Fast sequence-based microsatellite genotyping development workflow for any non-model species

Olivier Lepais, Emilie Chancerel, Christophe Boury, Franck Salin, Aurélie Manicki, Laura Taillebois, Christian Cyril Dutech, Abdeldjalil Aissi, Cécile Fanny Emilie Bacles, Françoise Daverat, et al.

GDR
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8, 9 et 10 octobre 2019

Forum des Pertuis, La Rochelle

Code **WIFI** Forum des Pertuis: **wififorum**

Bienvenue à La Rochelle

Merci de participer au 5ème colloque du GDR Génomique Environnementale. Cette édition a été réalisée avec le soutien du GDR GE, de La Rochelle Université (en particulier le laboratoire Littoral, Environnement et Sociétés, LIENSS, UMR7266) et de l'Université de Poitiers (en particulier le laboratoire d'Ecologie et Biologie des Interactions, EBI, UMR 7267), de la CDA de La Rochelle, la Région Nouvelle-Aquitaine, la Fédération de Recherche en Environnement pour le Développement Durable (FREDD, FR CNRS 3097), du CNRS et de l'INRA, de MP Biomedicals et France Génomique. Nous remercions nos équipes financières et administratives pour leur aide. Merci également aux intervenants invités.

Vous trouverez ci dessous le Programme Scientifique (versions courte et longue), les abstracts, et des informations pratiques pour se rendre au Forum des Pertuis et circuler à La Rochelle. En plus du bus traditionnel, nous avons accès au bus de de mer, qui relie le Forum au vieux port.

Nous vous souhaitons un excellent colloque.

Amélia Viricel
Eric Pante
Didier Bouchon

Programme résumé:

Mardi 08/10/2019	
12h30	*Accueil*
13h30	*Ouverture*
14h00	Session 1 - Invitée : Isabelle Domaizon
14h45	Présentations orales Session 1
16h05	*Pause café*
16h30	Présentations orales Session 1
17h30	Posters
18h50	*Cloture, soirée libre*
Mercredi 09/10/2019	
9h00	Session 2 - Invitée : Karine Van Doninck
9h45	Présentations orales Session 2
11h05	*Pause café*
11h30	Présentations orales Session 2
12:50	*Pause déjeuner (inclus)*
14h00	Présentation orale Session 2
14h20	Session 3 - Invité : Christoph Grunau
15h05	Présentations orales Session 3
16h05	*Pause café*
16h30	Présentations orales Session 3
19h00	*Cocktail dinatoire à l'Aquarium de la Rochelle*
Jeudi 10/10/2019	
9h00	Session 4 - Invité : Vincent Castric
9h45	Présentations orales Session 4
10h45	*Pause café*
11h10	Présentations orales Session 4
12h10	Présentation PCI : Thomas Guillemaud
12h30	*Cloture du colloque*
14h00	Table ronde entre chercheurs et lycéens
18h00	Conférence gd public : Sophie Arnaud-Haond

Programme détaillé:

Jours	Mardi 08/10/2019
Heure	
12:30	**Accueil**
13:30	**Discours d'ouverture du colloque**
. 14:00	**Session 1 – Génomique environnementale dans le temps – suivis et paléogénomique** Orateur invité : **Isabelle Domaizon** **Application of DNA High Throughput Sequencing in paleolimnology : new opportunities for investigating long-term changes in lacustrine biodiversity facing environmental pressures**
14:45	ALEXEY VOROBEV : Transcriptome reconstruction and functional analysis of eukaryotic marine plankton communities via high-throughput metatranscriptomics
15:05	BABETT GUENTHER : Limitations due to PCR-based metabarcoding short length fragments: A comparison with two possible alternatives, Capture by hybridisation and Nanopore sequencing
15:25	LUCAS SIRE : CLIMTREE: Quantifying changes in flying insect diversity and soil fauna along a gradient of climate induced forest decline using DNA metabarcoding
15:45	CHRISTO-FOROUX EUGENE : "Mollivirus Kamchatka : a second representative of the mollivirus familly provides better insights into molliviridae evolution"
16:05	**Pause**
16:30	GREGORY K. FARRANT : RoskoBaz - A unified database of genetic markers for marine exploration
16:50	RAFFAELE SIANO : Long-term dynamics of protist paleocommunities over 5000 years in the Bay of Brest (Brittany, France).
17:10	NILS GIORDANO : Co-activity networks reveal the structure of planktonic symbioses in the global ocean
17:30 18:50	**Session Poster**

Jours	**Mercredi 09/10/2019**
Heure	
09:00	**Session 2 – Biodiversité : structure et dynamique des populations et communautés incluant les taxons méconnus ou mal connus** Orateur invité : **Karine Van Doninck** **New insights into the genome structure and evolution of the bdelloid rotifer Adineta vaga and its DNA DSB repair dynamic**
09:45	DIDIER AURELLE : Individual, population and species differentiation in *Pocillopora* spp. Corals
10:05	ANAÏS MASSÉ : Microboring *Ostreobium* diversity in *Pocillopora* sp. coral skeletons from the Pacific Ocean
10:25	CAROLINE VERNETTE : The Ocean Barcode Atlas: A web service to explore plankton biodiversity
10:45	DIDIER BOUCHON: Viral DNA diversity in Isopods
11:05	**Pause**
11:30	JADE LECONTE : Populations structure of the microalgae *Bathycoccus prasinos* in the open ocean
11:50	LAURE SEGUREL : On the influence of urbanization on the human gut and oral microbiome
12:10	LAURIC REYNES : Genomic inferences on reproductive biology and population differentiation of the Mediterranean kelp *Laminaria rodriguezii*
12:30	SHUO LIU : New insights into selection under genome evolution and domestication of apricot
12:50	**Repas (inclus) sur place**
14:00	OPHÉLIE DA SILVA : Microbial populations metagenomics: insights and challenges
14:20	**Session 3 - Epigénétique et génomique fonctionnelle** Orateur invité : **Christoph Grunau** **A systems biology approach on (epigenetic) inheritance**
15:05	CHRISTOPHE DJEMIEL : Explorer les fonctions microbiennes à partir d'informations taxonomiques : un état de l'art des outils et des méthodes
15:25	DENIS LE PASLIER : Dégradation de la chlordécone : mise en évidence de cinq familles de produits de dégradation, au laboratoire et dans des échantillons environnementaux antillais, caractérisation de microorganismes impliqués.
15:45	JEAN PECCOUD : A la recherche du locus déterminant le sexe du cloporte commun, *Armadillidium vulgare*, par une approche de croisements et de séquençage par pools
16:05	**Pause**
16:30	KÉVIN ROBIC : Identification par Tn-seq des gènes essentiels à l'exploitation de l'hôte végétal par le pathogène émergeant *Dickeya solani*

16:50	MARIUS BREDON : La dégradation de la lignocellulose chez les isopodes : nouveaux éclairages sur l'adaptation à la vie terrestre
17:10	ULYSSE GUYET: Adaptation and acclimation strategies of picocyanobacteria unveiled by comparative genomics and meta-omic data analysis
17:30	LUCAS AUER : Adaptation fonctionnelle des communautés microbiennes en réponse à l'exportation massive de biomasse végétale en forêt : une analyse transcriptomique
19:00	**Cocktail dinatoire au Café de l'Aquarium**
21 :00	
Jours	**Jeudi 10/10/2019**
Heure	
09:00	**Session 4 – Session ouverte** Orateur invité : **Vincent Castric** **Evolution of functional and regulatory novelty at the self-incompatibility locus in *Arabidopsis***
09:45	BATTLE KARIMI : Biogeographical Design of Soil Microbial Habitats
10:05	AYMERIC ANTOINE-LORQUIN : Optimization of viral biodiversity detection: TINAP workflow
10:25	JEAN-FRANÇOIS BRIAND : Hydrodynamique et biocides façonnent les communautés de biofilms marins sur surfaces artificielles
10:45	**Pause**
11:10	ROMAIN BLANC-MATHIEU : Large DNA viruses of microalgae are predicted to enhance carbon export efficiency in the global sunlit ocean
11:30	STÉPHANE BOYER : A new DNA metabarcoding approach to describe the diet of social wasps and evaluate their impact on biodiversity
11h50	MARIE CARIOU : The stimulation of organic matter processing and nutrient cycling by tubificid worms in wetland sediments is associated with a reduction of bacterial diversity
12:10	**Intervention PCI : Thomas Guillemaud** **Peer Community in : un système public et gratuit de recommandations de preprints fondé sur le peer-reviewing.**
12:30	Clôture du Colloque
14:00	**Table ronde entre chercheurs et lycéens - Aquarium de La Rochelle** **Intervenants : Hélène Agogué, Amélia Viricel, Eric Pante**
18:00	**Conférence grand public, Aquarium de La Rochelle :** **Sophie Arnaud-Haond** **« Barcoding dans les abysses », identification par la génétique des espèces marines, du plancton à la baleine**

Liste des posters

Seul l'auteur présentant l'affiche est listé ici ; pour une liste complete avec affiliations, voir section "Abstract des Posters" dans la version en ligne.

Krick M.V. — Stress response in fish: an epiGBS approach

Pépin J.F. — Evaluation de la diversité des communautés microbiennes planctoniques au cours d'épisodes de mortalité des moules bleues en France : utilisation de l'approche de métabarcoding pour l'analyse de l'ADN environnemental dans les Pertuis Charentais

Cariou M. — Gene expression changes induced by long-term starvation in a cave amphibian (*Proteus anguinus*)

Theil S — UTOPIA: an automatically UpdaTed, cOmPlete and consistent ITS reference dAtabase

Barranger A. — Tolérance de la faune ingénieure du sol à la contamination résiduelle par les produits phytosanitaires dans les agroécosystèmes : approches omiques des mécanismes moléculaires en jeu

Olivier Lepais — Fast sequence-based microsatellite genotyping development workflow for any non—model species

Rifa E. — DAIRYdb: a manually curated reference database for improved taxonomy annotation of 16S rRNA gene sequences from dairy products

Morgane Ratin — Use of mutagenesis to characterize genes involved in a widespread chromatic acclimation process in marine *Synechococcus* cyanobacteria

Ferrieux M. — Cross-scale analysis of the adaptation to iron limitation and temperature in the marine picocyanobacterium *Synechococcus*

L. Garczarek — Environmental realized niches of the marine picocyanobacteria *Prochlorococcus* and *Synechococcus*

Chloé Vigliotti — Gut metagenomic signatures of Non-Alcoholic Fatty Liver Disease (NAFLD)

Theil S — ANOMALY: AmplicoN wOrkflow for Microbial community AnaLYsis

Notes

Abstracts des communications orales

Session 1
Génomique environnementale dans le temps – suivis et paléogénomique

Mardi 14h
Forum des Pertuis

Application of DNA High Throuphput Sequencing in paleolimnology : new opportunities for investigating long-term changes in lacustrine biodiversity facing environmental pressures

Isabelle Domaizon

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Lake sediments constitute natural archives of past environmental changes. The application of high-throughput sequencing for the analysis of sedimentary DNA has opened up many new areas of inquiry in paleolimnology. Ancient DNA preserved in sediments offers the possibility to consider taxa that were traditionally not accessible in paleo-reconstructions because they do not leave distinct morphological fossils. Recent applications that considered a diversity of biological groups illustrate how efficiently DNA-based methods complement classical paleolimnology proxies.
The knowledge gained from this approach is very diverse in scope, ranging from quantifying natural variability in population and community dynamics to understanding how these biological variables respond to anthropogenic disturbances. Such long-term environmental records are also essential to explore ecosystem reference conditions, enabling comparisons with current biodiversity and potentially providing more tightly constrained scenarios for the future.
Here, we illustrate recent applications aiming at characterizing the diversity of planktonic micro-eukaryotes and their turn-over in response to local anthropogenic disturbances (eutrophication) or more global pressures (temperature conditions). A large diversity of taxa is considered from phytoplankton (chlorophyta, bacillariophyta, …) to micro-heterotrophs (ciliophora, fungi, cercozoa…), allowing to explore co-occurences between taxa and the dynamics of ecological networks.
We discuss (i) the main methodological precautions to be taken into account for implementing this approach, and more globally (ii) the potential and challenges associated with the study of aDNA in paleolimnology to address critical research questions in lacustrine ecology.

Mardi 14h45
Forum des Pertuis

Transcriptome reconstruction and functional analysis of eukaryotic marine plankton communities via high-throughput metatranscriptomics

Alexey Vorobev(1,2), Marion Dupouy(1*), Quentin Carradec(1,2), Tom O. Delmont(1,2), Anita Annamalé(1*), Patrick Wincker(1,2), Eric Pelletier(1,2)

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Large scale metagenomic and metatranscriptomic data analyses are often restricted by their gene-centric approach, limiting the ability to understand organismal and community biology. De novo segregation of complex meta -omics data into specific biological entities remains a largely unsolved problem due to a variety of inherent biological and technical difficulties, particularly for large and complex eukaryotic genomes. Here we use a transcriptome reconstruction method based on binning co-abundant genes across a series of metagenomic samples. We investigated the co-abundance patterns of ~37 million eukaryotic unigenes across 369 metagenomic samples collected during the Tara Oceans expeditions to assess the diversity and functional profiles of marine plankton. We identified ~12 thousand co-abundant gene groups (CAGs), encompassing ~7 million unigenes, including 924 metagenomics based transcriptomes (MGTs, CAGs larger than 500 unigenes). We demonstrated the high effectiveness of our approach for reconstructing marine plankton transcriptomes by comparing MGTs with available references. We identified several key eukaryotic organisms involved in dimethylsulfoniopropionate (DMSP) biosynthesis and catabolism in different oceanic provinces, thus demonstrating the potential of the MGT collection to provide functional insights on eukaryotic plankton. We established the ability of the MGT approach to capture interspecies associations through the analysis of a nitrogen-fixing haptophyte-cyanobacterial symbiotic association. This MGT collection provides a valuable resource for an exhaustive analysis of the eukaryotic plankton in the open ocean by giving access to genomic content and functional potential of many ecologically relevant eukaryotic species.

Mardi 15h05
Forum des Pertuis

Limitations due to PCR-based metabarcoding short length fragments: A comparison with two possible alternatives, Capture by hybridisation and Nanopore sequencing

Babett Günther1, Pierre Peyret2, Sophie Marre2, Thomas Merzi3, Philippe Blanc3, Sophie Arnaud-Haond1

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The metabarcoding of environmental DNA (eDNA) opened large prospects for the future biomonitoring of marine environments. We dveloped a molecular pipe for metabarcoding standardized mitochondrial COI and ribosomal 16S, 18S barcodes, allowing inventory of biodiversity from bacteria until vertebrates. The recently improved bioinformatics pipelines allow more conservative and reliable assessments. Yet, Metabarcoding still relies on Polymerase chain reaction (PCR) of relatively short fragments, mostly by “universal” primers. This limits the reconstruction of robust phylogeny resulting in taxonomic biases. Here we present tests to adapt sequence hybridization capture methods for inventorying biodiversity in deep-sea sediment samples. This PCR-free method was expected to broaden the spectra of lineages captured in inventories, and obtain longer DNA fragments resulting in better phylogenetic reconstruction and enhanced taxonomic resolution, an essential improvement for environments still largely underrepresented in public databases. Results of the first tests on samples from a diversity of ecosystems partly fulfilled those expectations. We also compared testing with the long sequencing technology offered by Oxford Nanopore with the MinION device, which also has the advantage of allowing real-time analysis at sea. We will present a synthesis of the results obtained with the three methods 1) metabarcode (Illumina), 2) capture by hybridization and 3) MinION sequencing, and offer a set of criteria to choose the most adapted method depending on the main goal of biodiversity inventories.

Mardi 15h25
Forum des Pertuis

CLIMTREE: Quantifying changes in flying insect diversity and soil fauna along a gradient of climate induced forest decline using DNA metabarcoding

Sire, L (1); Schmidt Yañez, P (2); Fontaneto, D (3); Bouget, C (4) ; Rougerie, R (5); Larrieu, L (6); Monaghan, M (2); Yu, D (7) ; Herniou, E (1) ; Lopez-Vaamonde, C (1,8)

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Forests suffer from an increase in frequency and severity of summer droughts and infestations of pathogens and insects. Those factors cause high mortality of some keystone tree species (forest die-offs). Yet, how tree mortality and associated changes in forest composition will affect local diversity and ecosystem functions remains unknown.
CLIMTREE is an international projet funded by Belmont Forum to assess the impact of climate-induced tree diebacks on forest invertebrate biodiversity in France, Germany and China.
We have used a metabarcoding approach to measure changes in taxonomic structure of invertebrate communities along dieback and salvage logging gradients in silver fir forests in the French Pyrenees, Norway spruce in Bavarian Forest National Park (Germany) and Yunnan pine in Yunnan, (China). We examined patterns of variation in species diversity of flying insect assemblages collected by Malaise traps and soil fauna. Samples were sequenced using Illumina MiSeq and analyzed using the DAMe twin-tagging pipeline approach.
We found large species temporal turnover, as well as changes in community composition but no significant loss of species diversity along the forest decline gradient.
There is an urgent need to obtain detailed baseline data on species assemblages to quantify the impacts of climate change. Our study assessed biodiversity patterns on a scale and with a resolution that was previously impossible and provides data essential for evaluating future biotic change. Our workflow coupling metabarcoding and Malaise trapping is simple to use and provides an affordable, reliable, and verifiable way of monitoring forest biodiversity at a large geographical scale.

Mardi 15h45
Forum des Pertuis

Mollivirus Kamchatka : a second representative of the mollivirus familly provides better insights into molliviridae evolution

Eugène Christo-Foroux [1], Audrey Lartigue [1], Jean-Marie Alempic [1], Sebastien Santini [1], Matthieu Legendre [1], Jean-Michel Claverie [1], Chantal Abergel [1]

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eugene.christo-foroux@igs.cnrs-mrs.fr doctorant depuis octobre 2017

In a context of global warming, deep investigations of viruses retaining their infectivity in prehistorical permafrost layers led to the discovery in 2015 of a 30,000-y-old fourth type of giant virus, *Mollivirus sibericum*. The assessment of the infectious threat contained in Russian soil is still an ongoing project. The analyses of modern samples from the Kamchatka region using both metagenomic approach and giant virus reactivation experiments allowed us to isolate a new virus called *Mollivirus Kamchatka*. These two combined approaches permit a reliable appraisal of the residual infectious threat of both bacterias and DNA viruses contained in the melting permafrost.

We can already confirm that the *Mollivirus* familly has not gone extinct and has expanded at least accross the Russian Federation. Those two representatives of these Acanthamoeba-infecting large DNA viruses family are showing a similar nucleo-cytoplasmic replication cycle as previously described for *Mollivirus sibericum*. Virions display a characteristic spherical shape ~0.6 ¿m in diameter respectively enclosing a 648-kb to 651-kb fully syntenic GC-rich genome. Genetic features display 495 predicted proteins for *Mollivirus sibericum* and 480 proteins for *Mollivirus Kamchtka* of which an average of 62 % are familly-specific ORFans.

Strain specific genes shows recent horizontal gene transfers between *Mollivirus* and *Pandoravirus* family. Results suggest that most of the genome is under negative/purifying selection and must have thus significantly contributed to virus' fitness over the last 30,000 past years. As a conclusion we discuss the de novo gene creation process observed in Pandoravirdae1 and the relevance of current viral classification.

1. M. Legendre and al, Nat. Comm., 2018,9,2285-2297.

Mardi 16h30
Forum des Pertuis

RoskoBaz - A unified database of genetic markers for marine exploration

Farrant GK (1,2), Hoebeke M (2), Berney C (1), Corre E (2), DeVargas C (1), Guillou L (1), Jeanthon C (1), Vaulot D (1) and Garczarek L (1)

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Environmental genomics constitutes one of the pillars of marine ecosystems research at the Station Biologique of Roscoff (SBR). To study the biodiversity, ecology and dynamics of our vast and heavily contrasted oceans, environmental barcoding is currently the most widely used approach and requires reliable reference datasets for taxonomic assignment.
RoskoBaz aims at unifying four reference datasets developed at the SBR: PR2 (marine protists/18S), MicRhoDE (bacteria/proteorhodopsins), CyanoDB (marine picocyanobacteria/petB, 16S, etc.) and PhytoREF (phyto-eukaryotes/plastidial 16S). They are regrouped under a unified database schema focused on the sequences. For each sequence, the schema includes a description of the associated strain and its genome, of the sample of origin, of its spatio-temporal and physico-chemical characteristics, and of its curated taxonomy or functional ontology.
Unifying these banks of markers aims at ensuring their longevity through the development of methods to update their content. This is implemented by automatically recruiting newly sequenced variants available in public databases and through the development of common tools for the semi-automatic curation of the sequences, their taxonomy and their other metadata.

Mardi 16h50
Forum des Pertuis

Long-term dynamics of protist paleocommunities over 5000 years in the Bay of Brest (Brittany, France).

Siano R (1), Lassudrie M (2), Cuzin P (3), Mertens K (2), Schmidt S (4), Quintric L (3), Durand P (3)

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Metabarcoding of the ancient DNA of different sediment cores of the Bay of Brest allowed the characterization of protist community dynamics over 5-thousand years. Ancient DNA preserved in marine sediment cores mostly consisted in intracellular environmental DNA, suggesting that protist paleocommunities are mainly composed of species forming resting stages. The V7 (ca. 200bp) barcode region of the 18srDNA allowed the analysis of a higher Amplicon Sequence Variant number than the V4 barcode (ca. 390 bp), likely due to the degradation of the longer DNA fragment in ancient archives. Yet, the two barcode regions led to similar protist diversity patterns. Along the whole cores analyzed, the Alveolata was the dominant protist phylum, with the Apicomplexa often being the dominant group. This specific pattern has been also recorded in soil sediment archives, suggesting an interesting ecological parallel between aquatic and terrestrial habitats. Dinoflagellate (Alveolata) paleocommunities were a better indicator of ecosystemic changes that occurred in the Bay of Brest. Dinoflagellate paleocommunities were relatively stable until the 20th century, during which two major shifts were observed. Dinoflagellate genus dominance varied first during the 40's and then during the 80's. The latter variation corresponded to the expansion of the potential toxic genus *Alexandrium* in the Bay of Brest. These community shifts occurred in periods when the Bay of Brest suffered the devastation of the World War II bombing and the effects of the eutrophication of the area. Yet, the direct link between these historical events and the dinoflagellate community shifts remains to be demonstrated.

Mardi 17h10
Forum des Pertuis

Co-activity networks reveal the structure of planktonic symbioses in the global ocean

Giordano N (1,2), Chaffron S (1,2)

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Marine microbes play crucial ecological roles on our planet, forming the basis of the marine food web, sustaining Earth's biogeochemical cycles, and regulating climate. Limited by the fact that most microbes are difficult to isolate and cultivate in lab-controlled environments, meta-omic studies are instrumental to unravel the laws governing the complexity of their interactions. Today, the amount of data accumulated by large-scale environmental surveys is considerable and significant efforts have been made towards genome reconstruction from metagenomes. So-called Metagenome-Assembled Genomes (MAGs) improve the annotation of sequences by binning them into heritable and metabolically viable units. However, little is known about the biotic interactions structuring marine microbial communities. Here, we propose to uncover putative biotic interactions between MAGs by directly inferring genomic and growth traits from meta-omics data. Available metatranscriptomic data grant access to the expression of bacterial genomes in their environment, while new methods have emerged to infer bacterial replication rates based on differential coverage in a metagenomic sample. Across samples, these co-expression and co-growth signals can thus be exploited to reveal interactions between MAGs and link their activities to the environment. In addition, we can use the functional content of these co-active MAGs to predict potential dependencies, in particular if they deviate from general scaling laws that govern the functional content of genomes from lab-cultivated microbial organisms. Inferring and combining (meta-)genomic traits in a global framework can help to identify consortia of marine microbes and pave the way towards the functional understanding and the metabolic modeling of their interactions.

Session 2 – Biodiversité : structure et dynamique des populations et communautés incluant les taxons méconnus ou mal connus

Mercredi 9h00
Forum des Pertuis

New insights into the genome structure and evolution of the bdelloid rotifer *Adineta vaga* and its DNA DSB repair dynamic

Karine Van Doninck

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Mercredi 9h45
Forum des Pertuis

Individual, population and species differentiation in *Pocillopora* spp. Corals

Pratlong M(1,2), Magalon H(3,4), Bonhomme F(5), Haguenauer A(1,6), Adjeroud M(7), Toulza E (8), Brener K(8), Vidal-Dupiol J(8), Mitta G(8), Pontarotti P(2,9), Aurelle D(1,10,11)

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Genomic data allow in depth and renewed study of biodiversity at different organization levels. This is particularly useful in cnidarians, where the paucity of morphological characters, the impact of plasticity and reticulate evolution, make species delineation difficult. In a context of strong pressures on coral populations, a better characterization of their diversity is important to study their evolution and adaptive abilities. *Pocillopora* corals are ecologically important scleractinians from the Indo-Pacific. In this genus the use of mitochondrial DNA allowed to proposed primary species hypotheses, which have been refined in secondary species hypotheses thanks to microsatellite data. Here we used RAD sequencing to study genomic differentiation between mitochondrial lineages, and between populations from Oman and French Polynesia. RAD sequences were aligned on a draft genome of *Pocillopora*, and assembled with Stacks. Multivariate and clustering analyses were used to study the genetic structure. Site frequency spectra were used for evolutionary inferences. The main differentiation pattern was only partially congruent with mitochondrial lineages. No genetic structure was observed between sites in a given place. Interestingly, a few colonies displayed important genomic differences inside populations. These results are important to better understand the diversification of *Pocillopora* corals.

Mercredi 10h05
Forum des Pertuis

Microboring *Ostreobium* diversity in *Pocillopora* sp. coral skeletons from the Pacific Ocean

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The microboring alga *Ostreobium* (Ulvophyceae, Bryopsidale) is one of the major agents of carbonate dissolution in coral reefs (Tribollet et al. 2019). It dominates microboring communities in the skeleton of living corals and may also exchange metabolites with coral host tissue (Odum & Odum 1955; Fine and Loya 2002; Sangsawang et al 2017). Its diversity remains however underexplored in fast-growing branching corals compared to that of slow-growing massive corals (Gutner-Hoch and Fine 2011; Marcelino et al. 2017; Marcelino and Verbruggen 2016, 2018). The TARA Pacific expedition (2017-2018) has provided Pacific-wide sampling of the branching coral Pocillopora sp. We have analyzed *Pocillopora* skeletons from three South-West Pacific archipelagos (Gambier, Guam, Samoa) via amplicon sequencing of two taxonomic marker genes (rbcL and tufA) of the Ulvophyceae. Sanger sequencing of clones and Illumina amplicon sequencing MiSeq methods were compared. The results highlight clades (OTUs>98%) belonging to two families already referenced within the suborder Ostreobidinae, along with more genetically distant sequences that could correspond to new groups. The genetic diversity of *Ostreobium* is low at the colony (branch) scale (1-3 OTUs), but is diverse at the scale of reef sites and islands, with heterogeneous distribution and abundance of *Ostreobium* clades, depending on geography. Future studies will investigate environmental drivers shaping the patterns of *Pocillopora* coral-associated *Ostreobium* communities across the Pacific Ocean.

(we acknowledge partial funding from the Fondation pour la Recherche sur la Biodiversité)

Mercredi 10h25
Forum des Pertuis

The Ocean Barcode Atlas : A web service to explore plankton biodiversity

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The Ocean Barcode Atlas is a web service to explore the biodiversity and biogeography of marine planktonic organisms using metabarcoding. It allows users to query ocean ribosomal diversity (such as barcode catalogues) by submitting a barcode sequence or taxonomy. In one click, the abundance and location of the target barcodes are visualized on world maps as well as their taxonomic and diversity distribution. Interactive results panels allow for adjusting thresholds for alignment quality and display barcode abundance in the context of the environmental characteristics (temperature, nutrients, etc.) measured at the time of sampling. An intermediate page allows users to select the OTUs of interest. The taxonomic distribution of all the selected barcode sequences is represented by a krona and a phylogenetic analysis is computed. Usability makes it possible to explore quantitative and contextualized information on the barcode of interest in the global ocean ecosystem. In a search from a taxonomy, Shannon's index and richness are calculated and then presented on a map. In the future, beta diversity will also be calculated.
Currently, the Ocean Barcode Altas is deployed with eukaryotic 18S-V9 rDNA metabarcodes of comprising 380 000 OTUs collected during the expedition Tara Oceans and the V9-PR2 reference database (with 77 449 barcodes). Additional marine environmental datasets about prokaryotic or eukaryotic plankton biodiversity (such as 16S miTAGs or 18S-V4 rDNA) will be added upon availability that provides the required complement of barcodes and contextual environmental parameters. Ocean Gene Atlas is a freely-available web service at: http://oba.mio.osupytheas.fr/ocean-atlas/.

Mercredi 10h45
Forum des Pertuis

Viral DNA diversity in Isopods

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Hosts and their associated microbial genomes are now considered as holistic systems, or holobionts. This new paradigm and the rise of NGS technologies are revealing previously unknown biodiversity. A high-throughput metagenomics approach was used to analyze the complex interactions in the holobiont of terrestrial isopods [1, 2]. Terrestrial isopods are known to harbor highly diversified bacterial microbiota that influence their ecology and evolution [3-5]. However, little is known about the viral component of the microbiota associated with isopods. Apart endogenous viruses [6], only Reoviruses, Iridoviruses or Cruciviruses have been to date identified in isopods [7-9]. Here we investigate the metagenomes of five species of both terrestrial and aquatic isopods. More than 2 billion reads were generated from the five samples, and a virome catalog was assembled containing 298,982 viral contigs (> 1kb) representing from 27% to 57% (and among them from 3 to 27% of phages) of the final assemblies. From this virome catalog, 4,759 contigs were taxonomically identified corresponding to twenty-one families of viruses, most of them being newly identified in isopods. Detection and abundance quantification of viruses and phages are then performed according to tissue localization and host species.

We describe the general features of the isopod DNA virome, and test whether components of the virome differ between aquatic and terrestrial species. We discuss whether the virome component may impact the isopod microbiota composition. Our results highlight the vast and unexplored diversity of DNA viruses among isopods, an undersampled taxa.

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Mercredi 11h30
Forum des Pertuis

Populations structure of the microalgae *Bathycoccus prasinos* in the open ocean

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Marine micro-eukaryotes are critical actors in the biogeochemical cycles and trophic webs of Oceans. However, despite their importance, their enormous diversity remains largely unknown at the genomic level. Importantly, while they are being transported across long distance by currents, Plankton undergo very complex mixing between populations originated from different water masses and must thrive in contrasted environmental conditions.
The Tara Oceans expeditions, by collecting and sequencing thousands of metagenomics samples of plankton, allow us to better investigate this biodiversity and to analyze more precisely the biogeography as well as the structure of the populations. Here we interrogate the genomic diversity of the abundant and cosmopolitan microalgae *Bathycoccus prasinos* by developing multiple statistics genomics approaches to analyze marine metagenomics samples, allowing us a higher specificity and clearer biogeographical patterns. We analyzed *Bathycoccus* genomic diversity by studying single nucleotide variations and their impacts at the protein level finding a variant density going up to 1.96% and characterizing the most impactful amino-acid variants. Genomic Populations are segregated between hot and cold water, with a set of 2742 loci being considered significantly responsible for this pattern. This work presents a first large scale genomic survey of an environmental eukaryote across almost all latitude.

Mercredi 11h50
Forum des Pertuis

On the influence of urbanization on the human gut and oral microbiome

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Industrialization has been associated with a loss of human gut microbiota diversity. As a decreased gut microbiome diversity is also correlated with a number of modern diseases, understanding what factors drive this loss is vital for public health. It is also of great evolutionary interest to understand how gut bacteria are adapting to rapidly changing environments. However, industrialized and non-industrialized populations differ in many ways, making it practically impossible to disentangle the effects of diet, sanitary conditions, medical practices or other factors. Moreover, gut protozoa, who have likely shaped the human-gut microbiota interactions throughout their coevolutionary history but are virtually absent from industrialized populations, are rarely taken into account. Finally, even less is known about the effects of industrialization on other microbiomes, including the oral microbiome, another important health-associated microbial community. To address some of these limitations, we examined oral and gut microbiomes of 140 individuals from Cameroon along a small-scale urbanization gradient. Apart from metagenetic and metagenomic data, we collected a number of ethnological, medical, sanitary and parasitological parameters in order to identify factors that influence microbiome diversity and variation.
In addition, given the complexity of these microbial communities, we examined how our conclusions changed depending on the taxonomic and phylogenetic resolution scale used, as well as on the way we calculate diversity estimates. Such a comprehensive approach is more likely to identify the precise processes generating microbiome variation within and among individuals.
Overall, our results shed light on the link between various aspects of urbanization and human microbiome variation in a non-industrialized setting and highlight the importance of exploring various methodologies for inference and hypothesis generation in microbiome research.

Mercredi 12h10
Forum des Pertuis

Genomic inferences on reproductive biology and population differentiation of the Mediterranean kelp *Laminaria rodriguezii*

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Keywords: macroalgae, kelp forests, mating system, population genomics, RAD-sequencing

Deep-water forests of *Laminaria rodriguezii* are an endemic Mediterranean ecosystem, known only from a few localities, and with high conservation value. This kelp evolves under low light intensities at depths ranging from 50 to 120 m and temperature below 14°C. Recent molecular investigation of kelps, essentially based on microsatellite markers, allowed to investigate populations genetic. Although these studies are relevant for various macroalgae in shallow environments, deep-water forests still remain largely unknown. Moreover, most of kelps have invested in sexual reproduction through the creation of haploid meiospores while *Laminaria rodriguezii* evolved toward a dual mating system based also on vegetative propagation. However, how such original reproductive process impacts their population structure and genetic variability remains to be elucidated. Here, we conducted the first genomic investigation of the deep-water kelp *Laminaria rodriguezii* along the Mediterranean coasts of France. Through the development of ddRAD-sequencing libraries, 21 738 SNPs were selected across 49 individuals from four localities at 65-76 m depth. Our results revealed a significant heterozygote excess, involving negative FIS in each population. In addition, the detection of repeated Multilocus genotype and the presence of significant linkage disequilibrium revealed that asexual reproduction occurs frequently. Additionally, populations exhibited high levels of genetic differentiation, when the data set included repeated MLLs, but the elimination of repeated multilocus lineages, reduced the observed genetic divergence between populations. The kelp *Laminaria rodriguezii* requires effective and efficient management that account the effects of clonal reproduction and high level of genetic divergence across scales of tens of kilometers.

Mercredi 12h30
Forum des Pertuis

New insights into selection under genome evolution and domestication of apricot

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Long-lived perennials present evolutionary and domestication processes distinct from annual counterparts. Tree crop species tend to have been domesticated more recently, they are generally outcrossing, have extended juvenile periods, and are propagated clonally. While unravelling their histories of divergence is expected to provide insights into the processes of adaptation and diversification, selective sweep may help to identify the genomic bases underlying important agronomic traits during domestication.
Apricot, *Prunus armeniaca* L., is an excellent fruit tree for studying species evolution and domestication: while it is cultivated worldwide, it still exists in its wild form in natural populations of the Central Asian mountainous forests. We first illustrated the apricot history using microsatellite data and approximate Bayesian computation. We inferred that the origin center of European/Irano Caucasian cultivars was Central Asia and revealed that the wild species *P. armeniaca* and *P. sibirica* diverged ca. 8 to 16 Mya ago, followed by divergence of the two cultivated apricot clusters, Chinese and European/Irano-Caucasian from wild *P. armeniaca* in north Central Asia.
Based on the above demography history, we then switched to whole genome polymorphism to identify regions under selection during the domestication events. For this, we benefited, through ANR, France Génomique and University of Bordeaux's funding, from a high-quality apricot reference genome and from Next Generation Sequencing of hundreds sequences of wild and cultivated *P. armeniaca*. We implemented various methods to detect the selective signatures in the cultivated (European and Chinese) apricots as well as in Central Asian natural populations of *P. armeniaca*.

Mercredi 14h00
Forum des Pertuis

Microbial populations metagenomics: insights and challenges

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Populations genetics aims to study the genetic variability within a population and to identify the drivers shaping it (i.e. dispersal, environment). While most of population genetics studies have focused on fish and benthic species targeted by conservation planning, holoplankton has been underlooked, especially the ecologically crucial microbial eukaryotes. In parallel, high-throughput sequencing methods have gone through constant developments over the last decade allowing today an unprecedented access to the diversity and functions of natural communities. In particular, genetic diversity, which allows populations to adapt to a changing environment, can now be explored in depth for natural populations, including microbial eukaryotes. Thus, the aim of this study is to explore how large scale environmental samplings offer new insights into microbial populations structure and its drivers, as well as the raised challenges. We used the metagenomics samples collected in the Mediterranean sea during the Tara Oceans expedition to infer microbial population structure within this heterogenous pelagic environment. We took into account both environmental and dispersal variables (respectively environmental variables from climatologies and biophysical transport estimated from Lagrangian model simulations) to elucidate its drivers. Although our study has revealed several issues for microbial populations metagenomics (e.g. the lack of genomic references, the quantification of physical connectivity), we succeeded in detecting trends between population structures and forcing variables. This present population metagenomics study allowed making promising and innovative assumptions about mechanisms shaping metagenomic diversity of largely poorly studied but incredibly diversified microbial eukaryotes and could now be extended to other oceanic regions.

Session 3 - Epigénétique et génomique fonctionnelle

Mercredi 14h20
Forum des Pertuis

A systems biology approach on (epigenetic) inheritance

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Understanding the complex interactions between the environment and the genotype that bring about the phenotype are one of the central objectives but also one of the major challenges in evolutionary biology. Things have been further complicated by the idea that heritable changes in reaction norms cannot only be produced by genetic variations, but that a certain part might be due to epigenetic variants. A lively scientific debate has emerged around the question whether epigenetic changes (alone) can have any importance in evolutionary processes. We argue that both, and potentially other heritable elements, are necessary to convey information through time.
Genome and epigenome, the latter we will define tentatively as information unit that allows for heritable changes in gene function that is not based on changes of the DNA sequence, are tightly interrelated and interdependent. Neither genomes nor epigenomes can exist alone and they necessarily interact with each other as elements of an inheritance system. We define here a system as a collection of units (elements) that are linked and that influence each other through action and feedback (interactions), and that bring about over time observable effects (process).

Systems biology can be used as guide to identify interactions, interacting elements, strength of interaction, and the time course of interaction events in the generation of phenotypes. For operational reason, natural systems will need to be simplified, and systems biology allows for selecting elements and interactions that will have major effects from those that have minor.
Through interaction with environmental cues this inheritance system produces over time, in a developmental process phenotypes that can be selected for. In this systems approach to inheritance, elements such as genome or epigenome can only be operationally defined. It is then not only their relative importance but also the strength of reciprocal interaction that drives the production of phenotypes. The art of the experimenter will be to find the best operational definition of all elements of the inheritance system at identical levels of resolution either through molecular approaches or pedigree studies, and to evaluate their relative contributions to phenotypic variance. While this can now be done in many biological systems, major challenges remain to precisely characterize the interactions between genome and epigenome. But once this will be done, rational concepts can be developed and used to manipulate the inheritance system.

In the talk I will provide examples from our lab showing how epigenetic profiling can be used to (i) identify targets for pharmacological perturbation of the inheritance system, (ii) identify traces of environmental cues, and (iii) provide markers for specific phenotypes (e.g. parasite virulence) and molecular function (e.g. mRNA presence).

Mercredi 15h05
Forum des Pertuis

Explorer les fonctions microbiennes à partir d'informations taxonomiques : un état de l'art des outils et des méthodes

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À l'ère des Big Data, d'énormes quantités de données sont disponibles et constituent une occasion unique de développer des algorithmes de prédiction performants. En écologie microbienne, ce phénomène a joué un rôle majeur dans la façon dont nous abordons la biodiversité depuis l'apparition des NGS. L'étude des microbiomes environnementaux par les outils les méta-omiques a conduit à la découverte de nouveaux organismes, fournissant ainsi une source importante d'informations taxonomiques et fonctionnelles. L'un des futurs défis, est de réussir à associer une fonction à une diversité microbienne pour améliorer notre compréhension des fonctions du microbiome (British Ecological Society, 2016). Bien que certaines technologies renseignent sur les fonctions putatives ou réelles, elles restent fastidieuses et coûteuses à mettre en œuvre. L'approche de metabarcoding est couramment utilisée pour obtenir des informations sur la diversité microbienne avec un coût très abordable, mais elle ne permet pas directement d'obtenir des informations sur les fonctions microbiennes. Deux solutions vivement débattues au sein de la communauté scientifique émergent actuellement pour tirer des informations fonctionnelles à partir d'un profil taxonomique : (i) l'inférence fonctionnelle et (ii) l'assignation de traits écologiques. Si la plupart des outils disponibles sont utilisables uniquement pour les procaryotes, comme PICRUSt le plus connu, d'autres alternatives existent afin d'étudier les eucaryotes et notamment les champignons comme par exemple FUNGuild. Ainsi, nous présenterons un état de l'art des outils et méthodes disponibles, illustrés par différents exemples permettant de faire le lien entre la diversité des communautés et leurs fonctions ou traits écologiques en ciblant l'environnement sol.

Mercredi 15h25
Forum des Pertuis

Dégradation de la chlordécone : mise en évidence de cinq familles de produits de dégradation, au laboratoire et dans des échantillons environnementaux antillais, caractérisation de microorganismes impliqués.

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La chlordécone (C10Cl10O ou C10Cl10H2O2 sous forme hydratée) est un insecticide organochloré possédant une structure polycyclique bishomocubane. La chlordécone (CLD) est très toxique et a été interdite aux USA en 1976 et elle a été classée parmi les "Polluants Organiques Persistants". Elle a été massivement utilisée, avec dérogations, aux Antilles françaises pour lutter contre le charançon du bananier jusqu'en 1993. Son utilisation extensive, sa persistance, son accumulation dans la chaine alimentaire et sa résilience entraînent de graves problèmes socio-économiques et de santé publique. Elle était considérée jusqu'à peu comme non biodégradable.
Nous avons obtenu plusieurs consortia bactériens capables de transformer la CLD en anaérobiose. Une approche métagénomique de ces consortia n'a pas révélé l'existence de bactéries connues ni même de gènes connus pour réaliser une déhalogénation réductive. Puis, nous avons réussi à isoler plusieurs de ces bactéries en anaérobiose (1).
L'utilisation de réactions chimiques biomimétiques de dégradation de la CLD (en présence de vitamine B12 par exemple et de réducteurs) a permis d'obtenir les mêmes métabolites ou produits de transformation (PT) que ceux observés lors de la dégradation microbiologique avec les consortia microbiens ou les bactéries isolées. De plus, le développement de protocoles de purification et l'utilisation d'outils analytiques tels que la spectrométrie de masse et la résonance magnétique nucléaire ont permis l'obtention des principaux PT purs et l'identification de la structure chimique de 19 d'entre eux (2).
Finalement, cinq familles de PT de la CLD ont été décrites (2). Certains d'entre eux sont particulièrement intéressants car ont perdu jusqu'à 8 atomes de chlore et possèdent un noyau indène attestant de l'ouverture de la cage bishomocubane de la CLD.
Une étude du fractionnement isotopique du carbone de la CLD a été réalisée en comparant des transformations microbiologiques (consortium bactérien et Citrobacter isolé) et des réactions chimiques (en présence de vitamine B12 et de réducteurs ou de fer zéro valent). Cette étude a montré que les mécanismes mis en jeu lors des transformations biologiques ou chimiques sont différents. Nous avons également comparé le rapport isotopique de quatre lots historiques de

CLD (Kepone® et Curlone®). Ils s'avèrent être très similaires et suggèrent que la méthode développée pourrait être une façon d'évaluer si une transformation de la CLD a lieu dans les sols contaminés (3).
L'obtention des métabolites de la CLD avec une très grande pureté est très importante (étude de stabilité, solubilité, toxicité). Elle permet également la détection des PT de la CLD dans les matrices environnementales. Les analyses chimiques de différents types d'échantillons (eaux, sols, sédiments) provenant de Martinique ont révélé la présence de 19 PT dans les échantillons historiquement contaminés par la CLD. L'analyse taxonomique (ARNr 16S) des différents échantillons de sols a montré une grande diversité microbienne, chaque sol montrant des particularités. Les séquences de bactéries connues pour être impliquées directement ou indirectement dans la dégradation de la chlordécone (1) n'ont été retrouvées que très minoritairement et ce que dans certains sols. Plusieurs profils de pollution en PT ont pu être définis, généralement en lien avec la nature des sols (andosol, ferralsol, nitisol). Les capacités de dégradation de la CLD par les sols antillais ont été vérifiées en laboratoire.
Cette étude démontre que la CLD se dégrade naturellement et de manière significative dans les sols antillais historiquement contaminés. Les processus impliqués conduisent à une contamination généralisée en PT dans tous les compartiments environnementaux étudiés (sols, eaux, sédiments, mangrove). Les micro-organismes responsables de cette biodégradation sont en cours d'identification.
La découverte de cette "nouvelle" pollution aux PT de la chlordécone pose de nombreuses questions telles que la distribution réelle à l'échelle des Antilles de ces polluants "émergents", leur devenir dans l'environnement, la chaine alimentaire et l'imprégnation de la population, ainsi que la toxicité de ces molécules chlorées (sous forme purifiée ou en mélange au sein de l'exposome antillais).

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Mercredi 15h45
Forum des Pertuis

A la recherche du locus déterminant le sexe du cloporte commun, *Armadillidium vulgare*, par une approche de croisements et de séquençage par pools

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Les chromosomes sexuels d'une paire ne sont pas toujours très différents l'un de l'autre, à l'opposé du X et du Y des humains. En effet, une paire de chromosomes sexuels dérive d'autosomes ayant acquis une variation génétique contrôlant le sexe ; ils sont donc initialement indifférenciés au delà de ce locus. Par ce processus, les chromosomes sexuels se renouvellent assez fréquemment au sein de certains taxons. Cependant, hormis chez quelques groupes de vertébrés et d'insectes, cette dynamique de renouvellement, ainsi que les gènes mêmes déterminant le sexe, sont mal connus. Nous les étudions chez les cloportes (crustacés isopodes), dont les chromosomes sexuels présentent une forte dynamique de renouvellement. Nous nous focalisons sur le cloporte commun, *Armadillidium vulgare*, qui présente des chromosomes sexuels de type WZ (les femelles sont de génotype WZ et les mâles ZZ). En tirant partie du génome femelle du cloporte commun que nous avons récemment assemblé, nous identifions les régions génomiques portant le locus contrôlant le sexe par une méthode basée sur des SNPs, étant attendu qu'un SNP lié au locus contrôlant le sexe doit être hétérozygote chez les femelles WZ et homozygote chez les mâles ZZ. Ainsi, nous avons séquencé par pool (poolseq) les génomes entiers de fils et de filles de familles F1 de cloportes. Nous analysons les fréquences alléliques dans chaque sexe par une approche bayésienne, ainsi que les ratios de couverture de séquençage male/femelle, afin de sélectionner des régions génomiques candidates contrôlant le sexe chez le cloporte commun.

Mercredi 15h30
Forum des Pertuis

Identification par Tn-seq des gènes essentiels à l'exploitation de l'hôte végétal par le pathogène émergeant *Dickeya solani*

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Quelles sont les fonctions clés d'un pathogène impliquées dans la colonisation de son hôte ? Répondre à cette question constitue un enjeu important tant pour comprendre sa capacité d'adaptation à l'hôte que pour proposer de nouvelles cibles pour le contrôler. *Dickeya solani* est un phytopathogène qui a émergé au début des années 2000 en cultures de pomme de terre (*Solanum tuberosum*) en Europe et au-delà. Il colonise de manière asymptomatique les plantes, et peut, en conditions favorables, provoquer la macération des tissus végétaux, causant la maladie de la jambe noire sur tiges et celle de la pourriture molle des tubercules. Afin d'identifier les gènes essentiels intervenant dans la prolifération de ce pathogène lors de la colonisation de ces 3 niches écologiques (racines, tiges et tubercules), nous avons réalisé des expériences de transposon-sequencing (Tn-seq). Une population de *D. solani* mutants a été produite par insertion aléatoire d'un transposon avant d'être inoculée dans les 3 compartiments considérés. Le séquençage à haut-débit (Illumina) des populations de mutants avant et après colonisation des racines, tiges et tubercules a permis d'identifier les gènes de *D. solani* essentiels à la colonisation de ces 3 niches écologiques. Cette analyse montre que la colonisation et l'exploitation de chacun de ces compartiments de l'hôte font intervenir des gènes et des fonctions différents. Ces travaux permettent de comparer, pour la première fois, les modes de vie de ce pathogènes au cours de son cycle infectieux. Cette approche simple et puissante pourrait être déployée chez d'autres microorganismes qu'ils soient commensaux, pathogènes ou symbiotes afin de comprendre leur capacité d'adaptation.

Mercredi 16h50
Forum des Pertuis

La dégradation de la lignocellulose chez les isopodes : nouveaux éclairages sur l'adaptation à la vie terrestre

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D'origine marine, les isopodes ont aujourd'hui colonisé avec succès tous les environnements aquatiques et terrestres. Leur capacité à consommer diverses ressources alimentaires, en particulier celles issues de la biomasse végétale, pourrait être une des raisons de leur succès évolutif.
Tous les isopodes qui consomment des plantes et leurs dérivés, doivent être en mesure de dégrader la lignocellulose, le constituant majeur de la biomasse végétale. La plupart des arthropodes vivent en association avec des microorganismes qui leur permettent une digestion efficace de ce composé [1]. Parmi eux, les isopodes terrestres constituent un exemple particulier puisqu'à l'image des termites [2], ils décomposent la lignocellulose grâce une complémentarité de leurs CAZymes avec celles de leur microbiote [3, 4]. Leurs CAZymes propres ainsi que l'acquisition d'un microbiote digestif diversifié aurait aidé les isopodes terrestres à conquérir l'ensemble des écosystèmes terrestres.
Afin de mieux comprendre le succès des isopodes dans l'adaptation à la vie terrestre, nous avons caractérisé par des approches métagénomiques et transcriptomiques, le répertoire des CAZymes de l'hôte et de son microbiote impliqué dans la dégradation de lignocellulose d'un large spectre d'espèces d'isopodes aquatiques et terrestres. Les transcriptomes de 64 espèces montrent que le répertoire des CAZymes des isopodes terrestres est en expansion comparé à celui des isopodes aquatiques. Ce répertoire s'est enrichi grâce à l'acquisition de nouvelles enzymes par transfert horizontal et par des duplications de gènes qui ont conduit à l'apparition de nouvelles fonctions enzymatiques. Ces résultats apportent de nouveaux éclairages sur l'adaptation à la vie terrestre des isopodes.

Mercredi 17h10
Forum des Pertuis

Adaptation and acclimation strategies of picocyanobacteria unveiled by comparative genomics and meta-omic data analysis

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The marine picocyanobacteria *Synechococcus* and *Prochlorococcus* are the most abundant photosynthetic organisms on Earth and occupy a wide variety of environmental niches, an ecological success likely due to their large genetic diversity. However, processes governing their diversification remain poorly understood.
Here, 81 non-redundant genomes were used to evaluate the genomic diversity of both genera and how this relates to niche adaptation. 16S rRNA and amino acid identities between pairs of strains allowed us to clearly discriminate the 3 main *Synechococcus* deep lineages and all major phylogenetic clades. Despite the availability of several genomes by major clade, only a limited number of genes potentially related to niche partitioning were found and mainly concerned adaptation to salinity and/or nutrient limitations (N, P, Fe), while adaptation to temperature rather relies on amino acid substitutions. Prediction of genomic islands based on gained genes and comparison of their gene content between strains by a network approach led to the discrimination of islands shared by members of a same clade from potential lateral transfers between distantly related strains. Finally, use of these genomes as references to recruit picocyanobacterial reads from the Tara Oceans meta-omes allowed us to show that different ecologically significant taxonomic units (ESTUs, as defined by [1]) displayed distinct gene repertoires and expression patterns as well as to identify genes potentially involved in adaptation to various environmental niches. Altogether, these results allowed us to refine our understanding of the evolutionary processes involved in the diversification of key members of marine phytoplankton.

[1] Farrant GK et al. (2016). PNAS 113:E3365-74.

Mercredi 17h30
Forum des Pertuis

Adaptation fonctionnelle des communautés microbiennes en réponse à l'exportation massive de biomasse végétale en forêt : une analyse transcriptomique

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En forêt, les microorganismes du sol jouent un rôle majeur dans les cycles biogéochimiques. Cependant, divers facteurs peuvent affecter les services et fonctions liés aux processus microbiens dans les sols. Dans un contexte d'intensification de l'exportation de la biomasse forestière, nous avons étudié les effets de l'exportation de matière organique sur la diversité microbienne des sols d'une chênaie et sur le métatranscrit de ces communautés bactériennes et fongiques. A partir des ADN et ARN extraits de sols, nous avons analysé et comparé les séquences de barcoding microbien et de méta-transcrits issues deux conditions : *gestion forestière conventionnelle* et *exportation massive de matière organique*. Différentes ressources et bases de données ont été utilisées pour l'annotation experte de ces séquences méta-omiques. Les analyses de diversité montrent une forte augmentation des bactéries oligotrophes, mais aussi des levures et des champignons ectomycorhiziens, au dépend des microorganismes copiotrophes et champignons saprophytes dans les sols des placettes intensément exploitées. L'analyse fonctionnelle des différentes guildes écologiques révèle une répression de l'expression des familles de gènes (en particulier fongiques) associées à la décomposition des parois cellulaires végétales dans les placettes soumises à l'exportation de biomasse. De manière remarquable, cette répression est contrebalancée par une forte augmentation des transcrits bactériens impliqués dans la dégradation des parois cellulaires fongiques. Ces résultats mettent en lumière les conséquences des pratiques sylvicoles intenses sur la diversité et le fonctionnement des sols, mais aussi sur les modifications des réseaux d'interactions trophiques et leurs conséquences potentielles sur le stockage du C des sols.

Session 4 – Session ouverte

Jeudi 9h00
Forum des Pertuis

Evolution of functional and regulatory novelty at the self-incompatibility locus in *Arabidopsis*

Vincent Castric

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Self-incompatibility in plants of the Brassicaceae family is controlled by a highly diversified molecular lock-and-key system consisting of a large set of specific haplotypic combinations of two tightly linked genes : SCR, which is expressed in the anther tapetum and encodes the male recognition specificity and SRK, which is expressed at the stigma surface and encodes the female recognition specificity. This system has been a textbook example of natural (balancing) selection, in the form of a strong reproductive advantage for individuals expressing rare alleles. While the many highly divergent haplotypes segregating is one of the most defining features of self-incompatibility genes, the question of how so many lock-and-key combinations could arise raises a series of interesting theoretical and mechanistic problems. In particular, the emergence and evolutionary success of any novel haplotype from an ancestral form entails at least two individual mutations, one on each of the two genes. In this talk, I will first detail how we are investigating the conditions under which the fitness valley represented by single mutants can still be crossed in spite of the fitness penalty entailed by lack of self-recognition and ensuing inbreeding depression. I will then detail a set of ongoing experiments based on ancestral resurrection of ancient self-incompatibility genes in the plant *Arabidopsis thaliana* to put these theoretical predictions directly to the test and try and catch the diversification process in flagrante delicto. Overall, our data using this simple and experimentally tractable biological system provide insight into the broader issue of how functional and regulatory novelty can arise in natural populations.

Jeudi 9h45
Forum des Pertuis

Biogeographical Design of Soil Microbial Habitats

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(5) CEA / Institut de Biologie François Jacob / Génoscope, 2, Rue Gaston Crémieux, CP5706, 91057 Evry cedex

Since the beginning of 21th century, soil microbial diversity is intensively studied gathering a huge knowledge at local and global scales. Nevertheless, the microbial habitats have been poorly investigated, limiting our ability to link biodiversity description and regulation. In our study, we used a pyrosequencing approach targeting 16S rRNA genes directly amplified from soil DNA to have a comprehensive view of soil bacterial and archaeal community composition across the largest spatially explicit soil sampling available in France (2173 soils, area covered = 5.5x105 km2). Based on the multivariate regression tree (MRT) method, we designed 16 distinct terrestrial microbial habitats at the territory scale, delineated by the association of soil pH, C:N ratio, land use and minorly climatic conditions. The heterogeneous spatial distribution of habitats drew up a complex mosaic across France. As for plants and animals, each habitat hosts generalist and specialist taxa and a specific interaction network, directly or indirectly impacted by the Human activities. Overall, our results stressed the importance of the integration of microbial habitats for upgrading the biodiversity conservation policies in a context of global change.

Jeudi 10h05
Forum des Pertuis

Optimization of viral biodiversity detection : TINAP workflow

A. Antoine-Lorquin (1), S. François (3), L. Claude (2), D. Filloux (2), P. Roumagnac (2) & M. Ogliastro (1)

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Viral metagenomics is a powerful tool to analyze virus diversity and prevalence in ecosystems, allowing to highlight their abundance and the role they play in the functioning of many ecosystems. This approach can be used to explore virus diversity in insects and in plants which may ultimately help to improve the functioning and management of agrosystems. One major challenge of this approach remains virus identification, due to the lack of genes common to all viruses and the rapid evolution of the viral genomes. Such limitation requires to optimize bioinformatic methods.
Here we developed the TINAP workflow, which aims to improve virus detection from next generation sequencing by upgrading three fundamental steps: i) the linker identification: using a Kmer logic to identify linkers, we were able to double the number of identified sequences. ii) The sequence assembly: by including four complementary assembly steps, the TINAP workflow allows now the assembly of longer contigs, which facilitates their identification. iii) Virus sequence identification: we implement a double validation of the contigs based on nucleotidic and proteic identities (BlastN and BlastX respectively). This double validation allows identifying viruses at the species level, whereas a single validation only highlights similarity with already known species. Here we showed that improving these three steps, allows the TINAP workflow to optimize the viral metagenomic sequence analyses and help to describe a more accurate landscape of the viral diversity.

Jeudi 10h25
Forum des Pertuis

Hydrodynamique et biocides façonnent les communautés de biofilms marins sur surfaces artificielles

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La colonisation microbienne des surfaces immergées en milieu marin est un enjeu majeur d'un point de vue écologique et économique puisqu'il concerne des problématiques comme les coques des navires, les énergies marines renouvelables ou les plastiques1, 2, 5.
Ce projet avait pour objectif de comprendre les facteurs de forçage de la colonisation de substrats en zones côtières. L'importance relative des propriétés des surfaces (hydrophobie, rugosité, relargage de biocide), du mode d'immersion (statique vs dynamique) et des conditions environnementales (2 sites méditerranéens contrastés) a été déterminée sur la dynamique des structures de communautés des biofilms sur 1an (cytométrie et metabarcoding).
La colonisation en mode statique se traduit par des communautés denses et très diversifiées, dont la composition diffère significativement des communautés planctoniques dès les premières heures. La présence de biocides dans les revêtements sélectionne au contraire des communautés très peu diversifiées (2 OTU majoritaires pendant 20 jours). Le mode d'immersion dynamique limite clairement les densités et semble aussi accentuer les dissimilarités de structures de communautés, notamment en présence de cuivre. La rugosité ou l'hydrophobie des surfaces ne semblent influencer les communautés microbiennes qu'en mode dynamique et après une longue immersion alors qu'une convergence dans le temps des surfaces sans biocide a été observée en mode statique. Les surfaces immergées à Banyuls présentent des densités plus faibles et moins dissimilaires entre elles, ce qui pourrait s'expliquer par une hydrodynamique du site plus forte qui masquerait partiellement l'effet des revêtements. Nos résultats soulignent le rôle majeur des conditions hydrodynamiques dans ces processus de colonisation.

Jeudi 11h10
Forum des Pertuis

Large DNA viruses of microalgae are predicted to enhance carbon export efficiency in the global sunlit ocean

Romain Blanc-Mathieu (1), Hiroto Kaneko (1), Hisashi Endo (1), Samuel Chaffron (2), Lionel Guidi (3) and Hiroyuki Ogata (1)

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In the sunlit ocean autotrophic organisms transform inorganic carbon into organic matter that can be exported towards the ocean interior, in the form of particles via gravitational sinking. This process is known as the biological carbon pump (BCP). Viruses are thought to enhance the BCP by fostering primary production and facilitating the sinking of carbon-enriched materials. We leveraged deep-sequencing molecular data generated in the framework of Tara Oceans to identify and quantify diverse lineages of large dsDNA and smaller RNA viruses of the eukaryotic plankton. We found that the abundance of these viruses is associated with an indirect measure of carbon export efficiency (CEE) at sampling sites. The distant evolutionary relationship between cultured viruses and most of the viruses identified in environmental samples limits ecological interpretation such as their host organism. A host prediction analysis coupling co-abundance interaction networks with the phylogeny of viruses identified prasinoviruses infecting *Mamiellales* and *Mimivirus* relatives putatively infecting Prymnesiales among the lineages that are the most strongly and positively associated with CEE. This finding is the first to link viruses of the eukaryotic plankton with the BCP at a global scale.

Jeudi 11h30
Forum des Pertuis

A new DNA metabarcoding approach to describe the diet of social wasps and evaluate their impact on biodiversity

Marie-Caroline Lefort (1,2), Thomas E. Saunders(3), Jacqueline Beggs(3), Travis Glare(4), Stéphane Boyer (5)

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(5) IRBI, UMR 7261 CNRS/Tours University

For most invertebrates, it is difficult to access 'historical' samples such as older faeces due to the small size of the animals and the absence of permanent dejection sites. This project aimed at developing a method to study the diet of social wasps and provide an overall picture of their diet using the leftover prey DNA recovered in their nests. Our analysis also provides an overview of the resource partitioning in Polistine wasps in urban and sub-urban area in New Zealand and their potential impact on New Zealand native invertebrates.
The molecular method we developed allowed the amplification of 100% of the DNA samples collected from wasps' nest, with on average 80,334 DNA reads (±6,435 sem) per sample. The partitioning of the diet of the two Polistine species (i.e. *P. chinensis* and *P. humilis*) revealed that a large part of the diet is composed of lepidopteran and Thysanoptera species. Amongst the MOlecular Taxonomic Units (MOTUs) identified to species level, a significant number of reads of pest species were also reported, which supports MacIntyre and Hellstrom (2015) hypothesis that some wasp species can have positive effect on the control of other insect pests. On the other hand, this study also revealed that a large proportion of *P. chinensis* and *P. humilis'* diet is made of New Zealand native and endemic species (e.g. the moths *Ctenopseustis obliquana*, D*eclana floccose* or *Planotortrix notophaea*). The method develop in this study is readily transferable to the study of other social wasps.

Jeudi 11h50
Forum des Pertuis

The stimulation of organic matter processing and nutrient cycling by tubificid worms in wetland sediments is associated with a reduction of bacterial diversity

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Bioturbation activities of benthic tubificid worms has been recognized as a key process influencing organic matter processing and nutrient cycling in aquatic ecosystem, which likely influence microbial communities. Ingestion of fine particle at depth and egestion of fecal pellets at the sediment surface by tubificid worms modify sediment stratigraphy, but also bacterial abundances associated with faecal pellets (decreased after passage through the digestive tract). Nevertheless, the ecological consequences of bioturbators on microbial communities remain poorly studied in freshwater ecosystems. Existing studies used fingerprint approach and comparatively short term experiments. The present study aimed at evaluating the role of tubificid worms on bacterial community structure using NGS approach (16S metabarcoding) and long (6 months) laboratory experiments on 4 different sediments. Biogeochemical processes at the water-sediment interface were also measured to determine whether changes in bacterial community structure may control ecosystem processes. Measures of alpha diversity show that bacterial diversity is consistently reduced in presence of worms, whereas taxa whose abundance vary in presence of worms did not seems to be the same in the different sediments. Moreover, co-inertia analysis show a poor match between environmental parameter and bacterial communities.

Jeudi 12h10
Forum des Pertuis

Peer Community in: un système public et gratuit de recommandations de preprints fondé sur le peer-reviewing.

Thomas Guillemaud

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Afin d'offrir une alternative au système actuel de publication - qui est particulièrement coûteux et peu transparent - nous avons lancé le projet Peer Community in (PCI, https://peercommunityin.org). PCI vise à créer des communautés spécifiques d'éditeurs qui organisent l'évaluation et recommandent gratuitement des preprints dans leur domaine (des articles non publiés dans des journaux et déposés dans des archives ouvertes comme arXiv.org et bioRxiv.org) pour les rendre complets, fiables et citables, sans qu'il soit nécessaire de les publier dans des journaux " traditionnels " (même si les auteurs peuvent ensuite soumettre leurs preprints recommandés à des journaux). Lorsqu'un éditeur décide de recommander un preprint, il rédige un texte de recommandation qui est publié avec toute la correspondance éditoriale (reviews, décisions de l'éditeur, réponses des auteurs) par la PCI. La première PCI a été lancée en 2017 : PCI Evolutionary Biology (PCI Evol Biol). Plus de 700 collègues ont déjà rejoint PCI Evol Biol, PCI Paleontology, PCI Ecology, PCI Animal Science et PCI Entomology.

Jeudi 18h00
Aquarium de La Rochelle

Exploring extent and distribution of biodiversity in the largest biome on earth

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Ocean is the largest habitat in the biosphere, and the ocean seafloor in the abysses cover 65% of the surface of Earth. During the last decades, the emergence of high throughput sequencing and environmental DNA methods have led to large-scale exploration of the prokaryotic diversity. Large-scale expeditions such as Tara Oceans and Malaspina unravelled tens of thousands microbial lineages and offering promising avenues toward an enhanced understanding of the drivers of their distribution and dynamics. More recently, these efforts started to extend to the eukaryotic world, despite many specific technical challenges. The projects "*Pourquoi Pas les Abysses*" and "eDNAbyss" are large-scale initiatives aiming at developing and applying new standardized methods to inventory the living communities populating the seafloor, including microbial and multicellular compartments. These projects allowed defining standardized protocols from the sampling to the molecular and bioinformatic steps. The first results on a diversity of ecosystems from canyons and seamounts to hadal trenches demonstrate both the level of diversity still to be uncovered and the importance of adopting a standardized sampling scheme in the three dimension, highly structured oceanic environment.

Abstracts des posters

Stress response in fish: an epiGBS approach

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The evaluation of the molecular basis that mediates and modulates stress response in fish, e.g., the cascade of responses that occurs when facing and resisting an injury, including the re-establishment of homeostatic norms - has a long history in cell and tissue physiology. It has recently developed toward investigations of behavioral syndromes in individuals and the impact of disturbances on populations of both cultured and wild fish. With the development of next-generation sequencing technologies and the availability of genomic resources, studies that aim to identify genomic regions potentially involved in stress response have flourished. However, the genome-wide epigenetic landscape of any stress response has been far less studied in fish, while it may participate to the build-up of the molecular mechanisms that sustain stress resistance. Based on van Gurp et al. (2016), we designed an epiGBS (epiGenotyping By Sequencing) protocol in fish that allows for genome-wide representation of methylated regions within a genome. We hereby report key steps to implement the technique that will be used to investigate the molecular basis of differential stress response in European sea bass (*Dicentrarchus labrax*). This species, for which a genome assembly is available (Tine et al., 2014), represents an emblematic fish in European waters and a leader species for both aquaculture and eco-evolutionary studies (Vandeputte et al., 2019).

Key words: stress response, epigenomics, European sea bass.

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Tine M. et al. 2014 European sea bass genome and its variation provide insights into adaptation to euryhalinity and speciation. Nature Communications 5: 5770 (doi: 10.1038/ncomms6770)

Vandeputte M., Gagnaire P.-A., Allal F. 2019. The European sea bass: a key marine fish model in the wild an in aquaculture. Animal Genetics 50: 195-206 (doi: 10.1111/age.12779)

Van Gurp T.P. et al. 2016. epiGBS: reference-free reduced representation bisulfite sequencing. Nature Methods 13: 322-324 (doi: 10.1038/nmeth.3763)

ÉVALUATION DE LA DIVERSITÉ DES COMMUNAUTÉS MICROBIENNES PLANCTONIQUES AU COURS D'ÉPISODES DE MORTALITÉ DES MOULES BLEUES EN FRANCE : UTILISATION DE L'APPROCHE DE MÉTABARCODING POUR L'ANALYSE DE L'ADN ENVIRONNEMENTAL DANS LES PERTUIS CHARENTAIS

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Dans le cadre d'une étude associée aux épisodes de mortalité des moules bleues en France, visant à décrire et comprendre les facteurs qui peuvent favoriser ces mortalités, un ensemble de paramètres biotiques et abiotiques ont été suivis sur différents sites entre 2015 et 2018. Ce projet a été cofinancé par l'Ifremer et la DPMA (étude MORBLEU, MORtalité des moules BLEUes). Parmi les facteurs biotiques évalués, une approche basée sur l'ADN environnemental de la colonne d'eau a permis de décrire dans l'espace et dans le temps la dynamique et la diversité des communautés microbiennes planctoniques, procaryotes et eucaryotes (NGS, metarbarcoding) dans plusieurs secteurs des Pertuis Charentais. Nous détaillons la stratégie d'échantillonnage utilisée, les matériels et méthodes mis en œuvre au cours du projet, du prélèvement au séquençage ADNe et quelques résultats préliminaires.

Gene expression changes induced by long-term starvation in a cave amphibian (*Proteus anguinus*)

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The cave amphibian *Proteus anguinus* lives in complete darkness and has access to extremely limited food supplies. Among striking adaptations to these conditions, is its tolerance to starvation (up to 2 years). This exceptional resistance to long term fasting involves a drastic reduction of basal metabolism and activity, as well as a sequential use of energy reserves during nutritional stress (Hervant et al. 2001). These behavioral and metabolic processes are likely associated with strong changes in gene expression patterns that have yet to be described. Biochemical measures on the energy metabolisms and RNAseq data were obtained for 17 *Proteus anguinus* individuals among which 11 were starved during 18 months and 5 subsequently re-nourished (15 days). Our aim is to identify bio-marker genes and to relate them to changes in the energy metabolism. I will present first results concerning genes expression variations involved in resistance to nutritional stress and changes in metabolic pathways which likely underlie this adaptation.

F. Hervant, J. Mathieu, J. Durand (2001) J Exp Biol. 204:269-81.

UTOPIA: an automatically UpdaTed, cOmPlete and consistent ITS reference dAtabase

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Taxonomic assignment in metabarcoding analysis is a critical and challenging step. As more organisms being sequenced, taxonomy is evolving fast with multiple taxa rearrangement and thousand of new sequences uploaded each year. The internal transcribed spacer (ITS) is an ubiquitous sequence used as a barcode to identify fungi species in complex environmental samples.
Currently used databases like UNITE, offer a good and reliable reference, but update frequency is generally low, and new strain sequences can take several years to be integrated. UTOPIA provides a workflow that produce an updated ITS reference database directly from the NCBI genbank and taxonomy database.
Our workflow downloads all complete fungi ITS sequences from NCBI thanks to a formatted esearch query. Then homemade scripts extract sequences with their corresponding seven ranks taxonomy string. Post treatment consists on sequence quality filtering, dereplication and clustering. Taxonomy of each cluster are checked for consistency and incongruity are resolved by an homemade customizable script. Finally UTOPIA workflow generates two simple file, one fasta file containing sequences and a two columns tabulated file containing corresponding taxonomy that can be formatted for current assignment tools.
On our real dataset of 11000 ITS sequences, UTOPIA performs best in term of resolution and confidence on about 60% of sequences compared to UNITE. When UNITE fails to assign sequences, UTOPIA gives annotation up to 25% of these. But more interestingly, UTOPIA taxonomy is an exact copy of NCBI's, given the possibility to integrate latest sequenced fungal genomes.

Available at: https://forgemia.inra.fr/umrf/utopia

ANOMALY: AmplicoN wOrkflow for Microbial community AnaLYsis

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Bioinformatic tools for amplicon sequencing data analysis are continuously and rapidly evolving, thus integrating most recent techniques and tools is challenging.
We present an R workflow for 16S and ITS amplicons based sequencing. It is mainly based on the Dada2 and Phyloseq R packages. This workflow is based on several basic scripts in order to perform an analysis from fastq sequence files to final statistical analysis. The objective was to automate bioinformatic analyses to ensure reproducibility between projects trying to be versatile and simple to integrate new bioinformatic tools or statistical techniques.
ANOMALY use Amplicon Sequence Variant (ASV from Dada2 package) as taxonomic unit, allowing an easy and relevant sequence tracking between different environments and/or projects. Decontam package is included for an accurate and consistent detection of contaminant ASV and taxonomic assignment step relies on IDTAXA method. Our workflow is able to merge and check annotations from two taxonomic databases to unravel misannotation, discordance or inconsistency. The well known Phyloseq package provides the most common graphical representation, with additional statistics to assess significant impact of tested factors on microbial communities. The workflow incorporate multiple differential analyses (DESeq2 etc...) to reveal thin community contrast between conditions. Finally we are able to combine those results for cross-validation and thinner interpretation.
ANOMALY is a simple and customizable R workflow, that uses ASVs level for community characterization and integrates all assets of the up-to-date methods such as better sequence tracking, decontamination, merged taxonomic annotation, statistical tests, and cross-validated differential analysis.

Available at : https://forgemia.inra.fr/umrf/anomaly

Tolérance de la faune ingénieure du sol à la contamination résiduelle par les produits phytosanitaires dans les agroécosystèmes : approches omiques des mécanismes moléculaires en jeu

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Ce projet s'inscrit dans la nécessité de comprendre et de prédire in natura les effets subléthaux sur la biodiversité ingénieure des sols des pesticides utilisés en agriculture depuis l'après-guerre. Dans les agroécosystèmes, bien que la biodiversité des vers de terre soit en déclin, certaines espèces persistent en agriculture intensive, en particulier les espèces endogées. Ce constat suggère que ces espèces auraient développé des mécanismes de tolérance à long terme aux pesticides. L'étude vise à analyser les réponses moléculaires de tolérance de l'espèce *Aporrectodea caliginosa*, à la contamination résiduelle par les produits phytosanitaires. Il s'agira de savoir si la tolérance repose sur une acclimatation physiologique ou si elle met en jeu une adaptation, héritable de génération en génération. Une approche expérimentale de toxicologie évolutive multigénérationnelle (3 générations) a été mise en place. Deux populations ont été comparées, une population naïve (issue de parcelle biologique) versus une population pré-exposée (issue de parcelle conventionnelle). Un séquençage ARN de la génération F0 de nos deux populations a été réalisé, avant et après exposition à un fongicide d'intérêt, l'époxiconazole, afin d'obtenir un transcriptome de référence et une banque de protéines pour faciliter l'identification des protéines. Des protéines différentiellement exprimées ont ensuite été recherchées (LC/MS/MS) au sein des deux populations après exposition, aussi bien chez les adultes F0 que chez leurs descendants. Ce travail nous permettra d'identifier les voies métaboliques mises en jeu dans la tolérance et de prédire l'impact à long terme de l'exposition chronique des organismes ingénieurs du sol à des polluants multiples faiblement concentrés.

Fast sequence-based microsatellite genotyping development workflow for any non-model species

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Application of high-throughput sequencing technologies to microsatellite genotyping (SSRseq) has been shown to remove many of the limitations of electrophoresis-based methods and to refine inference of population genetic diversity and structure. However, early proof of concept and species specific development studies resulted in dispersed information making it cumbersome for prospective users to identify a clear path to SSRseq approach set up in species of new interest. To overcome these difficulties, we present here a streamlined SSRseq development workflow that includes microsatellite development, multiplexed marker amplification and sequencing, and automated bioinformatics data analysis.

DAIRYdb: a manually curated reference database for improved taxonomy annotation of 16S rRNA gene sequences from dairy products

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New sequencing technologies allowed the development of methods such as metabarcoding. They use 16S rRNA, the ubiquitous gene of the bacteria domain, as a biomarker to study bacterial communities from samples of complex environments.
The bioinformatic pipelines used to handle this type of data are well known but the taxonomic assignment is still a critical point. Misannotations are caused by short size sequences and high identity between bacterial species. Indeed, current technologies only allow to sequence two hyper-variable regions among the nine which compose the 16S rRNA. The available generalist databases (Greengenes, SILVA) do not reach enough accuracy to assign to the species rank. It is needed to create a curated reference database dedicated to the studied environment.
Here we introduce the DAIRYdb, a manually curated database composed of full length 16S rRNA sequences from samples of dairy products and close environments (cheese, milk, teat surface, starter, whey). The DAIRYdb was constructed using the 16S rRNA sequences deposited in EMBL and NCBI. After bioinformatic treatments, automatic and manual curative steps, DAIRYdb is finally composed of 10290 complete 16S sequences. It shows a higher assignment accuracy compared to other databases, at all taxonomic ranks and with any assignment tool tested. Depending on the variable region used, up to 90% of the tested sequences are reassigned to the species level with DAIRYdb.
DAIRYdb significantly improves taxonomic assignment accuracy for dairy environmental microbiome studies. It is available on public a repository (https://github.com/marcomeola/DAIRYdb).

Use of mutagenesis to characterize genes involved in a widespread chromatic acclimation process in marine *Synechococcus* cyanobacteria

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Synechococcus is the second most abundant phytoplanktonic organism of the world ocean and contributes significantly to global primary production. This cyanobacterium displays a wide diversity of photosynthetic pigments in their light-harvesting antennae (phycobilisomes), reflecting the variety of light niches colonized by this ubiquitous microorganism. Some strains are specialized in harvesting either green or blue light, while others can dynamically modify their light absorption spectrum to match the dominant color. This process called 'Type IV chromatic acclimation' (CA4) has been linked to the occurrence of a small genomic island existing in two configurations (CA4-A and -B). The analysis of 109 metagenomic samples from the Tara Oceans circumnavigation revealed that these CA4-capable populations globally constitute the most abundant pigment type and that CA4-A and -B occupy complementary ecological niches1. Recently, we characterized two phycobilin lyases, MpeZ and MpeY, i.e. enzymes covalently attaching chromophores on phycobiliproteins that are specifically involved in the CA4-A process2. Here, we use a combination of approaches including mutagenesis to characterize two additional lyases, MpeW and MpeQ, and demonstrate their critical role in the CA4-B process. While MpeW attaches the green-light absorbing phycoerythrobilin to cysteine-83 of the α-subunit of PE-II, MpeQ binds phycoerythrobilin to the same site in blue light and isomerizes it into the blue light-absorbing phycourobilin, in a mirror way as do MpeZ and MpeY in CA4-A strains. Our results therefore enlighten the key molecular differences between the two types of *Synechococcus* chromatic acclimaters.

1Grébert et al. (2018) PNAS 115:E2010-9 ; 2Sanfilippo et al. (2019) PNAS 116:6457-2

Cross-scale analysis of the adaptation to iron limitation and temperature in the marine picocyanobacterium *Synechococcus*

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The oceans are strongly impacted by global change, which is predicted to cause an increase of sea surface temperature but also an expansion of iron-poor areas, iron being an essential element for phytoplankton growth. In this context, one may wonder whether marine phytoplankton, and more specifically the marine picocyanobacterium *Synechococcus*, which contributes to almost 16% of the ocean's primary production, are able to adapt to such changes. The present study focused on the CRD1 clade that dominates iron-depleted areas and is composed of 3 distinct genetic groups (CRD1A to C), seemingly occupying different thermal niches in the Ocean. Here, we compared the physiology of representative strains of these 3 groups and of clades I to IV, which predominate in iron-replete areas of the world ocean. By acquiring various (photo)physiological parameters on strains acclimated to different temperatures, we validated the occurrence of 3 thermotypes within the CRD1 clade, but also revealed interesting features of their photosynthetic apparatus. A comparative analysis of 70 *Synechococcus* genomes, including 8 CRD1, showed that the occurrence of this clade in iron-depleted areas relies on a reduced number of genes encoding iron-rich proteins as well as a high number of genes encoding proteins using alternative metals and/or involved in acquisition and storage of iron. Finally, analysis of the Tara Oceans metagenomes revealed genes specifically present or absent in iron- poor niches that constitute good candidates for further understanding the mechanisms of adaptation to iron deficiency and temperature.

Environmental realized niches of the marine picocyanobacteria *Prochlorococcus* and *Synechococcus*

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The marine picocyanobacteria *Synechococcus* and *Prochlorococcus* are the two most abundant photosynthetic organisms on the planet and harbor a wide genetic and pigment diversity reflecting the variety of ecological niches colonized by these genera. By delineating Ecologically Significant Taxonomic Units (ESTUs), i.e. genetically related organisms occupying a given oceanic niche along the Tara Oceans transect using the high resolution taxonomic marker petB, we managed to improve the delineation of ecological niches occupied by picocyanobacterial populations and to show that their global distribution is tightly shaped by temperature, phosphate and iron availability [1]. Furthermore, the use of a combination of 3 genetic markers (cpcBA, mpeBA and mpeW) allowed us to establish the first global distribution map of all *Synechococcus* pigment types and to show that type IV chromatic acclimaters (CA4- A/B), which are able to dynamically modify their light absorption properties to maximally absorb green or blue light, were the most abundant pigment type oceanwide [2]. At last, analysis of the distribution of all known picocyanobacterial genes in the global ocean by recruitment of metagenomic reads on 81 genomes of marine picocyanobacteria also revealed that each taxonomic assemblage possesses a distinct gene repertoire. Correlation network analysis led to the identification of the most representative genes of each ecological niche and/or taxonomic assemblage, which constitute good targets to better understand the mechanisms involved in niche adaptation. Altogether, these studies provide important insights into the complex interactions between vertical phylogeny, pigmentation and environmental parameters that shaped the community structure and evolution of these organisms.

[1] Farrant GK et al. (2016). PNAS 113:E3365-74.
[2] Grébert T et al. (2018). PNAS 115:E2010-9

Gut metagenomic signatures of Non-Alcoholic Fatty Liver Disease (NAFLD)

Chloé Vigliotti, Phuong Le, Eugenio Belda, Quang Minh Dao, Edi Prifti, Jean-Daniel Zucker, Judith Aron-Wisnewsky, Raluca Pais, Vlad Ratziu, Elisabetta Bugianesi, Jorn Schattenberg, Jerome Boursier, Quentin Anstee, Karine Clément on behalf of the LITMUS consortium

Non-Alcoholic Fatty Liver Disease (NAFLD) and the more advanced Non-Alcoholic Steatohepatitis (NASH) and its associated fibrosis are increasingly becoming a clinical burden worldwide. Additionally, advanced stage NASH with fibrosis (cirrhosis) is a leading cause of liver transplants. Currently, the gold standard for NAFLD/NASH diagnosis is liver biopsy which can present notable risks and side-effects and is associated with variability. In this context, ongoing initiatives are looking into various ways to diagnose using non-invasive methods. Gut microbial organisms are associated with NAFLD/NASH (e.g. Fusobacteria, Proteobacteria, *Enterobacteriaceae, Pasteurellaceae)* may present a novel surrogate for diagnosis and/or prognosis. Using 209 biopsy-proven cases of NAFLD/NASH across 4 countries, we examined the associations between gut microbiome modifications with the progression of NAFLD/NASH and fibrosis progression.

We used an internally established bioinformatics pipeline and the 9.9M international gene catalog for human gut microbiota to produce bacterial genes abundances. After identifying potential confounders, logistic regression adjusted for BMI and type 2 diabetes (T2D) was applied on these abundances, and we confirmed previously discovered markers of liver disease progression such as Proteobacteria, *Enterobacteriaceae*, but also found new signatures such as *Coprobacter, Porphyromonas*. Additional explorations found new potential microbiome signatures of liver disease progression.

These results confirm potential microbiome-based biomarkers for NAFLD, NASH, and fibrosis progression, which will need further confirmation with additional and larger cohorts. Further explorations into microbial community analyses may provide additional insights of microbial ecosystems related to liver disease as well as mechanistic insights into the microbiota's role in liver disease pathology.

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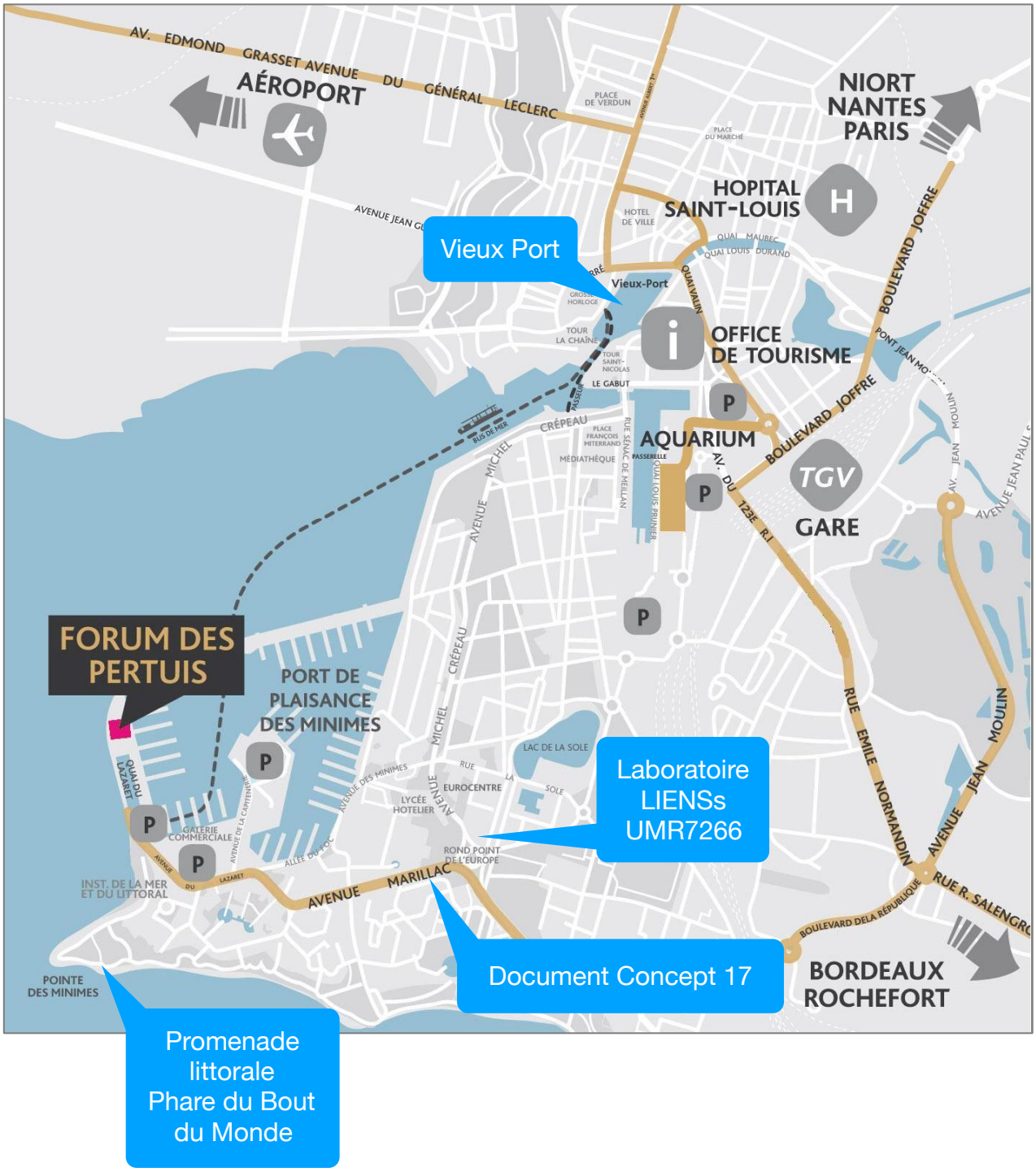

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A l'approche de La Rochelle, juste après le centre commercial, sortir direction « La Rochelle Gare ». Suivre cette direction jusqu'au rond-point situé entre l'Avenue Roger Salengro et la Rue Emile Normandin. Tourner à gauche et suivre ensuite « Port des Minimes – Forum des Pertuis ».

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- Posters : peuvent être affichés pour toute la durée du colloque (session poster : mardi soir) ; nous vous distribuerons des pinces pour les accrocher
- Code WIFI Forum des Pertuis: wififorum
- Accueil : vous recevrez un badge à l'entrée, merci de le garder pour toute la durée du colloque et de la recycler avant votre départ dans le carton prévu à cette effet.
- Si vous avez une question urgente: vous pouvez nous contacter au

  - 06 40 50 48 07 Amélia Viricel
  - 06 38 48 46 75 Eric Pante

- Pauses café : les rafraichissements sont couverts par vos frais d'inscription
- Déjeuner et diner de mercredi : sont couverts par vos frais d'inscription
- Si vous arrivez en voiture : y a 173 places de parking gratuit devant le Forum.

Notes