



The 6th International Marine Connectivity Conference

Organized by the iMarCo GDR, the COST Action SEA-UNICORN
and the Muséum National d'Histoire Naturelle, Paris



BOOK OF ABSTRACTS

Program

Monday 6th December

8h30: Registration

9h15: Introduction – Nicolas Puillandre (MNHN), Nicolas Bierne (iMARCO), Audrey Darnaude (SEA-UNICORN)

CHAIR: Audrey Darnaude

9h30: KEYNOTE SPEAKER: Sophie Arnaud-Haond – *Dark matter and obscure connectivity patterns in the deep sea.*

10h00: Marie Louis et al. – *Selection on ancestral genetic variation fuels repeated ecotype formation in bottlenose dolphins.*

10h20: Nicolas Oury et al. – *Same places, same stories: genomics reveals similar structuring patterns.*

10h40: Ophélie Da Silva et al. – *Are we ready for protist population metagenomics? Challenges to decipher drivers of genetic differentiation in marine planktonic populations.*

11h00: coffee-break

CHAIR: Magalie Castelin

11h30: Morane Clavel-Henry et al. – *Use of the connectivity concept as quantitative evidence for management actions against marine invasive species: a case study in Galway Bay, Ireland.*

11h50: Pierre Barry et al. – *Comparative population genomics of the Atlantic-Mediterranean suture zone reveals heterogeneous divergence patterns in marine fishes.*

12h10: Flemming Thorbjørn Hansen et al. – *Ranking of Danish harbours according to shipping activities and to the potential of natural dispersal of non-indigenous species.*

12h30: lunch break

CHAIR: Didier Aurelle

14h00: KEYNOTE SPEAKER: Maria Beger – *Operationalising marine functional connectivity in conservation and management*

14h30: Marlene Jahnke et al. – *Seascape genomics identify adaptive barriers according to tidal amplitude in the shore crab *Carcinus maenas*.*

14h50: Geneviève Lacroix et al. – *Can artificial structures increase connectivity of hard substrate species through stepping stone in the North Sea?*

15h10: Pierre De Wit et al. – *Fine-scale demographic patterns of the blue mussel species complex (*Mytilus* spp.) in Scandinavia – historical isolation, introgression and present-day barriers to gene flow.*

15h30: Costas Tsigenopoulos et al. – *Population genetics and phylogeographic studies for the identification of biological units for two fish and four crustacean species in the Mediterranean Sea: the MED_UNITS project.*

15h50: coffee-break

CHAIR: Christophe Lett

16h20: Rita Castilho et al. – *Range expansion and connectivity in a changing world.*

16h40: Céline Ellien et al. – *Connectivity between populations of the amphidromous goby *Sicyopterus lagocephalus* (Pallas 1770) in the southwest Indian Ocean, revealed by a modeling approach.*

17h00: Katell Guizien et al. – *Spatio-temporal variability in *Paramuricea clavata* population genetics reveals connectivity variability in Ligurian sea.*

17h20: Halvor Knutsen et al. – *The effect of pelagic larval stage on population genetic structure and demographic connectivity: a comparative study on coastal fishes.*

18h-19h30 Poster session with cocktail

Tuesday 7th December

CHAIR: Oscar Gaggiotti

9h30: KEYNOTE SPEAKER: Andy Foote – *Genomic insights into global connectivity and localised barriers to gene flow among killer whale populations*

10h00: Iraide Artetxe-Arrate et al. – *Otolith $\delta^{18}O$ composition as a tracer of yellowfin tuna (Thunnus albacares) origin in the Indian Ocean.*

10h20: Alan Le Moan et al. – *An introgression breakthrough left by an anthropogenic contact between two ascidians.*

10h40: Antoine Saint-Amand et al. – *Another kind of connectivity: Estimating the environmental footprint of a coal mine project on nearby marine ecosystems in the Great Barrier Reef.*

11h: coffee-break

CHAIR: Sarah Samadi

11h30: Sabrina Le Cam et al. – *Genetic connectivity inferred from male- and female-type mitochondrial DNA from Limecola balthica, a bivalve species characterised by DUI.*

11h40: Laura Meyer et al. – *Connectivity between ecotype pairs in coastal fish inhabiting the marine-lagoon gradient.*

12h10: Susanne E. Tanner et al. – *Evaluating movement and population dynamics of meagre (Argyrosomus regius) using an interdisciplinary approach*

12h30: lunch break

CHAIR: Federica Costantini

14h00: KEYNOTE SPEAKER: Marie Raynaud – *Population-based recombination rates estimates to study genetic connectivity.*

14h30: Vamara Koné et al. – *Modelling the seasonal retention patterns of the early life history of S. aurita in the Angolan upwelling system.*

14h50: Tanja N. Schwanck et al. – *Mitochondrial haplotypes reveal low diversity and connectivity in a critically endangered batoid population residing in a Scottish Nature Conservation Marine Protected Area.*

15h10: Vincent Muchi et al. – *Exploring connectivity in a deep-sea hydrothermal gastropod by elemental fingerprinting.*

15h30: Sarah M. Maes et al. – *Circumpolar population genomics of polar cod: connectivity in a changing ecosystem.*

15h50: coffee-break

CHAIR: Nicolas Bierne

16h20: Ane Pastor et al. – *Modeling eelgrass connectivity in the Kattegat Sea: A graph theory approach for eelgrass restoration.*

16h40: Thomas Dobbelaere et al. – *Disentangling coral disease and coral larvae connectivity to inform reef restoration in Florida.*

17h00: T rence Legrand et al. – *Coalescent connectivity through multi-generation dispersal modelling predicts gene flow across marine phyla.*

17h20: Adrien Tran Lu Y et al. – *Genome-wide analyses outline patterns of homogeneity and divergence of the deep-sea hydrothermal gastropod Ifremeria nautili but outlier loci reveal subtle limits to connectivity.*

17h40: Yael Teff-Seker et al. – *Do Alternative Dispute Resolution (ADR) and Track Two Processes Support Transboundary Marine Conservation? Lessons from six case studies of maritime disputes*

18h00: Closing words

19h00: Gala dinner at the “Belles Plantes” restaurant

Wednesday 8th December

9h-15h: Sea-Unicorn COST action meetings – Cross-Group meeting of the SEA-UNICORN COST Action.

During this meeting, the four Working Groups of SEA-UNICORN will present their advances and achievements since the launch of the Action (in November 2020), discuss their upcoming activities for 2022 and organize parallel brainstorming sessions on how to improve (1) the incorporation of data on Marine Functional Connectivity into models predicting the evolution of our Oceans and Seas and (2) the uptake of this knowledge by the stakeholders involved in Marine Spatial Planning for a Sustainable blue Growth.

ABSTRACTS (in alphabetic order of the first author's last name)

POSTER #1

Conservation management of polar ecosystems (COPE): using genomic approaches to study connectivity across spatial and functional scales.

Dorien Aerts^{1,2}, Henrik Christiansen¹, Anton P. Van de Putte^{1,2,3}, Filip Volckaert¹, Isa Schön^{2,4}

1 Laboratory of Biodiversity and Evolutionary Genomics, KU Leuven, Leuven, Belgium

2 Royal Belgian Institute of Natural Sciences, OD Nature, Brussels, Belgium

3 Université Libre de Bruxelles (ULB), Marine Biology Laboratory, Brussels, Belgium

4 University of Hasselt, Research Group Zoology, Diepenbeek, Belgium

Polar ecosystems are among the fastest changing regions on earth, causing a shift in species distributions, changes in food web dynamics and decreasing productivity. Rising pressures such as warming, acidification, pollution, and exploitation, make it imperative to understand and protect the unique cold-adapted fauna of the Southern Ocean. In this context, knowledge on speciation, adaptation, distribution, and connectivity supports sound Antarctic biodiversity management and conservation. The COPE project aims at contributing such information for two ecological model clades: the pelagic *Trematomus* fishes and benthic *Charcotia* amphipods. For both study systems, we will use occurrence records, environmental data and genotype information from thousands of genomic markers retrieved through reduced representation sequencing (RRS) techniques. Species distribution models and population genomic analyses are expected to provide insights into species identity, realized ecological niche, connectivity, and population structure. Here, we present a first overview of the data sourced so far, including genomic data from RRS. Preliminary analyses indicate that: 1) specimen identification with integrated molecular and morphological methods reveals considerable cryptic speciation (amphipods), 2) species distribution models are likely more suitable at a regional than circumpolar scale, 3) both target groups show various levels of spatial population differentiation. Our insights will contribute in the discussion of future management of the Southern Ocean.

POSTER #2

Evaluation of the impacts of climate change on the distribution of Florida stone crab larvae on the West Florida Shelf.

Lauranne Alaerts

UCLouvain, Croix du Sud 2, boîte L7.05.16, Louvain-la-Neuve, 1348, Belgium,
lauranne.alaerts@student.uclouvain.be

Ocean acidification and ocean warming are the two components of climate change that impacts marine life the most. The commercially important Florida stone crab, *Menippe mercenaria*, is one of the species that is going to be affected by those changes. In this study we investigated the impacts of climate change on the distribution of the stone crab larvae on the West Florida Shelf. To understand the dispersion of the larvae, we coupled SLIM3D, a multi-scale ocean model, with a larval dispersal model. We then conducted a connectivity study and evaluated the impacts of climate change analyzing three different scenarios, one presenting the dispersion of the larvae for present conditions and the two others presenting the dispersion for moderate and extreme climate change. The results show a clear impact of climate change on larval dispersal and on the subsequent crab distribution. In the future, climate change could result in stone crabs moving north or to deeper waters. The second impact would be the increase in the number of larvae settling in the non-fishing zone, where the water depth exceeds 30 m. The distance traveled by larvae is going to decrease, resulting in an increase of

self-recruitment and decrease of the size of sub-populations. The last impact we identified is the possibility of a shift of the spawning period earlier in the season. We also evaluated that the habitats in the non-fishing zone cannot serve as a significant source of larvae for the habitats in the fishing zone since there is very little exchange between the two zones. Overall, this work could help local authorities to better understand *M. mercenaria* and to take actions regarding the fishery management and its future considering the upcoming changes in the ocean conditions."

INVITED TALK

Dark matter and obscure connectivity patterns in the deep sea

Sophie Arnaud-Haond

MARBEC, University of Montpellier, Ifremer, IRD, CNRS, Sète, France.

The largest biome on Earth is by far the deep-sea floor, yet the biodiversity it encompasses, the way it distributes among biogeographic provinces, and the connectivity patterns in the three dimensions of the Ocean remain elusive. Thus far, studies on the deep sea mainly focused on ecosystems characterized by high biomass such as hydrothermal vents or cold-water coral reefs, despite they represent a minuscule part of the deep seafloor. Among the few population genetics studies realized in those ecosystems, many surprisingly revealed large scale dispersal and connectivity, questioning the mechanisms of passive or active dispersal susceptible to explain the connection among those small ecosystems scattered as oasis across the vast and still largely understudied abyssal plain. In the framework of the project Pourquoi Pas les Abysses (2016-2019), launched by Ifremer in 2016 and of the following France Génomique project eDNAbyss (2018-ongoing), we developed a series of standard protocols from sampling to bioinformatics analysis, to perform a standardized eDNA based assessment of benthic diversity of the deep-sea floor across the tree of life. Here I will present the results obtained through metabarcoding on a subset of samples mostly collected in abyssal plains and hadal trenches. These revealed a greatly structured distribution of highly diverse communities, made of largely unknown taxa, and largely driven by two depth factors (in the sediment and in the water column). Results also enlightened the sharing of some Operational Taxonomic Units (OTUs) and even Amplicon Sequence Variants (ASVs) across vast geographic distances suggesting intriguing mechanisms of connectivity still to be elucidated.

TALK

Otolith $\delta^{18}O$ Composition as a Tracer of Yellowfin Tuna (*Thunnus albacares*) Origin in the Indian Ocean.

Iraide Artetxe-Arrate¹, Igaratza Fraile¹, Jessica Farley², Audrey M. Darnaude³, Naomi Clear², David L. Dettman⁴, Campbell Davies², Francis Marsac⁵, Hilario Murua⁶

1 AZTI, Marine Research, Basque Research and Technology Alliance (BRTA), 20110 Pasaia, Gipuzkoa, Spain; iraide.artetxe@azti.es or i.artetxe73@gmail.com, ifraile@azti.es

2 CSIRO Oceans and Atmosphere, Hobart, Tasmania 7000, Australia; jessica.farley@csiro.au (J.F.), naomi.clear@csiro.au (N.C.); campbell.davies@csiro.au (C.D.)

3 Marbec, University Montpellier, CNRS, Ifremer, IRD, 34095 Montpellier, France; audrey.darnaude@cnrs.fr

4 Environmental Isotope Laboratory, Department of Geosciences, University of Arizona, Tucson, AZ 85721, USA; dettman@arizona.edu

5 Marbec, University Montpellier, CNRS, Ifremer, IRD, 34203 Sete, France; francis.marsac@ird.fr

6 International Seafood Sustainability Foundation, Washington, DC 20005, USA; hmurua@iss-foundation.org

Yellowfin tuna of the Indian Ocean is overfished, and a better understanding of the stock structure and connectivity is needed to enable sustainable management. Here, otolith $\delta^{18}\text{O}$ values of young-of-the-year fish from known nursery areas of the equatorial Indian Ocean (West, Central and East) were used to establish a reference isotopic signature to predict the origin of sub-adult and adult individuals. Sub-adult tuna otolith $\delta^{18}\text{O}$ values from Reunion Island were similar to the West nursery signature, but otolith $\delta^{18}\text{O}$ values of sub-adults from Pakistan were unlike any of the nurseries sampled. Therefore, $\delta^{18}\text{O}$ values from the Pakistan area samples were considered an additional nursery source for predicting the origin of adult tuna, using a multinomial logistic regression classification method. The western equatorial area was the most productive nursery for three fishing grounds sampled, with a minor contribution of Pakistan-like origin fish. Contribution of Central or East nurseries to the adult population was negligible. One adult otolith was analysed by secondary ion mass spectrometry along the otolith growth transect and results were compared with an isoscape approach to infer lifetime movements. This study is an important first step towards understanding the spatial structure and connectivity of the species.

TALK

Comparative population genomics of the Atlantic-Mediterranean suture zone reveals heterogeneous divergence patterns in marine fishes.

Pierre Barry¹, Thomas Broquet², Pierre-Alexandre Gagnaire¹

1 ISEM, Univ Montpellier, CNRS, EPHE, IRD, Montpellier, France

2 CNRS & Sorbonne Université, UMR 7144, Station Biologique de Roscoff, 29680, Roscoff, France

Delineating species boundaries is an important aspect of biodiversity and ecosystem conservation. Despite high potential for gene flow, marine fish species often display intra-specific genetic differentiation. Because evidence for genetic differentiation often relied on low coverage genome data and is rarely accompanied by phenotypic differences, these cryptic subdivisions are usually contentious. This result in difficulties in identifying biologically relevant units for the management and conservation of biodiversity. A genome-wide description of the extent and distribution of divergence is thus needed to better describe how genetic diversity is structured within species. Here, we described the partitioning of within-species genetic variation in the northeastern Atlantic and Mediterranean Sea suture zone for 20 various marine fish species. For each of them, we sequenced the whole-genome of 20 individuals and used genome-wide variation data to screen within-species subdivisions as revealed by highly differentiated genomic regions. Genetic subdivisions within the 20 species were distributed along a continuum of divergence, reflecting a variety of genomic architectures ranging from a few narrow-differentiated regions to high genome-wide divergence. Moreover, the spatial structure of divergence and gene flow varied considerably among species. These results raise questions about the eco-evolutionary drivers of species' heterogeneous responses to a shared biogeographical context and particularly whether species' life-history traits and genome architecture can shape genetic differentiation."

INVITED TALK

Implementing global conservation goals with connectivity in marine spatial planning.

Maria Beger^{1,2}, Anna Metaxas³; Arianna Balbar³, Jennifer McGowan^{2,4}, Remi Daigle^{3,5}, Caitie Kuempel^{2,6}, Eric Trembl⁷, Hugh Possingham⁸

1 School of Biology, Faculty of Biological Sciences, University of Leeds, LS2 9JT, UK;

2 Centre for Biodiversity and Conservation Science, School of Biological Sciences, University of Queensland, Brisbane, QLD 4072, Australia

3 Dalhousie University, Department of Oceanography, 1355 Oxford Street, Halifax, NS, B3H 4R2, Canada

4 The Nature Conservancy, South Brisbane, Queensland 4101, Australia

5 Université Laval, Département de Biologie, 1045, av. de la Médecine, Québec, QC, G1V 0A6, Canada

6 National Center for Ecological Analysis and Synthesis, University of California, Santa Barbara, 735 State Street, Suite 300, Santa Barbara, CA 93101, USA

7 School of Life and Environmental Sciences, Centre for Integrative Ecology, Deakin University, Geelong, Vic., 3220, Australia

8 The Nature Conservancy, South Brisbane, Queensland 4101, Australia

Connectivity describes dynamic flow processes of energy, materials, and organisms underpin the persistence of life on earth. Integrating them into biodiversity conservation decisions is key to confronting the biodiversity and climate crisis. Yet, when prioritizing conservation areas and actions, these flow processes are rarely incorporated. This lack in operationalization of the connectivity concept in spatial planning is largely because it is difficult to translate ecological and biophysical knowledge into how dynamic connectivity contributes to broad conservation goals, such as persistence. Connectivity is like God: it can be abstract and means different things to different people—hampering its conceptualization in conservation objectives.

Here, we tackle the urgent question of integrating dynamic flow processes into quantitative conservation planning objectives for connectivity. A key consideration in managing for persistence is that populations and communities do not exist in isolation, but typically interact within ecological networks and as meta-populations. We provide an outlook to understand how connectivity links to high-level conservation goals and to overcome barriers that currently obstruct progress towards designing spatial management areas that gain biodiversity benefit from dynamic flow processes with key examples.

POSTER #3

Coastal Management and Monitoring Network for tackling marine litter in Mediterranean Sea.

Sana Ben Ismail, Rym Ben Dhiab , Rafika Challouf , Olfa Chaeib , Hedia Hili , Emna Derouiche , Wael Kouched , Elisa Scocchera , Ali Harzallah

COastal Management and MONitoring Network for tackling marine litter in Mediterranean Sea (COMMON) project is a three-year funded project within the 2014-2020 ENI CBC "Mediterranean Sea Basin Programme", the largest Cross-Border Cooperation (CBC) initiative implemented by the EU under the European Neighborhood Instrument (ENI). The consortium is composed of 7 partners from three Mediterranean countries (Italy, Lebanon and Tunisia). COMMON aims at applying the ICZM principles to the marine litter management in 5 pilot coastal areas through a local coordination and the Mediterranean networking among different stakeholders by testing an integrated strategy for marine litter management and disposal at coastal level that could be transferred to the whole Mediterranean area. COMMON will contribute to build multi-stakeholder networks at basin-level for tackling marine litter in a coordinate and integrated manner. The INSTM is a leader of work package Institutional capacity building in tackling marine litter throughout ICZM plan which will enhance the capacity of public authorities in 5 pilot areas to plan for sustainable management, use and monitoring marine litter sources, treatment and consequences, employing an effective participatory approach involving relevant stakeholders and local communities. The activities of the project will be presented by highlighting our training plan during next 20 months and also it is occasion to present preliminary results about monitoring activities in Monastir and Kuriat Island the two pilot areas in Tunisia."

POSTER #4

Linking spatial connectivity to species trophodynamics in the seascape.

Blanco Andreu^{1,2,3}, Olabarria Celia^{2,3}, Begger Maria^{1,4}, Jeannot Laura-Li⁵, Domise Johanna⁵, Planes Serge⁵

1 School of Biology, Faculty of Biological Sciences, University of Leeds, Leeds, LS2 9JT, United Kingdom

2 Centro de Investigación Mariña, Universidade de Vigo, EcoCost, Facultade de Ciencias del Mar, Campus de Vigo, As Lagoas, Marcosende 36310 Vigo, Spain

3 Departamento de Ecoloxía e Bioloxía Animal, Universidade de Vigo, Campus As Lagoas-Marcosende, 36310 Vigo, Spain

4 Centre for Biodiversity Conservation Science, School of Biological Sciences, The University of Queensland, Brisbane, Queensland, Australia

5 CRIOBE-USR 3278, CNRS-EPHE-UPVD, Laboratoire d'Excellence 'CORAIL', 58 Avenue Paul Alduy, 66860, Perpignan, France

Maximizing biodiversity benefits from marine protected areas (MPAs) could result from ensuring both spatial and trophic connectivity within MPA networks (MPA-N). In this context, the project ORGANISE aimed to incorporate species trophodynamics into spatial connectivity data to support conservation management actions in a set of MPAs and non-protected areas along the western coast of the Iberian Peninsula. Firstly, the project evaluated the effects of protection on the trophic level of different species (from primary producers to secondary predators) at the bottom of the food web. Spatial connectivity was then assessed at small (shanny *Liphophrys pholis*) and large (common octopus *Octopus vulgaris*) scales. Preliminary results showed that protection has little influence on trophic levels of the studied species and were more related to local environmental factors and/or to poor implementation of MPAs. This homogenization in trophic levels was also evident in the genetic structure of both *L. pholis* and *O. vulgaris* populations that indicated high spatial connectivity and high larval dispersal at the scale of the studied MPAs network. Ensuring both horizontal (spatial) and vertical (in the food web) connectivity, will improve the MPA-N effectiveness and, ultimately, enhance ecosystem functioning, structure and services; however, this might not apply in upwelling areas (such as the study region) which are highly productive regions with strong currents. In addition, the high genetic connectivity of both species revealed panmictic populations and, therefore, either cascading or spill-over effect from MPAs towards unprotected areas could be evidenced. However, despite the genetic and trophic level homogenization, finer functioning processes (e.g. foraging movements between protected and unprotected areas) could be assessed through estimates of trophic connectivity, which still remains a challenge. Fitting such data in marine prioritization will help understand prey-predator dynamics and, hence, fisheries and conservation management."

POSTER #5

Streamlining crustacean larvae identification through DNA metabarcoding for fisheries assessment.

Marta Carreton¹, Ann Bucklin², Paola Batta-Lona², Joan B. Company¹, Luz B. Ferrer¹, Beatriz Nuño¹, Vadim Pisarenco¹, Guiomar Rotllant¹

1 Departament de Recursos Marins Renovables, Institut de Ciències del Mar (ICM-CSIC), Barcelona, SPAIN. mcarreton@icm.csic.es, batista@icm.csic.es, guio@icm.csic.es, luzferrer4b@gmail.com, beanuo@gmail.com, vadimpisarenco@gmail.com

2 Department of Marine Science, University of Connecticut, Groton, CT, USA. ann.bucklin@uconn.edu, paola.batta_lona@uconn.edu

Fisheries science relies on accurate field data to assess the state of exploited marine populations. The abundance of larvae in the plankton can be used as a proxy to estimate recruitment of commercially harvested deep-sea species, but morphological identification of larval stages of meroplanktonic organisms is complex and time-consuming. The molecular analysis of complex samples, known as DNA metabarcoding, is growingly being used for rapid and accurate species identification in abundance and

distribution surveys. In this study, we use a combination of DNA metabarcoding and morphological techniques to identify larvae of commercial species in zooplankton samples from the continental shelf margin of the northwestern Mediterranean Sea. We used a bongo net to sample 30 stations at depths of 119 to 427 m. For each pair of samples, one was processed using morphological microscopic methods to separate taxonomic groups of zooplankton (Cladocera, Copepoda, Ostracoda, Euphausiacea, Chaetognatha, Gastropoda, Pteropoda, Echinodermata, Polychaeta, Siphonophorae, Appendicularia, Doliolida, Salpidae and Foraminifera), as well as crustacean and fish eggs and larvae; shrimp larvae were identified to the lowest possible taxonomic level. The other sample was analyzed by DNA metabarcoding using two markers: V9 region of 18S rRNA, and cytochrome oxidase subunit I (COI). Comparison between the results of morphological and molecular analysis shows the potential of DNA metabarcoding as a streamlined method for larval identification of commercial species, allowing for efficient analysis of time series that can be used for monitoring and assessment.

TALK

Range expansion and connectivity in a changing world.

Rita Castilho^{1,2}, Joana I. Robalo³

1 Universidade do Algarve, Campus de Gambelas, 8005-139 Faro, Portugal

2 Centre of Marine Sciences, Campus de Gambelas, 8005-139 Faro, Portugal

3 MARE – Marine and Environmental Sciences Centre, ISPA Instituto Universitário, Lisboa, Portugal

Climate change is progressively displacing species from equatorial latitudes to temperate locations, resulting in the topicalization of fish communities. The putative consequence of these range expansions is the gradual loss of genetic diversity towards the expansion front with population differentiation, an expectation of the central-margin theory. Searching for emerging patterns in recent species displacements and expansion of distribution areas can reveal the species genetic connectivity profile. Here, we present results that partially contradict these expectations with no wholesale loss of genetic diversity but with strong population differentiation within the footprint of the marine northward expansion of the species. These high levels of differentiation hinder the evaluation of connectivity between locations, as most seldom share haplotypes. We discuss possible causes for hyper-diversity and lack of geographical structure and posit that the success of colonization may be related to these exceptional high levels of genetic diversity.

POSTER #6

Genomic differentiation and indications for local adaptation in an Antarctic fish.

Henrik Christiansen¹, Anton P. Van de Putte^{1,2,3}, Filip A. M. Volckaert¹

1 Laboratory of Biodiversity and Evolutionary Genomics, KU Leuven, Leuven, Belgium

2 Royal Belgian Institute of Natural Sciences, OD Nature, Brussels, Belgium

3 Université Libre de Bruxelles (ULB), Marine Biology Laboratory, Brussels, Belgium

Genetic differentiation depends on gene flow and local adaptation and provides crucial information for conservation. The Antarctic environment hosts a unique fish fauna, which faces rapid and locally opposing environmental change. West Antarctic fish populations are exposed to warming and sea ice reduction, while the sea ice cover recently increased in parts of East Antarctica. Here, we apply double-digest restriction-site associated DNA sequencing to investigate the genomic diversity and associations with environmental variables of the first Antarctic vertebrate with a sequenced draft genome. *Notothenia coriiceps* is an ecologically important and widely studied notothenioid fish species of the Southern Ocean. We genotype loci using both a de novo and reference genome mapping approach

and reveal that *N. coriiceps* is composed of at least two subtly (F_{ST} up to 0.024) differentiated sub-populations. While high connectivity across vast distances is realized through dispersal via ocean currents, we also observe genotype-environment associations that indicate some degree of local adaptation. However, incomplete sampling prevented us from disentangling effects from geographic distance and environmental variability. Genome scans for selection show that some loci are likely subject to recent, spatially-variable selection. One putatively adaptive SNP may be linked to a gene important for methionine biosynthesis and is correlated with ice cover. We also detect selection signatures in SNPs near anti-freeze glycoprotein genes. These loci should be investigated further, but already show that important genomic variability is distributed unevenly across the Southern Ocean. Conservation measures, such as marine protected areas, should consider these results to support population resilience and adaptation potential. Furthermore, we suggest that de novo SNP calling, even when a reference genome is available, can provide additional insights, for example through loci that are otherwise not recognized due to spatial ascertainment bias.

POSTER #7

Large-scale patterns of population structure of the key marine zooplankton *Calanus finmarchicus* and *C. glacialis* revealed by a new protocol of target-capture.

Marvin Choquet, Apollo Marco Lizano, Irina Smolina, Galice Hoarau
Faculty of Biosciences and Aquaculture, Nord University, Bodø, Norway

Zooplankton copepods *Calanus finmarchicus* and *C. glacialis* are key species for the North Atlantic and Arctic Ocean ecosystems, respectively, as main primary consumers and as prey for various predators including commercially important species. As a result of climate change, dramatic demographic reductions in *Calanus* spp. have been reported, as well as large-scale northward shifts, with expected impacts along the food webs. Despite well-documented life cycles, patterns of population connectivity in *C. finmarchicus* and *C. glacialis* remain unclear, and previous studies based on limited numbers of genetic markers and individuals have shown contradictory results. A thorough assessment of genetic population structure using genome-wide markers is therefore critical. To tackle the large genome sizes of *C. finmarchicus* and *C. glacialis* (6.5 Gbp and 12 Gbp, respectively) which have long hampered attempts to study population genomics in these species, we designed a protocol of target-capture coupled with next-generation sequencing to yield thousands of Single Nucleotide Polymorphism markers (SNPs) useful for population genomics. Contrasting patterns of population structure were characterized between the two species. No significant genetic differentiation was detected among *C. finmarchicus* from nine locations, while one location appeared as genetically isolated from others, suggesting overall high levels of gene flow. In *C. glacialis*, three major genetically differentiated groups were identified among 15 locations investigated, corresponding to the major ocean basins of North Atlantic, Arctic, and North Pacific Oceans.

TALK

Use of the connectivity concept as quantitative evidence for management actions against marine invasive species: a case study in Galway Bay, Ireland.

Morane Clavel-Henry¹, Rebecca J. Giesler¹, Tasman P. Crowe¹, Tomasz Dabrowski², Jonathan M. Yearsley¹

¹ UCD - SBES, Belfield, Dublin, Dublin County, D4 (Ireland)

² Marine Institute - Ocean Science and Information Services, Rinville, Oranmore, Galway County H91R673 (Ireland)

Knowledge of marine connectivity highlights the spatial transfer and/or exchanges of individuals between units of area. In the coastal waters of Galway Bay (Ireland), the concept of connectivity can be used to guide management actions that aim to limit and monitor the establishment and expansion of marine invasive species. To do so, our study relied on the estimated spatial distribution of marine invasive larvae at a competent age for settlement. It was carried out with an already-introduced marine invasive species, the Pacific oyster (*Magallana gigas*), and a species yet to be introduced, the eastern Asian shore crab (*Hemigrapsus sanguineus*). Their spatial distribution comes from running a species-specific larval transport model coupled with hydrodynamic information and habitat suitability. Modelling results were used as quantitative evidence to underpin tools to guide the development of efficient management plans. Priority areas to take action or to monitor were identified using the larval colonization rates, the type of connectivity from the larval sources (e.g., super spreader sites, exclusive spreader sites), and the sensitivity of the places in relation to biodiversity and socio-economic concerns. These management support tools were reported to stakeholders involved in the control of the coastal resources and provided an example that can be applied to the rest of the Irish coastal waters and to similar invasive species. This approach allows the efficient targeted allocation of resources to best monitor and manage the spread of invasive species.

POSTER #8

Characterising Fine-Scale Variability in Coastal Connectivity Patterns In the Iroise Sea, Western France.

Philippe Cugier, Martin Marzloff
IFREMER, DYNECO-LEBCO, 29280 Plouzané.

At the intersect between the Bay of Biscay and the English Channel, the bay of Brest and the bay of Douarnenez (which are located in western Brittany, France, and are geographically distant of only ~10 km) are dramatically different both in terms of oceanographic conditions and in term of benthic biodiversity. In parts due to the Crozon peninsula that acts as a barrier and prevents direct exchanges and also due to their different topographies, hydrodynamic characteristics of these two bays significantly differ: (1) the bay of Brest, connected to the Iroise Sea by a narrow bottleneck, is relatively well mixed due first to a strong tidal-driven renewal of its water masses, and to a lesser extent to freshwater flows from two watersheds. Conversely, the bay of Douarnenez is broadly open to the Iroise Sea and overall characterized by weaker tidal currents, which allow for thermal stratification in the summer. The two bays also present contrasted benthic community composition and dynamics: while mass proliferation of the brittle star *Ophiocomina nigra* occurred in both bays, the marine gastropod *Crepidula fornicata* only proliferated in the bay of Brest. Moreover, plankton monitoring network suggests that Pseudo-nitzschia blooms, which can produce ASP (Amnesic Shellfish Poisoning) toxin, appear in the bay of Douarnenez before reaching the bay of Brest where they may induce closures of shellfisheries. Thus, characterizing connectivity of these two bays is critical to better understand its contribution to observed differences in benthic biodiversity, or to phytoplankton bloom dynamics. Based on larval dispersal simulation with the hydrodynamics model MARS3D, we assess connectivity patterns in the Iroise sea with a specific focus on fine-scale variability in hydrodynamics flow between these two bays. We moreover identify the major factors that drive seasonal and interannual variability in these local connectivity patterns.

POSTER #9

Understanding marine connectivity of Scottish scallop populations with multidisciplinary approaches to inform marine management.

Simone D'Alessandro¹, Rob Ogden^{2,3}, Emily Humble², Babette Hoogakker¹, Doug C. Speirs⁴, Joanne S. Porter⁵, Michel J. Kaiser¹

1. The Lyell Centre, Heriot-Watt University, Edinburgh, United Kingdom
2. Royal (Dick) School of Veterinary Studies and the Roslin Institute, University of Edinburgh, Edinburgh, United Kingdom
3. TRACE Wildlife Forensics Network, Edinburgh, United Kingdom
4. Department of Mathematics and Statistics, University of Strathclyde, Glasgow, United Kingdom
5. International Centre for Island Technology, Heriot-Watt University Orkney, Stromness, United Kingdom

The aim of this study is to combine cutting-edge genomic and biogeochemical analysis to mapping scallop populations in Scottish waters, informing the appropriate spatial scale for a sustainable management of the fishery in a complex dynamic environment.

Effective marine management is currently limited by knowledge gaps and deficient data on the complex interactions at the ecosystem- and population- levels. Information available is often difficult to unravel and disentangle. Improving knowledge of connectivity is a crucial stepping-stone to understanding how marine species interact in a dynamic three-dimension environment. This will allow refining management and conservation strategies for commercial species at a national, regional, and local scale.

Scallop fisheries are of substantial social and economic importance in Scotland, landing around 10.000 tons and totaling almost £23 million in 2015 (Marine Scotland, 2016). However, despite their relevance, to date, there are knowledge gaps about their population structure and their meta-populations dynamics between different Scottish locations. Understanding marine connectivity between different scallop grounds is an important aspect in a sustainable exploitation vision, informing the appropriate spatial resolution at which to manage the fishery and delineating suitable actions management units. Indeed, overfishing of critical scallop grounds could potentially alter the connectivity between scallop grounds, thereby leaving the population more exposed to stock collapse. Here, we illustrate and discuss the future steps of our project, which is to determine the marine connectivity of patches of scallops in Scottish waters. We will examine the scallop population structure, as well as parental and geographic origins with a combination of approaches. Using isotopic signatures in the scallop shell, we plan to determine scallop age and use water temperature and shell chemistry signatures to investigate their geographic origins. Using contemporary genomic analysis, we will examine different cohorts within discrete scallop grounds to infer genetic population structure, levels of gene flow, and parental origins. Particular attention will be given to illustrate strengths, weaknesses, different spatial and temporal resolutions of the proposed methods in estimating marine connectivity of scallop grounds.

TALK

Are we ready for protist population metagenomics? Challenges to decipher drivers of genetic differentiation in marine planktonic populations.

Ophélie Da Silva^{1,2}, Enrico Ser-Giacomi³, Jade Leconte⁴, Eric Pelletier^{4,5}, Cécile Fauvelot^{1,6}, Amin Madoui⁴, Lionel Guidi^{1,5}, Fabien Lombard^{1,5,6}, Sakina Dorothée Ayata^{1,2}, Lucie Bittner^{2,6}

1 Sorbonne Université, CNRS, Laboratoire d'Océanographie de Villefranche, LOV, F- 06230 Villefranche-sur-Mer, France.

2 Institut de Systématique, Evolution, Biodiversité (ISYEB), Muséum national d'Histoire naturelle, CNRS, Sorbonne Université, EPHE, Université des Antilles CP 50, 57 rue Cuvier, 75005 Paris, France

3 Sorbonne Université, UMR 7159 CNRS-IRD-MNHN, LOCEAN-IPSL, 75005 Paris, France

4 Génomique Métabolique, Genoscope, Institut Français Jacob, CEA, CNRS, Univ Evry, Université Paris-Saclay, Evry, France

5 Research Federation for the study of Global Ocean Systems Ecology and Evolution, FR2022/Tara Oceans-GOSEE, Paris, France

6 Institut Universitaire de France (IUF), Paris, France

Since a decade, high-throughput sequencing has transformed the study of marine, planktonic communities and has highlighted the extent of protist diversity in these ecosystems. Still, little is known about their genetic diversity at the species-scale, and about their major speciation mechanisms. As data from large scale samplings are now available, we postulate that metagenomics could contribute to deciphering the processes shaping their genetic differentiation in the marine realm. As a proof of concept, we focused on the Mediterranean Sea and chose three abundant protist species: *Bathycoccus prasinos*, *Pelagomonas calceolata* and *Phaeocystis cordata*. We compared the genetic differentiation of each species in light of geographical, environmental and oceanographic distances. We highlighted that isolation-by-environment may shape the genetic differentiation of *Bathycoccus prasinos* whereas *Phaeocystis cordata* may be impacted by isolation-by-distance. At present time, the use of metagenomics to accurately estimate the genetic differentiation of protists remains challenging as resulting coverages are lower compared to traditional genetic populations surveys. However, we started here to shed light on ecological and evolutionary processes occurring within natural marine populations, and paved the way for future protist population studies exploiting metagenomics.

TALK

Fine-scale demographic patterns of the blue mussel species complex (*Mytilus* spp.) in Scandinavia – historical isolation, introgression and present-day barriers to gene flow.

Pierre De Wit¹, Malin Gustafsson², Malin Waern^{1,3}, Olga Ortega-Martinez¹, Marte Sodeland^{4,5}, Per Erik Jorde⁴, Anna-Lisa Wrangé², Ane Timenes Laugen⁵, Åsa Strand², Carl André¹, Halvor Knutsen^{4,5}

1 Department of Marine Sciences, Tjärnö Marine Laboratory, University of Gothenburg, Strömstad, Sweden

2 IVL Swedish Environmental Research Institute, Kristineberg, Fiskebäckskil, Sweden

3 Leibniz Institute for Baltic Sea Research, Warnemünde, Germany

4 Institute of Marine Research, Flødevigen Marine Research Station, His, Norway

5 Centre for Coastal Research, Department of Natural Sciences, University of Agder, Kristiansand, Norway

Blue mussels (*Mytilus* spp.) are frequently used as examples of organisms with complicated evolutionary trajectories. They have a history of multiple successive colonization events in the North Atlantic Ocean followed by wide-scale hybridization among evolutionary lineages in different geographic areas. The Scandinavian peninsula, in particular, has been shown to exhibit complex genetic patterns, with the Pacific *M. trossulus* lineage dominating inside the Baltic Sea; North Atlantic *M. edulis* on the western coasts; and occasional occurrences of the southern European *M. galloprovincialis* as well as *M. trossulus* on the northern part of the Norwegian coast, all of which are hybridizing with each other to some extent. However, these patterns have hitherto almost exclusively been studied using limited sets of genetic markers known to be diagnostic for the different evolutionary lineages. In this study, we investigate fine-scale genomic patterns by genotyping a large number of SNP loci randomly distributed throughout the genomes of *Mytilus* spp. in a dense geographic sampling effort along the Scandinavian peninsula. Our results show that there are two distinct *M. edulis* lineages along Scandinavia, one in Skagerrak and another in the North Sea, with a phylogeographic border in southwestern Norway. Demographic analyses indicate that these have arisen during a historical period of separation (probably during the last glacial maximum), and that secondary contact has resulted in large-scale introgression post glaciation. We also find consistent evidence of present-day barriers to larval dispersal in the Skagerrak lineage, separating fjord/bay populations from outer archipelago populations, both by interpolating genetic data geographically and by inferring dispersal potential in a biophysical transport model. Finally, we report *M. galloprovincialis* in the Skagerrak for the first time. With the most extensive study of mussel population genomics in

northern Europe to date, we here highlight the diverse scales upon which present-day and historical dispersal can shape species complexes in the marine environment."

TALK

Disentangling coral disease and coral larvae connectivity to inform reef restoration in Florida.

Thomas Dobbelaere, Daniel M Holstein, Erinn M Muller, Lewis j Gramer, Lucas McEachron, Sara D Williams, Emmanuel Hanert

thomas.dobbelaere@uclouvain.be | Earth and Life Institute (ELI), UCLouvain, Louvain-la-Neuve, Belgium

dholstein1@lsu.edu | Department of Oceanography and Coastal Sciences, College of the Coast and the Environment, Louisiana State University, LA, USA

emuller@mote.org | Coral Health and Disease Program, Mote Marine Laboratory, Sarasota, FL, USA

lew.gramer@noaa.gov | Cooperative Institute for Marine and Atmospheric Studies (CIMAS), University of Miami, Miami, FL, USA

luke.mceachron@myfwc.com | Florida Fish and Wildlife Conservation Commission, FL, USA

swilliams@mote.org | Coral Health and Disease Program, Mote Marine Laboratory, Sarasota, FL, USA

emmanuel.hanert@uclouvain.be | Earth and Life Institute (ELI), UCLouvain, Louvain-la-Neuve, Belgium

Over the last seven years, the Florida Reef Tract (FRT) has been experiencing an outbreak of the Stony Coral Tissue Loss Disease (SCTLD). First reported off the coast of Miami-Dade County in 2014, the SCTLD has since spread throughout the entire FRT and continues to propagate throughout the Caribbean. Although the causative agent for this disease is currently unknown, the hydrodynamics is highly explanatory of the SCTLD patterns of infection. The same hydrodynamics is also the driving mechanism of coral larvae dispersal and coral connectivity, which enhance the overall system resilience. Connectivity therefore appears to be a double-edged sword as it can both enhance and degrade coral populations. In the present study, we try to disentangle the respective effects of disease and larval connectivity in order to identify reefs best suited to restoration projects. We do that by computing larval and disease connectivity for three coral species in the entire FRT with a high-resolution biophysical model. Connectivity information is computed over 3 consecutive years and then analyzed using graph theory tools. This approach allows the development of reef-specific metrics to identify reefs with a high restoration potential for different degrees of disease susceptibility. These are the reefs that are both good larval suppliers and weak potential sources of disease agents. Using this indicator, we construct species-specific maps indicating reefs with best restoration potential for different disease susceptibilities, hence allowing the identification of favorable outplant sites with low probability of infection. These maps can support ongoing restoration projects and indicate, for instance, that some reefs selected for the "Restoring Seven Iconic Reefs" mission (Horseshoe Reef and Looe Key) are poorly protected against the SCTLD. Furthermore, our model brings new insight on the role played by hydrodynamics in the apparent stalling of the spread of the SCTLD in the western Florida Keys in 2020 and suggests that the Dry Tortugas were infected only in November or December 2020. By combining both larval and disease connectivity, this study has the potential to support restoration efforts in Florida by designing effective management strategies against the worst coral epidemic on record in the Caribbean."

POSTER #10

New insight in the genetic characterization of the pelagic blue shark *Prionace glauca* in the Mediterranean Sea: population structure and connectivity, and genetic vulnerability.

Violaine Dolfo, Matthieu Lapinski, Greg Nowell, Emilie Boissin, Serge Planes

The blue shark is the most abundant pelagic shark in the open ocean, yet its degree of vulnerability is not well understood. Although its population in the Mediterranean is facing a high population decline due to fishing, it is not fully characterized. Here we investigated the genetic diversity, demographic history, and population structure of the blue shark within the Mediterranean between the Gulf of Lion and Malta using mtDNA control region and 22 microsatellite markers. We included these data in an analysis of Atlantic-Mediterranean population structure. We assessed its genetic vulnerability in the Mediterranean basin by modelling its effective population size. Our results showed a degree of genetic differentiation between the Atlantic and the Mediterranean, with limited gene flow between the two basins, and distinct demographic histories. In the Mediterranean, no sign of population structure was detected, advocating for a single population in the Western and Central part of the basin. The low Mediterranean blue shark's effective population size highlights its high vulnerability, as it is not sufficient to ensure long-term conservation of the population. Finally, a nursery is suspected in the Gulf of Lion, which appears as an important area for the conservation of the species in the Mediterranean.

POSTER #11

Genetic structuring of *Octopus vulgaris* within and between NE atlantic and Mediterranean Sea.

J. Domise¹, C. Mouronvalle¹, C. Tardy¹, E. Boissin¹, C. Olabarria^{2,3}, M. Beger^{4,5}, M.F.L. Lemos⁶, J.N. Franco⁶, A. Blanco^{2,3,4}, S. Planes^{1,7}

1 PSL Research University, EPHE - UPVD - CNRS, USR 3278 CRIOBE, 66860 Perpignan, France

2 Centro de Investigación Mariña, Universidade de Vigo, EcoCost, Facultade de Ciencias del Mar, Campus de Vigo, As Lagoas, Marcosende 36310 Vigo, Spain

3 Departamento de Ecoloxía e Bioloxía Animal, Universidade de Vigo, Campus As Lagoas-Marcosende, 36310 Vigo, Spain

4 School of Biology, Faculty of Biological Sciences, University of Leeds, Leeds, LS2 9JT, United Kingdom

5 Centre for Biodiversity Conservation Science, School of Biological Sciences, The University of Queensland, Brisbane, Queensland, Australia

6 MARE – Marine and Environmental Sciences Centre, ESTM, Politécnico de Leiria, 2520-641, Peniche, Portugal

7 Laboratoire d'Excellence « CORAIL », 66860 Perpignan, France

Genetic tools have the potential to estimate the rate of exchange between populations and provide an indirect measure of connectivity, which may help to efficiently manage fisheries and conservation actions (namely marine protected area, MPA, networks). The common octopus, *Octopus vulgaris* (Cuvier, 1797), is a representative species that plays an important ecological role on marine food webs (both as prey and predator) and is a highly commercial species worldwide and, particularly, in the Mediterranean and the North-eastern Atlantic Ocean. In the present study, 16 locations in the Atlantic Ocean along the Western coast of Portugal and Spain (9 inside MPAs and 7 outside MPAs) were sampled in order to evaluate the potential network of MPAs of the region. Moreover, in order to assess the octopus population phylogenetic structure, four additional locations inside MPAs along the French coast of the Mediterranean Sea. As a result, the richest set of microsatellites (22 de novo highly polymorphic loci) for this species has been developed. Genetic diversity was high ($H_e = 0.841$ and $H_o = 0.777$) with an average allelic richness between 18 and 43 alleles. *O. vulgaris* showed a deficit of heterozygotes ($F_{is} > 0.1$). Such results indicate high inbreeding, which could be emphasized by overfishing and Wahlund effect by population fragmentation. A clear differentiation between the Atlantic and the Mediterranean was evidenced (F_{st} ranging from 0.02 to 0.46). Altogether, *O. vulgaris* of the NE Atlantic Ocean showed high genetic connectivity (high gene flow and high number of family links). However, additional information regarding the genetic differentiation of *O. vulgaris* between the Atlantic and the Mediterranean will be needed to accurately characterize and manage the stocks at the appropriate scale. Data provided here may be extremely useful for fisheries and conservation

managers in the study region (and, in extension, to other areas or other octopus species with similar life-history traits) in order to characterize and properly manage this valuable resource and, therefore, avoid overfishing (and the collapse of local stocks). Population dynamics in marine ecosystems is difficult to monitor and, therefore, genetic connectivity of representative species (such as *O. vulgaris*) provides a valuable tool for evaluating both fisheries and conservation actions.

TALK

Connectivity between populations of the amphidromous goby *Sicyopterus lagocephalus* (Pallas 1770) in the southwest Indian Ocean, revealed by a modeling approach.

Céline Ellien¹, Marion Leroulier², Stéphane Pous³

1 UMR BOREA (8067) 43 rue Cuvier 75005 Paris celine.ellien@sorbonne-universite.fr

2 Université Littoral Côte d'Opal) lerouliermarion@gmail.com

3 UMR LOCEAN, Campus de Jussieu, 75005 Paris spolod@locean-ipsl.upmc.fr

The amphidromous goby *Sicyopterus lagocephalus* (Pallas 1770) is widely distributed throughout the Indo-Pacific basin. Its particular life cycle is characterized by juvenile and adult stages inhabiting the rivers of tropical volcanic islands and a dispersive marine stage: the larval stage. In the South-West Indian Ocean region, this goby is present in the Mascarene and in the Comoros Archipelagos. A previous population genetics study showed that it was a single population. Then the question of connectivity relying on planktonic larvae, between these two archipelagos distant by 1500 km, arises. In order to evaluate the possibilities of larval exchange between Mayotte, Comoros, Reunion (represented in the model by 4 areas) and Mauritius (represented by 2 areas), the migration trajectories potentially followed by the larvae during their dispersal phase were simulated using a 3D hydrodynamic model coupled to a Lagrangian model of larval transport. Eight spawning areas, coinciding with the recruitment areas, were defined, and particles/larvae were emitted at a monthly frequency, in order to quantify the possible larval fluxes between populations and ultimately, to determine the most efficient region(s) to supply larvae to the different populations. A total of 168 simulations covering the periods 2005 to 2018 were realized with specific biological parameters (range of larval phase duration, vertical migration, spawning/recruitment areas) aiming at conducting a sensitivity study of migration trajectories to spawning date, including different realistic hydro-climatic scenarios. Based on the results of this study, all recruitment sites can receive particles/larvae characterized by an age at recruitment between 110 and 135 days, by self- and allo-recruitment. Our results show a very high inter-annual variability of the larvae trajectories and fluxes, without revealing any seasonal trend. It appears that Mauritius island and Comoros region have the highest recruitment rate, and Mauritius is also the "best contributor" to provide larvae to the other sites, which can be explained by its geographical position in relation to the direction of the currents. In Reunion, a balance between allo and self-recruitment is observed. The connectivity between Mascarene and Comoros archipelagos is validated by our study, mainly in the direction Mascarene towards Comoros, but occasionally from Comoros to Mascarene also, through the Mozambique Channel.

POSTER #12

Connectivity between reefs is key to effective marine conservation and management.

Irfana Diah Faryuni

UCLouvain, Croix du Sud 2, Ottignies-Louvain La Neuve, 1348, Belgium

The larval exchange between marine protected areas (MPAs) and other reefs improve the resilience of the entire marine ecosystem. Potential coral connectivity and other criteria such as reef size, habitat quality and productivity should be considered when planning spatial management policies to ensure

the persistence of coral reef systems. In this study, we modelled *Acropora millepora* and *Acropora gemmifera* dispersal in the Wakatobi islands, South East of Sulawesi, Indonesia, by using the high-resolution ocean model SLIM. We then used a Lagrangian particle tracker to model the coral larval dispersal. We analyzed the resulting connectivity matrices using a graph theory algorithm to explore the spatial connections and determine each site's importance to local and regional connectivity. In particular, we used Google's PageRank algorithm to identify the main source and sink reefs, as well as the reefs best suited for protection and restoration. Although it has some limitations, this quantitative study has the potential to provide insights into specific areas where government and marine managers should prioritize to plan science-based MPAs and better arrangement of the conservation program. Many reefs with a high PageRank protection index are outside existing MPAs, such as around Wangiwangi island, Kaledupa Island, Kapota reef, and Kaledupa reef. Areas best suited for coral restoration projects are north-Lintea island, south-Lintea island, north and south of Kapota reef, Koromaha reef, North, west, and south Kaledupa reef.

INVITED TALK

Genomic insights into global connectivity and localized barriers to gene flow among killer whale populations.

Andy Foote
NTNU University Museum

Darwin argued that biodiversity existed along a continuum from local varieties, geographically isolated populations and subspecies, through to species and higher taxa. The boundary between a polytypic species, or discrete, recognized subspecies is thus often blurred and subjective. Ecotype/morphotype formation can be a precursor to speciation and thus represents an important, but often neglected stage in the formation of biodiversity. The marine environment is characterised by patchy habitat and prey distribution, but also high dispersal potential and low cost of movement. These opposing characteristics provide increased opportunity for the colonisation of, and local adaptation to, novel ecological niches, whilst constraining divergence across the spatial scale of dispersal. Thus, speciation may be prolonged in the marine environment, or the ecotype stage may be the default taxonomic status beyond which many taxa fail to progress. The marine environment is thus particularly rich in disparate ecotypes, encompassing a wide range of taxonomic groups. Killer whales are currently considered a single polytypic species (*Orcinus orca*), for which a number of 'types' have been reported and described. Recent analyses of whole genome sequences have shed new light on the demographic and evolutionary processes underlying their formation. Killer whale types have histories that include genetic (and cultural) adaptation to ecological niche, and typically genetic signatures of founder effects. There is also variation among killer whale types in their demographic histories. In this talk I will present reconstructions of the demographic and evolutionary histories of different killer whale types. I hope to use this work to propose a response to the question: 'Why are there so many types of killer whale, but only one species?'

POSTER #13

Contrasted Biogeography of Pacific coral genera revealed using genome wide SNP sets.

Didier Forcioli¹, Eric Armstrong², B. Porro¹, Quentin Carradec², Emilie Boissin³, E. Roettinger¹, Tara Pacific Consortium⁴

1 IRCAN-CNRS-Université Côte d'Azur (Nice, France)

2 CNS Génomoscope (Evry, France)

3 CRILOBE-EPHE-UPVD-CNRS (Perpignan, France)

4 Tara Ocean Fondation (Paris, France)

Abstract: The question of resilience in the face of the ongoing global changes has become crucial for the reef building corals. The quest for resistant corals, or for markers to detect such, is on. But to build these essential tools for coral reef managements, one needs to elucidate first the genetic structure of the coral species. The resistance/susceptibility phenotypes arise from the genetic variability available in the relevant gene pool. And here lies an additional problem: what are the boundaries of this relevant gene pool? Even before detecting gene flow patterns and more or less isolated populations within species, the species themselves are to be delimited first. Indeed, cryptic species (reproductively isolated species without clear morphological differentiation) abound in the relatively less explored marine organisms. Ignoring the existence of such closely related but isolated gene pools can lead to false conclusions in studies of genetic diversity distribution, especially concerning the potential spread of beneficial genotypes in environmentally challenged species. The TARA Pacific research program took place within this context, and one of its aims was to identify markers of resilience for coral reefs, from the genetic constitutions and stress phenotypes of the coral hosts to the composition of their associated microbiome. To do so, colonies from three coral genera (*Pocillopora*, *Porites* and *Millepora*) have been sampled on three different sites from each of the 32 reefs/islands visited by TARA Pacific (from Panama to Japan, and from New Caledonia to Taiwan). We present here the species hypotheses obtained on a first third of the sampled islands, using SNPs defined from genomic sequencing for *Pocillopora* and *Porites* or from transcriptomic data for an arbitrary set of reference genes (for *Millepora*), and state of the art species delimitation tools. Although sampled in the same oceanographic context, the patterns of species richness and distribution differed among the three genera, probably because of their different relation to the environment.

POSTER #14

Genetic population structure of the Blackspot seabream (*Pagellus bogaraveo*): contribution of mtDNA control region to fisheries management.

Sara M Francisco¹, Joana I. Robalo¹, Karen Avellaneda¹, Rita Castilho², Inês Farias³, Ivone Figueiredo³

1 MARE – Marine and Environmental Sciences Centre, ISPA Instituto Universitario, Lisboa, Portugal

2 Faculty of Science and Technology, University of the Algarve, Faro, Portugal; Centre of Marine Sciences (CCMAR), Faro, Portugal

3 Portuguese Institute for Sea and Atmosphere (IPMA), Alges, Portugal;

Marine fisheries management models have traditionally considered biological parameters and geopolitical boundaries. The result is the existence of fisheries management units that do not match genetic populations. However, this panorama is changing with the contribution of genetic and genomic data. *Pagellus bogaraveo* is a commercially important sparid in the northeast Atlantic, with three stock components being considered by ICES: the Celtic Sea and Bay of Biscay, Atlantic Iberian waters and the Azores. The northern stock collapsed (1975–1985) and it is essential to characterize the genetic makeup of the species, particularly in the Iberian Peninsula, where it is managed as a single stock. The mitochondrial control region was used to screen the intraspecific diversity and population structure of individuals from six locations across the species range. The genetic diversity found is similar among sites, but the connectivity is limited, with differentiation being found between the Azores and the remaining locations."

POSTER #15

Lagrangian modeling to study the connectivity of *Aethotaxis mitopteryx* (Perciformes, Notothenioidei) populations between the Antarctic Peninsula and the Weddell Sea.

Martina Gastaldi¹, Geneviève Lacroix², Valérie Dulière², Leo Barbut², Luca Schiavon¹, Mario La Mesa³, Chiara Papetti¹

1 University of Padova – Biology Department, Via Ugo Bassi 58b, 35121, Padova, Italy. martina.gastaldi96@gmail.com

2 Royal Belgian Institute of Natural Sciences, Rue Vautier 29, 1000, Brussels, Belgium

3 CNR, Institute of Polar Sciences ISP, Bologna, Italy

Abstract: Under a climate change scenario, the Weddell Sea continental shelf (Antarctica) is likely to be a sink area of biodiversity and a refugium for highly cold-adapted benthic organisms. One of the plans that are currently underway in international waters is to establish a network of marine protected areas (MPAs) at a circum-Antarctic scale. In this perspective, including the Weddell Sea in the spatial planning of MPAs in the Southern Ocean will be essential. Considering that patterns of connectivity are increasingly recognized as relevant information to support spatial planning of MPAs, we generated connectivity data for *Aethotaxis mitopteryx* (nototheniid, pelagic), one of the less known fish species and endemic of the Antarctic environment, given its presence in the Weddell Sea and Antarctic Peninsula. The final aim was to compare the connectivity pattern with previous data about different species in order to understand whether core routes of dispersal may be identified in the area. Given the life-history traits of the target species and the hydrodynamics of the area, we generated some hypotheses of connectivity for both the larval and the adult stage and tested them by using the Lagrangian module of COHERENS to simulate particle dispersal (particles were proxy for larvae and adult organisms). The simulations highlighted a consistency of the dispersal pattern for both larvae and adults: connectivity from the Weddell Sea to the Antarctic Peninsula was present and evident for adults, while for larvae it was present only under certain conditions of particle abundance and hydrodynamics. This pattern of dispersal was consistent with results on other notothenioids connectivity and suggested the key role of currents in shaping the distribution of Antarctic fish."

TALK

Spatio-temporal variability in *Paramuricea clavata* population genetics reveals connectivity variability in Ligurian sea

Katell Guizien¹, Mariana Padron¹, Cécile Fauvelot²

1 CNRS-Sorbonne Université, Laboratoire d'Ecogéochimie des Environnements Benthiques, LECOB, Observatoire Océanologique de Banyuls sur Mer, 1 avenue Pierre Fabre - 66650 Banyuls sur Mer (FRANCE)

2 Laboratoire d'Excellence CORAIL, F-66100 Perpignan, France; IRD, Université de la Réunion, CNRS, IFREMER, Université de la Nouvelle-Calédonie, ENTROPIE, F-06230 Villefranche-sur-Mer, France; Sorbonne Université, CNRS, Laboratoire d'Océanographie de Villefranche, F-06230 Villefranche-sur-Mer, France

Paramuricea clavata individuals sampled in 20 locations spanning distances from 100 m to 400 kms in the Liguria region (NW Mediterranean Sea) and separated in three age cohorts were genotyped at 37 SNPs. Genotypes dissimilarity were analyzed spatially only (pooling the three age cohorts) and spatio-temporally. Genotypes spatial dissimilarities differed when analyzing per age cohorts and pooling the three age cohorts, although genotype dissimilarities between the three age cohorts in each location were subtle. The present study highlights a potential bias in connectivity patterns assessment due to sampling bias linked to individual size.

POSTER #16

Using environmental DNA biodiversity monitoring datasets for haplotype networks and phylogeographic analyses.

Babett Günther¹, Sophie Arnaud-Haond²

MARBEC, Univ Montpellier, CNRS, Ifremer, IRD, Sète, France, guenther.babett@gmail.com

MARBEC, Univ Montpellier, CNRS, Ifremer, IRD, Sète, France, sophie.arnaud-haond@umontpellier.fr

The Metabarcoding of environmental DNA (eDNA) is seen as the future biomonitoring of marine environments. However, especially for metazoans, this data can be used for large-scale connectivity analyses of marine systems. The eDNAbyss and iAtlas project tested and developed standardized sampling and analyses of sedimentary eDNA. The bioinformatics pipeline is based on the use of operational taxonomic units (OTUs), which are clustered amplicon sequence variants (ASVs). These are actually different perspectives of biodiversity offering various understandings, as examples to strategically analyze haplotypes and prepare phylogeographic analyses. During these projects, thousands of sediment samples were collected across the world, aiming for outstanding large-scale biodiversity inventories, furthermore allowing connectivity analyses across the tree of life within and across ecosystems as well as oceans. First examples will be presented, including cross Atlantic and Hadal/Abysal haplotype networks as well as further possible applications in research.

TALK

Ranking of Danish harbours according to shipping activities and to the potential of natural dispersal of non-indigenous species.

Flemming Thorbjørn Hansen, Aurelia Pereira Gabellini, Asbjørn Christensen

The Ballast Water Management Convention (BWMC) requires that ballast water (BW) meet certain standards before being discharged into the marine environment to reduce the risk of transferring non-indigenous species (NIS) between locations. The discharge of BW typically (but not exclusively) takes place during port visits following the load and un-load of cargo. To meet these standards, ship owners need to treat the BW prior to discharge by the use of on-board treatment technology. The BWMC provides an option for national authorities to grant exemptions to ships that operate exclusively between a fixed number of ports or exclusively within a limited geographical area. An exemption can be granted if a risk assessment can conclude that, the discharge of untreated BW only imposes a low and acceptable risk of transfer of NIS between locations. As a basis for future risk assessment there is a need for a better understanding on how NIS may disperse along Danish coastal areas and between ports, including the identification of the most likely hotspots for introduction and spread of NIS. Thus, the main objective of the present study is to contribute to the decision basis for granting exemptions to the BWMC by Danish authorities, by mapping the potential of introduction and spread of NIS to and from 28 major Danish cargo and ferry ports and identifying major hotspot for primary and secondary introduction of NIS in Denmark. The 28 major ports are ranked according to 1) the shipping activity, 2) the potential natural dispersal of pelagic life stages of NIS between ports, and 3) the potential natural dispersal of pelagic life stages of NIS to neighboring habitats.

The ranking of each port according to natural dispersal between ports was then done using three different methods: 1. Cluster membership analysis: The extent to which individual ports belong to groups of neighboring ports in areas with high larvae dispersal connectivity identified using cluster analysis techniques. 2. Dispersal probability analysis: The probability of natural dispersal between individual ports; and 3. Dispersal duration analysis: The dispersal duration between ports without considering species specific traits.

POSTER #17

Contrasting connectivity scenarios in a transcontinental ecosystem: assessment and management implications in the Alboran Sea.

M. Hidalgo¹, P. Abaunza¹, A. Cariani², M. Dominguez¹, M. Feki³, A. Ferrari², T. Filali⁴, A. Gaamour³, M. Galindo⁵, A. García¹, J. García-Lafuente⁶, J. Gil¹, A. Giraldez¹, M. H. Idrissi⁷, S. Jaziri⁷, C. Johnstone¹, S. Khemeri³, R. Laiz-Carrión¹, M. Mennad⁴, S. Mattiucci, I. Nadal⁶, K. Mokhtar Jamai⁷, J.M. Quintanilla¹, J. Rey¹, J.M. Rodríguez¹, M. Pérez¹, J.L. Pérez-Gil¹, J.C. Sánchez⁶, S. Sammartino⁶, M. Spiga², F. Wahbi⁷, M. Vasconcellos⁵, P. Hernandez⁵.

1 Instituto Español de Oceanografía (IEO), Spain

2 University of Bologna, Italy.

3 Institut National des Sciences et Technologies de la Mer (INSTM), Tunisia

4 Centre National de Recherche et de Développement de la Pêche et l'Aquaculture, Algeria

5 The Food and Agriculture Organization of the United Nations (FAO)

6 University of Málaga, Spain.

7 Institut National de Recherche Halieutique (INRH), Morocco.

Transboundary ecosystems are often complex socioecological systems in terms of ocean governance as cooperation and collaboration among countries to assess shared resources status and regulate harvest according to common measures or joint decision-making is critical and often difficult to achieve. This is even more complex in transcontinental systems such as in the Mediterranean Sea, where fisheries governance contrasts between European and north African countries. This is the case of Alboran Sea, the Strait of Sicily or Eastern Mediterranean where fish stocks are expected to be shared but connectivity processes are largely unknown.

Here, we present the contrasting connectivity scenarios observed for the three investigated species in the research project TRANSBORAN ('TRANSboundary population structure of Sardine, European hake and blackspot seabream in the ALBORAN Sea and adjacent waters: a multidisciplinary approach'): sardine, hake and blackspot seabream. The project has sampled 17 sites within Alboran and adjacent waters to combine information of: hydrodynamic modelling; genetics; stable isotopes, microchemistry and shape in otoliths; parasites composition; morphometry of body and meristic description fish-bone and gill rakers; fishery patterns, demography and life history traits; and a multidisciplinary oceanographic survey. I will present a synthesis of the most relevant results illustrating the contrasting connectivity patterns of the three species and discuss some implications in terms of fisheries assessment and management.

TALK

Seascape genomics identify adaptive barriers according to tidal amplitude in the shore crab *Carcinus maenas*.

Marlene Jahnke¹, Per-Olav Moknes², Alan Le-Moan¹, Gerrit A. Martens^{1,3}, Per R. Jonsson¹

1 Department of Marine Sciences, Tjärnö Marine Laboratory, University of Gothenburg, SE-45296 Strömstad, Sweden

2 Department of Marine Science, University of Gothenburg, Gothenburg, Sweden

3 current address: Institute of Zoology, University of Hamburg, Hamburg, Germany

A challenge for larvae of coastal species with a planktonic larval stage that may drift for weeks with ocean currents is to return to coastal nursery habitats. Shore crab (*Carcinus maenas* L.) larvae are known to show tidal rhythmicity in vertical migration in tidal areas and circadian rhythmicity in micro-tidal areas. Each behavioural strategy seems to increase successful coastal settlement in the respective environment. We studied genome-wide differentiation based on 24,000 SNPs of 12 native populations of shore crab sampled from a large tidal amplitude gradient from macro-tidal (ca. 8 m) to micro-tidal (ca. 0.5 m). Dispersal and recruitment success of larvae was assessed with a Lagrangian biophysical model, which showed a strong effect of larval behavior on long-term connectivity, and dispersal barriers that partly coincided with different tidal environments. The genetic population structure

showed a subdivision of the samples into three clusters, which represent micro-, meso- and macro-tidal areas. The genetic differentiation was mostly driven by 0.5% outlier loci, which showed strong allelic clines located at the limit between the three tidal areas. Demographic modelling suggested that the two barriers have different origins. Differential gene expression of two clock genes (*cyc* and *pdp1*) further highlighted phenotypic differences among genetic clusters that are potentially linked to the differences in larval behaviour. Taken together, our results imply that tidal regime acts as a strong selection force on shore crab population structure, consistent with larval behaviour affecting dispersal and recruitment success.

POSTER #18

Translocation in the millions: genetic population structure of cleaner fish used in aquaculture.

Eeva Jansson^{1#}, Ellika Faust^{2#}, Carl André², Dorte Bekkevold³, Kim Tallaksen Halvorsen⁴, Caroline Durif, Geir Dahle¹, Christophe S. Pampoulie⁵, Benjamin Whittaker⁶, Laila Unneland¹, Kevin A. Glover^{1,7}

These authors contributed equally to this work

1 Institute of Marine Research, P. O. Box 1870 Nordnes, N-5817 Bergen, Norway

2 Department of Marine Sciences - Tjärnö marina laboratorium, University of Gothenburg, 45296 Strömstad, Sweden

3 National Institute of Aquatic Resources, Technical University of Denmark, Vejlsovej 39, 8600, Silkeborg, Denmark

4 Institute of Marine Research, Austevoll Research Station, Storebø, N-5392, Norway

4 Institute of Marine Research, Flødevigen, Nye Flødevigveien 20, N-4817 His, Norway

5 Marine and Freshwater Research Institute, Hafnarfjörður, Iceland

6 Department of Integrative Biology, University of Guelph, ON, N1G 2W1, Canada

7 Institute of Biology, University of Bergen, P. O. Box 7803, N-5020 Bergen, Norway

Human mediated translocation of marine organisms can have large and long-lasting effects on populations, species and whole ecosystems. Similarly, farmed fish escaping aquaculture has been identified as a serious threat to wild fish populations as it may lead to genetic swamping and reduced fitness. Over the last decade the use of cleaner fish to combat sea lice infestations in salmon farms has grown exponentially. In Norway, the world's largest producer of Atlantic salmon, the number of cleaner fishes put into farms annually increased from 1.7 million in 2008 to 60 million in 2019, and now over 60% of all Norwegian salmon farms use cleaner fish to remove parasites. The high demand for cleaner fish has resulted in wild-caught wrasses being imported and translocated over thousands of kilometers from their source populations, which often are genetically highly diverged. In some species of wrasse researchers found evidence of escapees and extensive hybridization between the divergent populations in areas around the farms thereby raising concerns of increasing the use of cleaner fish. The use of wrasse in Norwegian aquaculture has declined in recent years as lumpfish (*Cyclopterus lumpus*) have become more common. In 2019 over 70% of cleaner fish used in Norwegian aquaculture were farmed lumpfish. Although, lumpfish used as cleaner fish are farmed, broodstocks are still essentially wild-caught, suggesting that the issues with translocation maybe equally applicable for this species. In this study we found that lumpfish may be more genetically structured than previously described, suggesting that translocation and subsequent escapees may also result in hybridization and altered populations. Consequently, genetic background should also be taken in consideration when choosing broodstocks for rearing this cleaner fish species."

POSTER #19

Genetic homogeneity in the shanny *Lipophrys pholis* throughout the Western Iberian Peninsula.

L.-L. Jeannot¹, C. Mouronvalle¹, C. Peyran¹, C. Olabarria^{2,3}, M. Beger^{4,5}, A. Blanco^{2,3,4}, S. Planes^{1,6}

1 PSL Research University, EPHE - UPVD - CNRS, USR 3278 CRIOBE, 66860 Perpignan, France

2 Centro de Investigación Mariña, Universidade de Vigo, EcoCost, Facultade de Ciencias del Mar, Campus de Vigo, As Lagoas, Marcosende 36310 Vigo, Spain

3 Departamento de Ecoloxía e Bioloxía Animal, Universidade de Vigo, Campus As Lagoas-Marcosende, 36310 Vigo, Spain

4 School of Biology, Faculty of Biological Sciences, University of Leeds, Leeds, LS2 9JT, United Kingdom

5 Centre for Biodiversity Conservation Science, School of Biological Sciences, The University of Queensland, Brisbane, Queensland, Australia

6 Laboratoire d'Excellence « CORAIL », 66860 Perpignan, France

The shanny *Lipophrys pholis* is an abundant intertidal fish widely distributed throughout the North-East Atlantic, with demonstrated capacity to biomonitor ecosystem health due to its restricted home range after larval settlement. This study describes the genetic structure of *L. pholis* across the Western Iberian Peninsula, covering over 550 km of coastline. Both large and small-scale connectivity were assessed by analyzing 519 samples and using 27 de novo highly polymorphic microsatellite loci. *L. pholis* showed no sign of genetic differentiation (F_{ST} ranging from 0.002 to 0.021) and was panmictic throughout the study range. Genetic diversity was high across all sites, with observed heterozygosity ranging from 0.0793 to 0.8935 and mean allele number between 14.3 and 20.1. Parentage analysis revealed long-range dispersal capabilities of several hundreds of kilometers between half-siblings originating from the same generation as well as between generations. In contrast, almost half of the related pairs were separated by less than 50 kilometers, suggesting that a significant proportion of larvae disperse over small distances. However, no finer scale processes could be detected in the *L. pholis* population structure, and the results showed that all shannies from the study area belong to a large genetically homogeneous population spanning the NE Atlantic coastline. This lack of structure as well as the large range of dispersal distances found among the samples can be related to the long pelagic larval duration of *L. pholis* coupled with high variability in ocean dynamics over the spawning period. The high connectivity of *L. pholis* between localities directly impacts population dynamics by maintaining high levels of genetic diversity and resilience in case of local disturbance. As a low trophic level species, *L. pholis* genetic diversity is paramount in preserving food web structure and stability and in ensuring trophic resilience, which will ultimately favor the long-term persistence of species reliant on *L. pholis* as a food source. Applying these findings to species with similar life-history traits can have important implications for the management and conservation of other NE Atlantic littoral fishes.

POSTER #20

Development of a genetic monitoring tool to assist conservation management of North East Atlantic benthic elasmobranchs.

Catherine S. Jones¹, Tanja N. Schwanck¹, Fenella Wood¹, James Thorburn², Jane Dodd³, Peter J. Wright⁴, David W. Donnan⁵, Leslie R. Noble⁶.

1 School of Biological Sciences, University of Aberdeen, Aberdeen AB24 2TZ, UK

2 Scottish Oceans Institute, University of St. Andrews, St. Andrews KY16 9AJ, UK

3 NatureScot, Cameron House, Oban PA34 4AE, UK

4 Marine Scotland Science, Marine Laboratory, 375 Victoria Rd, Aberdeen AB11 9DB, UK

5 NatureScot, Battleby, Redgorton, Perth PH1 3EW, UK

6 Faculty of Biosciences and Aquaculture, Nord University, Bodø, Norway

North-east Atlantic (NEA) elasmobranchs represent a minor but valuable component of marine fisheries, with many species suffering significant declines from targeting and bycatch. The protection and monitoring of genetic diversity in highly mobile elasmobranchs present management challenges across multi-legislative areas like the NEA. Genetic assessments are often rare and temporally separate, yet ongoing re-evaluation by workers in different states remains key to ensuring efficacy of protection. Declines in the critically endangered flapper skate (*Dipturus intermedius*) prompted

designation of a marine protected area (MPA) on the Scottish west coast, affording incidental protection to the endangered spurdog (*Squalus acanthias*), a benthic aggregating shark species. Yet knowledge of the genetic connectivity and variability of populations within and outwith the MPA is limited. Next-generation sequencing provides large numbers of genetic markers but often requires considerable quantities of high-quality DNA, a problem for wildlife monitoring where available material typically yields low-quality/quantities of DNA. Dedicated reduced marker panel assays could offer simple, cost-effective tools, for cross-laboratory comparisons for routine genetic monitoring. We are establishing reduced panels of Single Nucleotide Polymorphic (SNP) markers to allow high throughput genotyping to monitor flapper skate and spurdog populations. Monitoring the status of the current MPA population(s), and connectivity with individuals at other locations in the NEA, is important to affirm its current siting, and to assess the need and location of future MPA placements.

POSTER #21

Age and growth of the devil lionfish, *Pterois miles* (Bennet, 1828), in Kaş-Kekova MPA (Eastern Mediterranean).

Merve Karakuş¹, Coşkun Menderes Aydın¹, E.Mumtaz Tıraşın²

1 Mediterranean Fisheries Research Production and Training Institute, mervekarakus86@gmail.com

2 1 Institute of Marine Science and Technology, Dokuz Eylül University, İzmir, Turkey

This study reports the preliminary findings on the age and growth of the devil lionfish *Pterois miles* sampled during monthly scuba diving and spearfishing in Kaş-Kekova Marine Protected Area July 2018 and December 2020. A total of 1989 (988 females, 964 males and 1161 undetermined) *Pterois miles* specimens were collected at depths of 0-30 m. Total length and total weight of the sampled fish ranged between 7.1 - 41 cm and 3.3 - 988.3 g, respectively. The length-weight relationship for the whole sample was $W = 0,004L^{3,848}$ ($R^2 = 0.976$) and indicated a positive allometric growth. Age determinations were based on 464 otolith readings and ranged from 1 to 7 years. The von Bertalanffy growth parameters were: $L_{\infty} = 47,2$ cm, $K = 0.149$ year⁻¹ and $t_0 = -1.788$ year. Although (L_{∞}) obtained in the current study is higher than most of the other the growth coefficient (K) value is lower than the other regions. The reason of this may be that the Mediterranean is more nutritionally unproductive than other regions reported in the literature.

POSTER #22

Multi-faceted connectivity in a harvested metapopulation of the Western Mediterranean: implications for fisheries assessment and management.

Kerametsidis Georgios¹, Rossi Vincent², Hidalgo Manuel¹

1 Centro Oceanográfico de Baleares (IEO, CSIC), Ecosystem Oceanography Group (GRECO). Moll de Ponet s/n, 07190 Palma, Balearic Islands, Spain.

2 Mediterranean Institute of Oceanography (UM110, UMR 7294), CNRS, Aix Marseille Univ., Univ. Toulon, IRD, 13288 Marseille, France.

The efficiency of current management frameworks for marine fish stocks has long been questioned as they often fail to incorporate crucial biological processes that are space- and time-dependent. Consequently, there is a mismatch between the real spatial structure of wild exploited populations and the spatial units used for their management, which results in inaccurate portrayals of their spatiotemporal dynamics. To reveal the spatial structure of commercial resources and to explore their responses to fishing pressure, movements and connections among population sub-units must be examined. Here I present the objectives of my PhD project which addresses the different facets of functional connectivity among the subpopulations of an exploited species with high commercial value,

the red mullet (*Mullus barbatus*), in the Western Mediterranean Sea. First, the spatiotemporal variability of the different adult sub-units in response to contrasting environmental components will be explored utilizing spatiotemporal information from scientific surveys and port landings. Following, regional and small-scale (from spawning to settlement areas) connectivity will be assessed by using otolith chemical composition and ocean circulation models, respectively. Upon completion of the aforementioned tasks, a clearer depiction of the metapopulation structure will allow incorporating spatially explicit ecological processes and population sub-structures into spatially structured population dynamics models. This project will employ some state-of-the-art methods and is expected to have far-reaching applications in the assessment and management of marine stocks."

TALK

The effect of pelagic larval stage on population genetic structure and demographic connectivity: a comparative study on coastal fishes.

Halvor Knutsen^{1,2}, Diana Catarino², Lauren Rogers³, Marte Sodeland², Morten Mattingsdal², Marlene Jahnke⁵, Jeffrey A. Hutchings^{1,2,4}, Ida Møllerud¹, Sigurd H Espeland^{1,2}, Kerstin Johanneson⁵, Olivia Roth⁶, Michael M. Hansen⁷, Sissel Jentoft⁸, Carl André⁵, Per Erik Jorde¹

1. Institute of Marine Research, Nye Flødevigveien 20, 4817 His, Norway

2. Centre for Coastal Research, Department of Natural Sciences, University of Agder, 4630 Kristiansand, Norway

3. Alaska Fisheries Science Center, National Oceanic and Atmospheric Administration, 7600 Sand Point Way NE, Seattle, WA 98115, USA

4. Department of Biology, Dalhousie University, Halifax, NS, Canada

5. Department of Marine Sciences – Tjärnö, University of Gothenburg, 45296 Strömstad, Sweden

6. Marine Evolutionary Biology, Zoological Institute, Kiel University, Germany

7. Århus University, Department of Biology, 8000 Aarhus, Denmark

8. University of Oslo, Department of Biology, 0316 Oslo

What are the focal factors that impact spatial structuring of coastal ecosystems? Using a spatially consistent sampling scheme exploiting a time-series survey, we have collected tissue samples from three coastal fish species. We analyze these samples by combining modern genomics tools (ddRAD and full-genome sequencing), to characterize spatial correlations in genetics (indicating common ancestry) and spatial synchrony in population density changes (indicating population connectivity). Genomic data are further used to test for potential adaptive genetic differences among populations. We identify that the species with less larval drift, and patchy distributed habitat, are more localized and less connected to each other by dispersal. In combination, demographic and genetic methods are thus able to quantify the magnitude of dispersal in coastal systems for these species. We further find that all three species display a genetic discontinuity or ""break"", a potential ecosystem structure valid for many coastal species, at approximately the same geographic position at the coast, around the SW point of Norway. This genetic feature seems to be caused by a combination of unsuitable habitat (large, sandy beaches) and a tendency for the coastal current to leave the proximity to the coast around this area, thereby advecting pelagic eggs and larvae out into the open ocean.

POSTER #23

Phylogenetic diversity of Southern Ocean for better conservation planning.

Anna Kondratyeva, Marc Eléaume

MNHN, 57 rue Cuvier, Paris, 75005, France

For a long time our knowledge of marine biodiversity of the Southern Ocean has been constrained by the relative inaccessibility of the region, however, the publication of the Biogeographic Atlas of the Southern Ocean have shown that its marine biodiversity is more diverse as once thought. Since the beginning of biodiversity, studies in SO many particular species living in very specific areas have been observed and analyzed. In recent years the growing need of marine biodiversity protection in SO have become the primary objective for The Commission for the Conservation of Antarctic Marine Living Resources (CCAMLR). To develop more robust and integrative tool for marine biodiversity conservation we are measuring, for the first time, a global phylodiversity distribution for all animal taxa from the SO. Phyloregionalisation would be a powerful method unifying species distribution and phylogenetic relations reflecting species phylogenetic turnover between predefined biogeographic regions and determining priority areas for conservation, i.e. Marine Protected Areas."

TALK

Modelling the seasonal retention patterns of the early life history of *S. aurita* in the Angolan upwelling system.

Koné Vamara¹, Marek Ostrowski², Christophe Lett³

1 Centre de Recherches Océanologiques (CRO), Abidjan, Côte d'Ivoire.

2 Institut of Marine Research (IMR), Bergen, Norway.

3 Institut de Recherche pour le Développement (IRD), France.

The hydrographical regime off Angola is characterized by the cold northward-flowing Benguela current and the warm southward propagating waters of the Angolan current. These two currents meet at about 15°S at the Angola-Benguela front. The Angolan coastal upwelling is unique on the global scale since it occurs under calm wind conditions. Enrichment and high productivity occur in the absence of upwelling favorable wind, forced by low energetic processes such as lateral mixing or internal waves. Twice a year, upwelling is interrupted by a strong El Niño-like poleward current and downwelling conditions dominate along the entire coast. Small pelagic fish such as *S. aurita* has adapted their reproductive behaviour to this particular environment by forming highly contiguous aggregations aligned along topographic features and close to inshore. The alternation between upwelling and downwelling conditions strongly impact *S. aurita* seasonal distribution. We developed a biophysical model of *S. aurita* early life history by coupling offline a lagrangian model (Ichthyop) with the Coastal and Regional Ocean Community model (CROCO) in the Angolan upwelling system. We used this model to investigate the impacts of seasonal variability on retention of *S. aurita* early life stages in the Angolan upwelling region. Precisely, individuals were released from different spawning areas along the coast and tracked for a period of 28 days corresponding to their planktonic phase. Individuals that remained in the coastal recruitment areas at an age more than 7 days, at which they can supposedly actively retain themselves in a favorable area, were considered as recruited. Simulations show the importance of the spawning areas from the north (SGC, 3°S) to BNGELA (13°S) with the highest retention rates. CIAMBA and TOMBWA being the least favorable areas for retention. The spawning period also plays a key role in the recruitment success, with highest coastal retention obtained during the major upwelling period (June–September). These results are in general agreement with knowledge of *S. aurita* reproduction in the Angolan upwelling system.

POSTER #24

Investigating natal origin and trans-oceanic migrations of Albacore tuna (*Thunnus alalunga*) from the West Indian Ocean using otolith chemistry.

Maylis Labonne¹, Audrey M. Darnaude¹, Cécile Petit¹, Anais Médieu², Marianne Pernak², Natacha Nikolic³, Naomi Clear⁴, J. Paige Eveson⁴, Jessica Farley², Francis Marsac³, Campbell Davies⁴.

- 1 MARBEC, Univ Montpellier, CNRS, Ifremer, IRD, Montpellier, France
- 2 MARBEC, Univ Montpellier, CNRS, Ifremer, IRD, Victoria, Seychelles
- 3 MARBEC, Univ Montpellier, CNRS, Ifremer, IRD, La Réunion
- 4 CSIRO Oceans and Atmosphere, Hobart, Tasmania, Australia
- 5 MARBEC, Univ Montpellier, CNRS, Ifremer, IRD, Sète, France

Natal origin of 92 Albacore tuna (*Thunnus alalunga*) from the West Indian Ocean was investigated using trace elements in otoliths. Otoliths were collected from (i) 46 juveniles caught in 2 locations in South Africa (SA-North and SA-South) in 2018 and Tasmania (SWTS) in 2019, which are both known to be nurseries areas for the species, and (ii) 46 older fish caught in the Reunion island (SWI) during 3 sampling events in 2018. Otoliths concentrations in seven chemical elements (B, Mg, P, Cu, Zn, Sr and Ba) were analyzed by LA-ICP-MS at two points, near the core and at the edge, providing an elemental signal from the material deposited while the fish were close to their spawning grounds and from material deposited while they were in (or close) to their capture areas, respectively. Core and edge signatures for the same otolith were significantly different for most elements. At the edge, PCA identified different signatures (in Sr, Ba, and B) between the 3 main capture areas. Multi-elemental signatures for the Reunion samples were stable over the 3 sampling events. Those for South Africa samples split into 2 groups, the group of juveniles sampled in the Atlantic (SA- North) exhibiting signatures in B statistically different from those of all the juveniles from the Indian Ocean (SA-South and SWTS). The PCA on core signatures (from West Indian ocean and Atlantic ocean samples) identified some variation in spawning origin according to fish capture location. Based on the most relevant number of clusters, 2 putative spawning origins (SpO) with distinct chemical signatures in B and P were identified. All two SpO apparently contribute to the 3 sampling events investigated, but in varied proportions. Interestingly, although some overlap was found between SA-North and SA-South signatures, the two juvenile sampling locations mostly had different spawning origin. SpO-2 was identified as the main spawning source for the albacore analyzed (52%), principally in SA-S (76%), SWI-May18 (62%) and SWI-Dec18 (70%). SpO-1 apparently provides 47% of the fish sampled, principally in SA-N (69%) and SWI-Feb18 (85%). The samples collected do not allow to prove that these different spawning origins correspond to spatially discrete zones in the Indian or Atlantic Ocean. Nonetheless, these results bring evidence for trans-oceanic migrations in *T. alalunga*, which has strong implications for the management of its stocks.

TALK

Can artificial structures increase connectivity of hard substrate species through stepping stone in the North Sea?

Lacroix Geneviève, Kerckhof Francis, Barbut Léo, Vigin Laurence, De Mesel Ilse, Degraer Steven
Operational Directorate Natural Environment, Royal Belgian Institute of Natural Sciences, Rue Vautier 29, 1000 Brussels, Belgium

Pelagic life stages are crucial in determining invertebrate and fish dispersal and connectivity in the marine environment. Man-made structures, such as offshore wind farms (OWFs), are proliferating in the North Sea, possibly acting as stepping stones for fouling species and hence allowing species to expand their distribution range over large distances or increase connectivity between existing populations. Evidence-based marine management requires the understanding of how (man-made) hard structures are ecologically connected and what processes influence larval retention and dispersal. The transport of marine organisms from the spawning grounds to settlement areas is driven by hydrodynamic processes. However, the final dispersal pattern, larval survival and successful settlement of the larvae are affected by environmental factors, physiology, behaviour and reproductive strategies (spawning period/areas). Biophysical models help assessing the dispersal potential of marine species during their pelagic phase. Here, we use a particle-tracking transport model

coupled to a 3D hydrodynamic model (LARVAE&CO), to assess the larval dispersal of blue mussel (*Mytilus edulis*), European flat oyster (*Ostrea edulis*) and common limpet (*Patella vulgata*) in the North Sea and to quantify the increase of connectivity of populations owing to man-made structures. We comparatively analyses the stepping-stone effect of man-made structures for these three species with different larval life traits. Results showed that OWFs could potentially speed up larval dispersal of blue mussels and common limpets from existing natural populations to coastal areas and could allow for potential new colonization of coastal areas for the European flat oyster and common limpets. Our results contribute to a better understanding of the impact of man-made structures on larval dispersal and connectivity in the North Sea.

TALK

Genetic connectivity inferred from male- and female-type mitochondrial DNA from *Limecola balthica*, a bivalve species characterised by DUI.

Le Cam Sabrina, Brémaud Julie, Becquet Vanessa, Garcia Pascale, Viricel Amélia, Pante Eric
Laboratoire Littoral Environnement et Sociétés (LIENSs), UMR 7266, CNRS-La Rochelle Université, 2 rue Olympe de Gouges, F-17042 La Rochelle Cedex 01, France

Limecola balthica is among several bivalve species that show a remarkable exception to the maternal inheritance of mitochondria in metazoans: the doubly uniparental mode of inheritance (DUI). In this system, females transmit their mitochondria to all offspring, whereas mitochondria transmitted by males only persist in the male lineage (germ line and sperm). Males are therefore heteroplasmic. The female-transmitted mitotype (F-mtDNA) and the male-transmitted mitotype (M-mtDNA) are highly divergent in *L. balthica*, reaching 44%. This system is therefore potentially highly sensitive to mito-nuclear incompatibilities (MNIs), which may be expressed at several life stages in inter-population hybrids. In this study, we test whether male and female mitochondrial DNA presented a similar biogeographic scenario. Cox1 was partially sequenced for both mitotypes (cox1m and cox1f) across 313 males sampled from the Baltic Sea to the Gironde Estuary (the southern limit of *L. balthica*). Overall, cox1m showed a higher haplotype diversity (81 haplotypes compared to 37 at cox1f) and divergence level (Dxy between the Atlantic and Baltic lineages of 0.02 compared to 0.01 at cox1f). While the average nucleotide diversity and its range across sampling sites were similar between markers, a strong southward decrease of the genetic diversity was observed at cox1m only. The level of differentiation was 3.5 higher at cox1m compared to cox1f (global $\Phi_{ST} = 0.447$ and 0.126 respectively) and the geographic localization of the strongest genetic break was different at both markers, the Finistère peninsula for cox1f and the Cotentin for the cox1m. Both markers shared a common demographic history and π_{ns}/π_s was similar within each mitotype thus a higher mutation rate at the male mitotype could explain discrepancies in geographic patterns. Cox1m could therefore reflect a more recent representation of the genetic structure of the species. It is congruent with estimations based on nuclear markers which predicted that the hybrid zone was to shift northward within the next 80 yrs. On the other hand, mito-nuclear coadaptation is primordial to the mitochondrial function and might be primarily driven by FmtDNA since it is more prevalent in the organism. Significant linkage disequilibrium between the two markers in the southern populations due to preferential association of male haplotypes with F mtDNA suggested that MNIs might be occurring, limiting M-mtDNA gene flow past the Cotentin peninsula. In conclusion, within male individuals, the male and female mitochondrial lineages displayed contrasted phylogeographic patterns, the male cox1 being more congruent with previous results from nuclear markers (e.g. Microsatellites) than with the female cox1. Looking at both markers may offer two distinct windows into demographic events and selective pressures.

POSTER #25

Using metatranscriptomic datasets to infer population genetic structure in marine microbial eukaryotes.

Mickael le Gac¹, Gabriel Metegnier¹, Lou Mary¹, Raffaele Siano¹, Francisco Rodríguez², Christophe Destombe³, Marc Sourisseau¹

1 Ifremer, DYNECO, Plouzané, F-29280 France

2 Spanish Institute of Oceanography (IEO), Oceanographic Center of Vigo, Subida a Radio Faro 50, Cabo Estay, Canido, 36390 Vigo, Spain

3 Evolutionary Biology and Ecology of Algae, CNRS, Sorbonne Université, UC, UACH, IRL 3614, Roscoff, France

Microbial eukaryote census population sizes easily reach several billions of individuals. Traditionally, investigating population structure for these organisms starts from tedious and time-consuming single cell isolation that may then be turned into clonal cultures prior to DNA extraction. These mandatory steps considerably limit the number of individuals that may be genotyped and may potentially introduce biases if the ability to obtain clonal cultures depends on the genotype of the original cells. As an alternative, the possibility to investigate population structure from metatranscriptomic datasets was explored. Often used to determine community wide gene expression profiles, these datasets also contain genetic information, especially single nucleotide polymorphism data, that may be used to infer allelic frequencies at thousands of markers based on hundreds of thousands of individual cells. Although restricted to species reaching relatively high relative abundances in natural communities, such approach only requires minimal initial species-specific genomic resource and neither specific genetic marker development, nor targeted sequencing. The potential biases that may be introduced when allelic frequencies are determined using RNA and not DNA as well as the relationships between Fst precision and coverage were analyzed. Using the toxic dinoflagellate *A. minutum* as a case study, a strong genetic structure between populations from Galicia in Spain and Brittany in France was inferred and compared using 37 strains and 77 metatranscriptomic datasets.

TALK

An introgression breakthrough left by an anthropogenic contact between two ascidians.

Alan Le Moan^{1,2}, Charlotte Roby¹, Christelle Fraise³, Claire Daguin-Thiébaud¹, Nicolas Bierne⁴, Frédérique Viard^{1,4}

1 Sorbonne Université, CNRS, UMR 7144, Station Biologique de Roscoff, Place Georges Teissier, 29680 Roscoff, France

2 Department of Marine Sciences, Tjärnö Marine Laboratory, University of Gothenburg, Laboratorievägen 10, 452 96 Strömstad, Sweden

3 CNRS, Univ. Lille, UMR 8198 – Evo-Eco-Paleo, F-59000 Lille, France

4 ISEM, Univ. Montpellier, CNRS, IRD, Montpellier, France

Human-driven translocations of organisms have diverse evolutionary consequences, such as increasing connectivity among distant populations and promoting hybridization between previously geographically isolated taxa. This is well illustrated by tunicates from the genus *Ciona*. This genus encompasses several species which are commonly encountered within harbors and regularly translocated by boat across seas and oceans. In this presentation, I will show that such movements have multiple consequences on the population structure within species. I will describe this in *Ciona intestinalis*, a species native to Europe, which is now co-occurring with its introduced congener, *Ciona robusta* (native to the Pacific), within the English Channel. Despite their long allopatric divergence, the two species show partial reproductive isolation. Using genomic data, I will describe the chaotic genetic structure found 1) among *Ciona intestinalis* populations, and 2) within the introgression footprint left

by the anthropogenic hybridization between the native and introduced taxa. Both signatures are likely consequences of human-mediated translocations.

TALK

Coalescent connectivity through multi-generation dispersal modelling predicts gene flow across marine phyla.

Térence Legrand¹, Anne Chenuil², Enrico Ser-Giacomi³, Sophie Arnaud-Haond⁴, Nicolas Bierne⁵, Vincent Rossi⁶

1 Aix Marseille University, Université de Toulon, CNRS, IRD, Mediterranean Institute of Oceanography (UMR 7294), Marseille, France. (terence.legrand@mio.osupytheas.fr). Corresponding author.

2 Institut Méditerranéen de Biodiversité et d'Ecologie Marine et Continentale, CNRS (UMR 7263), Station Marine d'Endoume, Marseille, France. (anne.chenuil@imbe.fr).

3 Department of Earth, Atmospheric and Planetary Sciences, Massachusetts Institute of Technology, 54-1514 MIT, Cambridge, Massachusetts, USA. (enrico.sergiacomi@gmail.com).

4 Marine Biodiversity, Exploitation and Conservation, UMR 9190 IRD – IFREMER – UM – CNRS, Sète, France.

(sophie.arnaud-haond@umontpellier.fr).

5 Institut des Sciences de l'Évolution Montpellier, UMR 5554 UM – CNRS – IRD – EPHE, Station Marine OREME, Sète, France. 6 (nicolas.bierne@umontpellier.fr).

6 Aix Marseille University, Université de Toulon, CNRS, IRD, Mediterranean Institute of Oceanography (UMR 7294), Marseille, France (vincent.rossi@mio.osupytheas.fr).

Gene flow governs the contemporary spatial structure and dynamic of populations as well as their long-term evolution. For species whom migration is realized through propagule dispersal driven by atmospheric or oceanic flows, biophysical models allow predicting the migratory component of gene flow, which facilitates the interpretation of broad-scale spatial structure inferred from observed allele frequencies among populations. However, frequent mismatches between dispersal estimates and genetic diversity prevent an operational synthesis for eco-evolutionary projections. Here we use an extensive compilation of 58 population genetic studies of 47 phylogenetically divergent marine sessile species over the Mediterranean basin to compare genetic differentiation observations against gene-flow predictions obtained with Isolation-By-Distance, single-generation dispersal and novel multi-generation dispersal models. Unlike previous approaches, they unveil explicit parents-to-offspring links (filial connectivity) and, for the first time, implicit links among siblings from a common ancestor (coalescent connectivity). We find that genetic sampling strategy is determinant to predict accurately genetic structure and that 50 % of observed genetic differentiation variance is explained by coalescent connectivity over multiple generations, significantly outperforming other models. Our results offer great promises to untangle the eco-evolutionary forces that shape sessile population structure and to anticipate climate-driven redistributions, altogether improving spatial conservation planning.

POSTER #26

Population genomics of a highly vagrant pelagic species: the blue shark, *Prionace glauca*, within the Mediterranean and North Eastern Atlantic.

Agostino Leone^{1,2}, Rafaella Franch³, Dimitrios Damalas⁴, Antonella Zanzi⁵, Emilio Sperone⁵, Primo Micarelli⁶, Fulvio Garibaldi⁷, Persefoni Megalofonou⁸, Luca Bargelloni³, Massimiliano Babbucci³, David Macias⁹, Paulo A. Prodöhl¹⁰, Marco Stagioni¹¹, Ilaria Coscia¹², Stefano Mariani¹², Sophie Arnaud-Haond², Natacha Nikolic², Fausto Tinti¹, Jann Martinsohn⁴, Alessia Cariani¹

- 1 Department of Biological, Geological and Environmental Sciences, Laboratory of Genetics and Genomics of Marine Resources and Environment, University of Bologna, via S. Alberto 163, 48123, Ravenna, Italy.
- 2 MARBEC – MARine Biodiversity Exploitation and Conservation, Ifremer, University of Montpellier, IRD, CNRS, Avenue Jean Monnet - BP 171, 34203, Sète, France
- 3 Comparative Biomedicine and Food Science, University of Padova, Viale dell'Università 16, 35020, Legnaro, PD, Italy.
- 4 European Commission, Joint Research Centre, Directorate D - Sustainable Resources, TP051, 21027, Ispra (VA), Italy
- 5 Department of Biology, Ecology and Earth Science, University of Calabria, 87036, Arcavacata di Rende, Italy.
- 6 Sharks Research Center, Aquarium Mondo Marino, 58024, Massa Marittima (GR), Italy.
- 7 Department of Earth Sciences, Environmental and Life, University of Genova, 16132, Genova, Italy.
- 8 Department of Zoology-Marine Biology, Faculty of Biology, National and Kapodistrian University of Athens, Panepistimiopolis, 15771, Ilissia, Greece.
- 9 Instituto Español de Oceanografía, Centro Oceanográfico de Málaga, Puerto Pesquero s/n, 29640, Fuengirola, Málaga, Spain.
- 10 Institute for Global Food Security, School of Biological Sciences, Queen's University Belfast, Medical Biology Centre, 97 Lisburn Road, Belfast BT9 7BL, UK.
- 11 Department of Biological, Geological and Environmental Sciences, Laboratory of Marine Biology and Fisheries, University of Bologna, Viale Adriatico, 1/n, 61032, Fano (PU), Italy.
- 12 Ecosystems and Environment Research Centre, School of Environment and Life Sciences, University of Salford, Salford, Greater Manchester, M5 4WT, UK.

Defining the population genetic structure of highly vagile species is a challenging task, and frequently the results are in conflict with those from tagging studies. This is particularly the case of big pelagic species such the blue shark, *Prionace glauca* (L. 1758). Conservation and management of Mediterranean blue sharks still suffers from a lack of knowledge regarding population structure and the dynamics of connectivity with contingents in the adjacent North-eastern Atlantic. Here, we filled in this knowledge gap by estimating the genetic diversity and differentiation of >200 blue sharks sampled across the Mediterranean, and along the Atlantic continental slope of South- and North-western Europe, based on thousands of double-digest Restriction-site Amplified DNA (ddRAD) derived single-nucleotide polymorphisms (SNPs).

SNP variation revealed low genetic differentiation overall for this large pelagic predator but significant values of F_{st} between Western and Eastern Mediterranean, and between Mediterranean and Atlantic, suggesting the occurrence of subtle but significant genetic structure across the North-eastern Atlantic and the Mediterranean. Beyond the low but significant differentiation observed, the high amount of gene flow through the Strait of Gibraltar is in contrast with long term tagging data, which suggest that the blue shark very seldom cross the Strait of Gibraltar and reproduces on the other side.

Results also suggest that the Mediterranean BS population can be considered an extension of the North-eastern Atlantic population, which is in contrast with the current stock delineation and management

This observed pattern could be explained by a marine metapopulation model, in which genetic drift and gene flow determine the dynamics of local populations strongly dependent upon local demographic processes, but also influenced by a nontrivial element of external replenishment.

These contrasting results highlight the need to integrate multidisciplinary studies to better reveals the connectivity of highly vagile species, such as the blue shark, in order to take more appropriate conservation actions.

Biochemical traces of trophic connectivity across marine protected areas in Atlantic and Mediterranean ecosystems.

López-López Lucía¹, Preciado Izaskun², Martínez Regino¹, Molina Sebastián A.¹, García Encarnación³, García Rebollo José Miguel⁴, Vivas Miguel³, Esteban Antonio³, López Eduardo⁵, García Cristina⁶, Guijarro Elena³, Sánchez Francisco², Punzón Antonio², Hidalgo M¹

1 Centre Oceanogràfic de Balears. Spanish Institute of Oceanography (IEO,CSIC). Moll de Ponent, s/n. Palma, 07014 (Spain)

2 Centro Oceanográfico de Santander. Spanish Institute of Oceanography(IEO,CSIC). Promontorio de San Martín, s/n. Santander, 39004 (Spain)

3 Centro Oceanográfico de Murcia. Spanish Institute of Oceanography (IEO,CSIC). Varadero nº 1 Apto. 22 30740 San Pedro del Pinatar (Spain)

4 Centro Oceanográfico de Cádiz. Spanish Institute of Oceanography(IEO,CSIC). Puerto Pesquero, Muelle de Levante, s/n. Cádiz, 11006 (Spain)

5 Centro Oceanográfico de Málaga. Spanish Institute of Oceanography (IEO,CSIC). P.º de la Farola, 25, 29016 Málaga (Spain)

6 Centro Oceanográfico de Vigo. Spanish Institute of Oceanography (IEO,CSIC). Subida a Radio Faro, 50-52 36390 Vigo (Spain)

Marine protected areas hold the key for preserving rare, fragile and important species and communities, which inhabit these areas because of their unique biophysical conditions. Over the continental slope, submarine canyons are oceanographically dynamic environments, promoting higher productivity than adjacent areas and giving rise to feeding grounds for a suite of predators from different feeding guilds that are often candidates for spatial protection. Here, we investigate if these areas, in addition to an increased productivity, have a signature of higher habitat quality, which could be incorporated in the food web and effectively spilt over the surrounding areas. We investigated this hypothesis in the Aviles Canyons System (ACS) in the Southern Bay of Biscay, and the Submarine Valleys of the Mazarrón Slope (SVMS), in the western Mediterranean, and compared the results from both ecosystems. We used biochemical tracers, including stable isotopes ($\delta^{13}\text{C}$, $\delta^{15}\text{N}$ and $\delta^{34}\text{S}$) and several essential fatty acids, to investigate the trophic signatures of a range of marine species with different mobility and home ranges. Based on this data, we calculated several trophic indices as the trophic level, the percentage of pelagic vs. benthic production and the relative quality of the feeding habitat. As expected, the largest individuals within each species showed the higher trophic level, but we also found the percentage of pelagic production in the diet tended to increase along the ontogeny for most of the species investigated. Comparing the Atlantic and the Mediterranean MPAs, the trophic level was generally higher in the Mediterranean, while individuals of the same species and similar size had a higher reliance of benthic trophic routes in the SVMS (Mediterranean) compared with the SCA (Atlantic). The benthic shark *Scyliorhinus canicula* was the species showing a higher variability in terms of TLs, benthic: pelagic productivity and habitat quality, demonstrating its potential as an indicator species for trophic connectivity in these systems. Our results contribute to understand the degree of trophic connectivity within and across the limits of these MPAs and, more generally, to discuss how this functional perspective could be integrated into the current monitoring and management plans of MPAs.

TALK

Selection on ancestral genetic variation fuels repeated ecotype formation in bottlenose dolphins.

Marie Louis^{1,2,3,4}, Marco Galimberti^{5,6}, Frederik Archer⁷, Simon Berrow^{8,9}, Andrew Brownlow¹⁰, Ramon Fallon¹¹, Milaja Nykänen¹², Joanne O'Brien^{8,9}, Kelly M. Roberston⁷, Patricia E. Rosel¹³, Benoit Simon-Bouhet², Daniel Wegmann^{5,6}, Michael C. Fontaine^{3,14,15,*}, Andrew D. Foote^{16,17,*}, Oscar E. Gaggiotti^{1,*}

* these authors contributed equally

- 1 Scottish Oceans Institute, University of St Andrews, East Sands, St Andrews KY16 8LB, Scotland, UK
- 2 Centre d'Etudes Biologiques de Chize, La Rochelle Universite, 17000 La Rochelle, France
- 3 Groningen Institute for Evolutionary Life Sciences (GELIFES), University of Groningen, PO Box 11103 CC, Groningen, The Netherlands
- 4 Globe Institute, University of Copenhagen, Øster Voldgade 5, 1350 Copenhagen, Denmark
- 5 Department of Biology, University of Fribourg, Fribourg, Switzerland,
- 6 Swiss Institute of Bioinformatics, Fribourg, Switzerland
- 7 National Marine Fisheries Service, Southwest Fisheries Science Center, NOAA, 8901 La Jolla Shores Drive, La Jolla, CA 92037, USA
- 8 Irish Whale and Dolphin Group, Kilrush, Co Clare, Ireland
- 9 Marine and Freshwater Research Centre, Department of Natural Sciences, School of Science and Computing, Galway-Mayo Institute of Technology, Dublin Road, H91 T8NW Galway, Ireland.
- 10 Scottish Marine Animal Stranding Scheme, Institute of Biodiversity, Animal Health & Comparative Medicine College of Medical, Veterinary & Life Sciences, University of Glasgow
- 11 School of Medicine, University of St Andrews, North Haugh St Andrews, Fife, KY16 9TF, Scotland, UK
- 12 University College Cork, Cork, Ireland
- 13 National Marine Fisheries Service, Southeast Fisheries Science Center, NOAA, 646 Cajundome Boulevard, Lafayette, LA 70506, USA
- 14 MIVEGEC, Université de Montpellier, CNRS, IRD, Montpellier, France
- 15 Centre de Recherche en Écologie et Évolution de la Santé (CREES), Montpellier, France
- 16 Molecular Ecology and Evolution Bangor, Environment Centre Wales, School of Natural Sciences, Bangor University, Bangor, UK
- 17 Department of Natural History, University Museum, Norwegian University of Science and Technology (NTNU), Erling Skakkes gate 47A, Trondheim 7012, Norway

Studying repeated adaptation can provide insights into the mechanisms allowing species to adapt to novel environments. Here, we test for repeated evolution driven by habitat specialization in the common bottlenose dolphin and investigate the genetic origins of local adaptation. Parapatric pelagic and coastal ecotypes of common bottlenose dolphins have repeatedly formed across the oceans. Analyzing whole genomes of 57 individuals, we find that ecotype evolution involved a complex reticulated evolutionary history. We find parallel linked selection acted upon ancient alleles in geographically distant coastal populations. These alleles were present at low frequencies as standing genetic variation in the pelagic populations. Candidate loci evolving under parallel linked selection were found in ancient tracts, suggesting recurrent bouts of selection through time. Therefore, despite the constraints of small effective population size and long generation time on the efficacy of selection, repeated adaptation in long-lived social species can be driven by a combination of ecological opportunities and selection acting on ancestral standing genetic variation."

TALK

Circumpolar population genomics of polar cod: connectivity in a changing ecosystem.

Sarah M. Maes¹, Henrik Christiansen¹, Enora Geslain¹, Caroline Bouchard², Bart Hellemans¹, Felix C. Mark³, Magnus Lucassen³, Franz Mueter⁴, Filip A.M. Volckaert¹, Hauke Flores³

1 KU Leuven, Laboratory of Biodiversity and Evolutionary Genomics, Charles Deberiotstraat 32, B-3000 Leuven, Belgium

2 Greenland Climate Research Centre, Greenland Institute of Natural Resources, Kivioq 2, 3900 Nuuk, Greenland

3 Alfred Wegener Institute Helmholtz Center for Polar and Marine Research, Am Handelshafen 12, D-27570 Bremerhaven, Germany

4 University of Alaska Fairbanks, College of Fisheries and Ocean Sciences, Point Lena Loop Rd 17101, AK-99801 Juneau, USA

Climate-induced changes put an increasing pressure on the Arctic marine ecosystem and its endemic species, including polar cod (*Boreogadus saida*). This ecological key species is widely distributed in both open and ice-covered waters of the Arctic Ocean and its adjacent seas. Although connectivity patterns of polar cod are largely unknown, a high level of connectivity is suggested by the low genetic differentiation across its broad geographic range. On a circumpolar scale, four groups (Europe, US, Canada East, Canada West) were previously identified with little to no geographic differentiation within these groups using microsatellite markers. Here, we present a population genomic analysis of polar cod on a circumpolar scale with thousands of single nucleotide polymorphisms. We examine large and fine-scale genetic differentiation and connectivity patterns, and screen for putatively adaptive signals. Furthermore, we assess if the genetic exchange among polar cod populations in the Arctic Ocean could be facilitated by advection of under-ice juvenile polar cod hatched on the Siberian shelf to populations in the Barents Sea, Greenland Sea and Svalbard archipelago as formulated in the Transpolar Drift hypothesis by David et al. (2016). Understanding polar cod's spatial and temporal population dynamics, population diversity and adaptive divergence is crucial for its conservation and predictions about its future distribution."

TALK

Connectivity between ecotype pairs in coastal fish inhabiting the marine-lagoon gradient.

Meyer L, Bonhomme F, Bierne N, Barry P, Guinand B, Gagnaire P-A

Abstract: Species occupying the same ecological gradient provide interesting models to study the diversity of their evolutionary responses to similar selective pressures. Fish species inhabiting the marine-lagoon gradient sometimes exhibit genetic subdivision into distinct ecotype forms showing specific adaptations to each environment. The extent to which genetic connectivity varies amongst different ecotype pairs in different species remains unknown, as well as the potential eco-evolutionary drivers of these differences. Here, we use a multi-species comparative genomics approach to describe differentiation between ecotype forms in 5 species of coastal fish. Our objective is to understand which factors determine the level of gene flow between ecotypes, including demographic, selective and architectural factors (e.g. chromosomal inversions) potentially involved in maintaining ecotypic differentiation."

TALK

Exploring connectivity in a deep-sea hydrothermal gastropod by elemental fingerprinting.

Vincent Mouchi¹, Christophe Pecheyran², Fanny Claverie², Didier Jollivet¹, Thomas Broquet¹, Thierry Comtet¹

1 AD2M - UMR 7144, Station Biologique de Roscoff, Place Georges Teissier, 29680 Roscoff (France)

2 IPREM - UMR 5254, Université de Pau, 2 avenue du Président Angot, 64053 Pau cedex 9 (France)

Connectivity in deep-sea hydrothermal vent species is still poorly described due to challenging access and sampling. As ephemeral and patchy environments, colonization and exchanges between vent populations, as well as survival and persistence of these species, require larval dispersal. Moreover, little is known on larval dispersal of vent species in terms of duration and trajectory, although physical models provide information on water mass circulation. Therefore, the spatial scale at which hydrothermal vent populations are connected remains poorly defined. Population genetic approaches

are promising, but particularly challenging in species with large population sizes because they may be genetically homogeneous regardless of their connectivity.

To fill this knowledge gap, we investigated the potential of elemental fingerprinting to infer connectivity in a vent gastropod. As the shell forms, it incorporates chemical elements from the seawater, including the larval shell that thus should reflect the specific composition of its natal site. Validating this approach first requires to estimate differences in elemental fingerprints between sites. The gastropod *Shinkailepas tollmanni* is a model of choice for such an approach as females lay capsules containing larvae that form a shell prior to dispersal, thus incorporating an elemental signature specific of their natal site.

Encapsulated veliger larvae sampled at active sites in five hydrothermal vent provinces of the Southwestern Pacific Ocean were digested to obtain cleaned shells of approximately 100 µm in diameter. Such minute size and weight (a few tens of ng) required the use of a cutting-edge analytical technique to measure the elemental composition of individual shells. A triple-quadrupole inductively-coupled plasma mass spectrometer was used with a femtosecond laser ablation system. Using linear discriminant analysis, we assessed the elemental fingerprint of a series of individual *S. tollmanni* larval shells across the western Pacific vent fields, reaching an accuracy of over 80% in recovering their natal site.

TALK

Same places, same stories: genomics reveals similar structuring patterns for four *Pocillopora* coral species in the Southwestern Indian Ocean.

Nicolas Oury¹, Stefano Mona^{2,3,4}, Didier Aurelle^{2,5,6}, H el ene Magalon^{1,4}

1 UMR ENTROPIE (UMR 9220 – Univ. R union, IRD, Ifremer, Univ. Nouvelle-Cal donie, CNRS), Universit  de La R union, St Denis, La R union, France

2 ISYEB – Institut de SYst matique,  volution, Biodiversit  (UMR 7205 – CNRS, MNHN, UPMC, EPHE),  cole Pratique des Hautes  tudes, Paris, France

3 EPHE, Universit  PSL, Paris, France

4 Laboratoire d'Excellence CORAIL, Perpignan, France

5 IMBE – Institut M diterran en de Biodiversit  et d' cologie marine et continentale (UMR 7263 – Aix-Marseille Univ., CNRS, IRD), Universit  d'Avignon, Marseille, France

6 Institut M diterran en d'Oc anologie – MIO (Aix-Marseille Univ., Univ. de Toulon, CNRS, IRD), Campus de Luminy, Marseille, France

Knowledge of seascape and population connectivity ideally forms the basis for the definition of efficient management and conservation units. This is particularly decisive for scleractinian corals, key components of coral reefs, which are experiencing critical declines attributable both to global and local pressures. Yet their connectivity remains insufficiently documented. Here, we focused on four distinct species of the coral genus *Pocillopora* that are found in various habitats (reef slope, fringing reef, flat reef and/or lagoon) of the Southwestern Indian Ocean and adopt various reproductive strategies (with or without clonal propagation). We sequence-captured Ultra-Conserved Elements (UCEs) and exon loci from over a thousand colonies, sampled in 39 sites from nine localities, from which we called and filtered Single-Nucleotide Polymorphisms (SNPs) for each species separately. From the ca. 1,400 SNPs retained per species, Bayesian clustering methods and demographic statistics and inferences were applied to first infer the population genomic structure of each species, then the genomic diversity and demographic history of each population. Although sometimes living in distinct coral habitats or presenting different reproductive strategies, all four *Pocillopora* studied species display almost exactly the same population genomic structure, reflecting the sampled ecoregions (one cluster in Madagascar and surrounding archipelagos, one or two others in the Mascarene Islands). Moreover, the four species show similar demographic signals, including in the past, with smaller effective sample sizes for the clusters restricted to the Mascarene Islands. These results indicate reduced gene flow between both

sampled ecoregions, suggesting distinct connectivity networks that should be considered independently when setting up conservation plans. They also suggest that all four *Pocillopora* species share analogous demographic history, probably because they reacted similarly to the same pressures. One could expect it to be similar under current pressures, so it seems unlikely that one species functionally replaces the others in case of irreversible decline.

POSTER #28

Mito-nuclear coadaptation in bivalves with doubly uniparental inheritance of mitochondria may rely on alternative splicing.

Eric Pante, Valentine Watteau, Sabrina Le Cam

Laboratoire Littoral Environnement et Sociétés (LIENSs), UMR 7266, CNRS-La Rochelle Université, 2 rue Olympe de Gouges, F-17042 La Rochelle Cedex 01, France

Mito-nuclear incompatibilities (MNIs) can lead to a desynchronization of the machinery required for efficient cellular energy production (oxydative phosphorylation OXPHOS). Therefore, coevolution and coadaptation of mitochondrial and nuclear genes involved in this mechanism are primordial. In species with doubly uniparental inheritance (DUI) of mitochondria such as *Limecola balthica*, both males and females are able to transmit their mitochondria, the former to all their progeny and the latter to their male offspring, where the male mitogenomes (mt) are quartered in gametes. Two highly divergent mt-genome coexist within males, likely to disrupt mito-nuclear coadaptation. RNA-seq data from somatic tissues and purified gametes from 2 males and 2 females were produced to test if mitotype-specific nuclear alleles, paralogous nuclear genes, or alternative splicing could play a role in mito-nuclear coadaptation. Differential expression profiles showed oocyte specificity but also high variability between replicates. The *atp5c1* gene coding for the gamma subunit of the ATP-synthase FO/F1 complex, presented 9 isoforms which contained overall 32 different exons. These isoforms were composed of 10 to 21 exons and were differentially expressed between sexes. Sex-specific exons were genetically very close (89.3 to 92.9 % of identity). Inferring the tertiary structure of these isoforms revealed that sex-specific exons are likely in direct interaction with a mt-encoded subunit of the ATP-synthase. These results suggest the existence of a mutually exclusive alternative splicing mechanism in the expression of *atp5c1* between males and females. Additional analyses will be performed on additional samples and the other genes involved in the OXPHOS chain to test for the presence of alternative splicing.

TALK

Modeling eelgrass connectivity in the Kattegat Sea: A graph theory approach for eelgrass restoration.

Ane Pastor^{*1}, Andrés Ospina-Alvarez², Janus Larsen¹, Dorte Krause-Jensen³, Flemming Thorbjørn Hansen⁴, Marie Maar¹

¹Department of Bioscience, Aarhus University, 4000 Roskilde, Denmark

²Mediterranean Institute for Advanced Studies (IMEDEA-CSIC/UIB), C/ Miquel Marqués 21, CP 07190 Esporles, Balearic Islands, Spain.

³Department of Bioscience, Aarhus University, Silkeborg, Denmark

⁴Section for Oceans and Arctic, Technical University of Denmark, Kemitorvet, Building 201, 2800 kgs. Lyngby, Denmark

*e-mail address: apro@bios.au.dk

The inner Danish waters have suffered from a drastic decline in eelgrass *Zostera marina* coverage during the last decades. In 1901 eelgrass meadows covered ca. 15% of all Danish marine waters, which in 1930 was reduced to less than 8% due to the wasting disease. Currently the eelgrass distribution is

very limited and restoration efforts are being planned to recover eelgrass in the coastal areas of Denmark. In the present study, we developed a hydrodynamic model within the FlexSem framework coupled to an Individual-Based model, to study eelgrass dispersal in the Kattegat Sea. Floating particles simulated the dispersal of eelgrass reproductive shoots containing seeds during the flowering season July-September. We then use the graph theory approach to analyze the connectivity and identify key areas for eelgrass restoration. Our results identify fragile nodes and edges in the network, keystone areas and important sites to restore the network of patches. This study shows the possibilities of using such approach and the importance of collaborative work between researchers and practitioners in order to understand these complex systems and restore eelgrass beds in coastal areas.

POSTER #29

Marine connectivity in the South: an ecological, molecular and modelling perspective from the tip of Africa.

Francesca Porri^{1,2}, Bernardino S. Malauene^{3,4}, Thierry Hoareau^{5,6}, David Kaplan^{7,8}, Christophe Lett^{7,8}

1 South African Institute for Aquatic Biodiversity (SAIAB), Private Bag 1015, Makhanda 6139, South Africa

2 Department of Zoology and Entomology, Rhodes University, Makhanda, 6140, South Africa

3 Instituto Nacional de Investigação Pesqueira, Av. Mao Ts'e Tung 309, Maputo, Mozambique

4 Ocean Science and Marine Food Security, Nelson Mandela University, Port Elizabeth, 6001, South Africa

5 Department of Biochemistry, Genetics and Microbiology, University of Pretoria, X20, Hatfield, 0028, Pretoria, South Africa

6 Current address: Reneco International Wildlife Consultants LLC, Al Reem Island P.O. Box 61741, Abu Dhabi, United Arab Emirates

7 MARBEC, Univ. Montpellier, CNRS, Ifremer, IRD, Sète, France

8 Institut de Recherche pour le Développement (IRD), UMR MARBEC, av. Jean Monnet, CS30171, 34203 Sète, France

Pressure on living marine species is increasingly becoming unsustainable, threatening food security for communities that rely on these resources. Understanding the scales of connectivity of coastal populations is therefore a fundamental step towards the maintenance and resilience of these important ecological assets. The degree to which barriers and corridors effectively contribute to larval dispersal and connectivity remains however undefined for many regions. Here, we review the scales of connectivity in coastal waters surrounding the southernmost tip of Africa from ~ 100 ecological, molecular and modelling scientific papers. Results highlight the existence of long-standing, large-scale barriers driven by permanent and transient oceanographic features, for both the west (Lüderitz) and east (Natal Pulse) of South Africa. The complex regional oceanography also creates corridors, crafting a southern – western connectivity for several species. Small-scale, topographically-defined currents can also create localised nearshore barriers and corridors that influence larval dispersal and hence the genetic composition of coastal populations. This blending of large and localised barriers and corridors, mixed with temporal variability, makes the connectivity in this region complex, but it also depicts some clear hydrodynamic-driven synergies. In a climate change scenario, a close dependence on hydrodynamics is likely to tweak the strength of connectivity, reflecting the urge to focus on better understanding the possible threats and help ensure the maintenance of living resources in Southern Africa.

POSTER #30

Horizontal acquisition of Symbiodiniaceae in the *Anemonia viridis* (Cnidaria, Anthozoa) species complex.

Barbara Porro¹, Thamilla Zamoum¹, Cédric Mallien¹, Benjamin C.C. Hume², Christian R.Voolstra³, Eric Röttinger¹, Paola Furla¹, Didier Forcioli¹

1 Université Côte d'Azur, CNRS, INSERM, Institute for Research on Cancer and Aging (IRCAN), 28 avenue de Valombrose, 06107 Nice, France

2 Red Sea Research Center, Division of Biological and Environmental Science and Engineering, King Abdullah University of Science and Technology (KAUST), Thuwal 23955-6900, Saudi Arabia

3 Department of Biology, University of Konstanz, Konstanz, Germany

Deciphering the mechanisms of symbiont acquisition in a holobiont is essential to understanding the extent of its adaptive capacities. In Cnidarian, some species acquire their photosynthetic symbionts directly from their parents (vertical transmission) but may also acquire symbionts from the environment (horizontal acquisition) at the adult stage. In the snakelocks sea anemone, *Anemonia viridis* (Forskål, 1775), a Mediterranean Sea anemone with vertical transmission, the capacity for such horizontal acquisition is still unexplored. To unravel the flexibility of the association between the different host lineages identified in *A.viridis* and its Symbiodiniaceae, we genotyped members of animal host clones in five different locations in the North Western Mediterranean Sea. The composition of within-host symbiont populations was more dependent on the geographical origin of the hosts than their membership to a given lineage or even to a given clone. Additionally, similarities in host symbiont communities were greater among genets than ramets. Taken together, our results demonstrate that *A. viridis* may form associations with a range of symbiotic Dinoflagellates and suggest a capacity for horizontal acquisition. A mixed-mode transmission strategy *in A.viridis*, as we posit here, may help explain the large phenotypic plasticity that characterizes this sea anemone."

INVITED TALK

Population-based recombination rates estimates to study genetic connectivity.

Marie RAYNAUD, Pierre-Alexandre GAGNAIRE, Nicolas GALTIER
ISEM, Univ Montpellier, CNRS, EPHE, IRD, Montpellier, France

Marine connectivity measurement can be improved by studying the spatial decay of DNA fragments that are identical by descent (IBD). This information can be used to assess local variation in intragenerational dispersal distance across the landscape. The size of IBD fragments depends on the speed at which recombination erodes them through the time. Recombination rates vary along the genome, and therefore this variation must be taken into account for understanding the temporal dynamics of IBD fragment size reduction. Consequently, measuring recombination rate variation along the genome is a necessary prerequisite to estimate dispersal distances from IBD segments. Recombination rates can be estimated using genome resequencing population genetic data, using a sample size of only a few dozen of individuals. After reconstruction of the haplotypic phase, population inference methods based on linkage disequilibrium (LD) can be used to infer the population-scaled recombination rate parameter, $\rho = 4Ner$. These methods produce ρ estimates of the historical recombination rates of a population, and are very convenient to study non-model species for which laboratory crosses are difficult or impossible. These LD-based approaches should thus make it possible to use IBD fragments to improve connectivity studies in marine ecosystems.

POSTER #31

Understanding connectivity of pearl oyster populations within Tuamotu atoll semi-closed lagoons: Cumulative insight from genetics and biophysical modelling approaches.

Reisser Celine^{1,2}, Andréfouët Serge³, Le Gendre Romain⁴, Thomas Yoann⁵, Lo-Yat Alain¹.

- 1 UMR EIO, IFREMER Centre du Pacifique, Unité RMPF, BP49, Vairao, Tahiti, French Polynesia
- 2 MARBEC, Univ Montpellier, CNRS, IFREMER, IRD, Montpellier, France
- 3 UMR-9220 ENTROPIE (Institut de Recherche pour le Développement, Université de la Réunion, Ifremer, CNRS, Université de la Nouvelle-Calédonie), 101, promenade Roger-Laroque Anse Vata, BP A5, 98848 Noumea, New Caledonia
- 4 IFREMER, UMR-9220 ENTROPIE, IRD, Université de la Réunion, CNRS, Université de la Nouvelle-Calédonie, Campus IRD, BP32078, Nouméa, New Caledonia
- 5 Univ Brest, CNRS, IRD, Ifremer, LEMAR, F-29280 Plouzane, France

Connectivity affects species demography, (meta)population dynamics, evolution, phylogeny and biogeography. Various methodological approaches are applied to measure connectivity. Biophysical modelling can explore systematically the influence of atmospheric, oceanic and ecological forcing, while genetics measures connectivity patterns within the sampling strategy limit. In the Pacific Ocean pearl farming lagoons, the activity relies on spat collecting of the black lipped pearl oyster *Pinctada margaritifera* occurring after the larval dispersal phase, which follows spawning from wild or farmed populations. Biophysical 3D modelling and genomic studies have both separately brought insights on within-lagoon connectivity and on the origin of spats. Here, we combined previous genetics results with new realistic biophysical modelling scenarios to elucidate connectivity in Ahe Atoll lagoon. When combined, we identified the weather sequence likely explaining the realized connectivity observations.

POSTER #32

Genomic study of the connectivity of Mediterranean deep brown algae.

Lauric Reynes¹, Thierry Thibaut², Florian Holon³, Stéphane Sartoretto⁴, Aurélie Blanfune², Myriam Valero¹, Didier Aurelle^{2,5}

1 IRL 3614, Evolutionary Biology and Ecology of Algae, CNRS, Sorbonne Université, Université Catholique,

Université Australe du Chili, Roscoff, France

2 Aix Marseille Univ, Université de Toulon, CNRS, IRD, Institut Méditerranéen d'Océanologie, Marseille, France

3 Andromède Océanologie, Montpellier, France

4 Institut Français de Recherche pour l'Exploitation de la Mer, Zone Portuaire de Brégaillon, La Seyne-sur-mer, France

5 Institut de Systématique, Evolution, Biodiversité

(ISYEB), Muséum National d'Histoire Naturelle, CNRS, Sorbonne Université, École Pratique des Hautes Études, Paris, France

Dispersal is a central process that affects population growth, gene flow, and ultimately species persistence. Here we investigate the extent to which gene flow occurs between fragmented populations of the deep-water brown algae *Ericaria zosteroides* (Turner) Greville (Sargassaceae, Fucales). These investigations were performed at different spatial scales from the bay of Marseille (western Provence) to Corsica. As dispersal of zygotes is shown to be limited over distances beyond a few meters, we used a multidisciplinary approach, based on Lagrangian modeling and population genomics to test the hypothesis that drifting of fertile parts of thallus (eggs on fertile branches), mediated by ocean currents, enable occasional gene flow between populations. Therefore, we assessed the respective contribution of oceanographic connectivity, geographical isolation, and seawater temperatures to the genetic structure of this species. The genetic structure was assessed using 10,755 neutral SNPs and 12 outlier SNPs genotyped by dd-RAD sequencing in 261 individuals of *E. zosteroides*. We find that oceanographic connectivity is the best predictor of genetic structure, while differentiation in outlier SNPs can be explained by the depth of populations, as emphasized by the minimum seawater temperature predictor. However, further investigations will be necessary for

clarifying how depth drives adaptive genetic differentiation in *E. zosteroides*. Our analyses revealed that local hydrodynamic conditions are correlated with the very high divergence of one population in the Bay of Marseille. Overall, the levels of gene flow mediated by drifting were certainly not sufficient to counteract differentiation by local genetic drift, but enough to allow colonization several kilometers away. This study stresses the need to consider secondary dispersal mechanisms of presumed low dispersal marine species to improve inference of population connectivity.

POSTER #33

Population structure of the last untouched natural stock of flat Oysters (*Ostrea edulis*).

Chloé Robert¹, Homère J. Alves Monteiro², Åsa Strand³, Jakob Hemmer Hansen², Pierre De Wit¹

1 Gothenburg University

2. DTU Aqua

3. IVL Svenska Miljöinstitutet

The flat oyster *Ostrea edulis* is a native European species whose populations have declined in the past decades. These bivalves are extensively used in aquaculture, involving moving stocks between different countries, which potentially affect wild populations by genetic contamination from escapes. The Swedish populations have historically been protected from fishing and no translocation between different stocks have been documented, thus can be seen as the last untouched stock of European flat oysters. These Scandinavian populations are unique, but remain so far understudied. We have gathered low coverage whole genome sequencing data from twenty flat oyster populations in Skagerrak and Kattegat. We will present preliminary results and ideas for future analyses that will be performed to explore the connectivity among the Scandinavian populations of flat oysters. "

TALK

Another kind of connectivity: Estimating the environmental footprint of a coal mine project on nearby marine ecosystems in the Great Barrier Reef.

Antoine Saint-Amand¹, Alana Grech², Severine Choukroun², Emmanuel Hanert¹

1 Earth & Life Institute, UCLouvain, Louvain-la-Neuve, Belgium

2 ARC Centre of Excellence for Coral Reef Studies, James Cook University, Townsville, Australia

The Great Barrier Reef (GBR) is more than ever threatened by multiple stressors such as global warming, ocean acidification, tropical cyclones, etc. These global stressors are further compounded with local stressors such as coastal development. Recently, a new coal mine project has been proposed near Broad Sound bay, less than 10 km from the GBR World Heritage Area. This controversial project has been the object of several environmental impact assessments. However, the dispersion of sediments released by mining activities in Broad Sound bay has never been properly assessed. Here we show that sediments released from the mine would be directly connected to ecologically sensitive areas such as sea turtle nesting beaches, dense seagrass meadows and a dugong sanctuary. Those sediments could reach the GBR World Heritage Area through two rivers flowing around the coal mine and into Broad Sound. To evaluate the presence and the strength of those connections, we simulate the dispersal of sediments of various diameters thanks to the high-resolution hydrodynamic model SLIM. Sediments are released in the rivers and are then tracked for three months. The resulting sediment plumes are overlaid with ecologically sensitive receptor sites to derive the overall environmental footprint of mining activities on the neighboring marine ecosystems. Our results show that the intense tidal circulation within Broad Sound leads to non-isotropic and non-local sediment dispersion patterns that are concentrated in the western part of the bay. The resulting environmental footprints reach dugong feeding grounds and turtle nesting beaches more than 30 km away from the

river mouth. Our results suggest that this coal mine project, if accepted, would have a far-reaching impact on the GBR World Heritage Area and its iconic marine species.

POSTER #34

Comparative phylogeographic analysis of four mesopelagic fishes reveals different patterns of connectivity between the Greek Seas.

Sarropoulou X.¹, Tsaparis D.¹, Tsagarakis K.², Badouvas N.², Tsigenopoulos C. S.¹

1 Institute of Marine Biology, Biotechnology and Aquaculture, Hellenic Centre for Marine Research, 71003, Heraklion, Greece

2 Institute of Marine Biological Resources and Inland Waters, Hellenic Centre for Marine Research, 19013, Anavyssos, Greece

Mesopelagic fish constitute the most abundant group of vertebrates in the marine environment. Despite their unique biological and ecological traits, these species still remain largely understudied. The present study investigates the genetic diversity of four mesopelagic fishes (*Hygophum benoiti*, *Maurolicus muelleri*, *Benthoosema glaciale*, *Myctophum punctatum*) in the Greek Seas. Analyses of three mitochondrial genes (COI, 12S, 16S) from a total of 166 samples revealed a lack of genetic structure for *M. muelleri*, *B. glaciale* and *M. punctatum* across the studied area. However, *H. benoiti* specimens from the Corinthian Gulf were differentiated from the rest of the populations, suggesting that the limited connection between the Corinthian and neighboring seas may act as a barrier to gene flow. Furthermore, the observed shallow haplotype genealogy (high haplotype and low nucleotide diversity) in association with the significant number of low frequency private haplotypes can be considered as the result of the recent evolutionary history of these species in the Greek Seas."

TALK

Mitochondrial haplotypes reveal low diversity and connectivity in a critically endangered batoid population residing in a Scottish Nature Conservation Marine Protected Area.

Tanja N. Schwanck¹, Lili F. Vizer¹, James Thorburn², Jane Dodd³, Peter J. Wright⁵, David W. Donnan⁶, Leslie R. Noble^{1,7}, Catherine S. Jones¹

1 School of Biological Sciences, University of Aberdeen, Aberdeen AB24 2TZ, UK

2 Scottish Oceans Institute, University of St. Andrews, St. Andrews KY16 9AJ, UK

3 Scottish Natural Heritage, Cameron House, Oban PA34 4AE, UK

5 Marine Scotland Science, Marine Laboratory, 375 Victoria Rd, Aberdeen AB11 9DB, UK

6 Scottish Natural Heritage, Battleby, Redgorton, Perth PH1 3EW, UK

7 Faculty of Biosciences and Aquaculture, Nord University, Bodø, Norway

The stability and long-term persistence of a species relies heavily on its genetic diversity and gene flow between populations. Despite the association of marine animals with high dispersal capability, their populations can become fragmented and isolated for a myriad of reasons, including population declines caused by overfishing and bycatch. Genetic assessments of variability and population admixture of threatened animals can provide information crucial to the design of efficient conservation management. While the critically endangered flapper skate *Dipturus intermedius* receives extensive protection in the Loch Sunart to the Sound of Jura Nature Conservation Marine Protected Area (MPA) in Scotland, there is insufficient knowledge of genetic diversity across its range to ensure measures are sustaining the animal's existing genetic diversity and therefore its adaptive capabilities. Recent tagging studies in the MPA show it to be a mix of site attached (resident) and transient individuals, which raises concerns of restricted connectivity to populations outwith the MPA. Using a newly developed haplotype marker located in the mitochondrial DNA (mtDNA), this study used DNA sourced from fin

clips, mucus, and egg cases to investigate population structure and mitochondrial variability across several sites in the Northeast Atlantic, including the MPA. Extremely low haplotype diversity was revealed in the MPA, and what appears to be an almost exclusive haplotype, with significant population differentiation between the MPA and other sites. This apparent lack of admixture and likelihood of site fidelity in the population needs to be considered when evaluating and adapting flapper skate management measures. To better understand the population structure and potential isolation risks for the long-term persistence of the flapper skate, the contemporary connectivity of these sites is being analyzed further using nuclear markers."

POSTER #35

Juvenile movements in the yellow-legged gull (*Larus michahellis*) in relation to the natal colony.

Charly Souc^{1,2}, Thomas Blanchon², Marion Vittecoq^{2,3}, Rémi Choquet⁴, Karen McCoy^{1,3}

1 MIVEGEC, University of Montpellier-CNRS-IRD, Centre IRD, Montpellier, France.

2 Tour du Valat, Research Institute for the Conservation of Mediterranean Wetlands, Arles, France

3 Centre for Research on the Ecology and Evolution of Diseases (CREES), Montpellier – France

4 CEFE, University of Montpellier-CNRS-EPHE-IRD-Université Paul Valéry Montpellier, Montpellier, France,

The yellow-legged gull (*Larus michahellis*) is a common seabird species around the Mediterranean coast, well adapted to exploit human-associated resources. As this species can carry a range of infectious agents, some of specific public health concern, understanding its movement ecology can provide essential information for predicting disease risk and pathogen emergence. This study aimed to characterize movement in this species using a multi-event mark-recapture modeling framework. The data included the encounter histories of 5158 birds marked at fledging between 1999 and 2004 at 14 colonies in southern France and resighted for 10 years. Our results show that young individuals have a greater mobility than older ones; 53% of juveniles are migratory during the non-breeding period and move to areas more than 50 km from the natal colony compared to only 24% in older birds that return to the breeding colony. However, the spatial extent of juvenile movements depends on colony location, with a 45% difference in the proportion of sedentary individuals between colonies 50 km apart. These differences may be explained by colony quality or population dynamics. Indeed, young birds from colonies with strong juvenile survival probabilities (~0.75) appear to be more sedentary than those from colonies with low survival probabilities (~0.36). These results indicate that young birds are likely to frequent areas where exposure to pollutants is different from that of adults. These young birds are also likely to be more important dispersers of avian disease than older birds, and this propensity may be conditioned by local reproductive success, which may itself depend on the presence of parasites/pathogens and pollutants.

POSTER #36

Comparative seascape genomics at the local scale: marine mollusks of the Cretan coasts.

Loukia Spilani^{1,2}, Elena Sarropoulou², Aglaia Antoniou²

1 Biology Department, University of Crete, Greece

2 Institute of Marine Biology, Biotechnology and Aquaculture, HCMR, Crete, Greece

Marine invertebrates of coastal ecosystems, which are among the most highly threatened systems in the world, are key elements that face severe challenges while living in one of. Despite the occurrence of climatic change at a global scale, ecological impacts are often local, varying from place to place and confronted differently by each organism impeding successful generalizations on responses. Marine mollusks display various levels of phylogeographic and population genetic patterns, reflecting their life

history traits mostly related to development (direct versus indirect, lecithotrophic versus planktotrophic larvae) and/or responses to environmental pressures (local adaptation). In an attempt to disentangle the effects of life history traits from the environmentally induced adaptation, a comparative seascape genomics framework was employed. The genomic patterns of two marine mollusks (murex, *Hexaplex trunculus* and the abalone *Haliotis tuberculata*) with distinct developmental characteristics, which affect their dispersal abilities, and similar geographical distribution along the coastal ecosystems of the island of Crete (Greece) were studied by ddRAD genome-wide SNPs within the context of genetic - environmental association. Levels of population structure were distinct among the studied taxa complying to the species life history traits with the abalone having a pelagic larval stage, albeit short, and a high level of admixture and the murex having an intracapsular development and being highly structured. In both species a certain number of loci was detected with allelic frequencies that co-variated with environmental variables used in this study, interpreted as signals of local adaptation. Environmental variables that co-varied with most outlier loci differed between the species.

POSTER #37

Clutch relocation and shorter incubation duration impact morphology and fitness of the green sea turtle *Chelonia mydas*.

Steenacker Marion, Tanabe Lyndsey K., Rusli Mohd Uzair & Fournier Denis
Université libre de Bruxelles (ULB), Evolutionary Biology & Ecology, Brussels, Belgium
King Abdullah University of Science and Technology (KAUST), Thuwal, Kingdom of Saudi Arabia
Sea Turtle Research Unity (SEATRU), Institute of Oceanography and Environment, Universiti Malaysia Terengganu, Malaysia

The carapacial scute pattern of sea turtles is a conserved trait that provides taxonomic information. But non-modal scute patterns (NMSPs), i.e. intraspecific individual variabilities, are observed for almost all species and occur relatively often, particularly in hatchlings. These NMSPs could be associated with a reduced fitness and a lower survival rate of individuals. To better gauge their effects, we surveyed 156 clutches from 101 nesting green sea turtle females (*Chelonia mydas*) over an eight-week study duration on Redang Island, Malaysia. For a subsample of 67 nests, we collected 1,144 newly emerged hatchlings and compared their scute patterns, carapace size, mass, and their locomotor performances (self-righting ability, running and swimming speeds). We compared the scute pattern of hatchlings with the one of their mothers and found no link suggesting a significant maternal origin effect on scute pattern abnormalities. However, we found that short incubation duration (i.e. high incubation temperatures) and management techniques are the main drivers of scute pattern abnormalities and hatching success. Eggs hatched after a short incubation period and/or eggs that were relocated have a greater propensity to produce non-modal hatchlings. The proportion of hatchlings with NMSP in a nest is negatively correlated to the hatching success. Hatchlings that have been relocated, regardless of their scute patterns, are those with the lowest locomotor performances. Our work highlights the effects of incubation duration and invasive techniques on morphology and fitness of green turtle hatchlings and contributes to better informed management strategies as part of global research efforts to preserve an endangered species. Based on our findings we suggest applying clutch relocation exclusively to doomed nests.

TALK

Evaluating movement and population dynamics of meagre (*Argyrosomus regius*) using an interdisciplinary approach.

Susanne E. Tanner^{1,2}, Patrick Reis-Santos^{1,3}, Carlos M. Alexandre⁴, Ana Rita Almeida¹, Pedro R. Almeida^{4,5}, M. Judite Alves^{6,7}, M. Clara P. Amorim^{2,8}, José L. Costa^{1,2}, Isabel Domingos^{1,2}, Paulo J. Fonseca^{2,7}, André Jorge⁴, Maria João Lança^{9,10}, João Pedro Marques⁴, Catarina S. Mateus⁴, Nuno Prista¹¹, Marco Silva¹², Yorgos Stratoudakis¹³, Manuel Vieira^{2,7,8}, Bernardo Quintella^{2,4}

1 MARE – Marine and Environmental Sciences Centre, Faculdade de Ciências, Universidade de Lisboa, Lisbon, Portugal

2 Departamento de Biologia Animal, Faculdade de Ciências, Universidade de Lisboa, Lisbon, Portugal

3 Southern Seas Ecology Laboratories, School of Biological Sciences, The University of Adelaide, Adelaide, Australia

4 MARE – Marine and Environmental Sciences Centre, Universidade de Évora, Évora, Portugal

5 Departamento de Biologia, Escola de Ciências e Tecnologia, Universidade de Évora, Évora, Portugal

6 Universidade de Lisboa, Museu Nacional de História Natural e da Ciência, Lisbon, Portugal

7 CE3c - Centro de Ecologia, Evolução e Alterações Ambientais, Faculdade de Ciências, Universidade de Lisboa, Lisbon, Portugal

8 MARE – Marine and Environmental Sciences Centre, ISPA, Lisbon, Portugal

9 Departamento de Zootecnia, Escola de Ciências e Tecnologia, Universidade de Évora, Évora, Portugal

10 MED - Mediterranean Institute for Agriculture, Environment and Development, Departamento de Zootecnia, Escola de Ciência e Tecnologia, Universidade de Évora, Évora Portugal

11 Swedish University of Agricultural Sciences, Department of Aquatic Resources (SLU Aqua), Institute of Marine Research, Lysekil, Sweden

12 LAQV, REQUIMTE, Departamento de Química-Faculdade de Ciências e Tecnologia, Universidade NOVA de Lisboa, Caparica, Portugal

13 IPMA – Instituto Português do Mar e da Atmosfera, Lisbon, Portugal

Meagre (*Argyrosomus regius*) forms ephemeral spawning aggregations, which due to their large size and the species' high commercial value, lead to an increased risk of overexploitation. Data paucity together with the inability to apply classical fisheries assessment techniques and management measures due to the seasonally elusive dynamics of adult meagre, and the diffuse nature of artisanal fishing pressure, call for innovative alternatives that can inform fisheries management and safeguard the reproductive resilience of this iconic species. Here, we use an interdisciplinary approach combining a variety of techniques, ranging from molecular to behavioral tools. Molecular markers are used to assess population structure of meagre throughout its distribution range, with emphasis on the stocks associated with Portuguese estuaries. Genetic population structure is complemented by fatty acid composition of heart tissue phospholipids, a promising tool to assess population structure at small spatial scale. Otolith chemistry of meagre is used to reconstruct ontogenetic migration patterns and to determine natal or nursery origin of adults. Acoustic tags are used to study the movement patterns of juvenile and adult meagre, particularly to understand the use of estuaries as spawning and nursery habitats and to track movements along the Portuguese Coast. The distinct sounds produced by meagre are used in passive bioacoustics monitoring to delimit spawning aggregations and describe their dynamics within estuaries. This multifaceted approach aims to explore spatial population structure and assess connectivity at different spatiotemporal resolutions, and thus provide essential information for the sustainable management of meagre fisheries."

TALK

Do Alternative Dispute Resolution (ADR) and Track Two Processes Support Transboundary Marine Conservation? Lessons from six case studies of maritime disputes.

Yael Teff-Seker, Peter C Mackelworth, Tomás Vega Fernández, John McManus, Jungho Nam, Arthur Tuda, Drasko Holcer

Yael Teff Seker <yaelteff@gmail.com>

Peter Mackelworth <peter.mackelworth@gmail.com>

Tomas Vega Fernandez <tomas.vegafernandez@szn.it>
John McManus <mcmanus.john@gmail.com>
Jungho Nam <jhnam@kmi.re.kr>
Arthur Tuda <tudahke@yahoo.com>
Draško Holcer <drasko.holcer@hpm.hr>

Abstract: By definition, marine protected areas (MPAs) and other effective area-based conservation measures (OECMs) address spatial aspects of the ecological processes and marine features. Such a requirement is especially challenging in areas where there is no clearly defined jurisdiction. However, in these areas, assigning sovereignty and rights can be achieved through bilateral or multilateral agreements, or with the use of alternative dispute resolution (ADR) tools such as mediation and arbitration. In some cases, states may engage in transboundary marine conservation initiatives to provide an entry point to enable wider collaboration. These processes can also evolve into a form of 'environmental peacebuilding' while ideally maintaining ecosystem functioning and resilience as a core goal. Conversely, MPAs and OECMs can also be used to assert maritime sovereignty rights over disputed waters, under the pretext of conserving marine habitats.

This paper identifies emerging issues of conflict resolution and their interaction with transboundary marine conservation. While ADR focuses on negotiations and facilitated processes between state representatives ("track one diplomacy"), we also discuss other forms and levels of marine environmental peacebuilding and dispute resolution, particularly those between civil society organizations ("track two diplomacy"). The six case studies presented highlight areas of recent maritime conflict or border disputes in the Mediterranean Sea, the Red Sea, the West Indian Ocean, the Korean West Sea and the South China Sea. In all cases, high ecological value, vulnerable ecosystems, and the need to conserve ecosystem services provide a shared interest for cooperation despite on-going diplomatic difficulties.

The strategies used in these cases are analyzed to determine what lessons might be learned from cross-border collaborative marine initiatives in situations of territorial dispute. The use of ADR tools and their ability to support joint marine initiatives are examined, as well as how such initiatives contribute to formal border negotiations. Other forms of inter-state dialogue and cooperation between local or civil organizations, circumventing formal treaties and negotiations between state leaders ('track two') are also investigated. Finally, other influencing factors, including third-party involvement, stakeholder interests, power dynamics, economic context, and socio-cultural aspects, are considered."

TALK

Genome-wide analyses outline patterns of homogeneity and divergence of the deep-sea hydrothermal gastropod *Ifremeria nautiliei* but outlier loci reveal subtle limits to connectivity.

Adrien Tran Lu Y, Claire Daguin-Thiébaud, Stéphanie Ruault, Jade Castel, Pierre-Alexandre Gagnaire, Nicolas Bierne, Sophie Arnaud-Haond, Patrick Wincker, Aude Perdereau, Didier Jollivet, Stéphane Hourdez, François Bonhomme

CNRS, ISEM– Montpellier (France), adrien.tran-lu-y@umontpellier.fr

CNRS, SBR-Roscoff (France), daguin@sb-roscoff.fr

CNRS, SBR-Roscoff (France), stephanie.ruault@sb-roscoff.fr

CNRS, SBR-Roscoff (France), jade.castel@sb-roscoff.fr

CNRS, ISEM-Montpellier (France), pierre-alexandre.gagnaire@umontpellier.fr

CNRS, ISEM-Montpellier (France), nicolas.bierne@umontpellier.fr

Ifremer, Sète (France), sophie.arnaud-haond@umontpellier.fr

Genoscope, pwincker@genoscope.cns.fr

Genoscope, aperdere@genoscope.cns.fr

CNRS, SBR-Roscoff (France), jollivet@sb-roscoff.fr

CNRS, OOB-Banyuls-sur-Mer (France), hourdez@obs-banyuls.fr

CNRS, ISEM-Montpellier (France), francois.bonhomme@umontpellier.fr

Hydrothermal vents form archipelagos of ephemeral deep-sea habitats that are of great interest to understand the dynamics and evolution of their endemic fauna, which repeatedly recolonize active vents as soon as they appear. These metal-rich environments have also raised an appetite for their mineral resources formed by hydrothermal fluid circulation, raising recent conservation concerns. The evolutionary fate and demographic resilience of hydrothermal species strongly depend on the connectivity level of their fragmented metapopulations. In the deep sea, however, assessing connectivity is difficult and usually requires indirect genetic approaches. Improved detection of fine-scale genetic connectivity is now permitted using genome-wide screen for genetic differentiation. In the present study, we explored population connectivity in the hydrothermal vent snail *Ifremeria nautiliei* over the species range encompassing five distinct back-arc basins in the south-west Pacific. The global analysis based on 10 570 RAD-seq markers depicts two semi-isolated highly homogeneous genetic clusters. Demo-genetic modelling suggests that these two groups began to diverge about 70 000 generations ago, yet they still exhibit weak and asymmetrical gene flow. Furthermore, a careful analysis of outlier loci showed subtle limitation to connectivity between neighboring basins within both groups. This finding indicates that migration is not strong enough to totally counter-balance drift or local selection, hence questioning the potential for demographic resilience at this geographical scale.

TALK

Population Genetics and Phylogeographic Studies for the Identification of Biological Units for two fish and four crustacean species in the Mediterranean Sea: the MED_UNITS project.

C. Tsigenopoulos¹, R. Cannas², L. Zane², I. Marino², A. Cariani², F. Maroso², T. Manousaki¹, D. Tsaparis¹, R. Franch², S. Iori², L. Bargelloni², R. Melis², L. Carugati², R. Corti², A. Ferrari², F. Piattoni², E. Piazza², F. Tinti², V. Terzoglou¹, K. Ekonomaki¹, A. Tsakogiannis¹, M. T. Spedicato³

1 Hellenic Centre for Marine Research (HCMR), Greece

2 Consorzio Nazionale Interuniversitario per le Scienze del Mare (CoNISMa), Italy

3 COISPA Tecnologia & Ricerca, Italy

The principal “MED_UNITS” project’s objective was to identify biogeographical boundaries and population structure in six of the most important demersal species in the Mediterranean, included also among the priority species at GFCM level, namely the European hake (*Merluccius merluccius*), red mullet (*Mullus barbatus*), deep water rose shrimp (*Parapenaeus longirostris*), giant red shrimp (*Aristaeomorpha foliacea*), blue and red shrimp (*Aristeus antennatus*) and Norway lobster (*Nephrops norvegicus*). The study covered these stocks in the waters of the Mediterranean Sea’s Geographical Sub-Areas (GSAs) and investigated connectivity among and within sub-basins, thanks also to great support for the collection of samples from the FAO Regional Projects.

We first performed a literature review regarding the genetic structure of the 6-target species in the Mediterranean and Black Sea, contributing to identify biogeographical boundaries and population structure of the target species as well as a systematic and comprehensive review to illustrate the state of the art of the bioinformatics and genetic methods and tools used for stock identification and boundaries delimitation in fisheries. Then, a genetic sampling design was implemented which led to 210 sites and more than 10,000 specimens from 22 GSAs sampled for the genetic studies at the end of the project. However, only high molecular weight DNA samples (more than 7,500) were included in Double digest restriction-site associated DNA (ddRAD) library preparations and sequencing protocols with the majority of them successfully genotyped. More detailed phylogeographic analysis of the data will be presented and discussed for all species which finally showed different connectivity patterns. Last, we warmly acknowledge the EU Commission, DG MARE and CINEA together with the partner institutions involved in this project under the Tender EASME/EMFF/2016/032 for their financial support.

POSTER #38

The Invasion pathway, colonization and connectivity of lionfish (*Pterois miles* and *Pterois volitans*) in the Mediterranean.

Cemal Turan*, Servet Ahmet Dođdu, Mevlüt Gürlek, Deniz Ergüden
Molecular Ecology and Fisheries Genetics Laboratory, Department of Marine Sciences,
Marine Science and Technology Faculty, Iskenderun Technical University, Iskenderun,
Hatay, Turkey
*cemal.turan@yahoo.com

The widespread invasion of lionfish (*Pterois miles*) in the eastern Mediterranean and the western Atlantic Ocean has revealed that it is a successful invader and can have destructive effects on native species, having indirect ecological outcomes and economic effects on regional fisheries, tourism, and human health. In the present study, mtDNA cytochrome c oxidase subunit 1 (COI), cytochrome b, and 16S rRNA genes of lionfish from Turkish marine waters as well as sequence data from the whole distribution of the species including the Mediterranean, Atlantic Ocean, and the Pacific Ocean were analyzed to reveal invasion pathway, colonization and bottleneck effect, and connectivity of lionfish.

POSTER #39

Evaluation of the connectivity between shallow and mesophotic coral reefs in the United States Virgin Islands.

Constance Vandendorpe
constance.vandendorpe@uclouvain.be

Worldwide coral reefs being increasingly impacted by anthropogenic disturbances, identifying areas that can offer protection has become a priority. The Deep Reef Refugia Hypothesis states that mesophotic reefs (light-dependent reefs found between 30m and 150m) can act as substantial source of larvae for shallower reefs after a disturbing event. In this study, we assess the larval contribution of mesophotic *O. faveolata* habitats to shallow reefs in the northern USVI through late summer 2016, by the means of a biophysical model. In particular, we reproduce the study of Holstein et al. [2015] at a smaller habitat spatial scale with different modeling tools. To do so, we coupled the multi-scaled ocean model SLIM3D with a particle transport model. The resulting connectivity network was analyzed by the means of one-generational and multi-generational connectivity indicators. Our results suggest that more than half of the *O. faveolata* larvae arriving at shallow depths after the spawning event of August 2016 were spawned over mesophotic reefs. More specifically, most of these mesophotic larvae that could help repopulate shallow reefs originate from highly productive mesophotic reefs found between 30 and 40m depth. The deepest mesophotic habitat (40 - 50m depth) has the potential to act as a multigenerational corridor and thus increase the resilience of the entire coral reef network. All of this shows that mesophotic reefs can constitute significant sources of larvae for shallow reefs over several generations in the northern USVI. Despite some differences, Holstein et al. [2015] study and ours point towards the same direction, according to which mesophotic reefs have to be considered as a significant source of larvae for shallow reefs. While it has some limitations, the quantitative approach presented in this work has the potential to inform marine conservation in order to optimize resource allocation. We classified the reefs that constitute big exporters or that are part of multigenerational corridors as good candidates for restoration and localized them. The reefs north of St. Thomas have a high centrality value and are thus among the most important stepping stones for multigenerational larval connectivity. In the same way, big exporters found offshore at the south of St. Thomas have an important role regarding to the resilience of the network. Those reefs are however not part of any

conservation program. Our results suggest that they should be a target of future management actions."

POSTER #40

Investigating kinship in an aggregating small benthic shark, the spurdog, *Squalus acanthias*.

Fenella R. Wood¹, Tanja N. Schwanck¹, James Thorburn², Andrew Meharg³, Leslie R. Noble⁴, Catherine S. Jones¹

1 School of Biological Sciences, University of Aberdeen, Aberdeen AB24 2TZ, UK

2 Scottish Oceans Institute, University of St. Andrews, St. Andrews KY16 9AJ, UK

3 Biological Sciences, Queens University Belfast, Belfast, BT9 5DL, UK

4 Faculty of Biosciences and Aquaculture, Nord University, Bodø, Norway

Spurdog are a wide-ranging, highly mobile, small shark found in temperate seas across the globe. Once a commercially important species they experienced severe declines and are now listed as 'Endangered' in the Northeast Atlantic (IUCN red list). Since a zero total allowable catch was imposed in 2010, there have been positive indications of increasing population size, leading to discussions about reopening a limited spurdog fishery. However, as an aggregating species the catch can be large when spurdog are caught by commercial fisheries, as either target or bycatch. This can impact population size, with subsequent effects on genetic diversity. Previous research suggests aggregations may contain closely related individuals (perhaps sibships) and loss of such kin groups erodes selectable genetic diversity rapidly. Hence, understanding the origin of kinships and their biological characteristics within aggregations is crucial to assess the potential impact of their removal by fishing or bycatch on population sustainability. To better understand the biology of kinships, the extent of family relationships are being investigated within a biologically characterized spurdog aggregation caught in a single trawl net as bycatch off the coast of the Scilly Isles. Nuclear DNA markers are being used to identify 1st and 2nd order relatives within the aggregation, and to assess overall relatedness.