed imbalanced significantly increased their SMR while reducing their growth rate. This result suggest that homeostatic regulation costs increases with increasing mismatch between consumers and resources. To meet this higher energetic demands, individuals reallocate energy from growth to maintenance resulting in the reduced growth rate observed. Beyond this theoretical framework we showed that microcalorimetry is a powerful tool for monitoring small-sized organisms' metabolic rate. This method opens promising perspectives to understand the consequences of various environmental factors on organismal metabolism.

*Speaker

Morphological responses of the invasive species *Elodea canadensis* and *Elodea nuttallii* under salt pulses.

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Abstract

Salinization of freshwaters is of great ecological concerns, which is further intensified by changing climatic conditions and anthropogenic activities. In general, freshwater biota do not extend into saline or slightly saline water and most freshwater plants do not tolerate increasing salt concentration. The success of the invasion in inland waters will depend on the functional traits of the invasive macrophyte species (i.e. tolerance vs resistance to salt) and the habitat characteristics (salt level). Fluctuations in salt concentrations may affect the aquatic organisms in addition to high concentration because of difficulties in regulation of osmotic balance. Here, we determined the response (mortality rate, apical and lateral growth, production of roots) and the level of tolerance of two invasive macrophytes (*Elodea canadensis* and *Elodea nuttallii*) to salt pulses in spring via a laboratory experiment and their transplantation in a naturally salty river. Our main results showed that plant tolerance was higher when the plant was exposed to three salt pulses than one concentration and depended on species identity. In laboratory, we showed after a salt pulse exposure, a root inhibition (number and length) for *E. canadensis* at the salt concentration of 5 g.L⁻¹, whereas at a salt concentration of 1 g.L⁻¹ the number of roots of *E. nuttallii* increased and its root length was stimulated. In the field experiment, a higher mortality rate of the shoots was observed at 1 g.L⁻¹ than at 3 g.L⁻¹ of salt, as well as a root production inhibition. The influence of several abiotic factors (e.g. water temperature, velocity, and nutrient content) could explain the lowest performance of *E. canadensis* and of *E. nuttallii* in the field transplantation. It is difficult to determine the exact salt concentration that is toxic to a plant, due to the interactive effect of all of these environmental factors with salt pulses.

*Speaker

Metatranscriptomic profiling of microbial consortia during root colonization in a gnotobiotic system.

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Descriptions of plant rhizosphere and endosphere allowed to identify the factors driving microbiota assembly. In parallel, screening and transcriptome sequencing of individual microbial isolates have provided deep insights on the functions they provide to the plant and their impact on its phenotype. However, analyses of metatranscriptomes for complex microbial communities are still limited by the availability of annotated genomes. Using a gnotobiotic system combined with inoculation of synthetic microbial communities we aim at identifying microbial genes and metabolic pathways activated upon interaction with the host plant *Arabidopsis thaliana* in a complex community context. The use of microbial isolates from long-term culture collections established from natural soil allows to control precisely microbial identities in the system. Thus, reconstitution experiments with microbial consortia from genome-sequenced microbial isolates will enable simultaneous analysis of microbial community profiles (i.e. community composition) and metatranscriptomes during colonization of germ-free plants. In this case, the obtained data can be mapped against the corresponding annotated whole-genome, substantially facilitating data interpretation. To achieve this goal, we are currently developing an experimental protocol allowing the isolation and purification of prokaryotic (bacteria) and eukaryotic (plant, fungi) mRNA for dual RNAseq analysis of the microbial community and the host in a gnotobiotic system.

*Speaker

Evolution

Posters

Evolution

Evolution

Chronology of selection events during sheep domestication.

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Domestication represents a major turning point in human evolution, leading to the emergence of farming during the Neolithic. It is studied through the example of sheep (*Ovis aries*) which were domesticated 10,500 years ago in the Fertile Crescent. Domestication can be seen as a continuum of selective events of animals most adapted to human needs, environments and farming practices.

Several genomic regions are related to these events but it is still unknown which of them were involved in early domestication processes (i.e, unintentionally selected by humans) or in further improvements related to deliberate selection. Consequently, we used several methods to infer the chronology of selective events affecting these regions. They are based on linkage disequilibrium decay around a genetic variant to estimate the age of its selection. Such datings reveal some scenarios about sheep evolution and thus, about past civilisations. The results show a high proportion of recent selective events (a few hundred years) and only a few were very old (up to 10 000 years). This underlines the importance of replacement processes of primitive populations by modern breeds during successive waves of human colonization.

The next steps will be to specify the past demographic variations of each sheep population to clarify which estimations could be impacted by these kinds of factors. Then, we will compare the results obtained for the European part of colonization roads to the Asian ones to see potential differences of selection choices and timing in distinct human cultures.

Keywords: Evolution – Genomics – Domestication – *Ovis aries* – Chronology

*Speaker

Ecological distribution and local adaptations of egg parasitoids *Trichogramma* in a heterogeneous environment: Implications in evolutionary ecology and biological control

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All organisms are facing some environmental heterogeneity in time and/or space and, therefore, variations in the quality of their local environments. According to their biology (dispersal's ability, phenotypic plasticity, local genetic variability, etc.), the organisms respond differently, generating and/or maintaining inter- or intra-specific variations in life history traits. In this context, we firstly focus here on the geographical and ecological distributions of various *Trichogramma* species (oophagous endoparasitoids) along a small (less than 30km) but marked (from sea level to 1500m) altitudinal transect. We secondly investigate possible local adaptations linked to thermal biology for the most common encountered species using various laboratory or semi-field experiments.

*Speaker

Local adaptation of *Euchiloglanis* fish complex

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Determining how and why populations evolving is fundamental important in ecology and evolution. Studies usually focus on comparing phenotypic characteristics and detecting candidate local adaptation loci despite this task remains challenging. Here, we integrated multivariate morphometrics, geometric morphometrics, and population genomic data to test local adaptation in a recent evolutionary radiation of *Euchiloglanis* fish complex. The results from the morphological analysis indicated that *Euchiloglanis* fish complex had different degrees of morphological differentiation among rivers, and differences were mainly manifested in the head relative size, mouth size, origin of fins, anus position, length of dorsal and adipose fin, and caudal peduncle. Furthermore, a total of 6606 SNPs was identified using restriction site-associated DNA sequencing of 213 individuals from nine populations. Phylogenetic trees and cluster analyses based on the 6606 SNPs indicated that *Euchiloglanis* fish complex could be divided into four clusters according to rivers, while individuals from Dadu River and Yalong River had close relationships. The species delimitation analysis based on Bayesian coalescent supported that *Euchiloglanis* fish complex could be divided into three species. One was from Dadu River and Yalong River, another one was from Qingyi River, and the last one was from Jinsha River. Local adaptation was highlighted by outlier analysis using LOSITAN and ARLEQUIN. Selected sites shared by these two methods were ranged from 38-163 within each pairwise river systems. Cluster analysis based on climatic factors showed that difference of precipitation, temperature, and altitude might be the key climatic factors that caused local adaptation and speciation for *Euchiloglanis* fish complex. Taken together, we successfully elucidated the morphological differentiation and genomic architecture underlying adaptive changes of the *Euchiloglanis* fish complex in the Jinsha River basin.

*Speaker

Hybridization in the Mediterranean: a case study on *Cyclamens* sheds light on evolutionary drivers of plant speciation

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Hybridization plays a prominent role in plant evolution due to its influence on genetic diversity, fitness and adaptive potential. However, ecological mechanisms regulating hybridization remain unclear, and field-based evidence are of high interest to improve our understanding of hybrid persistence. We identified two disjunct sites in Corsica and Sardinia where *Cyclamen balearicum* (rare parent) and *C. repandum* subsp. *repandum* (common parent) are hybridizing. Hybrid populations on the two islands contain similar patterns of variation in flower color, with two parental and four hybrid phenotypes. However, the two islands probably differ in their evolutionary process of hybridization, as hybrid morphs dominate most Sardinian populations, whereas the common parent (*C. repandum*) is the most frequent morph in Corsica. Moreover, Sardinian hybrid populations occupy a wide territory while Corsican are highly localized in one single site. Ecological differentiation plays a major role in the process, as the ecological niche of hybrid populations is similar to the niche of *Cyclamen balearicum* (rare parent), both in terms of habitat and climatic conditions. Finally, a higher number of flowers per individual suggests that hybrid vigor may contribute to the maintenance of hybrid forms.

The two contrasting hybridization events provide evidences for mechanisms promoting the evolution of homoploid hybrids. Hybrid populations are found at the periphery of the common parent range, under marginal ecological conditions, which is supposed to limit parent's competitive ability. We discuss species distribution, especially regarding past events that could have bring the two formerly isolated taxa into contact. Finally we argue for the development of a conservation strategy for Mediterranean plants that integrates the need to protect hybrid populations where adaptive variation and species divergence are on-going.

*Speaker

Patterns of genomic divergence between parasitic and non-parasitic lamprey ecotype

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Investigating gene flow between closely related species and its variation across the genome is important to understand how reproductive barriers shape genome divergence before speciation is complete. The European river lamprey (*Lampetra fluviatilis*) and the brook lamprey (*L. planeri*) have distinct life histories: *L. fluviatilis* is parasitic-anadromous whereas *L. planeri* is nonparasitic and freshwater resident. Several studies have shown ongoing gene flow and a low reproductive isolation between these taxa that can be considered as partially reproductively isolated ecotypes. To characterise the genomic architecture of divergence, we first used Illumina short reads from shotgun sequencing of each ecotype to construct a de novo genome reference. Then, we used RAD sequencing from 192 individuals sampled in sympatry to identify outlier Single Nucleotide Polymorphisms and their distribution along the genome. We also analysed transcriptomic data from adults and juveniles *L. fluviatilis* and *L. planeri* to identify differentially expressed genes and measure expression variations across different stages of development. With this integrative approach combining genomic and transcriptomic data we hope to shed light on the relationship between life history differences and the genomic landscape of reproductive isolation in river and brook lampreys.

*Speaker

Maternal or paternal contributions to transgenerational plasticity of the freshwater snail *Physa acuta* in response to predation

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Global change poses adaptive challenges to organisms, which have to face new environmental situations. Species might be able to adapt to rapid environmental change if they have sufficient standing genetic variation and/or phenotypic plasticity to mount fast responses. Recently, the phenotypic plasticity process has been extended to an inter-generational scale called transgenerational plasticity that occurs when the environment experienced by parents influences offspring phenotypes and sometimes reaction norms. This form of phenotypic plasticity based on non-genetic inheritance mechanisms has been shown to be a highly effective mechanism that can buffer populations against rapid environmental change. However, many findings of transgenerational plasticity cannot disentangle the relative contributions of maternal vs. paternal effects to transgenerational plasticity. In the context of predation, we recently demonstrated that the environmental history of parents affects offspring induced defenses. Here, we wanted to estimate the relative maternal or paternal contributions to transgenerational plasticity in response to a predation risk. To address this question, we used a freshwater snail *Physa acuta* that is a good model as it has relatively short life span and is hermaphroditic. We submitted individuals of generation 1 (G1), from hatching to sexual maturity, to control (C) or predator-cue (P, crayfish odour) environment. We then realized reciprocal crosses using individuals G1 reared in the same or different environmental history to generate four experimental G2 lineages (C x C, C x P, P x C, P x P crossing) and raised offspring (G2) to the same two treatments (C or P) to test if maternal, or paternal exposure to predator cues, or both, are required / sufficient to trigger constitutive and/or induced defenses in offspring. We measured several traits susceptible to exhibit transgenerational plasticity (growth, morphology, thickness shell, behaviour).

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Posters

Global Changes and Biodiversity

Public knowledge and awareness of climate changes among people in China

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Measuring the public understanding, knowledge and perceptions towards recent climate change is become a growing research interest in the last two decades. The public understanding and knowledge can be measured through in-depth individual interviews, questionnaires and case studies. In the present study, the public awareness and knowledge towards climate change was measured using questionnaire which was distributed among 160 individuals in four regions of China (Shenzhen, Foshan, Zhuhai and Guangzhou). In general, the individuals showed moderate knowledge and understanding about climate change issue causes, impacts and suggested solutions. The items measuring "impacts of climate change" and "suggested solutions" were the only significant variables in the different regions. Other measures did not show significant different in their scores. The self-reported knowledge was high among the respondents (97.5%) which indicate dependence of individuals in the four regions for traditional knowledge to obtain the recent updates and information about climate change. It is concluded that the public understanding and knowledge among individuals in China is moderate and further efforts needed to be done to improve the general knowledge and perception about climate change issue in the different media resources such as TV and newspaper.

Plant-herbivore interactions in the context of climate change: Effects of elevated atmospheric CO₂ on grapevine and European grapevine moth

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The rising atmospheric carbon dioxide (CO₂) concentration is expected to influence interactions between plants and herbivorous insects. On the one hand, it may change the nutritional quality of the host plant and, on the other hand, affect insect phenology or biology. The European grapevine moth *Lobesia botrana* is considered as the key insect pest in European vineyards with increasing abundance worldwide. In order to anticipate future pest development and host plant response, we assessed the effects of elevated CO₂ on both *L. botrana* and grapevine, *Vitis vinifera* cv. Riesling, using climate chambers (400 and 700 ppm) and a free-air carbon dioxide enrichment (FACE; 395 and 460 ppm) system. In climate chambers, larval development of *L. botrana* was shorter and pupae were heavier under elevated compared to ambient CO₂ concentration, while the total lifespan as well as number of eggs or larvae were not affected. Whole transcriptome analysis of grapevine leaves showed that of the 14,763 genes identified, a substantial number was significantly differentially expressed during *L. botrana* herbivory. This is true for both sampling dates, fruit development and ripe berries, although the response was stronger regarding developing fruits. Altogether, more genes were differentially regulated during herbivory under elevated compared to ambient CO₂, indicating that the transcriptomic response of grapevine to *L. botrana* herbivory is CO₂-dependent. Among the respective genes, some are known to play a role in the biological processes "defense response" and "response to biotic stimuli" while the pathway of "biosynthesis of secondary metabolites" was significantly enriched. These changes are of particular interest for understanding future grapevine responses to herbivory under elevated CO₂. These results contribute to a better understanding of future grapevine-insect interactions in the context of climate change and, thus, help to identify potential consequences for future pest management strategies.

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Phytobiogeographic study of *Withania frutescens* in the Sebaa Chioukh and Middle Tafna stations in the Tlemcen region

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The nature and current composition of Mediterranean plant communities can not be understood without taking into account geological, paleo-climatic and anthropogenic factors; these have marked the genesis of the various ecosystems specific to this biogeographical zone.

The vegetation of the Tlemcen region is a good example of a study of plant diversity; and especially an interesting synthesis on the natural dynamics of ecosystems from the coast to the steppe. The study presented is only part of the objectives of the Plant Ecology Laboratory. It focused on the floristic diversity of *Withania frutescens* but also and above all on the control of the biological, morphological and phytobiogeographic capital of the two stations in the region. Tlemcen.

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The ecology of tropical temporary ponds at UWI Mona, Kingston, Jamaica

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Unlike a permanent body of water, which is inundated with some volume of water for a significant period throughout the year, a temporary body of water has a recurrent dry phase. As a unique habitat, temporary bodies of water may harbor rare species found in no other habitat. The project aims to identify the ecological interactions and significance of the fauna of tropical temporary ponds. The two temporary ponds being examined are located at the University of the West Indies, Mona. The first pond lies behind the Mona Information Technology System (MITS) building (18.00339181, -76.74462356), while the second lies near Mary Seacole Hall (18.0049006, -76.74409247). Data were collected weekly from November 2017 to present, including pond characteristics: pH, temperature, conductivity, dissolved oxygen, depth, area; biological samples and environmental data: air temperature, wind speed, light intensity, humidity and barometric pressure. Biological samples were collected by a 24 x 46 cm rectangular kick net by 1-3 large sweeps of the ponds and stored in jars of 10% formalin. Throughout the course of data collection particular patterns have been noted. Immediately after a rain shower in a dry pond area, adult dytiscid beetles, veliids and notonectids are found to in the ponds. With continuous rainfall such that the pond is not dried, dragonfly nymphs, ostracods and chironomid midge larvae become established. As the pond is kept inundated, tadpoles are able to develop, giving preliminary insight into the ecological succession of tropical temporary ponds. Data thus far has shown these two temporary ponds supporting 29 different aquatic species throughout their hydroperiods. The data, in association with future climate models, is relevant in predicting the prevalence of temporary ponds, their associated fauna and changes in ecosystem functions.

BELOWGROUND INTERACTION BETWEEN PLANTS DOES INCLUDE EXCHANGE OF NUTRIENTS

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Two distinct mechanisms of plants competition have been classically distinguished, competition due to exploitation, and competition due to interference. However recent literature suggests that interactions between plants are much more complex and include exchange of information, molecule and resources, through the mechanism of rhizodeposition.

We tested the hypothesis that competition between oak seedlings (*Quercus petraea*) and a common grass (*Molinia caerulea*) during forest natural regeneration does include a competition by exploitation of nitrogen (N) resources but also exchange of N between both species to the benefit of the grass.

Both species were cultivated together in pots, either directly in contact or separated by a membrane with different pore sizes, so that roots of both species can cross the membrane, or only hyphae of mycorrhiza, or only molecules. Oak seedlings were on a drip with a ¹⁵N enriched solution of urea (cotton-wick technique) at the beginning of the growing season. Oak, grass, and soil were harvested 2, 4, 6, and 10 months after start of labelling. Samples were analysed for N content and ¹⁵N excess.

The presence of grass reduced oak growth and the presence of oak favoured the grass growth. ¹⁵N was found in all oak organs, but also in the soil and grass organs. ¹⁵N was found in all grasses, meaning that ¹⁵N circulated in both sides of the membrane without any root contact, yet chemical forms of N has not been identified.

Those results suggest that beyond the exploitation of N by the grass to the detriment of oak, grass also benefited from a release of N by oak. The underlying mechanisms are not fully understood but they emphasize the important role of rhizodeposition, mycorrhizas, and microorganisms. They also suggest that exchange of nutrients, other molecules and information are much more common than suspected in belowground plant interactions.

Phytobiogeographic study of *Lavatera maritima* (malvaceae) in the coastal region of Rachgoune Ain-Temouchent Algeria

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The present work concerns a self-ecological study of *Lavatera maritima* (malvaceae) in the region of Rachgoune, for this study we rely on floristic criteria. The analysis of the plant structure takes into account the method of sampling and floristic surveys which obliges us to list all the plant species present. This floristic list changes from one station to another. The vegetation of Tlemcen is a good example of a study of biological diversity. This study allowed us to highlight the main families as well as the most dominant biological, morphological and biogeographic type. The calculation of the Disturbance Index is proportional to the dominance of therophytic species in our station. From our results, we note that biological and phytogeographic diversity is conditioned by climatic factors that play a vital role for a very large part of the vegetation in order to favor the process of biological recovery.

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Taking into account a diversity of environmental drivers for the analysis of biodiversity patterns: a methodological challenge

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Biodiversity management and conservation schemes need to be based on scientific knowledge. However, this important aim is still poorly achieved due mainly to the multi-dimensional character of the environmental drivers of biodiversity patterns, and, consequently, the lack of datasets accounting for this complexity. This multi-dimensionality presents two important detrimental consequences: 1/ it makes field data complicated and costly to collect/acquire, and 2/ it makes difficult to distinguish the proximate environmental variables which actually operate on biodiversity patterns while interdependency between variables may obscure data interpretation. This last point may cause two main pitfalls:

To set aside variables that actually impact the studied biodiversity because they are not considered. This can lead to a lower part of the variance explained by the model or to attribute the effect to a strongly correlated but not necessarily causally related variable.

To consider a variable as significant whereas it is another variable that actually impacts the studied biodiversity because both are correlated. In this case, the impacting variable can therefore explain a smaller part of the data or not being selected in the statistical model.

As part of a large-scale biodiversity monitoring program in a large floodplain of the Atlantic coast of France (The Marais poitevin), a large environmental dataset was acquired. We used this dataset to develop a framework for addressing this methodological challenge.

We developed a two-steps approach: (1) through a review, we identified the main environmental drivers impacting wetland biodiversity patterns. Then, (2) using the dataset, we compared the different analysis strategies used in the literature and proposed on this base a novel methodology. This novel methodology is intended to better identify environmental drivers of biodiversity patterns from field ecological data while taking into account the risks due to statistical co-variations.

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European tree species extinction and colonization across their ranges

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Climate is key driver of species distribution, and climate change may have a crucial impact on species ranges.

While huge work has been done to study the present species distribution and its dependencies to the current climate, yet few studies have attempted to understand the dynamics processes of colonization and extinction that control species ranges; methods to analyze this dynamic process are indeed challenging particularly for long-lived organisms such as trees.

We here propose an analysis of national forest inventories datasets covering the whole climatic gradient of Europe to calibrate a dynamic patch occupancy model accounting for extinction and colonization processes for the main species encountered in Europe.

The use of an observation model to account for different effects according to countries show that accounting for differences in observation between countries has a major impact on results.

Our results show that climate has a significative impact on extinction processes, while colonization remained difficult to predict.

Furthermore we explored the relations between colonization and extinction and species present distribution.

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The anthropogenic and climatic impact on the halophytic vegetation in Arid and semi-arid zones of western Algeria

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Algeria because of its geographical position presents a great diversity of biotope occupied by an important floristic richness. from Algeria. In addition, the drought in the Oran region has profoundly disrupted nature, leading to significant water stress and adaptation in plants. Important threats weigh on the heritage, which is subject to significant risks of impoverishment. And overall, the trend of decreasing biodiversity affects all natural ecosystems in Algeria. No ecosystem is characterized by a stabilization of biodiversity. The climatic actions responsible for the degradation of the vegetation are therefore recognized and have been the subject of several studies and across different regions. On the other hand, anthropogenic actions are less known because they reveal a social being whose behavior varies according to the regions and the social traditions of the latter.

The anthropogenic disturbances are to a large extent responsible for the current state of vegetation structures in the Maghreb (Qu'ézel et Barbero, 1990). In this context, and in order to better understand the effect of human action, which considerably affects the study area, it was considered necessary to study more or less detailed socio-economic data as well as their harmful impacts. of the urbanization of production and infrastructures on the environment, with the aim of evaluating the impact of the pressure of the man and his flock on the dynamics of the halophytic vegetation in the western region of Algeria.

Phenotypic plasticity in maize

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Adaptative response is a key mechanism to face changing environments over generations. As sessile organisms, plants evolution strongly rely on their adaptive response. Though, natural selection may not enable organisms to adapt fast enough to rapid climate changes. In this context, phenotypic plasticity (defined as the ability for an organism to change its phenotype in response to the environment) can allow organisms to cope with changing environments and interact with natural selection.

The interaction between these mechanisms, can be studied using an original plant material resulting from a Divergent Selection Experiment (DSE) for flowering time developed over the last 20 years. Within two maize inbred lines, Early- and Late-flowering populations, subsequently structured into families within populations, were formed.

Preliminary studies of growth and developmental phenotypes for Early and Late genotypes in different environments showed few differences between genotypes, but strong phenotypic plasticity. Further evaluation of the genealogy of selected populations will allow to compare the evolution of phenotypic plasticity (on several phenotypes) over 20 years of directional selection. In addition, a set of 7 maize lines (including parental lines of the DSE) exhibiting various drought tolerance levels were chosen and grown in two environments (Plateau de Saclay, France in 2016 and 2017). Several phenotypes were measured (such as yield, growth related traits, water content indexes, transpiration rates, chlorophyll content...). The study of the reaction norms of these phenotypes shows different phenotypic plasticity levels depending on the integration level of the phenotypes. This shows the need of characterizing intermediary phenotypes (molecular, physiological, developmental...) to better understand the many routes an organism can follow during its development to achieve its mature stage.

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Effects of tree species interactions and climate on water use efficiency of trees.

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In the context of biodiversity and ecosystem functioning relationships, mixed-species forests have been highly studied over the past decade. Forests with a high diversity of tree species are usually found to be more productive than monospecific ones. However, the mechanisms leading to these patterns are still not well understood. Furthermore, in the context of climate change, it is interesting to analyze whether these mechanisms can help mediate the effects of harsher climatic conditions such as drought.

The objective of this study was to characterize the influence of tree species interactions in mixed forests on water use efficiency of trees under various environmental conditions in South- ern France.

We estimated tree-level water use efficiency (WUE) with the carbon isotope composition ($\delta^{13}C$) of the wood in tree rings representing a five-year period (2003-2007) characterized by dry soil conditions. For each site, a triplet approach (3 different forest stands) was used to compare tree WUE in pure and two-species stands. Measurements were conducted along a latitudinal gradient in natural forests (5 sites in the South-East of France) in beech-silver fir or beech-pubescent oak forests.

In this poster, we present the results of this study. We expect that trees in mixtures should have a lower WUE than trees in pure stands because they were less exposed to water stress in mixtures due to a complementarity in water resource use. Furthermore, we expect that this effect should be stronger in the sites that are the most exposed to water stress.

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Rainwater deficit affects litter mass loss and microbial decomposer communities in a Mediterranean forest

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Decreasing rainfall is an expected consequence of climate change in the Mediterranean basin, which may severely affect nutrient cycling in terrestrial ecosystems. Here, we studied whether plant diversity and reduced precipitation affects litter decomposition and microbial decomposer community in a typical Mediterranean forest, equipped to exclude about 30% rain at the experimental site Oak Observatory of the Observatoire de Haute Provence (O3HP), France. Litterbags containing single- or multi-species leaf litter mixtures of *Quercus pubescens*, *Acer monspessulanum*, *Cotinus coggygria* or *Pinus halepensis* were collected after eight and twenty months of decomposition, following maximum periods of cumulated rain exclusion. We used a metabarcoding approach based on the v3-v4 region of the 16S rRNA gene and on the ITS1 intergenic region to characterize bacterial and fungal community compositions, respectively. As expected, litter decomposition was reduced in the rain exclusion treatment. The effects of litter mixture composition and of rain exclusion were significant for both bacterial and fungal communities. But bacterial communities were more diverse and subject to a higher turnover between sampling dates than fungal communities. Most remarkably, in bacterial communities, rain exclusion affected the dominance of Actinobacteria to the profit of Proteobacteria, Acidobacteria and Bacteroidetes. While, fungal communities mainly dominated by Ascomycota during early stage of litter decomposition, showed reduced domination of Schizoparmaceae to the profit of Gnomoniaceae. Our study provides evidences that combined climate and forest biodiversity changes, induced by human activities at a global scale, affect the functioning of forest ecosystems at a local scale.

Conservation of freshwater biodiversity in Tunisia in a global warming context: combining amphipod distribution data and molecular analyse to improve priorities

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The Mediterranean Basin is well known for its important biodiversity and is considered as a biodiversity hotspot. However, this biodiversity is threatened by human activities, particularly for freshwaters which are scarce, highly anthropized and highly threatened by climate change. It is hence very urgent to define conservation priorities.

In this study, we propose to use epigeal amphipods as model organisms to define conservation strategies for Tunisian fresh waters. This group is much diversified, widely distributed in all freshwater ecosystems and easy to collect. We visited more than 180 sampling sites widely distributed in all regions of Tunisia but amphipods were present only at 60 sites. We found all species already known/cited for Tunisia except for *Gammarus gauthieri* which is only cited for Tunisia and *Echinogammarus dactylus* for which additional samplings are required around the type locality and a new species for Tunisia, *Echinogammarus haraktis*. However, the barcoding of our samples revealed many, at least 12 according to the delimitation methods used, new Molecular Operational Taxonomic Units (MOTUs) that may represent different, even if cryptic, species.

There is a very strong spatial variation in the distribution of these species. Among climatic factors, the distribution is mainly explained by temperature. Considering the climate warming, we can argue that the group of *Echinogammarus simoni* and its related MOTUs, representing the only species occurring on 50% of all the sampling sites in Tunisia, are likely to be endangered. Moreover, occurring in the warmest part of Tunisia (mean water temperature around 28°C), they may already reach their physiological limits and thus be threatened by the global warming.

This study also provides new insights on the important contribution of molecular data to more detailed insight into biodiversity and to improve conservation strategies in a region of the world where reliable data are difficult to obtain.

Estimation of partial population replacement using spatiotemporally explicit simulations and ancient DNA

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Advances in sequencing technologies allow retrieving ancient DNA (aDNA) from fossils to provide snapshots of genomic diversity in past populations. Models used for the exploration of genetic relationships between samples from different periods usually consider a panmictic population and thus do not take into account the spatiotemporal dynamics of genes due to migration. Here, we present a new approach simulating genomic diversity, using a serial version of the program SPLATCHE2 and samples of different ages and locations, which takes into account population structure and migration over time. We apply our method to two ancient genomes from central Europe to investigate the genetic consequences of the change in human lifestyle that occurred during the Neolithic transition in this region. In order to understand if this event was accompanied by a population replacement, we estimated the amount of genetic continuity between Palaeolithic hunter-gatherers and Neolithic farmers. While previous approaches rejected the hypothesis of full population continuity, our method goes one step forward by estimating the most probable genetic contribution of local hunter-gatherers and immigrant farmers to the final Neolithic population in central Europe and by jointly estimating other demographic parameters such as carrying capacity, growth and migration rates. Our new approach constitutes a useful tool for the analysis of aDNA datasets, applicable to many species.

Posters

Halieutic and Marine Ecology

Genetic connectivity and local adaptation of a Mediterranean Brown seaweed.

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Marine species are usually characterized by a high dispersal potential and large effective population size, which result in weak genetic differentiation and high polymorphism. However, various marine species display a much stronger genetic structure, including at short distance. This is especially the case for the fucoids forest leading to the presence of clear spatial patterns of population structure. The endemic Phaeophyceae *Cystoseira zosteroides* is one of the most representative species of the Mediterranean marine forest of deep-water. This species exhibits a high survival rate, low recruitment, and low growth rate. Experimental approaches on *C. zosteroides* reproduction and zygotes also suggest very short dispersal distance. These life history traits suggest the possibility of significant genetic divergence at small spatial scales. Nevertheless, the oceanographic connection might counteract the low dispersal ability of these fucoids, by allowing the connectivity of distant populations. To our knowledge, no genomic researches have yet been carried in the genus *Cystoseira*. Previous connectivity studies on *Cystoseira* species were based on DNA markers (RAPD, microsatellite), and indicated a strong genetic differentiation. Analysing the genomic diversity of this species would be useful for management. It also provides an interesting biological model to study the adaptation to different marine environments. In the framework of the MarFor European project, we will investigate the effective dispersal of *C. zosteroides* by the development of RAD-sequencing (ddRAD). The use of a high number of DNA markers (SNPs) will be useful to understand the drivers of strong genetic structure in such species. Additionally, we will use RAD data and reciprocal transplant experiments to test for local adaptation according to depth. These results will offer a new perspective for the conservation and the management of the Mediterranean marine forests.

Mapping the kelp distribution area of the Sept-Iles marine reserve (Brittany, France) using hydroacoustics

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Kelp forests are present around temperate and polar coasts in all the oceans of the world. They are an important driver of global biochemical cycles and are one of the most productive habitat of the world, hosting numerous fauna and algae species. In Europe, kelp forests are dominated by *Laminaria* species, which are threatened by water turbidity or seabed substrate degradation due to global warming and human activities.

The Sept-Iles archipelago (320 ha, Brittany, France) is a marine reserve since 1976, highly colonised by kelp forests. Two hydroacoustic campaigns were conducted in 2006 and 2018 to evaluate the evolution of kelp distribution on the reserve area. Acoustic methods use the propagation capacities of sound into water to describe all the objects in the detection beam according to their echoes' characteristics. They offer non-intrusive monitoring tools that are less time-consuming than diving surveys. Acoustic data are recorded with a SIMRAD EK60 split-beam echosounder on both campaigns. Kelp echoes are identified on the echograms thanks to the specific shape of their signal. Furthermore, we analysed the area back-scattering coefficient (SA) recorded along transects between 50 and 500 cm from the seabed to map the kelp distribution. The comparison of both surveys shows that kelp forests' distribution on reserve has not dramatically reduced on the last decade. Results highlight that the kelp presence is highly driven by the bathymetry: as expected, their abundance decreases at depths higher than 20 meters. Comparison with diving observations shows that SA geographical patterns are able to distinct areas where kelp forests are well implanted from other with a patchy organization. Finally, unless further studies are essential to convert SA values into kelp biomasses or densities, hydroacoustic appears as a reliable and repeatable method to map the kelp forests and to evaluate temporal changes in their distribution area.

Sources partitioning in the diet of the shipworm *Bankia carinata* (Gray, 1827): an experimental study based on stable isotopes

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Adaptations that allow Teredinids to maintain and thrive on wood, a nutritionally unbalanced food, make these marine bivalves remarkable. Capable of filter-feeding, shipworm house endosymbiotic bacteria synthesizing cellulolytic enzymes for digestion of wood carbohydrates and providing nitrogen to their host through nitrogen fixation. To what extent does each of these nutrition modes contribute to the shipworm's metabolism remains an open question. In this experimental study, source partitioning was estimated through the determination of $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ values in original biological samples. To this purpose, pieces of common alder were immersed in a coastal station of the north-western Mediterranean Sea. Wood logs were rapidly infected by the shipworm *Bankia carinata*. Results from the stable isotope mixing models suggested that 72 to 81% of the carbon in the shipworms was derived from the digestion of wood carbohydrates. The approach permitted to determine estimates of nitrogen source contribution even though the number of sources was too large to get a unique solution from standard linear mixing models. Nitrogen in *B. carinata* mostly came from N₂ fixation (40 to 78%) and then from wood digestion (9 to 51%). These first semi-quantitative estimations suggest that the contribution of the endosymbiosis to nitrogen requirements of the shipworm is far to be incidental.

Towards faster and less efficient biomass transfers in marine food webs?

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Temperature affects metabolism of individual organisms and is a key abiotic factor determining the marine species distribution at large geographical scale. Consequently, ocean water temperature influences the structure and the flows of energy and biomass within the marine food webs. In the context of climate change and warming of the world Ocean, understanding temperature effects on the functioning of marine food webs is crucial to estimate their sensitivity to such changes and predict potential changes in terms of productivity and resilience. Here, using global fisheries catches and life history traits of marine species through a trophodynamic approach, we examined temperature effects on two characteristics of biomass transfers in coastal marine ecosystems. Within each coastal cell ($1^\circ \times 1^\circ$) of the world Ocean, we estimated the yearly values of two trophic indicators: (1) the Transfer Efficiency (TE) that represents the fraction of biomass or energy transfers from one trophic level to the next, and (2) the Time Cumulated Indicator (TCI) that indicates the residence time of the biomass in the food web. First, we showed that the speed of the biomass transfers has decreased between 1950 and 2010 while the efficiency of the transfers has increased over the same period. Secondly, using a generalized linear model, we tested the relationship between Sea Surface Temperature (SST) and the TE and TCI in each type of coastal ecosystem (tropical, temperate, polar and upwelling). Lastly, based on a selection of 70 published marine ecosystem models, and using biomass data, we tested the reliability of the observed patterns in various ecosystems. The findings suggest that warmer oceans are likely to result in faster and less efficient biomass flows, and these effects will be especially important in polar and tropical ecosystems.

Feeding marine ecosystem models from the space: improving realism of trophic models using satellite-derived zooplankton favourable habitats

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Variability of physical, environmental and oceanographic conditions as well as trophic interactions are crucial to understand marine species distribution. Representing ecosystems through complex food-webs and allowing modification of species foraging capacities according to ancillary factors such as depth, seabed substrate, temperature or salinity, Ecospace models (spatial version of Ecopath with Ecosim models, EwE) are powerful tools in this field. However, since such trophic models were originally designed to study fishing effects, they usually fail to accurately reproduce spatio-temporal dynamics of lower trophic levels. To address this issue, some studies have attempted to drive those dynamics by satellite-derived estimates of primary production (PP). To further increase realism of Ecospace models, we explored possibilities of also improving spatio-temporal dynamics of secondary production (SP), which provides a good proxy of the fraction of PP transferred to higher trophic levels. With this aim, we used outputs of a recently developed ecological-niche model for zooplankton. Calibrated on abundances data from the Continuous Plankton Recorder, this model uses daily detection of productive fronts from satellite sensors and 3D-hydrodynamic models results to predict suitable habitats of mesozooplankton. We successively (i) built Ecospace models of the Celtic Sea ecosystem for several strategic years over the 1997-2016 period (ii) implemented them with forced PP and habitat model of mesozooplankton (iii) compared results with/without such forcing functions cross-validated final outputs with abundance data from scientific surveys. In contrast to classical models, Ecospace models fed by satellite-derived information on PP and SP provided more realistic results and were able to reproduce great patterns of changes in species distribution over the last two decades, particularly for small pelagics and their consumer (e.g. hake). Such an approach, less complex than coupling EwE with biogeochemical or NPZD models, appears promising to improve assessment of anthropogenic impacts on marine species distribution and ecosystem functioning.

Trophic links between microbenthic invertebrates and demersal fish communities in the Mont Saint-Michel macrotidal estuary prior to dams removal on the Sélune river

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The restoration of the ecological continuity of rivers has today become a strong ecological issue. In some cases, it can lead to the dismantling of dams which ecological consequences must be known on downstream. In this context, we conducted a study to assess the initial state of the trophic functioning of a macrotidal estuarine ecosystem before the removal of two dams on a coastal river, Sélune, main contributor of this ecosystem. Fish (predator) and macroinvertebrate (prey) communities were sampled and characterized at two periods (late winter / late summer). A coupling analysis of stable isotopes (nitrogen and carbon) and analysis of digestive contents was conducted to understand the trophic functioning through the links between prey and predators. The results showed that the invertebrate and fish communities were typical of European estuaries and had low species richness due to the physical constraints (variable salinity, strong currents) prevailing in the area. The abundance of fish was much higher in late summer where the abundance of invertebrates was paradoxically rather lower. Two species of sand gobies (*Pomatoschistus microps* and *P. minutus*), juvenile sea bass (*Dicentrarchus labrax*) and juvenile flounder (*Platichthys flesus*) dominated the fish community, with each species showing particular feeding strategies. Harpacticoid copepods and amphipods (*Corophium arenarium* and *Bathyporeia pilosa*) were the main prey of fish. The overlap analysis between digestive contents of fish and benthic invertebrate communities indicated the existence of preferential feeding zones that evolved according to the period. The results of the mixing model showed that microphytobenthos constituted a major primary source of the food chain of this ecosystem, whatever the period considered.

*Speaker

Determining long-term ray community changes in the Bay of Biscay using grouped landings and limited species data

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Sustainable fisheries management requires the evaluation of the status of exploited populations and communities. Certain bycatch species such as rays are managed together which has led to overexploitation and conservation concerns for the most vulnerable ones. Traditional fisheries stock evaluation methods need species-specific input data while for ray species-specific landings have become available only recently in Europe. To overcome data limitations caused by grouped landings we developed a Bayesian multispecies biomass production model. In addition to the grouped landings the input data are shorter time series with species-specific information (landings and scientific biomass indices). Life history traits are used to define informative priors for intrinsic population growth rates. Applying the approach to the six main ray species managed together in the Bay of Biscay we identified long-term changes in community composition. Since the 1990s the small offshore cuckoo rays became increasingly dominant, while the contributions of the other five species declined, strongly for the largest species. In a prospective analysis, we found that all but the two largest species are expected to increase to biomass levels corresponding to maximum sustainable yield over the next decade under the current harvest rates while dedicated management will be needed to recover the strongly depleted largest species.

Posters

Holobiont and Extended Phenotype

New Insights into the Nature of Symbiotic Associations in Aphids: the Case of Gut-Associated *Serratia symbiotica*

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Symbiotic microorganisms are widespread in nature and can play a major role in evolution. A key question in evolutionary ecology is how mutualistic associations are established and evolve. The aphid-*Serratia symbiotica* bacterium interaction provides a valuable model to study mechanisms behind this question. Although this bacterium is usually considered as a true endosymbiont of aphids, some strains of *S. symbiotica* have been isolated from *Aphis fabae* and grown on a quite classic medium. In addition, a recent study has shown that these cultivable strains are very similar phylogenetically to other strains of *S. symbiotica* residing in the gut of field-collected aphids, suggesting that cultivable strains can be derived from the gut of aphids. To examine the mechanisms potentially involved in this route of infection, we have to simulate the environmental acquisition of these strains by aphids. After oral ingestion, we analyzed the infection dynamic of cultivable *S. symbiotica* during the host's lifetime and determined the immediate fitness consequences of these bacteria on their new host. We further examined the transmission behavior of cultivable strains. Our study revealed that cultivable *S. symbiotica* are predisposed to establish a symbiotic association with new aphid host, settling in its gut. Our experiments showed that cultivable *S. symbiotica* colonized the entire aphid digestive tract following infection, after which the bacterium multiplied exponentially during aphid development. Our results further revealed that gut colonization by the bacteria induce a fitness cost. However, it appeared that they also offer an immediate protection against parasitoids that should probably in some conditions compensate the costs. Moreover, cultivable *S. symbiotica* seem to be extracellularly transmitted, partly through the honeydew and the sap of the host plant. These findings provide new insights into the nature of symbiosis in aphids and the mechanisms underpinning these interactions.

Microbial interactions in mosquito microbiomes: Patterns in presence and absence of WNV infection

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Ecological relationships are a key factor shaping community structure in all environments. Interspecific interactions have been widely studied for plants and animals, while microbial interactions, particularly in microbiomes, have been widely overlooked. Although symbiont co-occurrence and co-exclusion have been previously described, they are not yet fully understood. Furthermore, these interactions may be also correlated with many aspects of the holobiont (e.g., ecological niche adaptation, vectorial capacity). It is known, for instance, that different symbiotic bacteria can affect, either positively or negatively, mosquitoes competence for virus infection and/or transmission. However, how microbial interactions may affect or be affected by virus presence in mosquitoes remains to be explored. Here we analyzed bacterial interactions within the microbiome of several field-sampled mosquito species from Toronto using 16S rDNA sequencing and interaction networks. Microbiota composition and diversity are host-specific, and thus bacterial interactions within the microbiome also vary among different mosquito species. In order to elucidate any particular microbial interaction patterns related to vectored pathogens, interaction networks including individuals naturally infected with West Nile Virus (WNV) were also constructed for populations of two of the mosquito species: *Culex pipiens* and *Aedes vexans*.

Posters

Interaction of Ecological and Social Aspects
in the Categorization of Spaces and
Species

A practical framework to analyse the resilience of socio-ecological systems

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The resilience is a central concept for the management of natural systems. Different metrics of resilience can help maintaining systems in sustainable states, can alarm about when critical thresholds are approaching, or may guide adaptive management actions. Although the multifaceted resilience concept originated from the system theory, it was first used by mathematical biologists and engineers, and it was further developed in human sciences.

One of the major challenges today is to identify measurable properties of socio-ecological systems, which are involved in determining the different dimensions of resilience.

Here, we develop a practical framework, based on fundamental elements of the system theory and inspired from ecological applications.

In particular, it will consider the multi-dimensional aspect of complex socio-ecological systems states as well as the multi-dimensional aspect of its resilience.

This framework intends to give a general quantitative approach that can be applied simultaneously to ecological and social measurable elements of the socio-ecological system of interest.

We illustrate the approach and its interest for comparative analyses by applying it on three socio-ecological systems in the French Alps.

This framework provides new opportunities for building comparative analysis as well as identifying vulnerabilities of managed natural systems across space and time.

National specific production system induce different perceptions of management impacts on soil biodiversity functions: comparison of five European countries

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Soil biodiversity across the European Union is under various threats through climate change, intensification of land use regimes or urbanization as general examples. Within the Biodiversa SOILMAN program, we investigated farmers' soil management practices in wheat cultivation according to the local constraints they identify and their perception of their inter-relation with soil functions driven by soil biodiversity in France, Spain, Romania, Sweden and Germany. We conducted five focus groups, one in each country, with a standardized protocol. In each focus group between six and seventeen farmers were present. Farmers were proposed to rank cards in order (i) to reflect which soil functions they consider as important for their cultures and (ii) to identify the practices they consider as influencing soil biodiversity and related functions. Results showed that each country is characterized by specific farmers' knowledge, reflecting different management strategies and needs. The national context and the economic development stage of farming, including institutions, market conditions and availability of different inputs, have a clear influence on how farmers manage and try to protect their soils. Furthermore climate conditions differed between countries. Different combinations of these factors seem to be the main drivers for soil management differences in the studied areas.

Effects of inter row soil cultivation in French vineyards - Benefits for earthworms and economic implications

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Ecosystem services related to biodiversity are essential for agriculture. They can be provided by organisms such as earthworms which play a major role in soil structure, stability and fertility. In vineyards, winegrowers keep bare soils in the inter-rows in order to prevent any loss in quality or yield of grapes. However, high management intensity, including high quantities of pesticides and high levels of mechanization, threatens soil biodiversity. Hence, conserving vine inter-row vegetation and landscape complexity to favour ecosystem services such as soil stability, biological pest control, and pollination can be defined as environmentally-friendly wine production. Wine consumers are more and more interested by this kind of wine production, which could change their purchasing habits towards "greener" wines.

The objective of this research work is to understand the ecological and economic impact of inter-row vegetation on (1) earthworm communities in vineyards, (2) viticulture landscapes attractiveness for tourism, and (3) the competitiveness of the vineries in France. Our hypotheses are that inter-row vegetation vs bare soil may (1) have higher earthworm abundance and species richness, (2) be visually more appreciated by visitors, and (3) be an asset for wine trading model developed at local scale. Earthworm abundance with respect to management intensity was investigated along with perception by tourists of management practices at the landscape scale and both were integrated in an economic analysis.

Overall, our results show that vegetation in the inter-rows has a positive ecological and economical effect on (1) earthworm abundance and species richness, (2) landscape attractiveness for tourism, and (3) vineries' competitiveness if they adopt a local marketing strategy promoting complex landscapes and biodiversity.

The outcome of this work allowed us to recommend extensive vineyard soil management promoting inter-row vegetation that could be beneficial for both vineyards soils and wine market.

Consumers' Awareness of Eco-designed Packaging: A Big Step towards Solving Ecological Issues

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Due to man's anthropocentric and irresponsible attitude towards the environment, serious ecological issues such as air, water and soil pollution, climate change, land degradation and bio-diversity loss, deforestation, the destruction of wetlands and other forms of land conversion, have occurred. Explosive population growth and the process of urbanisation, industrial and technological development, increased water consumption, air and noise pollution, the growth of solid waste generation, transport and mass tourism development, etc. are among the most important reasons for the situation. Humankind should make a balance between the desired industrial development and environmental capabilities. Nowadays, the conservation of the environment is one of the most important issues that increasingly attracts world attention. There are many forms of environmental conservation, from responsible practices of businesses and large corporations, to man's everyday habits in practice. The paper focuses on concern for the environment specifically related to consumers' buying patterns. This can be achieved by paying more attention to what we buy and not using resources unnecessarily. In this paper the authors describe the role of eco-designed food packaging in order to increase ecological consciousness and give a theoretical background of the concept. Moreover, the importance and types of ecolabelling are presented. In order to explore if consumers care about ecological issues while purchasing goods, and if we really consider their perception of eco-designed packaging as a part of their ecological consciousness, a survey on a sample of consumers from Croatia was conducted. The results suggested that Croatian consumers are more concerned about environmental changes and their purchasing behaviour has changed in this regard. There is a growing trend to support the environment by the preference of products that use eco-designed packaging, and moving away from disposable packaging to recyclable and reusable packaging has also increased.

Eco-anthropology in Lower Loire: waterfowl hunting and related knowledges

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The project takes place in France, in Loire'estuary (Loire Valley, west of the country). Islands, composed of wetlands (including swamps) can be found on this site. A specific flora can be observed in those islands, grazed by cattle, floristic species being submitted to salinity and submersion. Those factors depend on tides, the Loire and atmospheric pressure. Four islands are studied: Chevalier, Pierre-Rouge, Lavau and Pipy islands. In those islands take place a particular activity : hunting. Loire Valley is a shelter for many bird species, for their reproduction as for their migration; thousands individuals of Anatidae, Rallidae and Wader pass through the wetlands. The hunt of those species is called " waterfowl hunting ". Different ways to hunt exist and take place there, depending on the *environment*. We define " environment " as Tim Ingold does it. The different ways to hunt depend on many factor. Tides, climate, topography and eco-ethology of the hunted species must be considered by the hunters.

We try to answer different questions as i) how do hunters mobilize their knowledges, ii) how do they convey them, between hunters (if there is convey) or between generations, also iii) how did those practices modify the environment ? We also want to compare two different kind of knowledges : the ones known by hunters living in the swamps (Traditional knowledge in local conception, LTK) and the academic ones, known by people working and living in that same environment, like naturalist for example (Traditional knowledge in modernist conception, MTK). Considering the methods, qualitative interviews and participants' observations in a ethnographic way are used.

We expect hunters to mobilize their knowledges thanks to their field experiences. Those knowledges only make sense in the environment they are living in and they are not aware of them.

*Speaker

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Historical overview patterns of natural vegetation cover as support for the regularization of the compensation mechanisms from Legal Reserve established by the New Forest Act

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Compensation is one of the ways to comply with the liabilities provided from the Brazilian law as a counterbalancing mechanism for non-mitigable environmental impacts, which allows owners or holders of rural properties not to comply with their legal reserve (LR) compensate in another properties with surpluses of native vegetation. Non-Fulfilment to with liabilities leads to the owners punishment with administrative sanctions. However, according to article 68 of New Forest Act (NFA) (Federal Law 12.651/2012), owners that made a suppression before July 22, 2008, are required to comply with the liability in accordance with the legislation in force at the time, without administrative sanctions. The complexity of the understanding of the article in function of, for example, the different conceptualizations on vegetation contained in the previous laws, added to the difficulty of historical verification of the suppression in relation to the legal framework, makes the processes of deficit cover vegetation analysis and consequently the signing of a Term of Commitment foreseen in the Environmental Regularization Program (ERP) a weak process. This project aims to analyze an interpretation of the rules for demarcation of areas conserved in rural properties in laws prior to Federal Law 12.651 / 2012, to generate maps of native vegetation cover in the past based on this interpretations and existing models, as well as map of deficit and surplus of native vegetation for LR compensation, providing the public authority a tool for effective implementation of the ERP in São Paulo State and promote restoration in properties with environmental debts.

Posters

Landscape Ecology

Impact of urbanisation on plant compositional and functional diversity

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54 per cent of the world's population lives in urban areas, a proportion that is expected to increase to 66 per cent by 2050. Projections show that urbanization combined with the overall growth of the world's population could add another 2.5 billion people to urban populations by 2050. Yet, urbanization is known to lead to biodiversity decline and several studies show that urbanization leads to taxonomic and functional homogenization. Such effects are likely to impact the ecosystem services provided by biodiversity. This study is a component of the "Dynamiques" project, that aims to investigate how the process of urbanisation currently undergoing on the Plateau of Saclay will impact biodiversity dynamics and the associated ecosystem services. In this study, we examined how the taxonomic and functional diversity of plants vary along an urbanization gradient on the plateau of Saclay and Limours. More precisely, we studied the influence of the density of the impervious landscape, and of the green infrastructure on taxonomic diversity and the influence of urbanization on entomophile flora. Results have not been conclusive for the impact of the density of impervious landscape on taxonomic diversity. However, entomophile flora has underwent negative impact from agriculture but not from urbanization. The possible explanations are discussed.

Factors influencing the distribution of common herbaceous plants within vineyard landscapes

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Many anthropogenic factors influence the flora distribution, in particular in human-dominated landscapes. However, one challenge is to better understand the ecological processes involved and their related spatial scales. Vineyard landscapes are an example of cultural landscape, highly fragmented, and composed of many semi-natural habitats, usually of very small area. The aim of this study is to analyse the distribution of common herbaceous plants in relation to anthropogenic factors at local and landscape scale. Twelve one-km² study windows, with at least 33% vine cover, have been delimited in one region of the Loire valley: the Saumur-Champigny controlled origin appellation (AOC). The study windows were sampled according to four types of vineyard landscape common within in this study area: wooded (> 30% woodland cover), built-up (> 20% built-up), mainly vine (> 66% vine) and mixed situations (> 8% woodland and > 8% built-up). All semi-natural habitats within these 12 study windows (a total of more than 3 000 stations) have been mapped and visited in the field to record their local ecological characteristics and the presence-absence of eight herbaceous species. Several landscape ecology indices were calculated for each station in buffer zones ranging in size from 100 m to 500 m. These semi-natural habitats represent on average 10 % of the total area studied and are overwhelmingly dominated by herbaceous vegetation. Some local variables can explain the presence of several plant species (presence of trees or hedges for *Gallium aparine*, or neighbourhood of vineyard for *Capsella bursa-pastoris* for examples). However, landscape scale variables are also largely correlated to plant distribution. These results are discussed taking into account species dispersal strategies.

*Speaker

Role of host plant distribution at the landscape level on *Drosophila suzukii* (Matsumura) (Diptera:Drosophilidae) colonization in vineyards

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Insect movements are partly governed by landscape context and especially by abundance and spatial configuration of host patches. *Drosophila suzukii* (DS) is a polyvoltine invasive fruit fly species attacking several plants including grapevine. Our study aims at analyzing how the distribution of alternative host plants in the landscape affects the colonization of vineyard plots. We selected 20 vineyards in Saint-Emilion area to build a gradient of landscape composition in terms of alternative resources for DS. We digitalized the land use around each vineyard in a radius of 100 m and surveyed all patches of alternative resources. We calculated various landscape composition or configuration indices to quantify landscape context. Population monitoring of the flies was carried out by: i) trapping adults along a gradient of distance to the edge at 4 dates in 2016; ii) sampling bunches at 4 different dates up to harvest and at different distances in the plot to monitor infestation levels on grape. *Drosophila suzukii* accounts for half of the total number of flies caught. We found a significant positive relationship between the distance to alternative host plants in the landscape and the level of DS populations. The results were similar for cluster infestations with earlier and numerically superior attacks of DS when the distance to host plants was reduced. Our results suggest a significant flow of DS from alternative resources in the landscape within the main crop vineyards. Additional analyses incorporating other landscape variables as explanatory variables are in progress. This work should make it possible to define more precisely areas at risks of high DS pressure and will therefore guide landscape scale management strategy to limit the impact of DS on grapes.

Landscape effects on pollinator communities in grasslands and wet meadows along the Sélune river, France

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Pollinators provide a crucial ecosystem service by contributing to the reproduction of many wild plant species as well as crop plant species. Pollinators are facing pressures from multiple drivers leading to their declines with potentially serious implications for human food security and health, as well as ecosystem functions. Concern over pollinator declines has sparked a remarkable increase in studies assessing threats to pollinators and quantifying the impact of their decline on pollination services. Landscape changes have been identified as one of the major drivers of pollinator declines. Thus, understanding the effects of landscape composition and configuration on pollinators is crucial for the prevention of further pollinator loss and to help design strategies to protect pollinators in human-dominated landscapes.

Most previous studies examining the response of pollinator richness, abundance and composition to landscape composition showed a negative effect of the proportion of agricultural land. Landscape configuration can also play an important role: decreased patch size and reduced connectivity of landscape elements have been identified as important drivers of species richness declines. However, studies assessing the effects of landscape characteristics over time, even within a year, are less common. Furthermore, the majority of existing literature focuses on specific hymenopteran groups, but there is a lack of information on the effect of landscape on non-bee taxa and plant-pollinator interactions.

Here, we investigated the response of pollinator communities to landscape composition and configuration. To capture the intra-annual variability of plant-pollinator interactions, we surveyed both pollinators (honeybees, wild bees, bumblebees, syrphids and butterflies) and flowering plants, every 15 days from May to September 2018. Surveys were carried out in 7 grasslands and 7 wet meadows located along the Sélune river, Manche (France). Fields were selected to represent a gradient in landscape heterogeneity.

A methodological approach to consider ecological equivalence for native vegetation compensation in Brazil

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Most of the remaining native vegetation (53%) in Brazil is in private lands, protected by the Forest Act, reviewed in 2012. One of the main mechanisms to foster conservation is the "Legal Reserve", which is a percentage of native vegetation (varying from 20 to 80%) that each landowner is obliged to maintain in rural properties. When this percentage is not reached, landowners have two options for compliance: vegetation restoration within the property or compensation outside the property. According to the Forest Act, compensation is possible within the same biome and without the need to consider any ecological equivalence criteria. However, Brazilian biomes are large and heterogeneous, and compensation done exclusively based on economic criteria can be detrimental for biodiversity conservation. To avoid those negative impacts, the supreme federal court reviewed recently the Forest Act requiring now ecological equivalence for compensation. In this context, we developed a method to identify ecologically similar areas to guide *Legal Reserve* compensation and applied it to the State of São Paulo. We measured watershed similarity considering abiotic and biotic variables. For abiotic similarity, we used fourteen variables including soil, relief and climate characteristics, and applied an Euclidian distance and the Ward method to cluster similar watersheds. For the biotic similarity, we used species distribution models of 1,840 endemic and endangered species (mostly birds and vascular plants) and applied the Jaccard similarity index. The results showed that it is possible to calibrate the level of ecological equivalence to be required in order to allow a good balance between legal reserve deficits and surplus in a same ecological equivalent region, promoting local trade of legal reserves or the restoration of pasture areas with low agricultural aptitude. By considering ecological equivalence, it is possible to minimize biodiversity losses and guarantee a better spatial distribution of ecosystem services provision.

Key drivers of earthworm community and soil microbial biomass distribution at landscape scale and ecosystem service associated: SoilServ project.

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Soil biodiversity is strongly impacted by anthropic parameters such as land use and agricultural practices, and also by environmental factors such as pedological and climate contexts. Therefore, environmental context (natural and anthropic) are strong drivers of soil biota spatial distribution. For some taxa (e.g. microorganisms, earthworms, carabids) this spatial distribution has been assessed at field, regional, national and European scales, but the key drivers of this distribution depending on the studied scale are still unknown and models still need to be developed. In SoilServ project, one of the aim is to collect biological data in order to answer the following questions: (i) which are the environmental drivers (soil characteristics, land use management, agricultural practices) that affect soil biota? Are the drivers of soil biota spatial distribution the same when changing scale (i.e. how does soil biota structure change depending on studied scales)? In march 2018, 90 points were sampled on Naizin catchment (5 km²), on both crop fields and pastures; in may 2018, another campaign limited to crop field was done. Results presented in this study will focus on earthworm community and microbial biomass distribution and the relationship between soil organisms and infiltration rate.

Posters

Palaeoecology: How today's
ecosystems became what they are?

Palaeoecology: How today's ecosystems became what they are?

Micro-biodiversity patterns assessment of peat bog in Pays de Bitches (Moselle): consequences of environmental and biochemical changes?

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Peat bogs have an important role for the environment and the society (eg, carbon sequestration, water filtration, etc.) but they are sensible ecosystems easily affected by several external factors such as fire, climatic changes or land use changes. Therefore, since few decades they are heavily studied and significant conservation and restoration programs were developed. However, an important component of the peat bogs remains still poorly documented so far. Indeed, the composition and the richness of the microorganisms living into the organic sequences remains hardly reliable to any determinism, such as historical environmental or biochemical changes. When considering the key role that play microorganisms in the biogeochemical cycle of the peat bogs, such questioning appears to be a key issue to understand the functioning of peat bogs. And thus this questioning is crucial for conservation and/or restoration of the current state of such particular environmental. Therefore, we developed a research project that aims to assess the link between micro-biodiversity patterns in peat bogs to environmental and/or biochemical changes.

Our study area is in the Pays de Bitche, where we have got selected two study areas: the Katzenbruch peat bog, located in the military camp of Bitche, and the Horn peat bog, in the soundings of the camp. On both area we compare the biodiversity patterns of vegetation and microorganisms related to the occurrence of natural or anthropogenic disturbances and to the potential chemical contaminations due to the historical military activity on the area. To do this on each study site we analyzed 1) various biological indicators regarding both paleo-environmental and microbial fields, 2) several physical-chemical measures, and 3) we defined the chronological frame of the archives. We present here the first results of this innovative research project.

Palaeoecology: How today's ecosystems became what they are?

Investigating the long-term recurrence of nostocalean cyanobacteria through a 6 700 years core in a eutrophic Lake.

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Cyanobacteria are photosynthetic procaryotic organisms living mostly in aquatic ecosystems. Cyanobacterial proliferations are generally associated with excess input of nutrients, in relation to anthropic activities (adjustments on the catchment basin or direct emissions). In this context, Lake Aydat (Auvergne, France) has been for several decades particularly affected by proliferations of Nostocales (cyanobacteria with heterocysts). This cyanobacterial order has the distinctive characteristic of being able to produce resistant cells, called akinetes, which are able to persist in sediment. In order to determine the origin and recurrence of the cyanobacterial proliferations on this lake, the distribution of akinetes was analysed on a sediment core, which integrated a temporal sequence of 6700 years. Through the setting up of a sediment extraction protocol followed by microscopic observations of benthic akinetes, four morphotypes were discovered. Despite different temporal distributions, the highest abundances were found, for all the morphotypes, between 1,800 and 1,500 cal. BP, with numbers reaching 200 000 akinetes per gram of dry sediment (g.DW-1), thus concentrations that were equal to the second half of the 20th century. Simultaneously, the akinetes integrity was analysed, and also revealed substantial temporal fluctuations. The highest numbers of intact akinetes were reached at 5,500 cal. BP,

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Posters

Participative Sciences in Ecology

Impact of various land uses and the associated practices of management, on earthworm communities in the urban soils of Ile-de-France via an approach of participative science

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Urban soils are characterized by a strong spatial heterogeneity of their physical, chemical and biological properties (Béchet et al., 2009; Schwartz, 2009) and the hypotheses of spatial continuities usually used in pedology cannot thus apply (Franck-Néel et al., 2012). Although the publications concerning urban soils represent only 2 to 3 % of the articles of pedology (Ranjard, 2017), research initiatives multiply to understand their biological characteristics and their (dys-)functioning (Séré, 2007; Baize and Girard, 2009; Huot, 2013; Jangorzo, 2013; Morel et al., 2014).

To knowledge the distribution of earthworm communities into these specific urban areas and sensitize citizens to soil biodiversity conservation, University of Rennes 1 and the Regional Agency for the Biodiversity of Ile-de-France deployed "l'Observatoire Participatif des Vers de Terre" (https://ecobiosoil.univ-rennes1.fr/OPVT_accueil.php) on urban areas of Ile-de-France. This participative network is specifically turned towards earthworms because of their role as engineers in soil ecosystems and as bioindicators on land management and land use. The aim of this work is to understand which anthropological factors influence earthworms in these special ecosystems.

Participative Sciences in Ecology

Since 2016, more than 150 sites were sampled with two principal sampling protocols (Mustard and Spade test). 300 people attended the formation and the half contribute at this participative prospection. First results of 2016 and 2017 show large differences of abundance (from 0 to 1600 i/m²). Depending of the land cover, home gardens have the best abundance when lawn and agricultural grassland the worst. Despite these differences, urban soils reveal a very large diversity (32 taxa) on relatively small areas (territory from 70 to 100 km²). In home gardens, richness was significantly influenced by fertilisation especially for epigeic group. Novel results of 2018 will be discussed in comparison to the practices.

French national long-term monitoring program to assess earthworms' response to the agricultural practices in farmlands

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In order to assess the non-intentional effects of agricultural practices, particularly pesticides, on farmland, the French ministry for agriculture has been carrying out a biovigilance program since 2012. The objectives are i) to be able to detect changes in agricultural practices, including pesticides uses, through indicators of biodiversity, ii) to enhance knowledge of the mechanisms of biodiversity responses to agricultural pressures. Earthworms have been selected to be one of the four bio-indicators of this survey. At the national scale, 500 fields have been selected to achieve representativeness of the different regions, landscapes and pedoclimatic contexts in France. Three cropping systems were chosen Crops (winter wheat and corn), ii) vineyard and iii) market gardening. Earthworms are sampled by non-expert observers with the mustard method adapted by the OPVT (participative earthworm observatory). They are counted and identified according to their levels of development and their ecological categories (epigeic, epi-anecic, strict anecic and endogeic). Then they are kept in alcohol and sent to our laboratory of University of Rennes 1 who can confirm the field identification and proceed to a determination at sub-specific level. In addition to the constant variables (such as soil texture, climate zone...), a wide diversity of detailed information are collected each year like tillage (tools used, depth...), fertilizers, chemicals treatments (type of pesticide, active substance, quantity...) or crops rotation. Between 2013 and 2016, 1.869 sampling of earthworms have been done in 518 distinct. Earthworms' abundance is significantly impacted by land cover, administrative regions and the year of sampling. Earthworms' abundance is significantly lesser in market gardening crops than in vineyards or crops. Earthworm's richness increases with the decrease of soil work. The analysis of the impact of agricultural practices and cropping systems are in progress. Thanks to this monitoring we could know how each year influences earthworms' abundance.

The Herbonauts website: a citizen science project to acquire plant metadata over the four past centuries, from herbarium collections

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Natural History Collections allow tackling many questions in ecology and evolution, through the data provided by both the specimens themselves and the labels linked to the specimens, with rare advantages: data are real, spanned over time, checkable for accurate identifications, and the preserved physical objects make them not questionable. In particular, Herbaria represent millions of actual plants records collected in all continents since four centuries. However, such records linking a plant species to historical and ecological information (location, altitude, date, phenology...) are available for analyses only once all information has been read on herbarium labels, transcribed, and databased. Although it is challenging to complete such a task for large Herbaria, the Paris Herbarium (Muséum national d’Histoire naturelle, France) completed a first step toward the goal with the most ambitious digitization project ever conducted on the world’s largest Herbarium. All 6,000,000 specimens of vascular plants have been digitized with all images freely available online at <http://science.mnhn.fr/institution/mnhn/search>. As the second step, the Muséum launched in 2013 a participatory science project (<http://lesherbonautes.mnhn.fr>) to enrich the database with transcriptions of herbarium labels done by general public who read images and answer questions. To encourage participation, small subsets of the herbarium (called ‘missions’) are presented to the participants (named ‘herbonauts’), and are thought to provide a specific research project with data. Hence, the program has been successfully solicited by a diversity of projects aiming at e.g. studying endemism and macroecology in New Caledonia, or studying the genomics of local adaptation in parasitic weeds of major crops in Africa, or looking for phenological evidences of climate changes, or characterizing metal hyperaccumulator plant species, or defining Important Plant Areas for conservation, etc. The Herbonauts is a program of the national French Research infrastructure e-ReColNat, supported by the National Research Agency (ANR-II-INBS-004).

First Bioblitz on a French campus: Rapid biotic

Participative Sciences in Ecology

and abiotic inventory at Campus Beaulieu of the University Rennes

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The very first Bioblitz on a French campus took place at the Campus Beaulieu of Rennes University in June 2018, organized by the EcoBio lab. Infrastructures and green spaces on the campus have recently been modified by the construction of a new underground line.

While existing historical data provided an overview of past changes on the campus, this All Taxa Biodiversity Inventory (ATBI) in 24 hours, with the help of faculty members, students of the campus and local naturalist NGOs is the set off for a long-term monitoring program.

In perspective, teaching programs and citizen science events, such as this Bioblitz, will ensure the monitoring of the evolution of these areas.

Influence of taxonomical resolution on mutualistic network properties

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Citizen science has provided, over the past few years, a considerable amount of data to ecologists. It allows for more presence in the field over a larger geographic range than what individual research teams could collect on their own. In particular, when working on interaction networks, it takes a tremendous amount of effort to observe a satisfying portion of the network; citizen science could reach that effort much more easily. One problem that has been raised with citizen science is that, as participants are not specialists, they may be less able to correctly identify the observed species. This limitation is important when observing Plant-Pollinators interactions, and citizen scientists observations tend to be limited to the genus or even the family, while most properties of interaction networks have been studied and established on networks determined to the precision of the species.

Here, we examined whether taxonomical resolution influenced the properties of a mutualistic network. We used 49 mutualistic networks from the literature. We calculated classically used metrics for those matrices and the corresponding ones at the genus and family level. We then showed that, while the value of each metric varied from species to genus to family matrix, the relative order of the matrices' values was conserved.

This shows that we cannot use the naked values of the metrics for genus or family-level matrices. However, in a single study, it is possible to use genus or family-level networks to establish a trend of interaction network properties along a gradient. Thus, citizen science (or any photograph- based protocol, that only allows morphospecies identification at best) remains relevant and useful to build mutualistic networks and study the influence of diverse factors, such as urbanization or conservation efforts, on those networks.

Expeditionary Learning: High school students investigate aspects of landscape and marine ecology

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The project aims at involving high school students in ecological sciences and at broadening their understanding of ecological systems. The study regions are the coastal environments of Northern Germany. After a class has decided whether to focus on landscape or marine ecology, the students form groups, read up on topics they are most interested in and develop their own research questions. They plan their investigations, decide what kind of equipment they need and collect data in the field. Eventually they analyse their data, compare them with results from the literature and put them into a larger context. Finally the results are presented and ecological implications as well as alternative management measures are discussed. The project takes four to five days including one day of preparation at school. During the whole process the groups are supposed to work as autonomously as possible. Whenever necessary or requested, however, they are supported by scientists of the Kiel Science Factory. Besides evaluating whether the students gained a deeper understanding of ecological systems, it was also assessed whether their participation in the project changed their perception of scientists and scientific jobs and had an effect on their job perspectives. The Project is carried out by the Kiel Science Factory and is funded by the German Federal Environmental Foundation.

Posters

Population and Community Ecology,
From Micro- to Macroorganisms

Top-down control of prokaryotic population in temperate freshwater systems (French Massif Central)

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The relative importance of viral life strategy (lytic and lysogeny) and heterotrophic nanoflagellate grazing (top-down factors) on prokaryote mortality was determined in the euphotic zone of 19 freshwater lakes located in the same geographical region (French Massif Central). Flow cytometry indicated that viral abundance ranged from 0.5 – 26.3 x 10⁷ viruses mL⁻¹, exceeding prokaryote abundance by approximately 16-fold on average. Multiple regressions revealed that among the prokaryote subgroup, high nucleic acid content prokaryotes explained for significant variability in the total viral abundance and served as principle host target for viral proliferation. Among the viral life strategies, lytic infection contributing to 9 to 76% of prokaryotic mortality in June and August, whereas lysogeny (1 to 38%) was more evident in July in the majority of sampled lakes. High viral mediated prokaryotic mortality as observed in some of our lakes indicates that a significant prokaryotic fraction is recycled in the prokaryote–virus–DOM loop (viral shunt), contributing to carbon and nutrient cycling. The temporal shift in viral strategy was controlled by the availability of phosphate and chlorophyll concentration via host cell growth, with high concentrations favoring lytic infection and low concentrations supporting lysogenic infection. Antagonistic interactions between viral life strategies supports the hypothesis that lysogeny may represent a survival strategy for viruses in harsh nutrient/host conditions. The dominance of viruses over flagellates, or vice versa, as prokaryotic mortality factors differed among the lakes. The significant contribution of both the top down factors (34 to 89%) towards prokaryotic mortality indicates that viruses and flagellates are likely to act additively in their effects on prokaryotes by regulating the proportion of active members of the prokaryotic community. Such a combined effect of viruses and flagellates may strongly influence the planktonic food web and whole ecosystem functioning.

Population genetics structure of a desert- adapted Hindu sacred tree: *Prosopis cineraria*

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Prosopis cineraria, referred as Khejri in the northern Indian state of Rajasthan grows in semi-arid conditions. The tree has been praised for hundreds of years by locals (cf Bishnoi ethnic group) considering its enormous adaptability to scarce resources and desert conditions, and it yields a high nutrient enriched fodder. The tree is locally used in Ayurvedic medicine and agroforestry, but a scientific perspective is needed to unearth the ecology of the species behind the myth. A decline in the population density has been reported for the last 3 decades within important agricultural regions of Rajasthan, making it an urge to understand how the believed ancestral population of khejris in Rajasthan is genetically structured.

Prosopis cineraria's diversity is believed to be consistent with the distribution of 10 agro-climatic zones defined in Rajasthan.

As a part of my PhD research in which I aim to get a better knowledge of the ecological role of Khejri tree in Rajasthan, a large sampling campaign in partnership with Amity University Rajasthan of Jaipur was conducted in these 10 predefined zones. From May to November 2016, plant tissues from 414 individuals have been collected. The genomic resources of this species are scarce and I used 3 DAMD and 5 ISSR molecular markers already established to be polymorphic for this species to study the genetic diversity and its distribution (SPAR method).

Results showed a high level of genetic diversity neither evenly distributed through Rajasthan nor according to the agro-climatic zones. Khejri tree population maintains a high level of gene-flow and a potential local adaptation to the climatic diversity of North-East India.

The Ascochyta blight Complex on pea: Competition between different strains of two pathogenic fungi exhibiting different life history strategies

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The environmental heterogeneity and the genetic variability of the host plant population are key factors that govern the biology of the pathosystem, the epidemic dynamic and the interaction between the co-infecting species to take advantage of host resources. In a parasitic complex, the simultaneous presence of pathogens may affect the behavior of each of them through direct and host-mediated interactions. These interactions can affect pathogens virulence and transmission, and thus modify their epidemiological dynamics. Based on the example of ascochyta blight on pea we try to respond to two key questions (*i*) What Life History Trait(s) (LHT) contribute most to the interactions between the co-infecting species? (*ii*) Does the outcome of co-infection change with the varietal resistance and the evolution of plant organs physiological state? These issues are explored on detached stipules bioassays to evaluate different LHT (incubation period, latent period, necrosis development, spore production) from 28 strains of *D. pinodes* and 23 strains of *P. pinodella* on two pea cultivars (susceptible, and partially resistant). The analysis of LHT diversity allowed us to identify an interspecific diversity for most LHT. In particular we highlighted that the initiation and the colonization stages of the disease are faster for *D. pinodes* than for *P. pinodella*. Furthermore, this analysis underlined a trade-off between, on the one hand, spore length and the rate of bicellular spores and, on the other hand, the amount of offspring produced. The LHT study also showed an intraspecific diversity for both species with similar host exploitation pattern between strains belonging to different species. The selection of strains with contrasting LHT will allow us to control if LHT contribute in the same way as for the outcome of co-infection and if the outcome of these competitive interaction depends on species or individuals behavior patterns.

Transgenerational plasticity in response to competition in clonal plants

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In a context of global change, exploring the adaptive processes in response to rapid environmental variations is a major challenge. Plants are sessile organisms forced to cope with the locally fluctuating conditions of their environment. However, most of them produce new genetically identical individuals, through clonal growth (i.e. without meiosis or fecundation processes) limiting the possibility of genetic adaptation by selection. It is thus theoretically expected that clonal plants favor phenotypic plastic responses.

Phenotypic plasticity can be expressed in response to competitive interactions. Recent studies demonstrated that the parental environment can additionally affect the plastic response of offspring produced through sexual reproduction, and increase its fitness. This phenomenon referred as to "transgenerational plasticity" (TGP) has nevertheless never been tested on clonal generations in response to competition.

Our study aimed then at demonstrating TGP in six clonal plant species of wetlands in response to competition. These plant species were cultivated under controlled conditions in presence or absence of competitors for two clonal generations. Performance (individual biomass) and aerial traits (height, SLA, and LDMC) were used to characterize the individual plastic response to competition. We demonstrated varying patterns of response depending on the studied plant species, involving different aerial traits. Most importantly, we detected TGP. The ability of clonal plant species to display TGP would be related to their clonal growth strategy (either guerilla or phalanx). We argue that TGP is of particular importance in fluctuating environments and would act as equalizing mechanism supporting plant species coexistence.

Local foraging habitat selection as a tool for measuring spatial partitioning of two sympatric seal species *Halichoerus grypus* and *Phoca vitulina* in the Northeast Atlantic

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In the Northeast Atlantic, grey and harbour seals live in sympatry, with contrasted population dynamics. Although they share the same haulout as in the Firth of Tay (FoT) and in the Eastern English Channel (EEC) respectively in Scotland and France, little is known about their potential spatial overlap or partitioning at-sea. The habitat selection represents an important tool to evaluate the potential competition of interacting species. The objective of this study was to examine the foraging habitat selection and spatial usage of these two species in the FoT and EEC, depending on the influence of inter-specific interactions. We tagged 10 harbour seals and 8 grey seals in the EEC, and 9 harbour seals and 8 grey seals in the FoT. In both study areas, grey seals used more offshore areas: their median trip maximum extent were 15 Km from their haulout sites; while harbour seals performed trips in more inshore areas, with median values of 4 Km and 5 Km for the FoT and the EEC respectively. Moreover, mixed models revealed that these two species selected different foraging habitats in the two study areas. In the FoT, grey seals selected coarse sediments, and tidal currents faster than 0.4m/s; while this feature had a negative influence on harbour seals' foraging habitat selection. In the EEC, grey seals selected foraging habitat over muddy seabed with strong tidal currents (> 0.6m/s); while harbour seals selected low tidal currents over sandy seabed. These results suggested potential spatial and foraging habitat partitioning. This was quantified with the Bhattacharya Index, which supported the hypothesis of spatial partitioning as they were low representing 0.5 and 0.3 respectively for the EEC and the FoT. Spatial partitioning may represent the "ghost of competition past" allowing these two similar species to cohabit in part of their range.

Response of carabid communities to tree species mixtures in the context of climate change

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Community assembly theory posits that habitat composition and structure drive local species assemblages through resource availability and niche opportunities. In forests, which shelter the majority of terrestrial biodiversity, it is thus predicted that tree species richness and vertical stratification would be main drivers of animal diversity. Literature also suggests that microclimate is a local driver of soil macrofauna biodiversity, while it is increasingly acknowledged that forest diversity can also modify microclimatic conditions, buffering temperature variations and increasing soil and air moisture. We used a tree diversity experiment to test the effect of forest biodiversity on carabid communities through direct and indirect effects on habitat diversity and quality. In the ORPHEE experiment, eight blocks have been established with 32 plots of 100 trees in every block, corresponding to all possible combinations of one to five tree species (*Betula pendula*, *Quercus robur*, *Q. pyrenaica*, *Q. ilex*, and *Pinus pinaster*). Four blocks were irrigated during the tree growing season so as to suppress any summer drought, whereas the other four blocks are kept unirrigated so that plots experience chronic water stress conditions. We set pitfall traps to collect during six months (April to September) and evaluate the response of ground beetle communities to the irrigation x tree diversity interactions. We considered three sets of explanatory variables in interaction with the drought treatment: the height and composition of understory vegetation, of tree plots, and of surrounding plots as proxies of surrounding landscape heterogeneity. Results show that all tested variables are relevant to explain the species richness, abundance and diversity of carabid beetles but that their relative weights vary for dominant carabid species. Outcomes suggest that tree diversity would improve the resilience of forest carabid communities to the drought disturbances that will increase in severity and frequency as a result of climate change.

Use of sterols as biomarkers of trophic relationships in a mountain headwater stream.

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Sterols are precursors of compounds with a high physiological activity for freshwater invertebrates, such as ecdysteroids hormones involved in molting processes. It is noteworthy that arthropods are unable to synthesize sterols *de novo* and have to gain them from diet. In aquatic food webs, sterols mediate carbon transfers across autotroph-herbivore interface and thus represent essential compounds constraining bottom-up regulation in ecosystems structure. Concerning streams, most of the aquatic arthropods are polyphagous and must use sterols from allochthonous sources (leaf litter) or autochthonous primary sources. Important differences in sterol compositions occur between freshwater hyphomycetes with ergosterol being their major sterol, and leaf litter from riverine trees that contain a mixture of 24-ethyl sterols and 24-methyl sterols. In contrast, there is a larger diversity of sterol distributions in epilithic microalgae. In this context, sterols can be used as biomarkers to trace trophic links. They may be also useful for assessing the importance of the different food sources in meeting the arthropods need for essential nutrients. To gather information for the accuracy of these lipid biomarkers we conducted a study in a headwater stream containing a low diverse invertebrate community. Sterol distributions were characterized in basal sources (epilithic biofilm, leaf litter, fine organic particular matter and bryophytes) and three macroinvertebrate species assigned to different functional feeding groups (*Gammarus pulex*, *Heptagenia assimilis* and *Rhyacophila praemorsa*).

Comparison of species and individual fish habitat selection models in rivers

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Habitat selection depends on individual and species behaviour. Describing and understanding the process of habitat selection by organisms is crucial to better quantify biological responses to natural and anthropogenic habitat alterations. Fish habitat selection models in rivers, developed at the species level and at the scale of microhabitats around organisms, are frequently coupled with hydraulic models of stream reaches to predict potential changes in abundance due to modified flow regimes. Using current statistical developments, we developed habitat selection models for 31 fish species using very large data sets collected from 10 rivers (34 sites, 145 surveys). We linked abundance to hydraulic key variables (e.g. water depth) using a negative binomial distribution hypothesis to account for the overdispersion of abundance counts, and using mixed effects models to deal with the spatial and temporal variability of abundance and habitat selection between surveys. To improve models and prediction of environmental changes on species dynamics, individual behaviour component comprehension is required. Thus, we compared the individual and species levels of fish microhabitat selection for three species (barbel, n=5; catfish, n=6 and chub, n=7) of the Rhône River. These fish lived in a highly variable environment subjected to hydropeaking and locally warmed by the cooling system of a nuclear power plant. We used fixed acoustic telemetry technique in a 2-km reach to continuously survey individual over a three months period. Abiotic habitats were defined by current hydraulic conditions (e.g. water depth) and past hydraulic conditions (e.g. dewatering risk). Mixed-effects habitat selection models indicated that individual effects were as strong as specific effects. Models also indicated that fish selected both current and past hydraulic conditions. Although consistent with the static fish habitat selection models, our quantitative results demonstrate temporal variations in habitat selection, depending on individual behaviour and environmental history.

Vegetative sprouting responses of cork oak (*Quercus suber* L.) in relation to fire damage in the Beni Ghobri forest (North center, Algeria)

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The aim of this research is to contribute to the study of post-fire vegetative sprouting responses of cork oak. This type of study is needed in Algeria, due to the increasing number of fires raging in the cork oak forests, already heavily impacted by human action.

The selected study site is the forest of Beni Ghobri (Tizi Ouzou), mainly consisting of cork oak, affected by fire in September 2014.

According to a subjective sampling we selected 63 plots, each including an average of 30 trees, 2272 trees were sampled. For each plot, we noted the ecological (elevation, slope, aspect) and dendrometric parameters, such as (tree height, Bark thickness, Diameter at breast height (DBH), chair height).

Vegetative response in cork oaks was assessed 16 months after fire by the method proposed by Moreira *et al.*, (2009). We found six different types of tree responses: (A) shoots on the crown only, (B) shoots at the base and on the crown (C) shoots at the base only, (D) dead tree (no regrowth), (E) shoots on all parts of the tree (base, stem and crown), (F) shoots on the stem and crown; the latter two (E, F) are not described by this author.

Over 98,14 % of cork oak survived the fire, 59.20% of which have vigorously emitted shoots on the crown (A) and reconstituted it. Other types of response are as follows: B (21.79%), C (3.35%), E (9.15%) and F (4,53%). Dead trees (D) represent only 1.89% of the total .

Posters Session

Allergens in the City: Effects of novel plant communities on seasonal pollen allergies in urban areas

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Pollen allergies are a leading cause of chronic disease affecting over 20% of adults in Europe. Allergy prevalence have been on the rise in the past decades, particularly in cities. This increase seems largely driven by global changes: air pollution increase human sensitivity to allergens; warmer temperatures and increased atmospheric CO₂ increase yearly pollen production; and the introduction of plant species outside their native range spreads novel allergens – i.e. allergens previously absent from the resident flora. In this context, urbanization – where warmer temperatures, pollution and thriving neophyte invasions shape novel urban ecosystems– is a rapidly changing terrain of allergenic potential.

We investigated how allergenic properties of grasslands change with urbanization in Berlin, Germany. We expected the more urban and neophyte-invaded grasslands to exhibit the highest allergy risk. In 2017, we recorded plant species abundance in 56 plots of grasslands covering a double gradient of urbanization and neophyte invasion. We collected publicly available data on flowering phenology and allergenic properties of 234 plant species, including specific allergenic pollen molecules. Borrowing from trait-based community ecology, we developed new methods to characterize the mean allergenic potential, diversity and seasonal spectrum for each community along the urban-rural gradient.

Urban grasslands of Berlin were not more allergenic than rural ones. Neophytes and Natives were as frequently allergenic (35%). However, neophyte-rich urban grasslands produced a higher diversity of allergenic molecules. Both natives and neophytes contributed to a wider spectrum of molecules in the city, possibly affecting a wider range of people. Increasing human population densities in cities imply that novel allergens may cause more harm in urban than rural conditions. Cities may yet remain a relative haven for people suffering from hay fever, but efforts to identify novel risks and control them early should be a priority in urban nature management.

Challenges and Difficulties of sharing data on biological invasions management

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Since 2002, a working group on invasive alien species management is active in the French Loire watershed. Initiated by the Water Agency, its coordination was taken up by the Nature Conservancies Federation in 2007. The dynamic of the group relies on a structured, active and informed network of practitioners, exchanging information on management techniques and territorial coordinations. Gathering shared and comparable data on localisation and costs has been a target as well as a challenge during this period. In 2018 a new survey to detail the management costs was submitted to the working group and the practitioners' network. It revealed that if more and more species are managed and fought against on a regular basis, it is still very difficult to get any feedback on the elemental data of the projects as well as on the efficiency of the methods used on the site, except in "pilot" projects. The Nature Conservancies Federation proposes in response to these results the definition of a core of informations to gather, accompanied by a users guide for the motivation and voluntary use by the practitioners. It completes a range of tools developed *by* practitioners *for* practitioners, with the help of researchers and scientists : a management strategy at the Loire watershed level, an identification guidebook, another on management guidelines e.g. To perfect these useful and widespread tools, it will be proposed to the stakeholders financing the management projects to send the grid of minimal information and the users guide to the supported project holders, to maximize the return of information.

*Speaker

Restoration Ecology

REaménagement de Carrière ALLuvionnaire (RECALL): ecological diagnostic of alluvial quarries as part of their rehabilitation

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RECALL is a multidisciplinary research project that, through an approach of plant community ecology, geography and philosophy, addresses the issues related to the rehabilitation of alluvial quarries after exploitation. The project fits into the timing of regulatory rehabilitation of Pérouges alluvial quarry (Ain, France). The operator VICAT (aggregate extraction), the FRAPNA-Ain (association for environmental protection) and the communes of Pérouges and Saint Jean de Niost, collaborate to think the articulation between industrial activity, protection of the environment and cultural and recreational uses on the site which becomes an Ecophilopôle project. An ecological diagnosis is undertaken within the gravel pit of the Pérouges site and on a wider perimeter around it. Firstly, a diagnosis of the factors limiting the development of aquatic vegetation (dispersion and abiotic conditions) at the Pérouges gravel pit is realized via the study of the established vegetation, the propagule bank and deposition and the plastic response of the species relating to the environmental conditions (sediment characteristics) and constraints (waves). Secondly, the post-exploitation ecological state of about fifteen quarries which differ in their history and their environmental conditions is evaluated in a Lyon-plain of the Ain development gradient through the study of aquatic vegetation. The results of this work will provide recommendations for future rehabilitation choices and potential for ecological rehabilitation in a territorial coherence but also recommendations on ecological restoration techniques (e.g. shoreline management, sediment improvement, propagule supply) to remove the constraints to the establishment of the aquatic vegetation in large bodies of water.

Ecological restoration and plant succession of dry grasslands in the Haute-Durance valley following soil disturbance

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Large-scale ecological disturbance in grassland is increasing worldwide mainly due to land use changes and habitats destruction. The construction of high-voltage transmission lines in our study area, the Haute-Durance valley in the Southern French Alps, involves a degradation of soil and plant communities along transitory access tracks and construction platforms. In such disturbed ecosystems, restoration is limited by a lack of available propagules and low seedling recruitment due to soil degradation and/or strong summer drought. We focus on the restoration of species-rich dry to mesophilic grasslands covering a large part of the construction zone at an altitude of 1000 to 1400 m. Most of these grasslands are Natura 2000 priority habitats such as N6210 "Semi-natural dry grasslands of *Festuco-Brometalia* and scrubland facies on calcareous substrates" (EU directive habitat 92/43/EEC).

We will present the first results of a study analyzing (1) the appropriate reference community for ecological restoration, (2) hay transfer techniques to overcome dispersal limitation (3) soil preparation to facilitate establishment, (4) the required grazing intensity to favour grassland target species and to avoid the spread of ruderals and shrubs. In a second experiment, we test priority effects on plant succession and restoration by manipulating the arrival order of dominant and subordinate plant species. Due to differences in microclimate and soil conditions depending on slope, orientation of slope and bedrock, plant communities may change at relatively small scales. Additionally, management intensity affects species assemblages. The identification of the appropriate reference community is therefore the first crucial step for successful restoration using

Restoration Ecology

hay transfer but also to evaluate the success of restoration efforts. We will present results on environmental drivers of plant species composition. Based on these results we will discuss the required match of source and recipient site conditions in order to restore dry grassland communities in Southern French Alps.

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Indicators development to evaluate wetlands restoration actions for managers

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Wetlands are ecosystems on which efforts of conservation are being focused as their generalized and continued destruction is linked to water and environment quality. Their ecological functions are important to monitor on the long-term as well as the short-term, as numerous restoration projects are trying to better them. To answer the need of evaluation for the European Water Frame Directive and for the public policies in favour of wetlands, a project to develop indicators of the wetlands functions evolution was carried out. Natural areas managers, in close collaboration with scientists and researchers worked on a toolbox including 11 protocols and 13 indicators (RhoméO, 2009-2013), based on hydric, soil and biological indicators to monitor hydrological, physicochemical and biodiversity compartments. The field results analysis were calibrated for their use in the Rhône watershed, and the toolbox is now used to monitor on long and short-term the variability of wetland functions. Generalizing at the national scale the use of these protocols and indicators implies more questions than only transposing the tools in the monitoring methods, asks for the development of common tools and poses the challenge of the data securing. The national project (MhéO) aims at including a minimal toolbox in each major watershed toolbox, where other tools may be used already. However, the toolbox includes methods respecting several criterias that are not yet matched by these other tools : tested and optimized protocols, reference lists, calibrated indicator... This is why it is important to use the minimal common toolbox on the large scale. The MhéO tools are used today to construct the national French data referential (Sandré). Piezometric, soil and biological optimized inventories and monitoring will so work as a pattern to shape the future tools incrementing the watershed and national wetlands monitoring toolbox.

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Annual seed rain dynamics in degraded and preserved areas of a tropical grassland

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Seed rain, the number of seeds reaching an area, is a process that plays a key role in recruitment and regeneration in plant communities. A better understanding of seed rain dynamics is therefore a critical step for restoration practices. Here we present a seed rain study in a tropical grassland, represented by a mosaic of open vegetation on rocky outcrops that harbor a great biodiversity. While this ecosystem is highly resilient to endogenous disturbances, such as fire and seasonal droughts, it is not the case with exogenous disturbances, such as soil disturbance, which has a direct effect on seed dispersion limitation. We studied over one year, between May 2016 and April 2017, the dynamics of seed rain in pristine and degraded areas for gravel exploitation and thus soil disturbance for road construction. We choose three pairs of degraded and pristine areas, placing two types of seed traps (sticky and funnel), totaling six traps of each type per plot. We collected the samples monthly in order to record seeds richness and diversity. We found a total of 99 seed morphotypes and a significant difference between the richness and diversity of seeds between trap types, areas and over seasons. We found a positive relation between rainy months and the number of seeds captured in funnel traps, indicating the importance of water as a seed disperser in this ecosystem. Despite the fact that the total number of seeds found is much lower in relation to other seed rain studies in grasslands, the richness of seeds found is among the highest already reported in the literature. The small number of seeds captured indicate a close relation between the low resilience after as soil disturbance and seed dispersal limitation.

Restoration of Mediterranean dry grasslands in photovoltaic power stations – the effect of solar panels

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The construction of solar parks (photovoltaic power stations) requires shrub removal and soil levelling usually destroying the existing vegetation and degrading soil conditions. Additionally, solar panels change microclimate compared with open habitats. In the framework of an interdisciplinary research and development project (PIESO) we (1) analyse the influence of solar panels on plant performance and succession, and we (2) test methods to facilitate the re-establishment of (semi-)natural plant communities that do not compromise energy production.

The experiments were started in 2016 using a solar park close to the French Mediterranean coast (Roquefort-des-Corbières) as a model system. The experimental design comprises four restoration treatments, hay transfer from a nearby reference community (dry Mediterranean grassland), sowing a key grass species of this community (*Brachypodium retusum*), adding compost that favour earthworm and a control treatment. All treatments were tested under and outside solar panels in a randomised block design.

Photosynthetically active radiation (PAR) was 15 times lower under solar panels than outside. Although solar panels prevented the plots underneath from rainfall, soil humidity was mostly higher than outside. A lower flavonoid index of *B. retusum* obtained by multiple absorbance measurements (UV, visible spectrum) indicated a lower production of secondary metabolites under panels protecting leaves against UV radiation. The mortality of the species was higher under panels and total species richness was lower, whereas number and cover of target species (reference community) were not significantly different. Hay transfer was successful in establishing plant species of the reference community. Due to the dominance of *B. retusum* in the reference community monospecific sowing had also a positive effect on restoration. Observations in the following years will show whether restoration by hay transfer or sowing will be successful both below and outside solar panels.

Use of ecological and geomorphological processes to assess the resilience of stream ecosystem functions after hydromorphological restoration

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The restoration of freshwater ecosystems is a major goal in most of European countries with the EU Water Framework Directive in 2000. Several indicators have hence been developed recently in order to evaluate the ecosystem integrity and many stream restorations emerge everywhere in Europe. However, very few indicators focus on freshwater ecosystem functions underlying the ecosystem stability and promoting their resilience capacity. In order to fill this gap, we started to follow several low-order streams (Strahler ranks ≤ 3) in Brittany before their restoration which will be done either late in 2018 or in 2019. Different types of hydro-morphological alterations (e.g. damming, clogging, channalisation, degradation of banks) are followed and the resilience of ecosystem will be monitored over at least three years. To a better understanding of mechanisms behind the resilience of ecosystems, we choose a multidisciplinary approach using biological parameters (e.g. foodweb structure and leaf litter recycling) associated with physical parameters such as the hydrology and erosional processes (e.g. change in sediment, erosion of banks). We hence monitor the biological assemblages (invertebrates, fishes, and macrophytes), the topography (slope and resulting flow facies), the sediment characteristic (particle size and type), water flows at the surface (discharge, current velocity), water flows between the surface, the sediment, and the groundwater (piezometer). We also test the performance of functional indicators such as the measure of the leaf litter breakdown rate and conditions of oxygenation into the sediment via wood sticks (for clogging). For each parameter, a Before After Control Impact (BACI) approach will be used. Together with the scientific monitoring, we organized the formation of environmental managers to promote the use of simple but efficient tools to follow the effects of their restoration and to feed a regional database in order to improve the efficiency of restoration methods used.

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Posters

Soil Ecology

Spatial dependence of soil organic carbon, abundance, biomass and diversity of earthworms in 15 temperate agroforestry systems

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In temperate regions, silvoarable systems associating parallel tree rows and annual intercrops are the most widespread types of agroforestry systems. Earthworms are involved in numerous ecosystem services such as pedogenesis, soil structure, and nutrient cycling. In agricultural landscape, land occupation and management highly influence earthworm communities. The objectives of this study were to i) compare earthworm communities (abundance, biomass and diversity) between agroforestry tree rows, alley and agricultural control systems (treeless) and relate it to the spatial distribution of Soil Organic Carbon (SOC) stocks. We used a network of 15 agroforestry French sites arranged on a North/South gradient comprising an adjacent agricultural control plot. Agroforestry alleys and control plot have been strictly managed (soil tillage, crop rotation, fertilization) in the same way since the tree planting. Mean earthworm abundance and biomass were significantly higher in the trees rows than in the agroforestry alleys and the agricultural control system across the sites. Earthworm species richness in the tree rows was not significantly different from the agricultural control system but was higher than in the agroforestry alleys across the sites. Interestingly, adult earthworm.

Feeding behavior of epi-anecic earthworm species and their impact on soil microbial communities

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Earthworms contribute significantly to litter decomposition, providing numerous ecosystem services. Most of the studies focusing on the role of earthworms on litter decomposition were conducted by comparing distinct ecological categories (epigeic, epi-anecic, anecic strict and endogeic), whereas their specific contribution within a given ecological category remains largely unknown.

In this context, the aim of this study was to determine the contribution of four epi-anecic earthworms (*Lumbricus rubellus*, *Lumbricus festivus*, *Lumbricus centralis* and *Lumbricus terrestris*) to the decomposition of three plant litters with contrasted chemical and physical properties (*Lolium perenne*, *Holcus lanatus*, or *Corylus avellana*) located at both the soil surface and at a depth of 10 cm. The effect of these interactions on fungal and bacterial communities inhabiting epi-anecic burrows were assessed using T-RFLP analysis.

Epi-anecic species improved the litter mass loss solely at the soil surface, while, at 10 cm deep, litter mass loss was mainly due to microbial activity. Litter mass loss was correlated to the initial mass of epi-anecic species and its intensity depended on litter quality as the four epi-anecic species displayed a similar sensitivity to the quality of the litter added. Interestingly, *L. festivus* seemed to have a higher efficiency in surface litter mass loss that was linked to a stimulation of the fungal communities in its burrows. Fungal communities were thus impacted by both the litter type and the epi-anecic species whereas soil bacterial diversity and richness were stimulated in the earthworm burrows whatever the epi-anecic species. Overall, epi-anecic species contribute to enhance the diversity of the drilospheric microbiota.

Influence of organic matter and land use on the evolution of Technosols properties constructed with urban wastes

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Recycling urban waste into Technosols provide an alternative to the use of agricultural soils to build urban area. However, construction and demolition wastes are still poorly recycled because of insufficient techniques have been developed to transform them into reusable material. They represent a major waste in urban area (more than 10 million of tons per year in Paris region) and recycling them in situ would dramatically reduce pollution and economic cost associated to their transport and landfilling in peri-urban areas. Here, we present a large-scale experiment in which we tested the potential of excavated deep horizons of soil (EDH), a major demolition waste as a suitable material to create fertile soil. We tested if 1) the addition of compost and 2) the land use accelerate the pedogenesis of Technosols. Four compositions of substrate were settled in 2013 in an experimental site near Paris (France): EDH alone, EDH with green waste compost (GWC), EDH with crushed concrete from demolition sites (CC), and EDH with GWC and CC. We also tested the effect of land use using either wheat cultures, trees or meadow. The evolution of the physico-chemical properties (pH, C, N, P, texture), microbial communities (bacteria and fungi) and CO₂ emissions of Technosols were assessed after 3 years of experiment. The results showed a strong effect of the organic matter in interaction with the land use on all variables studied. Constructed Technosols represent interesting models to test the relative importance of biotic and abiotic factors on the dynamics of soil ecosystem since their composition can be easily manipulated by mixing different proportions of parent materials and introducing soil organisms.

The presence or absence of copper in the interactive arbuscular mycorrhizal fungi-microbial diversity-plant community relationships

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Pollution of environment with chemicals is a serious problem which has been known for many years. Each compartment of the ecosystem including plants and microbial species maybe disturbed by the unwanted addition of metals in soil. In this study, the effect of copper on arbuscular mycorrhizal fungi (AMF) in soil microbial diversity and their interactions on plant community in a microcosm experiment was investigated. Plant seedlings of two grass species (*Poa compressa* and *Festuca rubra*) and two herb species (*Centaurea jacea* and *Lotus corniculatus*) were planted in the experimental pots filled with post-mining soils, half of replicates artificially contaminated with copper. Treatments were bacteria, bacteria and saprophytic fungi, bacteria and protists, and their combined treatment (bacteria, saprophytic fungi, and protists) which were inoculated into test soils three months before the experiment started. At the start of the experiment, AMF was also inoculated into half of the pots both in the presence and absence of copper. After sixty days, plants were harvested and shoot and root biomass and microbial respiration and biomass were measured. In the absence of copper, above- and belowground plant biomass was significantly lower in the treatments with AMF. The effect was significant on aboveground biomass of grasses, especially that of *Poa compressa*, but not for herbs. However, in the presence of copper, higher above- and belowground plant biomass was observed in almost all treatments in the presence of AMF. Herbs, especially *Centaurea*, responded significantly to the soil inoculation with AMF, while grasses showed inconsistent patterns. Significant interactions between copper and AMF on plant biomass were resulted in enhancing plant growth in the presence of AMF. The results confirmed the importance of mycorrhizal fungi on plant community compared to other microbial diversity in the presence or absence of copper.

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Relationships between above ground and below ground soil biodiversity in agroecosystems - from functions to ecosystem services

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Relationships between soil organisms, especially between above ground and below ground biota, remain unclear. The objectives of this study, involved in SoilServ project, were to assess i) the services and dys-services provided by soil fauna, ii) the interactions, antagonist or synergy, between these organisms. In march 2018, 90 points were sampled on Naizin catchment (France, Britany) on both crop fields and pastures; in May 2018, another field campaign limited to crop field was done (30 points). For each point, several soil organisms were studied based on their relevance for providing soil ecosystem services related to biodiversity conservation: soil engineer (earthworm), pests (aphids, slugs and soil-dwelling larvae of click beetles-wireworms) and biological agents (carabid). In parallel, some ecosystem services were measured (water regulation, yield). This study will present i) the maps of soil biota distribution for the different taxa, ii) the relationships between soil fauna and ecosystem services, iii) the models of soil fauna distribution for the different taxa, according to soil characteristics and trophic interactions.

Posters

Spatio-temporal Dynamics of
Ecosystems

Faune des Hydrachnidia (Acari: Hydrachnellae) de la région de Collo (Nord-est Algérie): Répartition spatio-temporelle et corrélation avec les facteurs du milieu.

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Les Hydrachnidia sont des Arthropodes Chélicérates de la classe des Arachnides et de l'ordre des Acariens. Ils sont purement aquatiques, à téguments généralement mous et vivement colorés; souvent orange, jaune et rouge. On peut les considérer comme de véritables indicateurs écologiques du fait de leurs préférences d'habitat, mais aussi parce que ces organismes sont étroitement liés aux autres composantes biologiques de l'écosystème par des rapports complexes de prédation, de phorésie et de parasitisme. Les facteurs qui semblent agir sur la distribution des Hydracariens sont: l'eau, la température, les proies composant leurs source énergétique et les hôtes indispensables à l'accomplissement de la stase larvaire. Notre recherche consiste à déterminer la distribution spatio-temporelle des espèces des Hydrachnidia récoltées dans la région de Collo (Nord-est Algérien) durant trois années consécutives (2011, 2012, 2013). Quatre stations représentées par des gîtes temporaires des eaux pluviales, ont été retenues. Les résultats indiquent que la période d'apparition des Hydracariens est limitée à cinq mois (Janvier, Février, Mars, Avril et Mai). Les mois de Février, Mars et Avril marquent les valeurs les plus élevées, tandis que la valeur minimale a été enregistrée au mois de Mai. L'espèce *Eylais hammata* présente la densité la plus élevée, et persiste durant les trois années, comme, elle est présente dans presque toutes les stations. Ce qui pourrait être du au fait que la végétation existante au-dessus des gîtes, offre un microclimat favorable pour le développement des d'Hydracariens pendant les saisons pluviales. Alors que la diminution du niveau d'eau durant la période sèche, qui s'étend de Juin jusqu'à Décembre, conduit à leur disparition.

Spatio-temporal structural equation modeling in a hierarchical Bayesian framework: ecology of wet heathlands

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Structural equation models are highly suited for evaluating ecosystem-level hypotheses, but to be effective structural equation models need to be able to accommodate spatial and temporal data. Here, the importance of different abiotic and biotic drivers on wet heathland vegetation is investigated using a spatio-temporal structural equation model in a hierarchical Bayesian framework.

Ecological data from 39 Danish sites, each with several wet heathland plots, were sampled in the period 2007 to 2014. Including resampling over the years, 1322 plots were sampled. Plant cover was measured using the pin-point method and the joint distribution of the key plant species in the wet heathland ecosystem, *Erica tetralix*, *Calluna vulgaris*, *Molinia caerulea*, and an aggregate class of other higher plants was estimated assuming a Dirichlet-multinomial mixture distribution. The investigated drivers of wet heathland vegetation include nitrogen deposition, soil type, pH, precipitation and grazing.

The study demonstrated that important insight of ecosystem dynamics and regulation can be obtained by spatial and temporal structural equation modelling in a hierarchical Bayesian framework and that the proper statistical modelling of the joint species abundance is a key feature of such models. Furthermore, the advantages of partitioning different types of uncertainties become clear when the fitted structural equation model is used for predictive purposes at a specific site.

Hedgerow networks monitoring in France : from the map to the field

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”Bocage” is a typical Western European landscape consisting in a network of hedgerows surrounding agricultural parcels of variable size and geometry. There are many subcategories, depending on the type of land, the type of enclosure, the structure of hedgerows, the dominant tree species, the shape and scale of the field patchwork and the origins of the bocage. Some of these agro-pastoral lands are famous for a high level of biodiversity. But hedgerows have decreased globally in France since the 1950s. In parallel scientific community has demonstrated a decline of agricultural birds especially in the three last decades. In the same time, amphibians and reptiles seem to decline too. The French national hunting and wildlife agency (ONCFS) has studied wildlife in several sites dominated by bocage landscape for more than 20 years. In the 2000s, ONCFS supported government to define regional guidelines on wildlife and habitats, and then the organization created a bocage and wildlife expertise centre to encourage sustainable management of bocage environments.

The bocage center is preparing a national survey program on bocages to evaluate and monitor their structure and their quality (ecosystem approach). This new project has been thought with the French national geographic and forestry information institute (IGN) for one year and is divided into three phases :

1/ to create a first geographic layer with french hedgerows, 2/ to edit a new map of bocages in France,

3/ to define and set up a field monitoring on bocages (participatory sciences)

The first project partners are French Ministry for Agriculture and Food, the French Ministry for an Ecological and Solidary Transition and the French Biodiversity Agency. Indeed, the program could help to lead and evaluate both national agroforestry and biodiversity plans.

Posters

The Role of Aquatic Macrophytes in the
Functioning of Freshwater Ecosystems

Aquatic Plants Research, Teaching and Pedagogic Innovation: How several lanes could merge into a single one for mutual benefits.

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French Law is very restrictive concerning time and duration of internships: they had to end with the academic year (maximum early September, but usually mid-June) and could not last for more than 6 months. Such conditions could thus make research internships on aquatic plants very difficult in France where such vegetation type is developing from March-April till October-November.

The portion of a Master allocated to internship is usually limited to 6 months and correspond to the second semester (from January to June). Research internships on aquatic plants are thus quite problematic.

To address this issue, the Master "Biologie et Valorisation des Plantes" teaching staff has set up a pedagogic innovation named "Végé-LAB". This program allows to develop real research projects over 16 months spanning the first three semesters. Master students try to answer a question asked by a stakeholder. They are supervised by the teaching staff and stay in constant touch with their partner stakeholder.

This pedagogic program is very convenient to deal with aquatic plants research. It thus comes to no surprise that almost one third of the ecological research projects realized through this program involve aquatic plants.

Here, we will here present outcomes of 4 of these research projects:

- (1) Research of a new fractal approach to assess macrophyte complexity in lotic ecosystems
- (2) Allelopathic compounds activity in *Potamogeton lucens*
- (3) *Potamogeton coloratus*: a threatened bioindicator? Assessment of its'
- (4) *Hildenbrandia rivularis* as an indicator of hydromorphological functioning of rivers in the French Rhine alluvial plain.

All these four projects have already led to serious inputs in research programs (publishable results and/or great advances in broader research programs), testifying the mutual benefits that emerge from teaching and research real collaboration.

Reduction of wet grassland biodiversity due to Water Primrose proliferation in the ” Marais Poitevin ” (France)

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The floristic richness of the sub-halophilous grasslands of the River Lay is important with three protected species: *Damasonium alisma*, *Gratiola officinalis* and *Ranunculus ophioglossi- folius*. On the common marshes of Lairoux and Curzon, the colonization by *Ludwigia grandiflora* subsp. *hexapetala* endangers the pastoral use. Our aim is to verify and quantify this impact of *Ludwigia* at three complementary scales: experimental plots, the lower colonized habitats where the protected species grow, and the whole marshes. The study methods used were: detailed distribution analyzes by field surveys, floristic list on quadrats, some phytosociological records allowing linking the local observations to habitat booklet and bibliography. *Ludwigia* has progressed over 4 years (2014-2017): 1.2 ha in 2014, 2.8 ha in 2017. *Ludwigia* is absent from the meso-hygrophilous and mesophilous communities. At the level of the protected species, it is especially *Gratiola* which seems to compete with *Ludwigia*; for the other species the period of development as well as their ecology limiting their co-occurrence with *Ludwigia*. The specific richness in 4m² plots is highly inconstant, depending not only on *Ludwigia* cover, but also on the treatments carried out to try to regulate it. In the witness plots, it varies from 9 to 12 species (including *Ludwigia*). In the other plots, variations are much larger: between 1 (only *Ludwigia*) and 16. The effects on forage production are poorly understood, particularly regarding relationships between *Ludwigia* cover and forage value. Mapping *Ludwigia* will continue and if possible could be automatized, in order to assess its expansion and to be able to manage it as well as possible. This work on forage value and cartography constitutes the perspectives of this action research.

How physical heterogeneity of water masses in large shallow lakes shapes plankton community?

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Human activities strongly determine the flow of organic matter and nutrients in drainage basins, responsible for pollutions such as proliferation of primary producers in aquatic environments like cyanobacteria. Those blooms induce losses of biodiversity as well as socio-economic costs.

Physical forcing (mixing and convection) plays an essential role in biogeochemical and hydrosedimentary flows and the bloom dynamic, particularly in shallow lakes as they are highly vulnerable to climatic and anthropogenic changes. Moreover, in large lakes, the complexity of the basin, coupled with macrophytes areas, generates a large diversity of habitats, with specific physical and chemical conditions. This results in horizontal gradients that potentially initiate the formation of metacommunity, depending on the persistence of the gradients.

The Lake Grand-Lieu, which is one of the largest lowland lakes in France, show a strong spatial heterogeneity of phytoplankton biomass during sunny days and one can ask to what extent plankton communities also differ in species composition. A new project financed since 2018 by the Water Agency and European funds (FEDER), aims at measuring the biological responses of the lake at different scales to meteorological factors (wind, rain and radiations). The plankton communities will be characterized by two complementary methods: with microscopic identification and counting and with amplicon sequencing of the small subunit rRNA genes, while physical and chemical conditions will be monitored every three weeks.

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Posters

Theoretical Ecology

Modelling the dynamic of forest plant metacommunities.

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Present-day forests often consist of fragments of different quality, age, size and isolation, which are embedded in a more or less hostile matrix. In the context of accelerating global changes, many forest plant species have to migrate northwards to track their ecological niche, but this is expected a hard task for species that often are dispersal-limited. However, to which extent forest plant species can migrate among forest patches in lowland landscapes remains a poorly investigated question. In this study, we aim at filling this gap by building a spatially- realistic model of plant metacommunity dynamics. Community models are often too complex to be scaled up to the metacommunity scale (e.g. SORTIE-ND) or are unable to cope with species interaction. Here, we present a theoretical model of a forest plant community which can be easily scaled up to the metacommunity scale. We built a model which is simple enough to be mathematically analysed while accounting for the main (meta)community processes described in the literature (e.g. species-area relationship, species-time relationship, priority effect, source- sink relationship, mass effect). The dynamic of a local community is modeled according to the Wright-Fisher theory (1931). Wright-Fisher analysis gives the mean extinction time for species and we can specifically observe how this extinction time changes along with the variations of the community features. We then produce a spatially explicit metacommunity model by introducing a migration variable. The introduction of between-sites dispersal generates species diversity patterns that are similar as those commonly described in the literature. The neutral model can easily be enhanced to produce a model able to test all the different paradigms of a metacommunity. Our preliminary model thus pave the way for a complete metacommunity model which could be use as an efficient tool for nature management and landscape planning (e.g. designing ecological corridors).

Concepts and measures of diversity, rarity and originality in ecology and evolution

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The concept of biological diversity, or biodiversity, is at the core of many evolutionary and ecological studies. Many indices of biodiversity have been developed in the last four decades. Species has been one of the central units of these indices. However, evolutionary and ecological studies need a precise description of species characteristics to best quantify the inter-species diversity, as species are not equivalent and exchangeable. One of the first concepts characterising species in biodiversity studies was abundance-based rarity. More recently, the abundance-based rarity was completed by trait- and phylo-based rarity, called species' originality. The originality of a species represents its contribution to the overall diversity of a reference set of species. It can be also defined as the rarity of the species' characteristics such as the state of a functional trait, often assumed to be summarized by the position on a phylogenetic tree. We reviewed and compared various approaches to measure originality.

A measure of diversity is a property of a group of species. Alternatively, originality and rarity measures are the properties of an individual species in reference to a pool of species. Measures of diversity, rarity and originality are fundamentally connected, but have been independently treated in the past decades, with few attempts to bridge them. Using literature review and our own findings, we showed that trait-based and phylo-diversity indices can be written as a function of species rarity and originality measures.

Finally, analyzing studies using species' diversity, rarity and originality measures, we stressed the need of a joint use of these three types of indices to fully describe biodiversity and efficiently protect it.

Stabilizing niche differences are still required to maintain species-rich communities in temporally variable environments

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Explaining coexistence in species-rich communities of primary producers (e.g., tropical trees, phytoplankton) remains a challenge for ecologists because of the likely competition for shared basal resources. Following Hutchinson's seminal suggestion, many theoreticians have tried to create diversity through a fluctuating environment, which impairs or slows down competitive exclusion. There are now several fluctuating-environments models that allow coexistence, but they often produce only a dozen of coexisting species at best. Here, we investigate what it would take to create even richer communities in fluctuating environments using an empirically parameterized model. Building on the forced multi-species Lotka-Volterra model of Scranton and Vasseur (2016), we have investigated the effect of two coexistence mechanisms, namely the storage effect and stabilizing niche differences (SNDs). SNDs occur when intraspecific competition is stronger than interspecific (as opposed to neutral models where competition is symmetric), and we tuned the competition ratio based on empirical phytoplankton data. Although SNDs maintained more species than the storage effect (50 % w.r.t 25%), we show that none of the two coexistence mechanisms considered could, by itself, ensure the coexistence of all species present at the beginning of our simulations. Realistic seasonal environments only aggravated that picture, as they decreased persistence relative to white noise. Our results suggest that combining different mechanisms for biodiversity maintenance into community models might be more fruitful than trying to find which explains best the observed diversity levels. Our results on community composition (formation of clumps, biomass distribution) in the different scenarios give further hints on how to empirically weight the influence of coexistence mechanisms.

Posters

Trait-based Approaches in Ecology

Trait-based approaches in aquatic ecology: a common language for freshwater and marine ecologists?

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Functional traits are phenotypic characteristics of organisms influencing individual fitness, such as size, trophic regime or resource acquisition strategy, reproduction mode, or abilities of escaping predation. Functional traits drive both the response of organisms to perturbations

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(response traits) and they effects on ecosystem functioning and associated ecosystem services (effect traits). They have been used for a better understanding of ecosystem functioning and for ecosystem management and monitoring.

In this poster, we focus on trait-based approaches in aquatic ecology and argue that they could be a common language for freshwater and marine ecologists. Firstly, methods for measuring or estimating functional traits are presented, including in situ observations, dedicated experiments, literature review, or more recent technics such as automatic imaging and molecular approaches. Trait-based models are also discussed. Secondly, future research questions and opportunities are described. They encompass the estimation of aquatic functional diversity at various spatio-temporal scales, the study of aquatic food webs, community interactions, and biogeochemical cycles, and the investigation of potential effect of anthropogenic and natural pressures on aquatic ecosystems.

Diversity-function relationships in contaminated soils – A functional trait approach

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Litter decomposition is a key ecosystem process allowing the recycling of organic matter.. This process, ensured by both decomposer micro-organisms (fungi & bacteria) and detritivorous invertebrates, is influenced by many biotic and abiotic parameters. In France, and more generally in Europe and North America, industrialization has left many sites with multicontaminated soils. Despite high levels of contamination, diverse forest ecosystems have been able to develop on these wastelands. However, since these soils often contain high levels of trace metal elements (TMEs), trees accumulate these contaminants that are found in twigs and leaves, ultimately producing litter enriched in available ETM. By impacting the different communities of litter consumers, TME toxicity could modify the recycling of organic matter, disrupting biogeochemical cycles. Yet, our recent work has shown that litter decomposition rate was not affected by soil contamination. In this context, the main goal of the ECOBIOS project is to understand how the functioning of contaminated soil (here, the litter decomposition) can be maintained at

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the same level as on uncontaminated soil. In relation to this objective, several questions arise. One of them would be to understand how soil contamination modifies diversity – function relationships? To answer this question, we will try to highlight, in decomposer microorganisms and detritivorous invertebrates communities living along a contamination gradient, the functional traits related to litter decomposition and to the soil contamination level. Several non-exclusive hypotheses of the contamination effects on decomposer and detritivorous communities can be proposed. For example, organisms could be smaller (invertebrates) or have a lower biomass (invertebrates and / or micro-organisms) or have a lower assimilation rate (invertebrates) or decreased enzyme capacity (micro-organisms) at contaminated sites compared to uncontaminated sites. Our poster will present and discuss the first results of this project.

Using ecomorphology and functional traits to understand the efficiency of a selective device in a multi-species fishery

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Improving selectivity of fishing gears is one strategy to significantly reduce by-catch of non-commercial species or undersized individuals. The efficiency of selective device has mainly been estimated by comparing the biomass and length spectrum of caught individuals and escapees while the morpho-anatomical and functional parameters of species are rarely accounted for. Using an innovative technical device to reduce catches of undersized individuals in a multi-species bottom trawl fishery in the Bay of Biscay, we measured a set ecomorphological and functional traits on both captured and escaped individuals of 18 species. Using a Principal Component Analysis and K-means partitioning, we clustered species into six groups illustrating six different locomotion modes. We identified ecomorphological and functional features related to body size, visual ability and locomotion, differing between the two. As expected, escapees were smaller on average but also tended to be more streamlined, with a relatively bigger eye and fin characteristics involved in manoeuvrability and propulsion. Here, we demonstrate how ecomorphological and functional traits can shed light on the biological parameters influencing the efficiency of selective devices.

Growth success of seedlings of different populations of *Ludwigia hexapetala* and *Ludwigia peploides* subsp. *montevidensis*.

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The water primroses *Ludwigia hexapetala* and *Ludwigia peploides* subsp. *montevidensis* are emergent perennial species native to South America. They became invasive in France and in California, where they cause severe damages in wetlands. In previous studies, the two species showed high germination percentage. Thus sexual reproduction could contribute to their high invasiveness. To investigate the growth success of sexual propagules of populations of *Ludwigia hexapetala* and *Ludwigia peploides* from different climate zones, a comparative analysis was undertaken on seedlings grown in greenhouse. Fruits of *L. hexapetala* were collected from three populations in California and from three populations Western France. Fruits of *Ludwigia peploides* were collected from three sites in California, from two sites in Western France and from three sites in Southern France. We grew 20 seedlings per population and measured their survival, the shoot length, the number of lateral shoots, and the shoot and root biomass. Our results showed that seedlings of both species have a high survival percentage. Populations of *L. peploides* had longer shoots, greater shoot biomass and higher production lateral shoots than those of *L. hexapetala*. Statistical analysis also revealed a significant trait variability among populations. Furthermore, the apical and lateral growth and the root biomass of populations of *L. peploides* from California were greater than those of the populations from France, although the survival rate of seedlings was lower. Moreover, the populations of *L. hexapetala* from California produced significantly less lateral shoots than populations from France, but their biomass was higher. These results highlighted strong differences between the two invaded ranges for both species, independent on climate experienced by mother plants. Population from California were particularly vigorous compared with those from France. They showed the influence of the source of the populations in the success of exotic species through sexual reproduction.

Posters

Tropical Ecology

Patterns of within and between-population genetic diversity across a high species richness riverine network: describing the multi-species fishery of the Upper-Maroni in East Guianas.

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Multi-species datasets for comparative phylogeography represent a cornerstone to study the relative influence of biological, environmental and anthropic factors on genetic diversity and evolution. However, the availability of such datasets within a particular region remains limited. The Maroni, an Atlantic coastal riverine network in French Guiana, harbors a high fish species richness, which is of high scientific but also cultural and economic interest for native human communities. Therefore, assessing the currently unknown levels of genetic diversity in these species is critical to put in place a sustainable subsistence and commercial fishery.

Consequently, we studied within- and between-population genetic variability for 18 fish species from the Upper-Maroni, displaying contrasted biological characteristics and fishing interest; sampled along a gradient of decreasing fishing pressure and distance to the river mouth. Firstly, we developed molecular resources for each of these non-model, even though locally emblematic species using a custom, highly simplified RAD-Seq design and *in silico* protocol at low-cost. 110 to 156 RAD-Seq derived, specific SNP markers enabled to cost- and time-effectively build a comprehensive multi-species dataset covering the whole study area. Secondly, within- and between-population diversity indices highlighted a range of genetic variability profiles across species. These could be associated with some of their documented biological characteristics – sometimes in an unexpected way, but also with habitat features, revealing the influence of both riverine dendritic-network and habitat availability. Results were also interpreted regarding the downstream fishing gradient, leading to discussion on the relative influence of habitat and anthropic pressure within the area.

Our work supports comparative population genetic approaches and will contribute to develop our knowledge about Neotropical fish species, partly filling the gap between the phylogenetic and evolutionary understanding of this highly rich fauna. Such applications may be particularly relevant within the current context of large-scale biodiversity loss linked with anthropic pressures.

Predictive models for freshwater fish communities reveal spatial factors more important than seasonal factors in determining species distributions in two contrasting tropical ecoregions in India

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Despite their rich biodiversity, ecosystems (especially stream fish communities) in India are largely understudied. Here, we explore freshwater fish communities in very contrasting landscapes and investigate similarities in community structure. Tropical systems operate differently than temperate systems and our work focuses on investigating this difference.

20 stream sites were sampled in the states of Madhya Pradesh 'MP' (central India) and West Bengal 'WB' (Himalayan foothills, eastern India). Fish sampling was conducted during winter, pre-monsoon and post-monsoon seasons from 2015 to 2017. Environmental data was also collected on site during each sampling round. Results show that despite the sites being more than 1000kms apart, they show relatively equivalent species richness (SRWB=80, SRMP=72) and share 40% of the species. Diversity is highest during the pre-monsoon, in comparison to winter and post monsoon. GLMMs were used to predict SR and Shannon's diversity index (H) based on a combination of environmental variables. Variance inflation factor was used to remove correlated variables. Variable selection was performed using stepwise regression based on AIC values and their ecological relevance. Season was taken as a random factor in the models (null models had no random factor). Likelihood ratio tests (LRTs) were performed to assess the importance of random factor to the models.

While chemical factors (pH, dissolved oxygen, total dissolved solutes) were more significant in MP, physical factors (stream width, stream depth, altitude, etc.) showed higher significant effects in WB. Variations in dissolved oxygen, stream depth, water velocity and pH were found to be significant common factors that affected both regions. Interestingly, LRTs showed no effect of season in the model. Our results reveal that similar environmental factors determine fish diversity and composition in these two regions, despite their geographical contrasts. This indicates likely occurrence of common mechanisms that drive fish community structure across diverse eco-regions.

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Seasonal and Spatial Variations in Physico-Chemical Water Quality of a Tropical River at some of its Natural Points

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This study was carried out at six selected sampling stations over the three reaches of Osun River along its main axis to determine seasonal and spatial variations in the general physico-chemical water quality parameters of the river water. From each sampling station, surface water samples were collected bi-monthly for an annual cycle, the samples were treated and analyzed for physico-chemical water quality parameters using applicable standard procedures. The river showed an increasing clarity from its headwaters to the lower reach with regard to mean transparency, turbidity and colour and was also clearer in the dry season than in the rainy season. The water was generally moderately alkaline (pH: 7.41 ± 0.11 - 7.61 ± 0.16) but significantly ($P=0.05$) more alkaline in the dry season than in the rainy season. It can be classified as a dilute salt bicarbonate freshwater with mean conductivity at the three reaches ranging from $128.92 \pm 1016 \mu\text{S}/\text{cm}$ to $141.79 \pm 27.29 \mu\text{S}/\text{cm}$. Ca^{2+} and HCO_3^- were the dominant cation and anion respectively in all stations investigated and in both seasons. The mean values of most parameters determined were within permissible limits making the river water suitable for most probable domestic and industrial uses and livestock support.

Ecology of the genus *Millettia* (Fabaceae) for land restoration and its valorization on oil production in Madagascar

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Here, a consortium formed by scientists, industrialists and local population associations focus a special emphasis on studying the potentiality of the genus *Millettia* in Madagascar, in the process of ecological restoration and for long term oil (biodiesel) production. First, to identify the suitable habitat for their growth, the distribution and ecological characteristics of the *Millettia* in Madagascar will be described. Second, to domesticate *Millettia* in Madagascar for a large scale production, we will use several propagation methods (cutting propagation, seeds inoculation...). Third, to study the behavior of domesticated species at the transplant site, we will follow the survival and the growth in nursery and at the transplanting sites regarding the climate conditions and soil quality. Fourth, to evaluate the potential of seeds for oil production, we will compare the oil production rates among all nine *Millettia* species.

According to the distribution seen during bibliography, the study sites will be in the eastern, the northern, the western and the south-western parts of Madagascar. We started our field work in the north of the Island. *Millettia pinnata*, the only species which is not endemic of Madagascar was found there. They grow well on sand near the ocean as well as on soil with low sand content even on soil with stone. They can develop with other native species or alone. The nodules were observed on these root samples. And now, our laboratory work is concentrated on the description of the symbiotic status, the physico-chemical analysis of the soil and on oil extraction from the seeds.

These preliminary data indicate that *Millettia* indeed can have major potentials for land restoration. Our ongoing study on the nine *Millettia* in Madagascar will allow us to achieve our aims of using these species in land restoration and oil production in Madagascar.

*Speaker

Habitat loss and frugivores defaunation in Réunion island (Indian Ocean)

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Abstract

Whereas human settlement on Mascarene islands occurred only recently during the 17th century, the native insular biota experienced a drastic extinction of the vertebrate fauna mainly explained by rapid habitat transformation. At archipelago scale, La Réunion is the last of the Mascarene islands with large areas of untransformed habitats still covering 40% of the island area (2512 km²). Conversely, Mauritius native forests covers less than 1% of the initial area (1872 km²) but still retain several native frugivore species that went extinct in La Réunion during early human settlement (fruit bats, skinks, pigeons). In order to explain these patterns, we compare habitat transformation history between both islands using past and present vegetation maps, subfossil archives and reports of early travellers. We also question the consequences of native frugivores extinction at island scale. Preliminary results of forest dynamics studies confirm the lack of recovery of native plant communities after natural disturbance that can be explained by dispersal limitation of most native trees, new plant invasions and drastic changes in frugivores community composition.

*Speaker

Lack of evidence of fragmentation effects on necromass stocks and heterotrophic respiration in Brazilian Atlantic forest

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Fragmentation is an important processes on tropical forests, responsible for carbon changes. Plant necromass plays an important role on carbon cycle in tropical forests, and its stocks and release, by heterotrophic respiration, can be altered by human impacts. The aim of this study was to assess the stocks of fine and coarse necromass, and estimate its heterotrophic respiration rates of Atlantic forest fragments in Rio de Janeiro. We tested the hypothesis that those processes are dependent on fragment size and that necromass stock is higher and the heterotrophic respiration is lower in the edge than in the interior of the fragments, as re- sult of the edge effect. Five forest fragments were selected, one biggest and more preserved (2300ha) and four neighbours' smaller (19-155ha) fragments. Sampling were carried out during the wet season, in two 100m transects at the edge and at the interior of each fragment. The coarse necromass was sampled every 20m, by the LIS (Line Intersect Sample) method and the fine necromass in 50x50cm quadrats. The heterotrophic respiration was measured using a portable closed-chamber infrared CO₂ gas analyzer system (EGM-4). There was no edge effect on the stocks of the coarse (Mg/ha,edge=5.24±3.80;interior=3.05±2.01) or fine (Mg/ha,edge=5.16±1.53;interior=4.61±0.74Mg/ha) necromass in the forests. Also, the heterothophic respiration (µgCR/gCN/min) of necromass, was similar between the edge (coarse=2.61±1.54;fine=5. and interior (coarse=2.49±0.62;fine=4.31±3.80) of the fragments. But, heterotrophic respiration of the necromass was positively related with its moisture, although it did not differ between the edge and interior. The fragment size also did not affect necromassa stock neither respiration. No edge or size effect on necromass was detected for the moist Atlantic forest fragments studied, indicating that not always fragmentation effect is evident, even though alterations in functioning of carbon stock and release, is expected.

Vegetation carbon stocks of mangroves in Futian Mangrove National Nature Reserve, China, based on UAV images

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Mangroves are well-known for their ecological, social and economic ecosystem services, which are regarded as the one of the richest carbon (C) pools in the tropics. There is an increasing interest in the conservation of mangroves as they become involved with incentive programs for climate change mitigation. However, accurate assessments of mangrove C stocks at the local scale are lacking. Recently, the availability of Unmanned Aerial Vehicles (UAV) has provide an operationally efficient approach to investigate the distribution of vegetation and estimate C stocks at a fine scale. In this study, we employed the lightweight UAV as a useful supplement to field inventory for estimating vegetation C stocks of mangrove forest in the Futian Mangrove National Nature Reserve, China. We generated extreme high-spatial-resolution image (0.02m) from UAV technology, and then we applied a traditional inventory for each mangrove assemblage based on its distribution derived from UAV images. The total area of mangrove forest is 82 ha, and the vegetation C density for mangrove assemblages ranged from 6.65 Mg ha⁻¹ to 192.05 Mg C ha⁻¹. The total vegetation C stocks estimated for the seven assemblages, weighted based on their spatial distribution, was 9.19×10³ Mg with average of 112.69 Mg C ha⁻¹. The error bounds from the 95% confidence interval are ±5% of our estimate, which is well within acceptable levels of uncertainty. Our study suggests that UAV technology is able to obtain accurate estimation of C stocks by local government, for management and conservation practices.

Urban Ecology

Severity of human-rhesus macaque conflict in urban landscape and possible mitigation strategies in Delhi NCR, India

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Human-monkey conflict is a serious threat to urban and suburban societies of Delhi- NCR, northern India. Urban rhesus monkeys (*Macaca mulatta*) have been trans-located to Asola- Bhatti wildlife sanctuary which is situated at the tri-junction border of Delhi, Faridabad and Gurgaon city. We interviewed 1568 respondents in nearby localities in and around Asola-Bhatti Wildlife Sanctuary from 2016 to 2017 and obtained qualitative and quantitative information on conflict incidents. We recorded on average 14.74% cases of attack, 12.01% cases of injury, 11.15% cases of bites, 15.56% cases of snatching foods, 11.23% cases of threatening, 11.49% cases of entering into the houses, 11.36% cases of property damage and 8.27% cases of littering. We also analyzed the seasonal changes of conflict incidents in and around the sanctuary. We recorded the different conflict types from each and every site of occurrence from January to December and later summarized the data to get the cumulative result. We calculated 34.04% conflict cases in summer (March-June), 16.57% in monsoon (July-September), 26.28% in post monsoon (September-November) and 23.16% in winter (December-February) months. We collected data throughout the year covering all the seasons from all the 7 different sites and One-way ANOVA showed that there was significant difference ($p < 0.001$) among the study sites on the occurrence of conflict incidents. Attack ($12.46 \pm SE 3.33$), injury ($10.21 \pm SE 1.61$), bites ($9.72 \pm SE 1.89$), snatching ($11.62 \pm SE 1.47$), threatening ($8.60 \pm SE 0.92$), entering into houses ($9.77 \pm SE 2.12$), breaking and damaging properties ($8.23 \pm SE 1.09$), telephone line disruption ($1.15 \pm SE 0.66$) and littering ($7.34 \pm SE 0.82$) was calculated throughout the year. Mitigation strategies to reduce conflict by population management and improvement of co-existence between local people and rhesus monkeys in the urban areas suggested.

Characterization of earthworm communities in reconstituted anthropic soils of urban areas

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To create a fertile environment, reconstituted anthropic soils are formed using transported pedological material. Consequently it is subjected to a high level of constraints from extraction until the installation in urban or semi-urban areas. Almost nothing is known about the response of the biological compartment and especially about the earthworm communities to such perturbations. A panel of reconstituted anthropic soils in two cities near Paris has been sampled because of solid knowledge of the constraints and the processes used to engineer them.

Saclay (91) is characterized by very young soils (0 to 4-year-old) and Saint-Quentin-en-Yvelines (78) by older ones (20- year-old). The thirty different sites selected are characterized by a use, an age, a succession of horizon, a type of material and a human disturbance degree of the environment. They are divided in five use groups: planting trees of roadways, urban parks, hydraulic infrastructures, soils stored in windrow and environmental mitigation areas. Each individual collected was identified to the species level and weighed in the laboratory of Rennes University.

The abundance of earthworms seems to be twice as high in the very constraints areas as the natural control group. Earthworms have been found in an elevated and isolated soil of 70 cm wide, separating a bus lane and a road. The lindens planted in this soil are coming from the same tree nursery and are possibly a source of biological sowing. Pedological material stored in windrow contains earthworms after one year in good conditions of storage. It has to be noted that the bioturbation after two years is particularly well-developed in the windrow after two years and reaches 15 to 20 centimeters deep.

A second part of the study will focus on the bioturbation description to make the link between abundance, biomass, diversity and soil functioning.

Impact of urbanisation on entomophile plants and pollinators

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The human impact on landscape has changed over time and we currently assist to a tendency to urbanise areas that previously classified as rural, a tendency likely to impact biodiversity dynamics. Urban areas have been shown to harbor less diverse communities, that are very homogenous between distinct urban areas. But communities in rural areas are currently undergoing decline, both in terms of abundance as of the diversity hosted. We examined whether the interface between rural and urban areas could result in positive synergy leading to higher diversity. We have addressed this question by examining flowering plants and visiting insect diversity along a gradient of both urbanisation and rurality at the Plateau de Saclay by adapting a citizen science protocol, the Spipoll. This protocol is part of the MNHN Vigie Nature program and allowed us to observe and identify insect morphotaxons in 35 field quadrats

We observed that entomophile plant diversity and insect diversity increased with open urban habitat (private gardens, parcs, cemeteries), but decreased with imperviousness. Furthermore, insect diversity was higher when floral resources were more abundant.

From weeds to cultivated flora :turnover of floral resources in domestic gardens is linked to environmental rather than human characteristics

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Domestic gardens account for a substantial part of urban green spaces. They are increasingly considered as suitable places for urban biodiversity conservation. Regarding pollinators, domestic gardens may offer a variety of floral resources as well as welcome specific honey flower planting. At the same time, domestic gardens may be source places for non local, maybe invasive, plant species. Human related dynamics also act within domestic gardens, highly appropriated spaces, along with environmental dynamics. Understanding floral resources, their characteristics and their turnover in domestic gardens requires to take into account social and ecological components. We related four floral indexes in 30 peri-urban domestic gardens to (1) urbanization degree, (2) ecological characteristics of gardens and (3) environmental psychology variables describing their human inhabitants connection with nature, in order to understand the nature and dynamics of domestic gardens floral resources. Flowers' diversity, rarity, cultivated nature and origin are driven by ecological characteristics of gardens and urbanization degree but not by inhabitants' connection with nature. Altogether, domestic gardens host a variety of flowers which may succeed in providing continuous resources to pollinators through turnover from spontaneous common to cultivated rare flowers. Those rare cultivated flowers are also more likely to be non-native flowers. The unexpected absence of relation between floral indexes and inhabitant connection with nature may indicate a deeper relation, which could not be grasped here through the limited variables used. The existence of a floral turnover needs to be further investigated in order to know if pollinators are indeed using the successively flowering plants as resources.

Remote sensing in ecology

Posters Remote sensing in ecology

Assessment of Worldview 2 imagery for long term monitoring of fast evolving Natura 2000 coastal habitats

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The Camargue's former saltworks is a 6500-ha, located in South of France, the site was purchased in 2009 by the Conservatoire du Littoral, a French public organization created in 1975 to ensure the protection of outstanding natural areas along the coast. The site comprises a wide range of Natura 2000 habitats, including coastal lagoons, salt-tolerant Mediterranean thickets, meadows, beaches and dunes. Multiplication of breaches in inner and sea-front dikes translates into a fast-evolving site of increasingly difficult access for ground survey, calling for a synoptic and spatially explicit monitoring. Mapping all habitats considering their heterogeneity is necessary for monitoring. We explored mapping capacities of Worldview 2 images (2m pixel size, 8 spectral bands) on 2016 using images acquired in September 2010, 2013, 2015 and 2016. Field samples were used to build and validate statistical models using a classification tree algorithm (CART) on 7 habitats. Several approaches for discriminating vegetation communities have been tested using spectral indices either or without the integration of DTM to evaluate the interest of taking into account the topographical variability of the site. Models without topographic data provided an overall accuracy over 93 % for each habitat. Models with topographic data provided an overall accuracy over 95% showing that the integration of the micro-topography can greatly help to map the distribution of the vegetation species. However, the acquisition of accurate topographic information can be very expensive. Our results suggest that the fast evolving change of the site that modifies the phenology of the vegetation species due to random sea water input periodicity hinder the inter-annual resistance and robustness of the models. It may imply that the site has not yet reached its dynamic equilibrium.

Remote sensing in ecology

Large scale monitoring of grassland biomass dynamics with Sentinel-2 satellite images

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1

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Abstract

I will present ongoing works to use the novel Sentinel-2 satellite images for grassland biomass monitoring at the plot scale with unprecedented temporal resolution (up to 2 days). Tests of the precision of the biomass estimates are currently performed with field references. I will present the results of these tests, as well as a comparison of several data imputation methods to estimate missing data that are frequently linked to cloud masks. Potentialities of these novel massive data will be discussed with special reference to 1) feeding phenomenological models of grassland growth as a function of pedological and climate forcings; and 2) assessing agricultural practices at large scales.

Session Ecosystem services in Agricultural Landscape

An economic comparison of adaptation strategies towards a drought-induced risk of forest decline

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Abstract

Drought is a stress affecting forest growth and resulting in financial losses for forest owners and amenity losses for society. Due to climate change, such natural event will be more frequent and intense in the future. In this context, the objective of the paper is to compare, from an economical perspective, different forest adaptation strategies towards drought-induced risk of decline. For that purpose, we focus on a case study of a forest of beech in Burgundy (France) and, we studied several adaptation options: density reduction, reduction of the rotation length and substitution by Douglas-fir. We also considered two levels of risks (intermediate and low soil water capacity), two climatic scenarii from IPCC (RCP 4.5 and RCP 8.5) and two types of loss (financial and in terms of carbon sequestration). We combine a forest growth simulator (CASTANEA) with a traditional forest economics approach (Fautsmann's LEV and Hartman's LEV). The results showed that adaptation provided the best economic return in most of the scenario considered. Combining strategies appears as a relevant way to adapt forest towards a drought-induced risk of forest decline. The interest to consider two disciplinary fields was also demonstrated with beneficial scenarii in an ecological perspective that were not in an economic one and reversely. The results are discussed taking into account the financial balance and the carbon balance.

*Speaker

Effect of plant genetic diversity on biomass production, structuration of species in sown grassland communities and microbial diversity in soil

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Abstract

Many studies highlighted the importance of species diversity in ecosystems functioning and supplying of the ecosystems services. The diversity effect on ecosystem functioning has been largely described at species level, but remains little investigated at within-species level (*i.e.* genetic diversity). In our experimental approach, at INRA in Lusignan, we highlighted a genetic diversity benefit on biomass production and its stability over years, and on species composition of sown grasslands. We also observed an increase in species equitability with genetic diversity. Currently, we are studying plant genetic diversity effect on soil microbial diversity.

*Speaker

What interactions between ecosystem services linked to soil functioning?

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Abstract

Agricultural ecosystems contribute significantly to water flow in hydrosystems, but are also important water consumers. This situation reveals possible trade-offs risk among green and blue water regulation services, especially areas affected by water deficit. The main objective of this work is to analyze and quantify interactions (trade-offs or synergies) between different ecosystem services provided to farmers and society. Analysis focus in particular on the interactions between green water, blue water, soil quality, and climate regulation. This question is addressed at two spatial scales: at French national scale and in two areas where water management is a priority (Beauce groundwater and Adour-Garonne hydrographic basin); and is addressed at three temporal scales: the cultural season, the year, and a three decades period. Taking into account the spatial and temporal dimension of interactions between services make possible to assess the response time of agro-ecosystem change, and to evaluate the temporal dynamics of synergies or trade-offs between services. To do this, this work is based on conceptual and methodological frameworks and on the important modelling and simulation device (using the STICS crop model) developed as part of the INRA (French National Institute for Agricultural Research) EFESE-EA study. Ultimately, this work aims at understanding and modelling agro-ecosystems functioning at different spatial and temporal scales, and to quantify, map, and evaluate the services provided.

^{*}Speaker

Crossing boundaries: flux of aquatic winged insects toward agricultural lands and its potential contribution to ecosystem services

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Abstract

Linkage between aquatic and terrestrial habitats aroused scientific interest on ecological subsidies, *i.e.* how the transfer of matter and energy between adjacent ecosystems can modify their own functioning. Freshwater ecosystems are widespread in agricultural landscapes, however the possible implication of aquatic subsidies is rarely considered. To fill this knowledge gap, we carried out a field work to study winged aquatic insects emergence and dispersal from twelve second-to-third order lowland streams in an intensive agricultural landscape in the northwest of France for one year. The contribution of aquatic insect emergence to ecosystem services in agricultural landscapes is discussed.

*Speaker

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Influence of landscape heterogeneity and agricultural practices on biological control of pests: Detailed literature review from 1993 to 2017.

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Abstract

The effect of landscape heterogeneity on pest and natural enemy communities and the resulting service of biological regulation have been investigated in several meta-analysis and reviews.

However, those analysis have been conducted on studies taking place in very variable contexts (tropical and temperate climate, cereals and orchards), and using a wide variety of indicators to describe local and landscape-scale factors, and pests and natural enemies communities' status. While those reviews were able to demonstrate general tendencies of the effect of landscape simplification on natural enemies and pest communities, they are not sufficient to provide reliable predictions of the level of biocontrol in a given field, based on its landscape. They also tended, for statistical reasons, to aggregate a lot of indicators into more general proxies, preventing the provision of specific recommendations for landscape management.

Here, we propose a detailed review of the influence of landscape heterogeneity on the biological control of pest. The results obtained in 36 articles, published from 1993 to 2017, were analyzed, and gathered in a database. We recorded information on crops, pest and natural enemy species studied, scales, and indicators. We use this information to propose a detailed view on the effect of specific landscape features (composition and configuration aspects) and agricultural practices on pest and natural enemy communities' status and the level of biocontrol. An exhaustive and non-ambiguous ontology of the indicators used to describe the landscape and the communities' responses was also built. The goal of this work is to provide sufficient information for the conception of a simulation module of biological control intended to be implemented in the MAELIA platform (<http://maelia-platform.inra.fr/>).

*Speaker

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Ecosystem services and ecological compensation, an approach to favour agroecological transition

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Abstract

We aimed at defining possible means to combine the ecological compensation obligation and the related environmental added-value with the agroecological transition. Our approach meets two current objectives of environmental and agricultural public policies: the agroecological transition that implies a material change in agricultural practices, and the effective implementation of ecological compensation, that aims at achieving at least no net loss of biodiversity and even net positive impacts. We describe and assess the various relations among agricultural lands, ordinary nature, ecosystem functions and services, and to come up with concrete methodological proposals to construct operational bioindicators based, in particular, on the ecosystems services.

*Speaker