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Vast panmixia in the widely distributed blue shark (*Prionace glauca*)

Diane Bailleul, Alicia Mackenzie, Olivier Sacchi, Francois Pompanon, Sophie
Arnaud-Haond

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FIRST MEETING of the INTERNATIONAL MARINE CONNECTIVITY NETWORK - iMarCo



UNIVERSITY OF ST ANDREWS
27 – 29 JUNE 2016



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Methods in Ecology and Evolution





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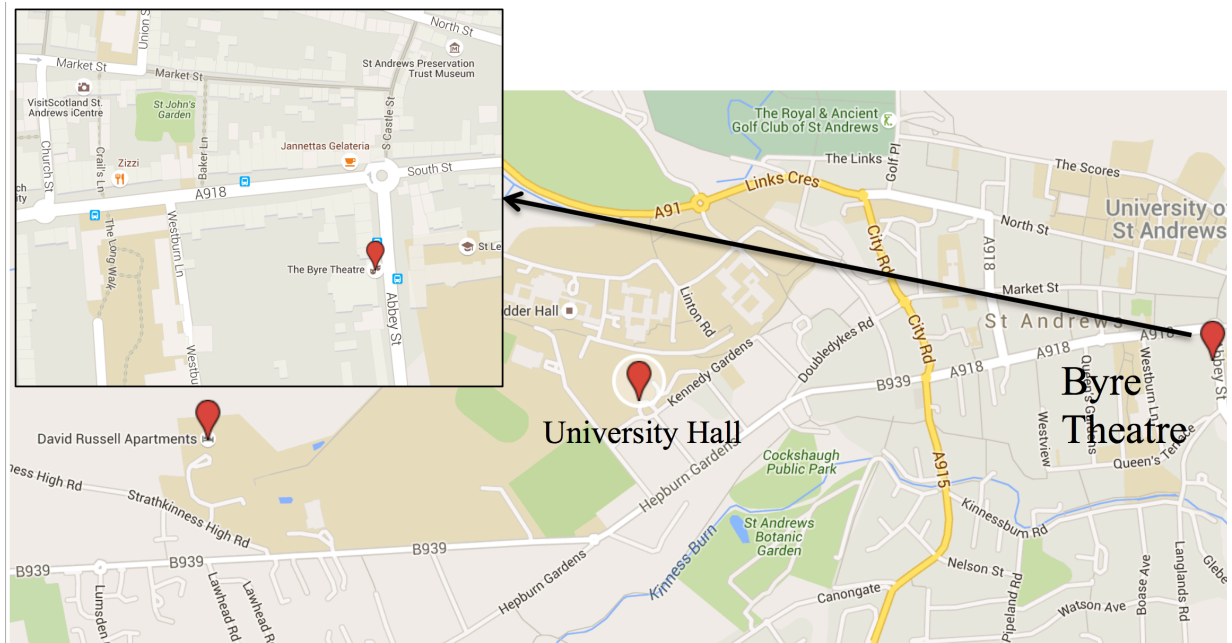
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DIRECTIONS



SPONSORS

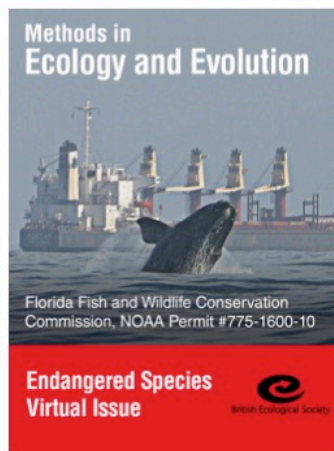
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PROGRAMME

MONDAY 27 JUNE 2016

14.00-14.10 OPENING REMARKS

- | | | |
|-------------|------------------|--|
| 14.10-14.30 | Colin Moffat | Linking connectivity to delivering our vision for our seas |
| 14.30-14.50 | Magalie Castelin | A new integrative framework for large-scale assessments of biodiversity and community dynamics, using littoral gastropods and crabs of British Columbia, Canada. |
| 14.50-15.10 | Barbara Porro | One <i>Symbiodinium</i> to rule them all? The genetic diversity of a symbiotic dinoflagellate in the temperate sea anemone, <i>Anemonia viridis</i> |
| 15.10-15.30 | Sabrina Le Cam | Genetic diversity of the Thornback ray (<i>Raja clavata</i>) in the North East Atlantic assessed by RAD sequencing |

15.30-16.00 BREAK

- | | | |
|-------------|-------------------|---|
| 16.00-16.20 | Ronan Becheler | Out of the Mediterranean: a phylogeographic assessment of the hypothesis of a post-glacial recolonization of Atlantic reefs following the Mediterranean outflow water |
| 16.20-16.40 | Florentine Riquet | The genetic chaos under the sea |
| 16.40-17.00 | Jon Yearsley | The impact of collective dispersal on genetic diversity and population differentiation |

17.00-19.00 DRINKS RECEPTION





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TUESDAY 28 JUNE 2016

9.00-9.20	Alejandro Gallego	Bio-physical modelling-based connectivity studies in Marine Scotland Science: past, present and future
9.20-9.40	Henrique Queiroga	Accounting for uncertainty improves cross-validation of independent estimates of larval dispersal and population connectivity in a spatially structured marine metapopulation.
9.40-10.00	Geneviève Lacroix	How is connectivity of flatfish impacted by reproductive strategy?
10.00-10.20	Leo Barbut	Modelling larval transport and connectivity of sole: using ICES survey assessment for parameterization
10.20-10.50	BREAK	
10.50-11.10	Filip Volckaert	Regional population structure of a top predator in the Northeast Atlantic Ocean
11.10-11.30	Alan Fox	Marine connectivity and climate variability, a case study of <i>Lophelia pertusa</i> in Scottish marine protected areas
11.30-11.50	Didier Aurelle	Differentiation and adaptation along depth gradients in the red coral <i>Corallium rubrum</i> : insights from RAD-Seq data
11.50-12.10	Grégory Charrier	Relative role of phylogeography, contemporary demographic processes and selective forces on the population genetic structure of the European flounder (<i>Platichthys flesus</i>) over its distribution range
12.10-14.00	LUNCH	
14.00-14.20	Galice Hoarau	<i>Calanus</i> population genomics
14.20-14.40	Emma Carroll	Hierarchical circumpolar population structure and reduced connectivity between ocean basins in the southern right whale
14.40-15.00	Diane Bailleul	Vast panmixia in the worldwide distributed blue shark (<i>Prionace glauca</i>)
15:00-15.20	Panagiotis Kasapidis	Comparison of the global connectivity patterns of swordfish (<i>Xiphias gladius</i> , L.), as revealed by microsatellite DNA and ddRAD analyses





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15.20-15.50 BREAK

- 15.50-16.10 H el ene de Pontual European sea bass population connectivity: what can we learn from archival tagging of adults and IBM modelling of larval dispersal?
- 16:10-16.30 Sophie Delerue-Ricard Dispersal, a survival strategy – genomics and otolith shape of sole of the North Sea
- 16.30-16.50 Thomas Regnier Direction and range of dispersal in sandeel (*Ammodytes marinus*)
- 16.50-17.10 David Stirling Investigating the dispersal dynamics of the rare mussel fan, *Atrina fragilis*

WEDNESDAY 29 JUNE 2016

- 9.00-9.20 Antoine Saint-Amand Combining high-resolution modelling with graph theory tools to identify COTS epidemic hotspots in the Great Barrier Reef
- 9.20-9.40 Tom Adams Connecting dispersal and population models with sea lice management
- 9.40-10.00 Alexis Simon What secondary contacts can tell us about marine connectivity? From theory to the field

10.00-10.30 BREAK

- 10:30-10:50 Federica Constantini Multilocus phylogeography of *Patella caerulea* reveals differential connectivity patterns across the Eastern-Western Mediterranean transition
- 10.50-11.10 Aur elien De Jode Phylogeography of the Bryzoa *Myriapora truncata* (Pallas 1766), at the Mediterranean scale
- 11.10-11.30 George Gkafas Biogeography pattern of the marine angiosperm *Cymodocea nodosa* in the eastern Mediterranean Sea related to the Quaternary climatic changes
- 11.50-12.10 **CONCLUDING REMARKS**





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ABSTRACTS

**CONNECTING DISPERSAL AND POPULATION MODELS WITH
SEA LICE MANAGEMENT**

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In modern salmon aquaculture operations, sites are managed within areas. These areas may be configured primarily for the control of spread of diseases or parasites, but their layout may also be designed to satisfy a range of other operational requirements.

Where control of disease spread is the principal goal, boundaries between units may be defined by some representation of hydrodynamic process. However, only recently have sufficiently advanced hydrodynamic models been available to allow description of regional scale dispersal processes while also representing the complex topography inhabited by the majority of salmon farm operations. It is therefore unclear how effective current management arrangements may be.

We used the latest advances in hydrodynamic modelling to describe the dispersal of sea lice between aquaculture sites on the west coast of Scotland. We found that coordinated management, even within small units, has the potential to reduce external sea lice connectivity by over 75%. We also demonstrate how incorporating connectivity estimates into population models may allow optimisation of chemical treatment and fallow schedules, and minimisation of sea lice abundances.

**DIFFERENTIATION AND ADAPTATION ALONG DEPTH
GRADIENTS IN THE RED CORAL *CORALLIUM RUBRUM*:
INSIGHTS FROM RAD-SEQ DATA**

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Understanding the evolution of populations in heterogeneous environments, including neutral and adaptive differentiation, is a major question in marine biology. The red coral *Corallium rubrum* is a good model in this context: it is a long-lived sessile species which is present in very different thermal conditions from less than 10 m to 800 m depth. We used RAD sequencing to study the genetic structure of *C. rubrum* according to depth in three areas used as geographical replicates: Corsica, Marseille and Banyuls. Our results indicate a significant differentiation between regions and between depths inside regions. We will discuss the potential implication of some loci in local adaptation.





VAST PANMIXIA IN THE WORLDWIDE DISTRIBUTED BLUE SHARK (*PRIONACE GLAUCA*)

Diane Bailleul^{1,2*}, Alicia MacKenzie^{1,2}, Olivier Sacchi¹, François Pompanon^{1,2}, Sophie Arnaud-Haond^{1,2}

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Prionace glauca is thought to be one of the most common and studied pelagic sharks, and yet few is known about its population structure. Blue sharks are fished, mainly as bycatch, across their nearly worldwide (except at polar latitudes), distribution area. The estimated removal of 20 million individuals per year by fisheries classifies blue sharks as near threatened (IUCN, 2009). However, the lack of knowledge of population size and structure, the high fecundity and early maturation of *P. glauca* as well as its apparent stable catch rate make it difficult to forecast the long term consequences of such a huge removal on this top-down predator itself, and on its trophic network. Tags studies identified stocks in North Atlantic and in Pacific Ocean with few migrants capable of ten thousand kilometers travels and previous genetic studies concluded to panmixia at the scale of the Pacific Ocean. Here we will present worldwide genetic results on mitochondrial and nuclear DNA with 258 blue shark samples from eight regions.

MODELLING LARVAL TRANSPORT AND CONNECTIVITY OF SOLE: USING ICES SURVEY ASSESSMENT FOR PARAMETERIZATION

Léo Barbut^{1,2*}, Sigrid Lehuta⁴, Sophie Delerue-Ricard²⁻³, Andreas Vanden Bavière³, Gregory Maes¹, Johan Robbens³, Filip A.M. Volckaert², Geneviève Lacroix³

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Sole has a low population structure in the North Sea and a high inter-annual variability of recruitment. For many fish taxa, recruitment and dispersal pattern are determined in early life stages. Indeed for sole in the North Sea, a Lagrangian larval transport model, coupling a physical model with an Individual-Based Model (IBM), has shown that hydrodynamics explains part of the year-to-year variability of sole larval recruitment (Lacroix et al. 2013). IBMs require a good knowledge of the biological processes governing larval dispersal while they may be highly sensitive to some parameters. In particular, parameter estimates may strongly influence larval connectivity / retention and successful migration. Various assumptions about larval traits and behaviours (different vertical migrations, mortality levels, larval durations, spawning periods...) can be simulated and tested by comparing simulation results with field data. Here, after a sensitivity analysis of the model to determine most critical factors, hundred test cases with various parametrizations were simulated. Results were compared to ICES (International Council for the



Exploration of the Sea) recruitment assessments to identify the most plausible model parameterization. Finally, the connectivity patterns estimated by the best model are confronted to those derived from genetic markers.

OUT OF THE MEDITERRANEAN: A PHYLOGEOGRAPHIC ASSESSMENT OF THE HYPOTHESIS OF A POST-GLACIAL RECOLONIZATION OF ATLANTIC REEFS FOLLOWING THE MEDITERRANEAN OUTFLOW WATER

R. Becheler^{1*} & S. Arnaud-Haond²

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The cold-water corals *Lophelia pertusa* and *Madrepora oculata* are the two main engineering species of the worldwide distributed deep-reefs. These ecosystems are hotspots of deep biodiversity and play a crucial role in biogeochemical cycles, notably for the carbon storage. Within the NE-Atlantic, geological records reported a stop of the growth of CWC-reefs during the last glacial maximum (20-12 000 yrs BP), while the growth of Mediterranean reefs remained active. Atlantic reefs re-found a growing dynamics after the LGM (10-12 000 years BP), initially around the Gibraltar and Cadiz' Gulf. This dynamics progressed then northward. These geological considerations have led to formulate the following biogeographic hypothesis: the Mediterranean has played the role of glacial refugia during the Ice Ages of the Pleistocene, and constitutes the source of the gradual northward recolonization of the Atlantic since 12 000-10 000 years, CWC larvae following the Mediterranean Outflow Water. Demographic history and populations expansions can leave strong and persistent signatures in the genetic structure of the species. We aim at testing the hypothesis of Mediterranean recolonization by examining the patterns of genetic diversity structure of both *Lophelia pertusa* and *Madrepora oculata* populations, from Mediterranean, to South of Iceland. We used two distinct kinds of nuclear markers (ITS and microsatellites). Bayesian inferences will be also conducted on order to infer the more likely demographic scenario having led to the observed genetic pattern.

GENETIC DIVERSITY OF THE THORNBACK RAY (*RAJA CLAVATA*) IN THE NORTH EAST ATLANTIC ASSESSED BY RAD SEQUENCING

Sabrina Le Cam^{1,2*}, Florence Cornette¹, Grégory Charrier², Pascal Lorange³, Gérard Biais⁴, Eric Stéphan⁵, Adeline Bidault², Jean Laroche², Florianne Marandel³, Verena Trenkel³, Sylvie Lapègue¹

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At the ecosystem level, sustainable exploitation of fisheries resources depends not only on the status of target species but also on that of bycatch species, some of which are even more sensitive to





exploitation. It is especially the case for Elasmobranchs species whose abundance declined during the 20th century. Further, their biology is still poorly known. This study aims at measuring the genetic diversity of the thornback ray (*Raja clavata*) and its distribution in the Northeast Atlantic using a Radseq approach. Over 500 individuals sampled in the North Sea, the Celtic Sea, the Bay of Biscay, down to the Azores islands and the Mediterranean Sea will be analysed. Genomic resources obtained for this study will also be used to apply recent genetic-based methods for absolute population abundance estimation as traditional fisheries stock assessment methods using fisheries catches and scientific survey data for estimating abundance are challenging due to the small numbers observed in this type of species

HIERARCHICAL CIRCUMPOLAR POPULATION STRUCTURE AND REDUCED CONNECTIVITY BETWEEN OCEAN BASINS IN THE SOUTHERN RIGHT WHALE

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Understanding the relative roles of recent and historical demographic events in shaping patterns of genetic diversity and connectivity can be critical. We examined contemporary and historic gene flow in southern right whale (*Eubalaena australis*) wintering grounds, in the context of its documented decline due to whaling. We compiled a circumpolar dataset of 1327 mitochondrial control region (mtDNA) sequences (380 bp) and microsatellite genotyped 222 samples (up to 17 loci) collected from southern right whales on their wintering grounds in the Indo-Atlantic (Argentina and South Africa) and Indo-Pacific (Australia and New Zealand). Hierarchical population structure was detected; AMOVA analyses indicated there was greater variation among ocean basins (mtDNA F_{ST} : 0.126; Φ_{ST} : 0.132; microsatellite F_{ST} : 0.024; $p < 0.01$) than among populations within ocean basins (mtDNA F_{ST} : 0.052; Φ_{ST} : 0.084, microsatellite F_{ST} : 0.004; $p < 0.01$), confirming previous work based solely on mtDNA data. Two clusters were identified using the microsatellite data in the Bayesian clustering program STRUCTURE, corresponding with ocean



basins. However, both mtDNA and microsatellite-based fixation indices and multivariate statistical analyses suggested additional sub-structuring within these two clusters. The median migration rate estimate from the Indo-Atlantic to the Indo-Pacific was 0.021 (95% HPD <0.001, 0.064) and 0.037 (95% HPD 0.007, 0.084) in the reverse direction, based on a BayesAss analysis. A Bayesian phylogeny of the 62 unique mtDNA haplotypes, constructed in MrBayes, showed a Type II phylogeographic pattern, as previously described. The above findings are consistent with either high levels of gene flow and large effective population sizes, or a period of isolation followed by secondary contact; two contrasting hypotheses we are currently assessing with approximate Bayesian computations, which will also provide insights into historical effective population sizes and migrations rates, as well as changes therein.

A NEW INTEGRATIVE FRAMEWORK FOR LARGE-SCALE ASSESSMENTS OF BIODIVERSITY AND COMMUNITY DYNAMICS, USING LITTORAL GASTROPODS AND CRABS OF BRITISH COLUMBIA, CANADA

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Improving our understanding of species responses to environmental changes is an important contribution ecologists can make to facilitate effective management decisions. Novel synthetic approaches to assessing biodiversity and ecosystem integrity are needed, ideally including all species living in a community and the dynamics defining their ecological relationships. Here we present and apply an integrative approach that links high-throughput, multi-character taxonomy with community ecology. The overall purpose is to enable the coupling of biodiversity assessments with investigations into the nature of ecological interactions in a community-level data set. We collected 1,195 gastropods and crabs in British Columbia. First, the General mixed Yule-coalescent (GMYC) and the Poisson Tree Processes (PTP) methods for proposing primary species-hypotheses based on *cox1* sequences were evaluated against an integrative taxonomic framework. We then used data on the geographic distribution of delineated species to test species co-occurrence patterns for non-randomness using community-wide and pairwise approaches. Results showed that PTP generally outperformed GMYC and thus constitutes a more effective option for producing species-hypotheses in community-level datasets. Non-random species co-occurrence patterns indicative of ecological relationships or habitat preferences were observed for grazer gastropods, whereas assemblages of opportunistic omnivorous gastropods and crabs appeared influenced by random processes. Species-pair associations were consistent with current ecological knowledge, thus suggesting that applying community assembly within a large taxonomical framework constitutes a valuable tool for assessing ecological interactions. Combining phylogenetic, morphological and co-occurrence data enabled an integrated view of communities, providing both a conceptual and pragmatic framework for biodiversity assessments and investigations into community dynamics.



RELATIVE ROLE OF PHYLOGEOGRAPHY, CONTEMPORARY DEMOGRAPHIC PROCESSES AND SELECTIVE FORCES ON THE POPULATION GENETIC STRUCTURE OF THE EUROPEAN FLOUNDER (*PLATICHTHYS FLESUS*) OVER ITS DISTRIBUTION RANGE

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The impact of ongoing climate change on marine populations cannot be understood without considering an evolutionary perspective, since genetic variation of species is structured by the contribution of phylogeographical history, modern demographic processes and contemporary selective forces. In order to address this issue, the population genetic structure of the European flounder (*Platichthys flesus*) was investigated over its distribution range: 26 population samples, including temporal replicates (965 individuals, sampled between 2003 and 2015) were analysed using 12 microsatellites and six candidate gene SNPs (Single nucleotide Polymorphism). Overall, data revealed a strong population differentiation, with four main population groupings identified using the 11 neutral microsatellites: Iberian Peninsula, Bay of Biscay, East Channel - North Sea, and Baltic Sea. This population structure appeared highly congruent with phylogeographical patterns found in other subboreal species. Moreover, low genetic diversity and high temporal variability in the southern peripheral population (Mondego) suggested effects of demographic bottlenecks. One microsatellite seemed to be under selection. Five of the SNPs exhibited a significant population differentiation, but distinct structuring patterns, that were probably induced by contrasted environmental pressures. Overall, this study confirms that the combination of neutral and non neutral loci conduct to deeper insights in genetic structuring of fish populations.

MULTILOCUS PHYLOGEOGRAPHY OF *PATELLA CAERULEA* REVEALS DIFFERENTIAL CONNECTIVITY PATTERNS ACROSS THE EASTERN-WESTERN MEDITERRANEAN TRANSITION

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The Mediterranean Sea is acknowledged to be a biodiversity hotspot, hosting a wide variety of habitats and organisms resulting from its complex past history and present day processes. Although several biogeographic areas are defined within it, a comprehensive description of the main connectivity patterns between these areas is still lacking. In the present work we aim to describe the main features structuring past and present genetic diversity and connectivity in the shallow subtidal limpets populations across the whole Mediterranean Sea. Genetic diversity and structure of 32 populations of the common and widespread limpet *Patella caerulea* were analysed using two mitochondrial markers (COI and 16S) and five nuclear microsatellite loci. Two main evolutionary units were detected according to both mitochondrial markers. The main phylogeographical break in the Mediterranean Sea was located between the southern tip of Sicily and Calabria peninsula,



however the full transition occurs up to the eastern Ionian Sea. Highly variable nuclear markers revealed a limited gene flow across the detected phylogeographic break, as well as further differentiation across the Siculo-Tunisian Strait and in the Thyrrenian and Ligurian Seas. All three markers fit an isolation by distance genetic pattern only in the Eastern basin. The major genetic discontinuity between Eastern and Western Mediterranean populations is located between the Siculo-Tunisian Strait and the eastern limit of the Ionian Sea. Rather than a barrier separating different evolutionary units, in this area admixture of genotypes occurs, reflecting the complex interplay of past and present connectivity processes.

DISPERSAL, A SURVIVAL STRATEGY – GENOMICS AND OTOLITH SHAPE OF SOLE OF THE NORTH SEA

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Fisheries managers should monitor fish stocks at an ecologically meaningful scale. Better understanding of population structure and movements of individuals between populations would be helpful. However it is difficult to measure connectivity between populations, especially because early-life stages cannot be tagged physically. Therefore we resort to information embedded in the genome and the otoliths. Population structure of adult sole *Solea solea* seems to be low but meaningful at the European scale. However this is less clear at the regional level of the North Sea. Our research focuses on Young of the Year sole caught off the Belgian coast in 2013 and 2014. We trace the spawning origins of juveniles reaching the Belgian nursery. What is the contribution of the different spawning grounds to the Belgian nursery? Is there a reproductive strategy favouring different cohort origins throughout the season? In order to assess connectivity, 150 juveniles have been genotyped using ddRAD sequencing. First, we computed population genetic measures and observed variation in population structure between years. Then, the genomic data were combined with otolith shape using Fourier descriptors. Our research reveals origins of fish contributing to the Belgian nursery stock, hence improving management perspectives

MARINE CONNECTIVITY AND CLIMATE VARIABILITY, A CASE STUDY OF *LOPHELIA PERTUSA* IN SCOTTISH MARINE PROTECTED AREAS

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A Lagrangian particle tracking model suggests that dispersal of larvae from sub-populations of *Lophelia pertusa* and connectivity between sub-populations are crucially dependent on the atmospheric state. Laboratory observations have revealed that *L. pertusa* larvae have sufficient





vertical swimming ability to reach near-surface waters, exposing the larvae to stronger and more variable currents than at depth. When this behaviour is introduced into a larval particle tracking model, the resulting dispersal of larvae from sub-populations in the NE Atlantic shows strong correlation with the North Atlantic Oscillation, the dominant mode of inter-annual atmospheric variability in the region. Positive NAO state is correlated with a more connected, though directional west to east, network. Negative NAO results in a less connected network, though with more larvae transported from east to west. A long-term shift towards either more positive or more negative NAO state would result in loss of connections, potentially isolating sub-populations.

The modelling study is described. Results predict connectivity of a network of *L. pertusa* sub-populations in marine protected areas around Scotland, largely consistent with known genetic connectivity and recent population expansion. Results from a modelling study are presented and the major sources of uncertainty discussed.

BIO-PHYSICAL MODELLING-BASED CONNECTIVITY STUDIES IN MARINE SCOTLAND SCIENCE: PAST, PRESENT AND FUTURE

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Scientists in Marine Scotland Science (MSS) and its previous incarnations have used bio-physical modelling tools quite regularly to investigate marine connectivity patterns for nearly 20 years. This talk will present a very brief overview of those activities, with applications to zooplankton ecology (Calanus, jellyfish), population dynamics and the ecology of early life stages of fish (cod, haddock, herring, sandeel, salmon), disease and parasite dynamics in relation to aquaculture (sea lice, viruses), and connectivity within the Scottish nature conservation Marine Protected Area network. Bio-physical modelling tools have been used for a wider range of applications outside connectivity studies, including some highly unusual examples! With the recent availability of state-of-the-art hydrodynamic models to force particle-tracking applications, such as the “Scottish Shelf Model”, there is a promising future for bio-physical modelling methods to study marine connectivity in Scottish waters.

BIOGEOGRAPHY PATTERN OF THE MARINE ANGIOSPERM *CYMODOCEA NODOSA* IN THE EASTERN MEDITERRANEAN SEA RELATED TO THE QUATERNARY CLIMATIC CHANGES

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Demographic and evolutionary mechanisms always influence genetic diversity and population dynamics within and among species. Historical alterations could potentially affect biogeography patterns on response to future adaptation or dispersal ability of the species. Here it is presented how a high clonal organism, the marine angiosperm *Cymodocea nodosa*, responded to the climatic oscillations in the Quaternary period. We tested to what extent different multilocus lineages can lead to significant increases in diversity and levels of demographic fluctuations could be related to





species dynamics and species fitness. Microsatellites data indicate a rather expansion of the species distribution in the eastern Mediterranean Sea from Late Pleistocene to early Holocene epoch with a relatively high connectivity between certain geographical habitats.

CALANUS POPULATION GENOMICS

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Calanus is a genus of copepods, present in all oceans as part of the zooplankton. In North Atlantic and Arctic, *Calanus* plays a fundamental role for the food webs linking primary production to higher trophic levels including commercially important fish, mammals, birds... The main species are *Calanus finmarchicus* in the North Atlantic, *Calanus glacialis* in the Arctic, and *Calanus hyperboreus* in deeper part in Arctic Ocean. Despite their huge ecological importance, very little is known about species boundaries and genetic structure. We are using next generation sequencing technologies to investigate *Calanus* species identification, thermal stress response and population genetic structure.

PHYLOGEOGRAPHY OF THE BRYZOA *MYRIAPORA TRUNCATA* (PALLAS 1766), AT THE MEDITERRANEAN SCALE

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Coralligenous habitats are bioconstructed, emblematic habitats of the Mediterranean Sea which present a remarkably complex 3D structure resulting of the permanent dynamics between bioerosion and bioconstruction. The main builders of these habitats are corallines red algae but other marine invertebrates such as bryozoans also contribute to the frameworks of the habitats as they build their own calcareous skeletons. This highly complex framework represents an habitat for around 1600 species (Ballesteros 2006) and is so considered as one of the most important biodiversity hotspot of the Mediterranean Sea. *Myriapora truncata* (Bryozoa, Cheilostomata), considered one of the most important animal builders of the coralligenous habitats, is present in all the Mediterranean Sea (Gautier, 1962) and produces lecithotrophic larvae by sexual reproduction with a short pelagic existence (Ferretti et al. 2007). Here we present a phylogeographic study based on the COI gene of the Bryozoa *M. truncata* at the scale of the Mediterranean Sea. It shows important genetic structure even at a small spatial scale and indicates the probable presence of different cryptic species under the name *M. truncata*. Nuclear markers on samples from the bay of Marseilles are also analyzed to assess the presence of gene flow between mitochondrial lineages.



COMPARISON OF THE GLOBAL CONNECTIVITY PATTERNS OF THE SWORDFISH (*XIPHIAS GLADIUS*, L.), AS REVEALED BY MICROSATELLITE DNA AND DDRAD ANALYSES

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The swordfish is an epipelagic fish found in all oceans around the world. Despite its high migratory potential, various studies have revealed significant genetic structure between Mediterranean, Atlantic and Indo-Pacific, but also within Atlantic. In the current study, we compare the connectivity patterns that were revealed using microsatellite DNA and ddRAD analyses. In the first case, 2610 specimens from Mediterranean, Atlantic, Indian and Pacific stocks, were genotyped for fifteen microsatellite markers and analyzed using a Bayesian cluster analysis. The results suggested the presence of three clusters that correspond mainly to Mediterranean, Atlantic and Indo-Pacific regions, with extensive mixing between the two latter. Heterogeneity tests and pairwise F_{ST} 's further supported the genetic differentiation between north and south Atlantic. For the ddRAD analysis, 140 individuals, corresponding to nine sampling localities from the aforementioned oceans, were sequenced on an Illumina platform. The analysis is still undergoing and the results will be compared with that of the microsatellite DNA analysis to see whether the novel genomic approaches have higher resolution in revealing population structure and connectivity patterns of the swordfish.

HOW IS CONNECTIVITY OF FLATFISH IMPACTED BY REPRODUCTIVE STRATEGY?

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Connectivity throughout the life cycle of flatfish remains a poorly charted question, especially during the early life stages which are strongly influenced by larval retention and dispersal. But we need better knowledge on the underlying mechanisms that influence connectivity to understand the population dynamics of commercially important flatfish species. The transport of flatfish larvae from the spawning grounds to the nurseries is driven by hydrodynamic processes, but the final dispersal pattern and larval survival is affected by environmental factors, physiology, behaviour and reproductive strategies (spawning period and spawning grounds). Here we use a particle-tracking transport model (LARVAE&CO) coupled to a 3D hydrodynamic model to assess the connectivity pattern between spawning grounds and nurseries of six flatfish species in the North Sea. We analyse comparatively the impact of different life traits on connectivity of sole (*Solea solea*), plaice (*Pleuronectes platessa*), turbot (*Scophthalmus maximus*), brill (*Scophthalmus rhombus*), flounder (*Platichthys flesus*) and dab (*Limanda limanda*).



EUROPEAN SEA BASS POPULATION CONNECTIVITY: WHAT CAN WE LEARN FROM ARCHIVAL TAGGING OF ADULTS AND IBM MODELLING OF LARVAL DISPERSAL?

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Despite the economical and societal value of European sea bass, little is known concerning its spatial structure and dynamics at the population scale. From 2010 –2012, we deployed 246 DSTs off the west coast of Brittany and a more 1200 DSTs are being deployed (2014 - 2016) from Southern North Sea to Southern Bay of Biscay. We developed a geolocation model predicting daily probability distribution of positions issued from a Hidden Markov Model. Reconstructed tracks of fish with long time at liberty (one year) show strong site fidelity to summer feeding grounds. Fidelity on winter spawning areas is also evidenced on available long time series (8 months). These new results support the hypothesis of a fine scale spatial structuring of the population, a key issue poorly addressed by current management frameworks. In a second approach, we started modelling the connectivity between spawning and nursery grounds for a better understanding of population structure and recruitment variability. Models simulating transport and bioenergetics of eggs and larvae were coupled in order to investigate the impact of contrasted hydroclimatic conditions on nursery settlement. Maps of larval dispersal as well as connectivity matrices between spawning grounds and coastal/estuarine nurseries showed significant spatio-temporal variability due to environmental variations.

ONE *SYMBIODINIUM* TO RULE THEM ALL? THE GENETIC DIVERSITY OF A SYMBIOTIC DINOFLAGELLATE IN THE TEMPERATE SEA ANEMONE, *ANEMONIA VIRIDIS*

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Over the world, there are 9 clades of *Symbiodinium*, all of them involved in symbiotic relationship with various organisms including cnidarians. In contrast to the high clade diversity of tropical seas, Mediterranean sea and North-eastern Atlantic ocean harbour a single clade: the temperate A clade. However, significant genetic diversity can still be found within a single clade. In order to explore



this diversity, we chose, as a model study, a symbiotic cnidarian distributed over the same geographical range and involved in a mutualistic endosymbiosis with *Symbiodinium*: the temperate sea anemone, *Anemonia viridis*. This relationship is particularly interesting because of the wide distribution of *A. viridis*, the diversity of habitats it inhabits (lagoon, seashores, standard or low pH values) and its morph diversity (5 morphs with putatively different adaptive strategies). What is the genetic diversity of *Symbiodinium* between the English channel anemones and the Mediterranean ones? Is there a correlation on the distribution of this diversity with environmental conditions or with the morphs of *A. viridis*? Is there a link between life history traits in the host anemone and its symbiotic population? To address these fundamental questions, we propose to characterize the distribution of genetic diversity of *Symbiodinium* populations by sampling 3 morphs of *A. viridis* (with a total of 384 individuals) from the English channel and the Mediterranean sea (France and Italy). We assess genetic diversity combining information from microsatellite markers (genotyped by NGS sequencing) and sequence markers (ITS2, cp23S) commonly used in phylogenetic studies. The structuring factors for symbiont genetic diversity will be compared with the ones for the host, as the host genetic diversity will be assessed in parallel in the lab, through the study of EPICs and RADseq markers

ACCOUNTING FOR UNCERTAINTY IMPROVES CROSS-VALIDATION OF INDEPENDENT ESTIMATES OF LARVAL DISPERSAL AND POPULATION CONNECTIVITY IN A SPATIALLY STRUCTURED MARINE METAPOPULATION

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Several reviews and syntheses advocate the use of multiple methodological approaches to describe population connectivity in marine species with a bi-phasic life cycle (most benthic macroinvertebrates and fishes). This necessity derives from the difficulty in tracking minute marine larvae in an unbounded environment subjected to considerable variability, which impacts on larval dispersal pathways and survival. The underlying rationale is that the application of multiple methodologies would characterize and bracket the uncertainty associated with an elected connectivity matrix. In the present study we explicitly account for the statistical uncertainty in the construction of alternative observed connectivity matrices derived from elemental chemistry of mussel shells, and compare these with predictions from a biophysical model simulating the observed levels of uncertainty. We manipulate the observed connectivity matrix by applying different confidence levels to the assignment of recruits to the source populations, which results in a variable number of recruits classified as unknowns. In the model, we simulate the intrinsic variability of the geochemical signal and the inability of geochemical method to assign recruits to unsampled sources, and also assigned these to an unknown source. We demonstrate that the correlation between the observed and modelled matrices increases as the number of observed recruits classified as unknowns approximated the misclassification rate of the larvae. We also demonstrate that the increase in matrix correlation is significantly different from that obtained with



a random classification of observed recruits into an unknown origin. The highest correlation coefficient ($r=0.96$) was obtained for a 95% confidence level and a spatial partitioning of the connectivity matrix where each cell corresponds to 20-40 km-long stretches of coast. This resolution is higher than that obtained from a standard jackknifed classification of recruits into the source population based exclusively on their elemental signature. A literature review of 40 studies using more than one methodology (from an universe of >500 studies) indicates that accounting for uncertainty results in an unprecedented degree of convergence between different methodologies. We argue that this approach could be generalized to other methods and result in improved descriptions of connectivity pathways.

DIRECTION AND RANGE OF DISPERSAL IN SANDEEL (*AMMODYTES MARINUS*)

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Knowledge of dispersal range of marine species, and, connectivity between patches of suitable habitat, is critical for the design of successful networks of Marine Protected Areas (MPAs). In particular, identifying the direction and scale of dispersal would allow adapted management practice in a twofold objective of (i) preserving local diversity by protecting self-recruiting units and (ii) favour the replenishment of depleted area through an enhancement of dispersive life stages production in identified major sources. In many fish, dispersal is limited to planktonic early life stages, making movement tracking a difficult task. In the present study, we use otolith microchemistry to estimate the range and direction of dispersal in a key forage fish, the lesser sandeel (*Ammodytes marinus*). Considering the elemental signature of the larval region of the otolith in a clustering analysis allowed the assessment of the degree of connectivity between the most important sandeel grounds situated around the Scottish coast.

GENETIC CHAOS UNDER THE SEA

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Chaotic genetic patchiness is a surprising pattern observed in some marine species that show genetic structure far below the dispersive range of pelagic larvae. After having described the chaotic genetic patchiness patterns, we will discuss three of the four mechanisms involved in explaining such patterns: selection, sweepstakes reproductive success and temporal shifts in local population dynamics. Collective larval dispersal is another mechanism that will be further detailed by Jon Yearsley in another talk of this symposium. Selection can be responsible for locus-specific signatures, while sweepstakes reproductive success and population dynamics are neutral processes that can leave genome-wide signatures. We conclude that neutral processes require that 1) drift is strong enough to create genetic differentiation between cohorts of larvae, and 2) dispersal is not efficiently homogenizing the genetic variability in space across the study area.

COMBINING HIGH-RESOLUTION MODELLING WITH GRAPH THEORY TOOLS TO IDENTIFY COTS EPIDEMIC HOTSPOTS IN THE GREAT BARRIER REEF

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One of the most significant causes of reef decline in the Great Barrier Reef (GBR) is certainly the outbreak of Crown-of-Thorns Starfish (COTS), which feed on coral. COTS populations tend to boom very quickly causing devastation of entire reefs. Our goal is to evaluate the connectivity of COTS in the GBR in order to identify the epidemic hotspots. By using the high-resolution unstructured-mesh coastal ocean model SLIM we are able to simulate the complex and multi-scale currents with a spatial resolution of ~100m over the scale of the entire GBR. This model is coupled with a biophysical model of larval dispersal to track the position of virtual larvae of COTS. Connectivity matrices are then generated from the positions of the particles at the start and at the end of the simulations. Finally, we use graph theory tools such as community detection and “Google algorithms” (for e.g. PageRank and Influence Rank). This allows us to identify clusters of reefs strongly connected between each others and connectivity hotspots presenting the highest dissemination potential. Our results highlight the reefs that should be surveyed in priority in order to tame the outbreak in its early stages.

WHAT SECONDARY CONTACTS CAN TELL US ABOUT MARINE CONNECTIVITY? FROM THEORY TO THE FIELD

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Contacts between divergent lineages are a source of information for the understanding of evolutionary processes driving adaptation and speciation. Recent contacts and experimental crosses give access to the initial phase of a secondary contact. The recent introduction of the mediterranean mussel *Mytilus galloprovincialis* in the Channel where it can hybridize with the local species *Mytilus edulis* is an opportunity to investigate introgression mechanisms of secondary contacts that



can have an impact on the spread of an invasive species. We investigated two questions: (i) Did *M. galloprovincialis* expand in Normandy? (ii) What are the genomic patterns of recent secondary contacts? Results showed that *M. galloprovincialis* did not expand its range in the Channel and stayed localized in Cherbourg. Secondly, we theoretically predict a heterozygous advantage and global monocus and bilocus distortions in F2 crosses that have been verified in experimental and natural crosses. Even though predictions of the model are globally verified, strong disparities persist on some loci presenting segregation distortions compatible with the existence of Dobzhanski-Muller incompatibilities. The more incompatible pair of loci seems to be still active in Cherbourg and it would be interesting to follow its evolution in time.

INVESTIGATING THE DISPERSAL DYNAMICS OF THE RARE FAN MUSSEL, *ATRINA FRAGILIS*

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Measuring dispersal in rare sessile benthic species is of key importance in the development of conservation measures such as MPA networks. Larval dispersal dynamics are dependent on the complex interplay between abiotic (hydrodynamic regime, settlement substrate) and biotic (pelagic larval duration (PLD), behaviour and spawning time) features. Efforts to understand dispersal dynamics for many species of conservation concern are hampered by a lack of fundamental life-history information and hydrodynamic data of sufficient resolution. Using hydrodynamic data from the recently developed Scottish Shelf Model and incorporating new observations of key larval traits, we investigate the dispersal dynamics of a rare bivalve mollusc of conservation concern, the fan mussel *Atrina fragilis* (Pennant 1777), within a Lagrangian particle tracking framework. Specific larval behaviours are likely important in determining the range of dispersal distances, but the long PLD for this species will facilitate dispersal between MPAs.

REGIONAL POPULATION STRUCTURE OF A TOP PREDATOR IN THE NORTHEAST ATLANTIC OCEAN

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Fish with larval dispersal and good (sub)adult swimming capacity have a large potential for dispersal leading to subtle genetic patterns. However, dispersal being non-random, there is a good chance for philopatry and hence adaptation to regional oceanographic conditions. Moreover, some species have expanded their range to higher latitudes due to global warming, which raises the question whether these colonisers represent a random population sample. We test the hypothesis that dispersal in an open marine environment does allow for constrained connectivity, partially mediated by biotic and abiotic factors. We also test whether there is evidence for genetically differential range expansion. We genotyped with a large array of molecular markers a range-wide collection of European sea bass *Dicentrarchus labrax* from the Northeastern Atlantic Ocean. In total 496 wild-caught fish were genotyped at 1044 ddRAD sourced and mapped SNP markers. Neutral markers showed a homogenous profile along most of the West and South European coast. However, we detected introgression from the Mediterranean clade in the Eastern Atlantic Ocean off the Strait of Gibraltar, while a subset of putatively adaptive markers suggested clinal population structure. Additional questions such as the impact of range expansion and the nature of markers under selection are currently under study.

THE IMPACT OF COLLECTIVE DISPERSAL ON GENETIC DIVERSITY AND POPULATION DIFFERENTIATION

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There is growing empirical evidence of collective dispersal in a broad range of marine species. The population genetic implications of this collective dispersal have received relatively little attention. I will present theoretical predictions for the effect of collective dispersal on genetic diversity and population differentiation in a finite island model. These results show that collective dispersal reduces mixing between demes, decreasing expected coalescence times and increasing population differentiation. The effects are strongest in systems with high migration rates. Some effects of collective dispersal are surprising, such as increasing migration rates increasing population differentiation. We also demonstrate with simulations and analytical theory the strong similarity between the effects of collective dispersal and anisotropic dispersal. This has applied consequences for the interpretation of genetic structure (e.g., chaotic genetic patchiness) and estimation of migration rates from genetic data.



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