Book of Abstracts

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Advancing research for improved management

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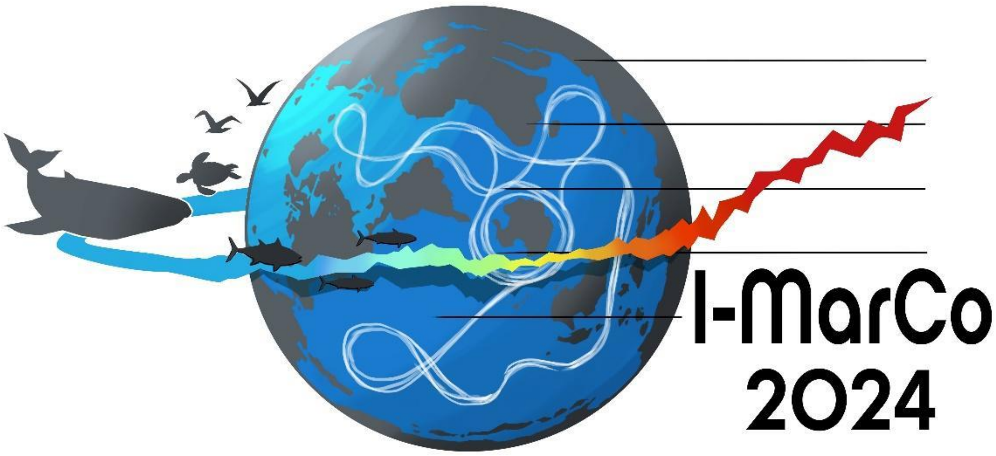
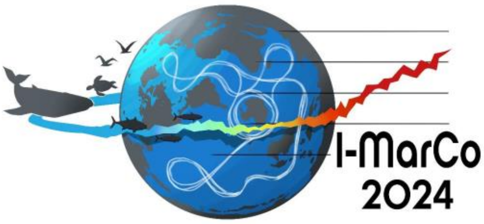


Session 1

Multi-disciplinary approaches in Marine Functional Connectivity research



Conveners:

Katell Guizien (France)
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Anna Sturrock (UK)
Susanne Tanner (Portugal)
Filip Volckaert (Belgium)

Session 1

Keynote

Oscar Gaggiotti

Marine Connectivity: Opening the black box of marine ecology using all available sources of information

Oscar E. Gaggiotti*,
Centre for Biological Diversity, University of St Andrews, UK

Connectivity, broadly defined as the exchange of individuals among local populations, is one of the main drivers of the persistence and resilience of populations and influences the extent to which species can adapt to local conditions. Its understanding is essential for effective spatial management and design of protected areas. However, marine species pose difficult challenges because of their complex life histories and the limitations of the individual methodologies currently used to infer connectivity. The most popular techniques include genetic markers, geochemical signatures of calcified structures and biophysical models. Most studies use a single methodology or ad-hoc methods aimed at evaluating the congruence of two different approaches. I will present a framework to overcome current limitations by simultaneously harnessing the leading empirical methods in connectivity research and rigorously integrating the independent datasets they generate to increase the statistical power for quantifying demographic connectivity in even the most challenging marine species.

LOCAL-SCALE CONNECTIONS AND LARVAL COMPETENCY STRONGLY INFLUENCE FUNCTIONAL CONNECTIVITY AND MARINE METAPOPULATION DYNAMICS

Treml Eric A. *[1]
1. Australian Institute of Marine Science (AIMS) and UWA Oceans Institute, The University of Western Australia, Crawley, WA, Australia

The relationship between metapopulation persistence and connectivity has long been studied, yet rarely explored in complex real-world seascapes. Understanding this relationship, and the influential physical and biological drivers, is essential in managing all marine metapopulations and minimising the impacts of climate change. Here we quantify the impact that local connectivity and larval life history have on metapopulation persistence across several complex seascape in Australia and the Indo-Pacific. Our work combines network-based approaches, Eigenanalysis, and metapopulation modelling to efficiently estimate persistence, as well as the patch-level contributions. Biophysical larval dispersal models were used to quantify species-specific metapopulation connectivity for a variety of benthic invertebrate and fisheries species. Network analysis and Eigenanalysis helped quantify regional and global persistence and determine the unique importance of individual sub-populations and communities. Across species and across seascape, the number of local outgoing connections was found to have one of the largest impacts on local persistence, implying these strong connectivity hubs may be the most influential for real-world metapopulation dynamics and regional persistence. Results also suggest the length and characteristics of the pre-competency period may be critical in accurately estimating local retention and metapopulation persistence in complex seascapes. Finally, we highlight important knowledge gaps that are inhibiting our capacity to identify the most ecologically relevant and geopolitically feasible locations for management actions.

PLASTICITY IN MOVEMENT BEHAVIOUR OF EUROPEAN FLOUNDER INFERRED BY OTOLITH CHEMISTRY AND GENETICS

Tanner Susanne E. *[1], Ferreira-Araújo Thais [2], Kemppainen Petri [3], Gillanders Bronwyn M. [4], Momigliano Paolo [3], Reis-Santos Patrick [4]
1. MARE - Marine and Environmental Sciences Centre/ARNET - Aquatic Research Network Associated Laboratory, Department of Animal Biology, Faculty of Sciences, University of Lisbon, Lisbon, Portugal
2. Faculty of Biological and Environmental Sciences, University of Helsinki, Helsinki, Finland
3. School of Biological Sciences, Faculty of Science, The University of Hong Kong, Hong Kong
4. Southern Seas Ecology Laboratories, School of Biological Sciences, The University of Adelaide, Adelaide, Australia

Plasticity in life-history traits allows species to adapt to varying conditions throughout their distribution range as well as to stochastic variations in local environments. Furthermore, it can increase species' adaptation potential to rapidly changing environmental conditions and resilience to exploitation. European flounder (*Platichthys flesus*) is known to exhibit plasticity in several traits, including differential movement behaviours along the marine-freshwater gradient. Here, we used otolith core-to-edge chemical profiles (Mg:Ca, Mn:Ca, Sr:Ca and Ba:Ca) and genetic markers (SNP markers) to investigate movement patterns and genetic diversity of adult and sub-adult flounder sampled near the northern limit of its distribution in a freshwater lake and two nearby fjords. Otolith chemical transects showed several distinct patterns including life history profiles of freshwater and marine residents and migrants. A time-series clustering algorithm identified clearly distinct clusters from the life history profiles of otolith chemistry. Genetic data provided evidence for weak genetic differentiation between lake and fjord samples. The majority of fish from the lake showed genotypes with no admixture to neighbouring populations, while the remaining lake and fjord samples showed admixed genotypes. Integrating information from both markers suggested that part of the lake flounder are residents in freshwater and may even spawn there given the non-admixed genotypes, however for several individuals from the lake and the fjords the information obtained using the two markers is contradictory (e.g., otolith freshwater signature and admixed genotype). Different scenarios potentially explaining the observed movement patterns and genetic differentiation as well as implications on individual growth are explored.

METHODOLOGICAL ADVANCES IN THE STUDY OF ACTIVE DISPERSAL ABILITIES OF REEF FISH LARVAE

Ruiz Eliot *[1], Thomas Raphaël [2], Barrier Nicolas [1], Cordonnier Sébastien [2], Rault Pierre-Louis [2], Chatagnon Amélia [2], Dromard Charlotte [2], Chaput Romain [3], Lett Christophe [1], Pellissier Loïc [4], Albouy Camille [4], Panfili Jacques [1], Pascal Pierre-Yves [2], Leprieur Fabien [1]
1. MARBEC, Montpellier/Sète, France
2. Université des Antilles, Pointe-à-Pitre, France
3. Cawthron Institute, Nelson, New Zealand
4. ETH, Zürich, Switzerland

A growing number of studies demonstrate that coral reef fish larvae have exceptional active dispersal abilities, allowing them to remain close to their native island despite strong currents, or travel thousands of kilometers in an oriented manner. Due to the difficulty of studying these behaviors in situ, very little is known about them, and their implications for conservation and biogeography are generally overlooked, despite a probable predominant effect on the population connectivity of most coral reef fishes. First, we will describe a newly developed in situ tracking methodology involving various miniaturized sensors to precisely reconstruct high-frequency 3D tracks of larvae followed by a diver, enabling us to obtain orientation and speed measurements. Second, we will present how to enrich current larval swimming speed databases for modeling purposes from various morphometric predictors using gradient-boosting random forest in a bootstrapping framework. Third, we will give an insight into how to implement various behavioral strategies using field measurements of orientation and swimming speed into the widely used ICHTHYOP model through a newly developed module. In the future, coupling these technical, statistical and modeling advances may be crucial to develop biophysical models matching the observed connectivity between populations. As a perspective, we will finish by presenting our current advances in the development of a genetically calibrated model to assess the effectiveness of Marine Protected Areas in the western Indian Ocean to preserve major larval sources, in order to ensure sufficient stock replenishment.

MODELLING MARINE FUNCTIONAL CONNECTIVITY: STATE OF THE ART AND RESEARCH GAPS TO BRIDGE

Addamo AM.*[1], Lopez L. [2], Hidalgo M. [3], WG2-DMI team [4], Darnaude A. [5]
1. Nord University, Norway
2. COST-IEO, Spain
3. COB-IEO, Spain
4. Several institutions, several countries
5. MARBEC Montpellier, France

Marine functional connectivity (MFC) is still an emerging but very dynamic field of research. Its complexity has led to the application of multidisciplinary approaches at various levels of biological organisations that collectively challenge the transfer of information and communication on MFC to managers and stakeholders. Thus, we performed an expert judgement-based review to assess the integration of empirical data in various modelling approaches used to study MFC under multidisciplinary frameworks. To do so, a review protocol was established, defining specific categories for model classification and empirical data inputs, which ensured an integrated approach for the participation of a large number of experts in different fields, and covering complementary aspects of marine functional connectivity (from ocean circulation and biogeochemical cycles to larval dispersal, molecular ecology, demography, or paleoecology). By applying this review protocol to more than 250 papers selected by experts in different research fields, key gaps in past and current approaches within MFC were identified. Preliminary results showed that most data/model integration were applied on larval dispersal, molecular ecology and demography of marine species with single-species and species distribution models. Our review also identified combination of MFC methods and modelling where research is scarce and whose development could contribute to advancing marine functional connectivity research. Finally, we discuss new perspectives regarding the advantages and drawbacks, identifying the necessary components for closed-system development in future research where gaps on data-modelling integrative efforts require further work of such integrative approach.

UNRAVELLING MEAGRE POPULATION CONNECTIVITY: A COMPREHENSIVE STUDY COMBINING GENOMICS, BIOPHYSICAL MODELLING, AND BIOTELEMETRY

Abecasis David *[1], Afonso Pedro [2], Gandra Miguel [1], Ogden Rob [3], Winkler Alexander C. [1,4], Assis Jorge [1,5]
1. Centre of Marine Sciences (CCMAR), Universidade do Algarve, Portugal
2. Ocean Sciences Institute (Okeanos), Universidade dos Açores, Portugal
3. Royal (Dick) School of Veterinary Studies and the Roslin Institute, University of Edinburgh, UK
4. Department of Ichthyology and Fisheries Science, Rhodes University, South Africa
5. Faculty of Bioscience and Aquaculture, Nord Universitet, Norway

We employed a comprehensive approach integrating genomics, biophysical modelling, and biotelemetry to elucidate the population structure and connectivity of meagre, an important fishery resource across its distribution. Genetic samples from known Atlantic spawning sites (Gironde, Tejo, Guadalquivir, Banc D'Arguin) and two additional regions (Algarve and Senegal) were subjected to genome-wide SNP-genotyping and mitochondrial DNA analyses. Biophysical models were utilized to examine larval dispersal and connectivity from known spawning locations, while biotelemetry provided insights into the movement patterns and connectivity of adult individuals. Our results revealed a pronounced differentiation between European and African populations, with a significant isolation of known Atlantic spawning sites. Limited connectivity between these subpopulations was observed, suggesting that adults, capable of extensive movements and connecting sites up to 500 km apart as demonstrated by biotelemetry, play a crucial role. In contrast, larval dispersal, as inferred by biophysical modelling, appeared more restricted. The results emphasize a clear and distinct population structure, particularly between Africa and Europe, and within Europe itself, suggesting the necessity of managing the meagre as separate stocks. The observed limited connectivity and substantial genetic differentiation highlight the importance of recognizing these distinct populations for effective spatial conservation and fisheries management strategies. Our multidisciplinary approach provides a robust overview of meagre Atlantic population dynamics, contributing valuable insights for informed decision-making in the realm of marine resource management.

ASSESSING DIRECTIONAL POPULATION CONNECTIVITY FROM SNPs DATA: A BENCHMARK OF COMMONLY USED METHODS AND TOOLS ON SIMULATED DATASETS

Sant Camille *[1], Forcioli Didier [3], Irisson Jean-Olivier [1], Fauvelot Cecile [1,2]
1. Sorbonne Université, CNRS, UMR LOV, Villefranche-sur-Mer, France
2. Institut de Recherche pour le Développement (IRD), UMR ENTROPIE, Nouméa, New Caledonia
3. EUR Life, Université Côte d'Azur, 65 avenue Valrose, Campus Valrose, 06108 Nice, France

Population connectivity - the exchange of individuals between geographically fragmented populations - has a major impact on population persistence. Thus, accurate and reliable estimates of connectivity are crucial for effective ecosystem management. Recent technical advances in molecular biology have made obtaining SNPs easy even for non-model species. Such data are increasingly used to estimate connectivity rates. To do so, a wide variety of methods are available, based on gene flow inference, clustering of individuals, or parentage assignment. However, to our knowledge, no systematic study of the reliability of those approaches exists. To fill this gap, we analyzed 3240 datasets of SNPs from three virtual populations, simulated using various demographic parameters (population size and migration rate) and various sampling efforts (both for individuals and SNPs). We applied a broad range of methods to estimate connectivity matrices and evaluate their concordance with the theoretical simulated migration rates. We found that the best-performing method highly depends on the demographic scenarios and subsampling rates. With high sampling rates of individuals and SNPs, either clustering or parentage assignment methods were the best-performing ones depending on the demographic scenarios, though with a drastic decrease for the later one when the rate of sampled individuals drops. Conversely, with low SNP and/or individual counts, gene flow methods showed the greatest stability, making them the best-performing ones. Overall, our study highlights the importance of carefully selecting the method to assess connectivity from SNPs data and consequently, we offer some guidelines to choose the most appropriate tool for a given dataset.

CONNECTIVITY OF MESOPHOTIC HYDROIDS FROM FRENCH OVERSEAS TERRITORIES IN THE SOUTHWESTERN INDIAN OCEAN USING POPULATION GENETICS

Ory David *[1,2], Bourmaud Chloé [1,2], Chabanet Pascale [1,2], Gravier-Bonnet Nicole [3], Boissin Emilie [2,4]
1. UMR 9220 ENTROPIE (UR , IRD, UNC, IFREMER, CNRS), La Réunion, France
2. Laboratoire d'Excellence CORAIL, France
3. Association Poisson Lune, La Réunion, France
4. UAR 3278 CRIOBE (PSL Research University, EPHE-CNRS-UPVD), Perpignan, France

In the context of global warming and anthropogenic pressures that threat coral reef ecosystems, scientific interest about the mesophotic zone has increased considering its potential for shallow reef resilience. Located between 30 and 150 meters of depth, mesophotic coral ecosystems (MCEs) remain largely unknown, in terms of their biodiversity as well as their relationships with euphotic ecosystems. In the Deep Reef Refugia Hypothesis (DRRH), MCEs have been proposed to act as potential sources for recolonization of degraded shallower reefs. However, the prerequisite to this hypothesis is the existence of connectivity between shallow and deep reefs: a vertical connectivity along the depth gradient. This study aims to test the vertical genetic connectivity, among hydroid populations, a neglected group with a high diversity of traits in terms of morphs, skeletons, habitats, and reproduction modalities. Through 50 dives at mesophotic depths in the French overseas territories of the southwestern Indian Ocean (La Réunion & Mayotte), more than 2600 samples were collected. These samples were genotyped using microsatellite libraries for 8 target species (6 newly developed for this study) to perform a comparative population genetics approach . A combination of several methods (estimation of genetic differentiation indexes, Structure and AMOVA analyses, Mantel tests and estimation of gene flow) was used to investigate population genetic patterns at different scales of complexity. Results show contrasting patterns of connectivity depending on species and reproduction strategies. This study brings new information about the links between mesophotic and euphotic populations which could contribute to the conservation of reef ecosystems.

LARGE-SCALE CONNECTIVITY OF THE BLACK LIPPED PEARL OYSTER (*PINCTADA MARGARITIFERA*) ACROSS FRENCH POLYNESIA USING AN INTEGRATIVE APPROACH FROM GENOMIC DATA, BIOPHYSICAL MODELS AND GRAPH THEORY

Gradel Antoine OJ. *[1,5], Legrand Térence [2], Tran Lu Y Adrien [3], Dorant Yann [4], Planes Serge [5], Reisser Céline MO. [1]
1. MARBEC Montpellier, France
2. CCMAR Faro, Portugal
3. ISEM Montpellier, France
4. LEMAR Brest, France
5. CRIOBE Perpignan, France

Marine connectivity has been at the center of a lot of studies in the last decades. With the improvement of indirect techniques to estimate the flow of individuals from one place to the next, conservation planning as well as management was successfully improved. *Pinctada margaritifera* is exploited to produce the tahitian black pearl, and the industry relies on the natural spat that is collected and farmed. However, spat collection is declining and became increasingly erratic in the last years, leading to intra-archipelago spat transfers from producing atolls to farming atolls, and pushing the government to consider the implementation of hatcheries. Here, we combined genetics, physical dispersal modeling and larvae physiological models to assess the diversity and connectivity of natural populations of the pearl oyster *P. margaritifera* across the five Polynesian archipelagos (the Marquesas, Society, Tuamotu, Gambier and Australe). Where the genetic results placed the Marquesas as an outlier and the Australe as a mix of others, the biophysical modeling, transformed into a multigenerational dispersal matrix gave opposite results, with a weak unidirectional (but existent) connection between the Marquesas and the Tuamotu/Society/Gambier and a complete isolation of the Australe. Both techniques however agreed on the levels of connection among the Tuamotu, the Society and the Gambier archipelago, with an existing genetic signature of each archipelago. Inconsistencies between the two methods will be discussed (from model calibration to demographic history). Our study provided the French Polynesian government with a description of the management units that could be used for sustainable pearl farming.

DECODING ESTUARINE FISH CONNECTIVITY: A MULTI-DISCIPLINARY APPROACH

Reis-Santos Patrick *[1], Sarakinis Koster [1], Donnellan Steve [2], Earl Jason [3], Ye Qifeng [3], Gillanders Bronwyn [1]
1. The University of Adelaide, Australia
2. South Australian Museum, Australia
3. South Australian Research Development Institute Aquatic Sciences (SARDI), Australia

The chemical information stored in otoliths reflects individual lifetime variations in growth, movements, and responses to environmental conditions, providing multi-layered pathways to unravel connectivity patterns. This information can be boosted by incorporating complementary genetic markers, allowing us to reconcile individual life histories and movement patterns with gene flow. Here we present a multi-disciplinary approach to unravel the complexities of the connectivity of an estuarine fish. Through the integration of Single-Nucleotide Polymorphisms (SNPs), otolith shape, isotopic and elemental composition, we provide a comprehensive assessment of population structure, lifetime migrations and multigenerational connectivity of black bream Acantopagrus butcheri across its distribution range in southern Australia. Otolith chemical information confirmed variations in movement patterns for this partial migrant species, emphasising variations in environmental histories as well as diverse migratory patterns within and across estuaries. Despite movement between estuaries and coastal areas, genetic markers reveal population structuring at small spatial scales, highlighting estuarine dependency with limited movement, connectivity, or gene flow even among nearby estuaries. Overall, we highlight how otolith-derived chemical information combined with genetic markers provide critical insights into the spatial scales of movement and gene flow, and can resolve uncertainties in population dynamics and connectivity.

RESULTS OF THE SEAMOBB EUROPEAN PROGRAM: ALPHA AND BETA DIVERSITY ANALYSES OF NW MEDITERRANEAN BENTHIC COMMUNITY INFERRED BY PHOTO AND METABARCODING FROM A VARIETY OF SAMPLING SYSTEMS

Chenuil A *[1], Boucherau E [1], Dubut V [1], Haguenauer A [1], Marschal F [1], Marschal C [1], Meglecz E [1], Zuberer [2], Abbiati M [4], Appolis A [1], Calvert [1], Chemin C [1], Chenesseau [1], Guillemain [2], Legrand T [5], Mirleau F[1], Mirleau P[1], Mugnai F [4], Ortuno [3], Ruitton S [5], Selva [1], Vanbostal L [2], Costantini F [4], Gutierrez JM [3], Leduc M [6], Rossi V [5]
1. IMBE (Institut Méditerranéen de Biodiversité et d'Ecologie), Marseille, FRANCE
2. Institut Pytheas, Marseille, FRANCE
3. Taxon, Murcia, FRANCE
4. UNIBO (University of Bologna), ITALY
5. MIO (Mediterranean Institute of Oceanology), Marseille, FRANCE
6. Stareso, Calvi, FRANCE

Monitoring biodiversity requires both standardizable methods of assessing community composition (or genetic diversity) and a relevant network of sites with respect to connectivity. The seamobb european project was dedicated to test methods of community diversity assessment, in a set of North-western Mediterranean sites. It allowed the collection and characterization of thousands of samples for both their community diversity and species (genetic) diversity. We analysed how (alpha- and) beta diversity was structured by oceanic distance, physical barriers, but by year (and immersion duration) for various types of samples. This original field protocol had the advantage of allowing the parallel sampling and analysis of both community composition and genetic diversity for a number of species, an experimental scheme favorable to disentangle the effects of niche (natural selection) from neutral processes like connectivity. Two (to three) yearly samplings of rocky bottoms at 20m depth were performed in 28 sites from 8 regions from Murcia (Spain, Mediterranean) to Rovinj (Adriatic Sea). They were collected from scraping of natural substrate, from ARMS (artificial reef monitoring structures), and from ASUs (artificial substrate units). Thousands of image analyses (from sessile fractions on ARMS) and metabarcoding (from all fractions and sampling systems, > distinct 1000 samples) were carried out to obtain community composition tables. In this presentation we will focus on community composition (but a candidate-poster will present a pilot study describing within species genetic diversity from the same sites, in addition, RAD-sequencing of two additional species are ongoing and may, though it is uncertain, be ready to be presented in addition). For community, alpha and Beta diversity analyses revealed effects of sampling fraction, region, site, and some environmental variables. Fractions, and approaches (image versus metabarcoding) are compared with respect to their relevance for monitoring, ... among other conclusions and perspectives.

APPLICATION OF EYE LENS ISOTOPES TO INFER LIFE-LONG MOVEMENTS OF LARGE OCEANIC SQUID (*THYSANOTEUTHIS RHOMBUS*)

Sakamoto Tatsuya *[1]
1. Instituto Português do Mar e da Atmosfera, Portugal

Knowledge of the movements of marine organisms is essential for effective conservation schemes. Here, we investigated the lifetime habitat use of diamondback squid, Thysanoteuthis rhombus, collected in the western North Pacific and its marginal seas, whose migratory ecology is poorly known, using bulk stable nitrogen and carbon isotope ratios in eye lenses. From the eye lens isotope profiles, the chronology of the isotopic baseline of squid habitat was estimated by removing the effect of size-dependent changes of trophic position. Then, the baseline estimates were compared to the isoscapes of particulate organic matter. The baseline chronologies showed fluctuations during the paralarval and juvenile stages, becoming stable during the adult stage, suggesting that significant movements mainly occur during the early life stages due to current transport, with adults potentially not undertaking long-distance migrations. The squids in the marginal seas mostly originated from outside the subtropical gyre, while the squids in the subtropical gyre had various sources, including outside the gyre and southern and northern parts within the gyre, revealing a complex mixing pattern of the species. These results show that isotope chronology combined with baseline isoscapes are effective tools to understand animal migrations, which can help managing various cephalopods and fish.

PREDICTING HIGH-RESOLUTION OTOLITH ISOTOPE RATIOS ALONG PASSIVE DRIFT TRAJECTORIES TO SHED LIGHT ON EARLY LIFE HISTORY MIGRATIONS: A CASE STUDY WITH EUROPEAN EEL

Yuan Tian Chou *[1,2], Robert Marsh [2], Ewan Hunter [4], Clive Trueman [2]
1.Eastern Marine Biology Research Center, Fisheries Research Institute, COA, Taiwan
2. School of Ocean and Earth Science, University of Southampton, UK
3. Centre for Fisheries and Aquatic Science, UK
4. Agri-food and Biosciences Institute (AFBI), Belfast, UK Affiliations

Despite significant efforts, our knowledge of the spawning grounds, larval migration behaviour, and pathways of European eels remain limited due to sampling difficulties. However, understanding the behaviour and pathways of eel larvae is essential for effective management and conservation strategies, especially since long migrations may make eels more vulnerable to the effects of climate change. This study aimed to investigate the potential use of otolith isotopes to verify European eel spawning locations and test hypotheses about the impact of ocean dynamics, specifically swimming behaviour and NAO index, on eel larvae migration. The study used virtual particle trajectories to predict the drift of eels from four subareas of spawning locations at different depths, with the highest success rate observed in May at a depth of 200 meters. The study also found that during NAO+ periods, eels required a longer time for migration and had a lower migration success rate. Otolith δ18O was used to distinguish successful and failed drifts and verify the hypothesis that NAO affects eel migration. Moreover, the study found that otolith oxygen isotope ratios can distinguish the characteristics of spawning locations during NAO+ periods. This study demonstrates the possibility of using a combined model and otolith analysis for validating each other's findings and highlights the potential of using stable isotopes to address questions about the recruitment success of migratory species.

A MULTI-METHOD APPROACH TO IDENTIFY THE CONNECTIVITY PATTERNS AND CRITICAL HABITATS OF A COMMERCIALLY IMPORTANT FISH

Sturrock Anna M. *[1], Taylor Michelle [1], Cameron Tom [1], Hyder Kieran [2], Dawson Joseph [1], Freeman Howard [1], Ciotti Ben [3], Martinho Filipe [4], Bradley Kirsty [2], Hunter Ewan [5]. Wright Serena [2]
1. University of Essex, UK
2. Centre for Environment, Fisheries and Aquaculture Science, UK
3. University of Plymouth, UK
4. University of Coimbra, Portugal
5. Agri-Food and Biosciences Institute, UK

European sea bass (*Dicentrarchus labrax*) represent a commercially important recreational and commercial fishery that has experienced large fluctuations and recent declines in recruitment, particularly around the UK which represents its northerly range margin. Most mortality in marine fishes occurs at early life stages, so understanding the processes driving selection in the first few years – and how to plan nursery area protection and restoration measures in a targeted way – is critical to boost the productivity and resilience of the adult fishery. Here, we sampled 0-2 year old juveniles from 16 estuaries (22 sites) around the UK and mainland Europe in 2022 and 2023, and characterised estuary-specific fingerprints using otolith multielemental signatures, eye lens stable isotopes (carbon, nitrogen, sulphur) and SNPs. We assessed within- vs between-estuary and among-year stability in provenance assignments to assess the necessity for annual reference libraries and cohort matching to adults. We then sampled adults through (1) commercial fishers, (2) a citizen science campaign among recreational fishers and (3) a data storage tagging programme, and performed a proof of concept study estimating the contribution rates of different nursery areas. Finally, we showcase the diversity in adult movement patterns revealed by various tagging efforts, and discuss the implications of these lifetime connectivity patterns on the stability of the stock. A key take home is how the combination of markers and tissues increased the accuracy of provenance assignments, and how combining methods can provide unique insights across different spatial and temporal scales.

THE BIOGEOGRAPHY OF COASTAL MARINE CONNECTIVITY

Legrand Térence *[1], González-Trujillo Juan David [2,3], Araújo Miguel B. [2,3], Fragkopoulou Eliza [1], Gouvea Lidiane [1], Campoy Ana [1], Serrão Ester [1], Costello Mark J. [4], Assis Jorge [1,4]
1. Centre of Marine Sciences, University of Algarve, Faro, Portugal
2. Rui Nabeiro Biodiversity Chair, MED -Mediterranean Institute for Agriculture, Environment and Development & CHANGE –Global Change and Sustainability Institute, University of Évora, Évora, Portugal
3. Department of Biogeography and Global Change, National Museum of Natural Sciences, CSIC, Madrid, Spain
4. Faculty of Bioscience and Aquaculture, Nord Universitet, Bodø, Norway

A better understanding of the extent to which species disperse and establish connections across seascapes is instrumental for marine conservation and management, as well as biogeography and climate change research. This understanding is particularly relevant for projecting the dynamics of species' geographical ranges. However, a comprehensive perspective on the elemental structures and patterns of species connectivity along coastlines is currently lacking. To address this gap, we present a mechanistic biophysical approach designed to reveal communities in connectivity networks for a broad spectrum of taxonomic groups, including fishes, corals, molluscs, crustaceans, and keystone species of macroalgae, seagrasses, and mangroves, on a global scale. This approach is grounded by 21 years of ocean current data and tuned by empirical information on species dispersal capacity, with kernels spanning from local to long-distance dispersal events. We delineate well-connected communities as distinct biogeographic units, explaining observed community composition derived from species range maps (approximately 3,000 species globally). These units' composition aligns with existing biogeographic regionalisations based on both expert knowledge and biodiversity data. We identify the location of weak and strong connectivity barriers and the directional putative connectivity pathways at the global scale, revealing a global network between units for each taxonomic group under consideration. By expanding connectivity analysis to the biogeographic scale, our findings establish baselines to enhance our understanding of the mechanisms controlling species dispersal and ongoing range shifts due to climate change. Additionally, they provide standards for the development of effective conservation and management spatial strategies for marine coastal species.

MULTI-DISCIPLINARY CONNECTIVITY INVESTIGATION OF FLAME SHELL (*LIMARIA HIANS*) BEDS IN SCOTTISH WATERS USING BIO-PHYSICAL MODELLING AND POPULATION GENOMICS

Sloan Danielle A. R. *[1], Rabe Berit [2], Noble Leslie R. [3], Jones Catherine S. [1]
1. School of Biological Sciences, University of Aberdeen, UK
2. Scottish Government Marine Directorate, Aberdeen, UK
3. Faculty of Biosciences and Aquaculture, Nord University, Bodø, Norway

Marine Protected Areas (MPAs) are designated to protect and conserve nationally important species and habitats, known as Priority Marine Features (PMFs). Understanding how PMFs are connected and their relationship with species and habitats outside the MPA network is critical to the provision of effective spatial management. Flame shells, *Limaria hians*, are a nest building bivalve that can create dense biogenic beds which support rich associated communities. Given their size and the habitat's global scarcity, Scottish flame shell beds are of international importance and are protected within several MPAs as a PMF. Due to difficulties sampling benthic species, such as the flame shell, limited information is available on the connectivity of benthic biogenic habitats around Scotland. By combining coupled particle tracking and hydrodynamic models with mitochondrial DNA analyses, this multi-disciplinary project investigates the connectivity of Scottish flame shell beds. Here we use FISCM, a Lagrangian particle tracking model, coupled with the hydrodynamic Scottish Shelf Model to model larval dispersal, investigating the oceanographic mechanisms behind the connectivity of these benthic populations which rely on the pelagic larval phase for transportation to other areas. Regions of the cytochrome c oxidase subunit 1 (COI) mitochondrial gene sequenced from over 200 flame shells across nine populations were used to explore population structure, providing insight into the connectivity and genetic differentiation between and within populations. We present the findings of this study which will help inform future evidence-based management of flame shell beds and establish an integrative approach for analyses of other information limited benthic habitats.

FROM THE MEDITERRANEAN TO THE INDIAN OCEAN: UNDERSTANDING CONNECTIVITY OF MARINE VERTEBRATE TO IMPROVE RESOURCE MANAGEMENT: A MULTI DISCIPLINE – SPECIES – OCEANS APPROACH

Bourjea Jérôme *[1], Forget Fabien [1], Mignucci Alexandre [2], Derridj Olivier [1], Villeneuve Remy [1], Thambithurai Davide [1], Ciccione Stéphane [3], Ballorain Katia [4], Dalleau Mayeul [5]
1. MARBEC Sète, France
2. Terres Australes et Antarctiques Française, France
3. Kélonia, l’observatoire des tortues marines de La Réunion, France
4. Centre d’étude et de découverte des Tortues Marines, France
5. Biotope, France

Human activities impact marine ecosystem health and resilience and the ability of oceans to provide essential ecosystem services, such as food biodiversity conservation, and marine ecological connectivity is an essential factor influencing ecological resilience. Despite ecological connectivity being a multidimensional concept, tackled by researchers from multiple disciplines such as physical oceanographers, geneticists and ecologists, its knowledge has generally been produced for a limited number of species or functional traits, under specific environmental conditions, within relatively smaller geographical areas, and with limited integration across disciplines. Based on contrasted species life traits and individual movement from Mediterranean fish (Acoustic telemetry; array of hydrophone > 200; Seabass, Seabream and Salema N>600 from 2019 to 2023) and western Indian Ocean sea turtles (satellite telemetry; Green, Hawksbill and Loggerhead turtles, N>300 from 2010 and 2023), along with population genetic and dispersal passive modelling approaches, we aim to show the importance of investigating population structure and migratory corridors via different scientific approach and its impact on resources management via a multi-disciplinary approach. The results and associated numerical models (network analysis, Movement-based Kernel Density Estimation), show that marine megafauna do not have the monopoly of large-scale migrations structured in space and time. They also show how important it is to know the fine and large-scale connectivity of different species in order to better assess the relevance of current MPA networks and their future planning.

POPULATION CONNECTIVITY OF THREE CORAL SPECIES REVEALS PERSISTENT VS. SEASONAL ENVIRONMENTAL BARRIERS AROUND THE ARABIAN PENINSULA

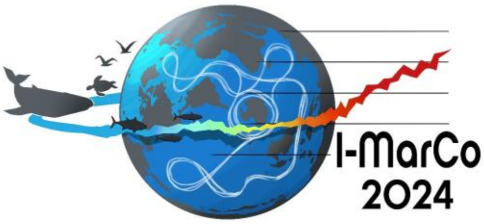
Oury Nicolas *[1,2], Wang Yixin [3], Terraneo Tullia I. [2], Barreca Federica [2], Delgadillo Nathalia [1,2], Raimundo Inês [1,2], Vimercati Silvia [1,2], Berumen Michael L. [1,2], Eweida Ameer A. [4,5], Peixoto Raquel [1,2], Rodrigue Mattie [6], Paulay Gustav [7], Hoteit Ibrahim [3], Benzoni Francesca [1,2]
1. Marine Science Program, King Abdullah University of Science and Technology (KAUST), Saudi Arabia
2. KAUST Red Sea Research Center, King Abdullah University of Science and Technology (KAUST), Saudi Arabia
3. Department of Earth Science and Engineering, King Abdullah University of Science and Technology (KAUST), Saudi Arabia
4. Marine Conservation Program, NEOM, Saudi Arabia
5. Center of Carbonate Research, University of Miami, USA
6. OceanX, USA
7. Florida Museum of Natural History, University of Florida, USA

Identifying barriers to gene flow and, ultimately, informing stakeholders to implement effective conservation efforts, is the paradigm of connectivity studies. The latter should ideally use multi-species and multi-disciplinary approaches to accurately reveal and understand connectivity patterns. This is becoming increasingly urgent for coral reefs, which are experiencing critical declines. Yet, their connectivity remains insufficiently documented, especially around the Arabian Peninsula, surrounded by different water masses, each with unique oceanographic conditions providing potential barriers or corridors for marine organisms. Here, to understand the role of these conditions in shaping the diversity, distribution and connectivity of scleractinian corals, we assessed for the first time ever the population genomic connectivity of different non-model corals with different life history traits and distributions around the Arabian Peninsula. We revealed distinct genetic structuring patterns among species, likely related to specific reproductive cycles and strong seasonality of currents and environmental conditions within this region. To further test this hypothesis, we deployed a Lagrangian particle tracking model based on currents and environmental conditions from validated regional models to simulate the seasonal larval dispersal around the peninsula. Combined with existing observations on spawning periodicity among the targeted species, this model provided insights to better understand the specific structuring patterns. We subsequently investigated whether distance, currents and environmental conditions correlated with gene flow among populations for each species. All together, these findings advance our understanding of connectivity patterns around the Arabian Peninsula, an understudied region undergoing unprecedented coastal development yet aiming to establish an effective network of marine protected areas.

Talks

Session 2

Marine Functional Connectivity research and the global functioning and health of the Ocean



Conveners

Stéphanie D'Agata (France)
Amber Childs (South Africa)
Manuel Hidalgo (Spain)
Thomas Lamy (France)
Fabien Leprieur (France)
Lucía López López (Spain)

Session 2

Keynote

Renato Morais

ENERGETIC CONNECTIVITY, DARWIN AND THE CORAL REEF PARADOX THAT NEVER WAS

Morais, Renato A.*[1], Parravicini, Valeriano [1], Valerio, Larisa P. [2], Narvaez, Pauline [1], Brandl, Simon J. [3]
1. Université Paris Sciences et Lettres, École Pratique des Hautes Études, CRIOBE, UAR3278, Perpignan, France
2. The University of Queensland, School of Environmental Sciences, Joint Remote Sensing Research Program, St Lucia, Queensland, Australia
3. The University of Texas at Austin, Marine Science Institute, Department of Marine Science, Port Aransas, Texas, USA

For decades, coral reefs have been touted as an ecological enigma: despite dwelling in nutrient-poor, oligotrophic tropical waters, they exhibit remarkably high internal productivity. This observation, attributed to Charles Darwin in his 1842 book (‘The structure and distribution of coral reefs') and frequently termed the ‘Darwin’s paradox’, has spurred ample research in ecology, oceanography, and ecophysiology. Ignoring several decades of research highlighting pathways energetically connecting coral reefs and surrounding habitats, coral reefs continue to be viewed as isolated 'marine oases' in unproductive tropical oceans. Given the growing popularity of the “Darwin's paradox” concept, it is surprising that it has, to date, remained largely unappraised. In this talk, I will present historical and empirical evidence that the “Darwin’s paradox” is neither Darwinian, nor truly paradoxical. Coral reefs occur in diverse oceanographic conditions ranging from oligotrophic to eutrophic yet skewed toward high production. Furthermore, key nutrient concentrations in waters surrounding coral reefs are similar to, not lower than, background tropical oceans including regions where coral reefs are absent. As part of larger connected seascapes embedded in relatively productive waters, most coral reefs and their consumers face ample opportunities to harvest external energy and nutrient subsidies. I will then present case studies where external subsidies have been identified as critical to power reef consumers. I will argue that abandoning the implied dichotomy of the ‘Darwin’s paradox’ will further our understanding of reef functioning, emphasising the need to extensively quantify the complex energetic connections that coral reefs maintain with neighbouring ecosystems.

A ROLE FOR MARINE CONNECTIVITY IN THE SECONDARY EXPANSION OF LESSEPSIAN IMMIGRANTS IN THE MEDITERRANEAN SEA?

Andrello Marco *[1], D'Amen Manuela [2,3], Azzurro Ernesto [3]
1. Institute for the study of Anthropic impacts and Sustainability in the marine environment, National Research Council - CNR-IAS, Rome, Italy
2. Italian Institute for Environmental Protection and Research – ISPRA (PRES-PSMA), Rome, Italy
3. Institute of Biological Resources and Marine Biotechnologies, National Research Council - CNR-IRBIM, Ancona, Italy

With the opening of the Suez Canal in 1869, dozens of marine species native to the Red Sea and Indian Ocean found a passageway to enter the Mediterranean Sea and expand their range. Several of these Lessepsian species (named after Ferdinand de Lesseps, the French entrepreneur who promoted the construction of the canal) established large, permanent populations in the eastern Mediterranean. The spatio-temporal spread dynamics vary widely: some species develop successful populations and spread over large geographical areas, whereas others remain rare for long periods before spreading, or even fail to establish. Some species also spread to more distant areas, and in few cases to the entire Mediterranean basin. The post-establishment secondary spread westward in the Mediterranean Basin is mediated by connectivity in various life stages of the species (larval, juvenile, and adult) and is likely aided by ongoing climate change that brings the environmental conditions of the Mediterranean closer to species native range. In this study, we seek to quantify the different role of marine connectivity and habitat suitability in Lessepsian fish invasions by comparing different simulated dispersal pathways against the species observation from the georeferenced ORMEF database. Using spatiotemporally explicit occupancy models and a statistical model comparison approach, we seek to (i) identify the processes that structure the connectivity of these species through the spatiotemporal process of invasion; (ii) quantify the effect of environmental variables on the colonization of local sites; and (iii) account for the uncertainty deriving from imperfect species detection.

THE ROLE OF POTENTIAL CONNECTIVITY IN SHAPING TROPICAL CORAL BIOGEOGRAPHY AND RESPONSES TO RAPID ENVIRONMENTAL CHANGE

Vogt-Vincent Noam S. *[1,2], Burt April J. [3,4], McManus Lisa [2], Mitarai Satoshi [5], van der Ven Rosa M. [6], Turnbull Lindsay A. [3], Johnson Helen L. [1]
1. Department of Earth Sciences, University of Oxford, UK
2. Hawai'i Institute of Marine Biology, University of Hawai'i at Mānoa, USA
3. Department of Biology, University of Oxford, UK
4. Seychelles Islands Foundation, Seychelles
5. Marine Biophysics Unit, Okinawa Institute of Science and Technology, Japan
6. Marine Animal Ecology Group, Wageningen University and Research, Netherlands

Integrated over many spawning events, low-probability, long-distance dispersal can establish connectivity between isolated coral reefs. Based on a 2 km resolution ocean model, we predict potential connectivity between all shallow-water coral reefs in the tropical southwest Indian Ocean for a variety of broadcasting corals, across thousands of simulated mass spawning events. Despite considerable short-term variability in potential connectivity, we identify robust long-term clusters of reefs that consistently retain larvae over many generations of dispersal. These clusters are shaped by large-scale oceanography and are generally consistent with regional assessments of biogeography (for both reef-building corals, and marine taxa as a whole) and coral population genetic structure. In contrast, we show that short-term, recent gene flow between isolated reefs in Seychelles is practically impossible to predict using oceanographic models alone, due to the dominant role of stochastic connectivity in setting ecological connectivity. By integrating reef potential connectivity into an eco-evolutionary meta-community model, we find that there is already tentative evidence for a large-scale coral community evolutionary response to climate change. Preliminary results suggest that this response will be driven by local selection rather than a mass effect of thermally-adapted immigrants, but inter-reef connectivity may play a key role in maintaining genetic variance in response to strong selective pressure.

DEFINING TRAIT-BASED FUNCTIONAL GROUPS OF MARINE CONNECTIVITY

K. Guizien [1], A. Chenuil [2], F.R. Barboza [3], M. Beger [4,5], A. Blanco [6], L. Chaoui [7], C. Clay [4], F. Costantini [8], B. Edvardsen [9], A. Fernández-Alías [10], S. Gran-Stadniczeñko [11], T. Guy-Haim [12], M. Hidalgo [13], G. Kerametsidis [13], L. López-López [14], A. Pérez-Ruzafa [15], CMO. Reisser [16], M. Sanz-Martín [13], S.E. Tanner [17], A.M. Darnaude [16]
1. CNRS, Sorbonne Université, Laboratoire d'Ecogéochimie des Environnements Benthiques, LECOB, F-66650 Banyuls-sur-Mer, France
2. Aix Marseille Univ, Avignon Univ, CNRS, IRD, IMBE, Station Marine d'Endoume, Chemin de la Batterie des Lions, F-13007 Marseille, France
3. Estonian Marine Institute, University of Tartu, Mäealuse 14, 12618 Tallinn, Estonia
4. School of Biology, Faculty of Biological Sciences, University of Leeds, Leeds, LS2 9JT, UK.
5. Centre for Biodiversity and Conservation Science, School of the Environment, The University of Queensland, St. Lucia, QLD 4072, Australia.
6. Centro de Investigación Mariña, Universidade de Vigo, Future Oceans Lab, 36310 Vigo (Spain)
7. Laboratoire bioressources marines, Université d'Annaba Badji-Mokhtar, Annaba, Algérie
8. Dipartimento di Scienze Biologiche, Geologiche e Ambientali, Università di Bologna, Campus di Ravenna, Ravenna, Italy
9. Department of Biosciences, Section for Aquatic Biology and Toxicology, University of Oslo, Oslo, Norway
10. Department of Ecology and Hydrology and Regional Campus of International Excellence "Mare Nostrum", University of Murcia, 30100 Spain
11. Section for Aquatic Biology and Toxicology, Department of Biosciences, University of Oslo, P.O. Box 1066, Blindern, Oslo 0316, Norway
12. National Institute of Oceanography, Israel Oceanographic and Limnological Research, Tel-Shikmona, Haifa, Israel
13. Oceanographic Centre of the Balearic Islands, Ecosystem Oceanography Group (GRECO), Spanish Institute of Oceanography (IEO-CSIC), Moll de Ponent s/n, 07015 Palma de Mallorca, Spain
14. Oceanographic Centre of Santander.Ecosystem Oceanography Group (GRECO), Spanish Institute of Oceanography (IEO, CSIC), Avda. Severiano Ballesteros, nº16, Santander C.P.39610 Spain
15. Department of Ecology and Hydrology and Regional Campus of International Excellence "Mare Nostrum", University of Murcia, 30100, Spain
16. MARBEC, Univ. Montpellier, CNRS, IRD, Ifremer, Montpellier, France.
17. MARE - Marine and Environmental Sciences Centre, ARNET - Aquatic Research Network (LA) Department of Animal Biology, Faculdade de Ciências, Universidade de Lisboa, Lisboa, Portugal

Connectivity plays a key role in marine ecosystem functioning and resilience, becoming progressively a requisite for the design of marine biodiversity conservation actions and implementing maritime spatial planning. However, many aspects of marine connectivity remain unknown–including the biological scope and drivers of connectivity as well as the functional scope of action, which is expected to be taxonomic- and ontogenetic-dependent. In particular, despite the known importance of species traits as indicators of functional scope in general, the life history traits and functional groups associated

with dispersal and movement of marine organisms have not been evaluated, from a connectivity-oriented perspective. Here, we tackle this challenge and identify functional groups and key traits of marine dispersal and movement across the marine tree of life. Using an expert elicitation approach from within our authorship, all global experts in the dispersal and movement of marine phyla/taxa, we identified a set of 20 core traits to define functional groups of connectivity. Species for which speed values were found in either existing traits database or literature were selected. Using the traits of all dispersive life stages (propagules up to adults), we classified functional groups with cluster analyses, and identified which traits drive the categorisation. We identified 528 species, from phytoplankton to mammals, that span the tree of life and had information for most of the core traits. We identified clear functional groups across these species; these functional groups did not systematically match taxon boundaries. Given the disparate dispersal abilities of life stages, the functional groups rarely contain all life stages of one species. Those functional groups will be useful to facilitate connectivity concept implementation and the definition of connectivity indices for decision-making in marine conservation or management as it requires integrating multi-specific connectivity estimates at the multi-specific, or community or even ecosystem level.

IDENTIFYING COMMUNITIES FROM CONNECTIVITY PATHWAYS IN THE TROPICAL SOUTHWEST ATLANTIC

Tosetto Everton G. *[1,2,3], Lett C. [1,2], Koch-Larrouy A. [3,4], Bertrand A. [1,2,3,5]
1. MARBEC, University of Montpellier, CNRS, IFREMER, IRD, Sète, France
2. Institut de Recherche pour le Développement, Sète, France
3. Departamento de Oceanografia, Universidade Federal de Pernambuco, Recife, PE, Brazil
4. Laboratoire d'Etudes en Géophysique et Océanographie Spatiales (LEGOS), Toulouse, France
5. Departamento de Pesca e Aquicultura, Universidade Federal Rural de Pernambuco, Recife, PE, Brazil

Because most marine taxa have planktonic life stages that are transported by currents, dispersal is more intense in the ocean than on land. Species dispersal is therefore expected to strongly influence the composition of marine communities. Here we propose a novel, community-based, approach of connectivity, based on Lagrangian simulations of plankton dispersal, to identify marine assemblage zones that characterise spatial areas that are particularly likely to receive and retain similar animal assemblages from a regional species pool through passive dispersal. We apply this approach to communities (coast, outer shelf, slope, seamounts and islands) of the tropical southwest Atlantic. Specifically, according to biological characteristics (planktonic life duration and spawning habitat) of representative planktonic communities, we first classified the modelled particles into 15 categories. Then, from a hierarchical clustering of the multivariate matrix containing the number of particles from each category that arrive in each of the model cells, we identified 14 assemblage zones. Finally, we show that the boundaries, dispersal and connectivity patterns of these zones match local and regional in situ distribution and abundance patterns. This approach, coupled with knowledge of other processes shaping community structure and distribution, provides important insights for regions and animal groups for which knowledge is limited or absent. More generally, it allows a comprehensive overview of the distribution of different communities and connectivity pathways along marine environments.

EXPLORING CONNECTIVITY PATTERNS OF SEAGRASS SPECIES IN THE CHANGING EASTERN MEDITERRANEAN SEA

Garcia-Escudero Catalina A. *[1, 2], Litsi-Mizan Victoria [1, 2], Tsigenopoulos Costas S. [3], Apostolaki Eugenia T. [2]
1. University of Crete, Biology Department, Voutes University Campus, P.O. Box 2208, GR-70013, Heraklion, Crete, Greece.
2. Institute of Oceanography, Hellenic Centre for Marine Research, PO Box 2214, GR-71003, Heraklion, Crete, Greece.
3. Institute of Marine Biology, Biotechnology and Aquaculture, Hellenic Centre for Marine Research, PO Box 2214, 71003 Heraklion, Greece.

Global environmental change threatens to alter the presence and distribution of seagrasses in the Eastern Mediterranean Sea. The endemic seagrass Posidonia oceanica is exhibiting signs of decline, while the exotic *Halophila stipulacea* appears to be expanding, potentially aided by the rising sea temperature and its tropical origin and life traits. By leveraging datasets from both seagrass species, and employing long-established genetic and emerging genomic tools, we assessed seagrass population dynamics to understand the intricacies of species adaptability and resilience in the face of changing environmental conditions. In particular, we studied the genetic diversity, population structure, and connectivity of *P. oceanica* meadows along the understudied Greek Seas, using microsatellite markers and Lagrangian models. Similarly, we assessed the genetic patterns of *H. stipulacea* in its native (Red Sea) and exotic range (Italy, Greece, Cyprus) using SNP markers from double-digest RAD sequencing. Our findings revealed substantial gene flow between P. oceanica along the Greek Seas, indicating well-connected populations. Some meadows exhibited high clonality, low genetic diversity, or distinct genetic characteristics, linked to oceanographic connectivity patterns, in conjunction with historical and evolutionary processes. On the other hand, *H. stipulacea* exhibited considerable genetic structure, especially between major geographical discontinuities. Despite a 130-year invasion history, it exhibited lower genetic diversity compared to native populations, and higher clonality, which potentially influenced its Mediterranean spread. These new genetic insights serve as a catalyst for future research into species' invasion dynamics, aiming to identify suitable areas as management units to effectively conserve seagrass ecosystems and their invaluable services.

EFFECTS OF CLIMATE CHANGE ON LARVAL DISPERSAL CONNECTIVITY OF MEDITERRANEAN COASTAL FISHES

Mirzaei Reza *[1], Quattrocchi Giovanni [2], Cucco Andrea [2], Sinerchia Matteo [2] and Andrello Marco [1]
1. Institute for the study of Anthropic Impacts and Sustainability in the marine environment, National Research Council, Rome, Italy
2. Institute for the study of Anthropic Impacts and Sustainability in the marine environment, National Research Council, Oristano, Italy

Climate change is affecting the ecology of marine species, influencing how organisms disperse and the connectivity of their populations. This study aims to explore changes in larval dispersal patterns and connectivity for coastal fishes in the Mediterranenan sea, shedding light on the potential ecological consequences in the region. To achieve this, we run Lagrangian larval dispersal simulations in Ichthyop using outputs of a high-resolution ocean circulation model (POLCOMS, 0.1 degrees spatial resolution) forced with two climate change scenarios (RCP4.5 and RCP8.5) for the coastal areas of the Mediterranean Sea, over the range of pelagic larval duration (PLDs) of most coastal fishes (60 days). We compare larval dispersal distances and connectivity between present (2020-2029), mid-century (2050-2059), and end of the century (2090-2099) decades. This study offers valuable insights into the ecological effects of climate change on Mediterranean marine ecosystems, providing crucial information for the design of a future-proof network of well-connected marine protected areas and the maintenance of larval supply to fished areas in the face of global climate change.

EXISTING KNOWLEDGE ON ESTUARINE-MARINE CONNECTIVITY OF IMPORTANT FISHERY SPECIES IN SOUTH AFRICA

Murray Taryn S. *[1], Childs Amber-Robyn [2], Bennett Rhett H. [1,3], Næsje Tor F. [1,4], Grant Gareth [1], Mukhari Dinah L. [1,2], Ziko Bantony [1,2], Padare Godfrey [5], Mxo R. Vuyolwethu [1,6], Cowley Paul D. [1]
1. South African Institute for Aquatic Biodiversity, South Africa
2. Rhodes University, South Africa
3. Wildlife Conservation Society, South Africa
4. Norwegian Institute for Nature Research
5. South African Environmental Observation Network Elwandle Node, South Africa
6. Nelson Mandela University, South Africa

Many fish species make use of estuaries throughout their lives, with others using these environments predominantly during their juvenile life stage. This is due to these environments providing abundant food resources, and multiple habitats for shelter and refuge. Many species are able to tolerate the extremely large fluctuations in environmental variables typical of estuarine environments; however, movement can also be used as a coping mechanism to these changes. The movements of several important estuary-associated fishery species, including representatives of the sciaenid, haemulid, sparid, carangid and mugilid families, have been studied for the past 20 years in South Africa using acoustic telemetry. While these studies have provided incredibly valuable information on the movements of fishes within different estuaries, it has also allowed for the connectivity between different habitats, such as the estuary and the sea, to be assessed, including the drivers behind these movements. What makes understanding this kind of connectivity so important is the changes facing both estuaries (heavily impacted by anthropogenic activities) and the adjacent marine (changes in water temperatures with a changing climate) environments. Here, we provide an overview of existing information on estuarine-marine connectivity of important fishery species in South Africa, and touch on how this connectivity may change given the changing climate.

A TRANSDISCIPLINARY APPROACH TO ASSESS SPATIAL CONNECTIVITY OF SOUTH AFRICA'S MARINE SHORE-BASED FISHERY

Childs Amber *[1], Potts Warren M. [1], Farthing Matthew [1], Winkler Alexander C. [1,2], Bova Chris [1], Hewitt Kyle [1], Parkinson Matthew [2], Du Toit Montagu [1], Kaplan David [3], Mlotshwa Nonhle [1,3], Ngcefa Samkele [1], James Nicola C. [2], Murray Taryn S. [2], Henriques Romina [4], Olivier Wilfred [4], Smith Kyle [5], Sink Kerry [6], Mann Bruce Q. [1]
1. Department of Ichthyology and Fisheries Science, Rhodes University, South Africa
2. South African Institute for Aquatic Biodiversity (SAIAB), South Africa
3. MARBEC, University of Montpellier, CNRS, IRD, Ifremer, Montpellier, France
4. University of Pretoria, South Africa
5. South African National Parks (SANParks), South Africa
6. South African National Biodiversity Institute (SANBI), South Africa

Marine shore-based fisheries provide considerable economic and livelihood benefits, yet their governance is poor, particularly in developing countries, with the overexploitation of most stocks attributed to excessive harvest. South Africa's inshore fishery resources are heavily exploited by a large marine shore-based recreational fishery which has reduced the abundance of these species and the opportunities for a growing small-scale fishery. Research on this fishery has focused on life history and stock assessment of some species, but critical knowledge gaps on the ecological, human dimensions and governance aspects of the fishery still exist. While compliance is poor with most fisheries regulations (i.e. traditional output controls), closed areas appear to be relatively well respected by shore-based recreational anglers, suggesting that other area-based management strategies may yield considerable benefits for species targeted in this fishery. Knowledge on the connectivity and spatial distribution of fish and fishers is critical for spatial-based management and conservation strategies. This presentation highlights the valuable role that both traditional and innovative methods, such as fishery catch data, species distribution modelling, ecophysiology, population connectivity, acoustic telemetry and angler perceptions and attitudes can play in assessing marine connectivity and contributing to improved management of this important fishery.

POPULATION CONNECTIVITY OF TWO COLD-WATER-CORAL SPECIES, *DESMOPHYLLUM PERTUSUM* (*LOPHELIA PERTUSA*) AND *MADREPORA OCULATA* IN THE ATLANTIC OCEAN AND MEDITERRANEAN SEA

Adrien Tran Lu Y *[1], Emilio Egal [1], Christine Felix [2], Jean-Marc Aury [3], Alexis M Weinning [4], Cheryl Morrison [4], Claudia Vaga [5], Santiago Herrera [6], Andrea Quatrini [7], Murray Roberts [8], Covadonga Oreja [9], Marie-Claire Fabri [10], Ricardo Tomás Pereyra-Ortega [11], Ann Larsson [11], Marcelo Visentini Kitahara [5], Nicolas Bierne [12] & Sophie Arnaud-Haond [1]
1. MARBEC, University of Montpellier, IRD, Ifremer, CNRS, Sète, France
2. MARBEC, Université de Montpellier, CNRS, Ifremer, IRD, Montpellier, France
3. Génomique Métabolique, Genoscope, Institut François Jacob, CEA, CNRS, France
4. U.S. Geological Survey, Eastern Ecological Science Center at the Leetown Research Laboratory, USA
5. Centre for Marine Biology, University of São Paulo, Brazil
6. Department of Biological Sciences, Lehigh University, Bethlehem, PA, USA
7. Department of Invertebrate Zoology, Smithsonian Institution, Washington, DC, U.S.A.
8. Changing Oceans Research Group, School of GeoSciences, University of Edinburgh, UK
9. Centro Oceanográfico de Gijón, Instituto Español de Oceanografia (IEO-CSIC), Spain
10. Institut Français de Recherche pour l'Exploitation de la MER (Ifremer), France
11. University of Gothenburg, Gothenburg, Sweden
12. ISEM, University of Montpellier, CNRS, IRD, Montpellier, France

Ongoing anthropogenic activities and climate change pose significant threats to ecosystems and organisms, including deep-sea species. Cold-water coral reefs, constructed by species like *Desmophyllum pertusum*, *Madrepora oculata*, and *Solenosmilia variabilis*, play a vital role in providing habitat for numerous species in the Atlantic Ocean. Despite their ecological importance, these deep-water reefs are understudied due to their remote locations, especially when compared to their shallow tropical counterparts. Previous genetic studies using microsatellite markers revealed partitioning into two large lineages for *D. pertusum* and *M. oculata* in the Northeast Atlantic and Mediterranean Sea. However, unclear signals persisted in the Atlantic populations, prompting the need for further research. To address these gaps, we realized a genomic study, generating reference genomes and conducting population genomics with 100 whole-genome re-sequencing samples for each species from the Mediterranean Sea and Northeast Atlantic. International collaboration facilitated by iAtlantic extended our analysis to include samples from the Western and Southern Atlantic regions. Our findings at the European region scale uncovered surprising results. *D. pertusum* exhibited multiple lineages with subtle genetic differentiation. At the Atlantic scale, a notable east-west genetic divergence emerged, revealing a closer relationship between US and Brazilian populations than European populations. Intriguingly, *M. oculata* demonstrated highly divergent lineages across the Atlantic and Mediterranean Sea, indicating a complex of cryptic species rather than distinct populations. Notably, a significant differentiation was observed between at least two Atlantic groups of populations, lacking geographic coherence and suggesting a complex history with possible partial reproductive isolation. Furthermore, our whole-genome analysis suggested the non-negligible role of clonal reproduction in these species. Overall, our genomic approach provides valuable insights into the biology, distribution, connectivity, and management of these crucial deep-water coral reefs amid the challenges of climate change and human activities.

ASSESSING FISH SPACE USE AND HABITAT CONNECTIVITY IN A CONTEXT OF OFFSHORE WIND ENERGY DEVELOPMENT USING ACOUSTIC TELEMETRY

Couturier Lydie I. E. *[1], Labourgade Pierre [1, 2], Trancart Thomas [2], Bourjea Jérôme [3], Woillez Mathieu [4], Stephan Eric [5], Gonse Marine [4], Laurans Martial [4], Reubens Jan T. [6], Lenfant Philippe [7]
1. France Energies Marines, France
2. CRESCO, Muséum National d'Histoire Naturelle, France
3. MARBEC Sète, France
4. DECOD (Ecosystem Dynamics and Sustainability), IFREMER, INRAE, Institut Agro, France
5. Association pour l'Etude et la Conservation des Sélaciens (APECS), France
6. Flanders Marine Institute (VLIZ), Belgium
7. Université de Perpignan, CEFREM, France

In France, the increasing demand for decarbonized energy production has led to a rapid expansion of offshore wind farm (OWF) deployment. The introduction of these anthropogenic structures in the marine environment are likely to influence space use and habitat connectivity of fish. OWFs can act as artificial reefs for certain fish communities with species exhibiting high residency and/or site fidelity patterns for these new habitats. Alternatively, pressures generated by OWF, such as noise emissions, may repel certain species and modify movement and migration behaviour. Considering the ecological functions and socio-economic importance of fish communities, species responses to OWF need to be assessed through comprehensive and long-term monitoring to improve our understanding of impacts at ecosystem level. The collaborative FISHOWF project uses acoustic telemetry to identify how mobile fish species use and connect different habitats across OWF development areas in the Channel, Atlantic and Mediterranean Sea. This project relies on dedicated receiver arrays deployed within OWF, combined with the region-wide acoustic telemetry networks FISHINTEL (Channel), CONNECT-MED & RESMED (Mediterranean) to track over 400 fish/crustaceans (including sea bass, pollack, lobster, sharks and rays). Here we will present 1) how OWF may influence fish habitat connectivity, 2) how fish movements within and across OWF are monitored through the FISHOWF project and, 3) what information our preliminary results have brought on habitat connectivity for mobile species after 2 years of monitoring. Results will be used to better assess and understand the effect of habitat modifications induced by OWF from the seafloor to the surface.

POPULATION STRUCTURE AND CONNECTIVITY PATTERNS OF DEEP-SEA SPONGE GROUND FORMING SPECIES IN THE NORTH ATLANTIC

Taboada Sergi *[1], Arias María Belén [2], Gracia-Sancha Carlota [1], Mitchell Alex [2], Cranston Alex [2], Whiting Connie [3], Koustouvelli Vasiliki [4], Cárdenas Paco [5], Wang Shuangqiang [6], Ríos Pilar [7], Cristobo Javier [7], Davies Andrew J. [8], Rapp Hans Tore [9], Kenchington Ellen [6], Mienis Furu [10], Drewery Jim [11], Xavier Joana R. [12,9], Riesgo Ana [1]
1. Museo Nacional de Ciencia Naturales de Madrid, Spain
2. Natural History Museum of London, UK
3. University College London, UK
4. GEOMAR Helmholtz Centre for Ocean Research Kiel, Germany
5. Uppsala University, Sweden
6. Bedford Institute of Oceanography, Canada
7. Instituto Español de Oceanografía, Spain
8. University of Rhode Island, USA
9. University of Bergen, Norway
10. NIOZ Royal Netherlands Institute for Sea Research, The Netherlands
11. Marine Scotland Science, UK
12. CIIMAR-Interdisciplinary Centre of Marine and Environmental Research, University of Porto, Portugal

Deep-sea North Atlantic sponge grounds are crucial components of the marine fauna providing a key role in ecosystem functioning. These aggregations also provide important ecosystem services, since they represent complex habitats for many marine species, including commercial fish. Given the importance and fragility of these habitats and the anthropogenic threats they are currently facing, deep-sea sponge grounds have been recognized as Vulnerable Marine Ecosystems (VMEs). However, population connectivity and genetic diversity patterns in deep-sea species forming sponge grounds are poorly known in the North Atlantic, which is crucial to proper develop effective conservation and management plans. Here, we present our latest results on three species of deep-sea sponge ground forming species from the North Atlantic using a combined population genomics approach (ddRADseq) with 1000s of SNPS, with microbial community analyses. Our results for *Phakellia robusta* and *Phakellia ventilabrum* detected long distance genetic connectivity in samples collected from the British Islands to the North of Norway, despite samples were collected from a moderate bathymetric range. Interestingly, a clear genetic break was observed between samples from the Cantabrian Sea and the northernmost areas. Our results for *Geodia hentscheli*, covering the whole distribution of the species (>6000 km), detected two distinct genetic clusters segregated by depth, identifying a 1,300 m isobath as a potential dispersal barrier, as well as substructure in the shallower cluster, separating samples from the West and East North Atlantic-Arctic. The molecular connectivity and the genetic breaks observed are discussed in the light of major oceanographic currents in the area.

Talks

Session 3

Marine Functional Connectivity knowledge use for improved environmental policies and sustainable development

Conveners

Maria Beger (UK)
Andreu Blanco (Spain)
David Goldsborough (the Netherlands)
Ewan Hunter (UK)
Yael Teff-Seker (USA)
Ant Türkmen (Italy)

Session 3

Keynote

Anna Metaxas

ECOLOGICAL CONNECTIVITY IS ESSENTIAL TO MEET CONSERVATION TARGETS IN THE GLOBAL OCEAN

Metaxas, A.
Dalhousie University, Canada

The importance of ecological connectivity is being recognized in most major international fora dealing with biodiversity conservation, such as the Global Biodiversity Framework, the agreement on Biodiversity Beyond National Jurisdiction, and the regional environmental management plans for deep-sea mining by the International Seabed Authority. However, this recognition is currently not well-coupled with implementation in the oceans. I will present the current state of the incorporation of marine ecological connectivity in global conservation targets, and address some of the gaps and limitations for moving forward. Using some of our own research, I will provide examples of studies on connectivity that have direct implications for the design of networks of marine protected areas. I will present some tools and approaches that we have implemented and provide ideas on future directions to address the gap between the science of connectivity and its implementation in ocean management and conservation.

EXPERT SURVEY: THE NEXT STEPS FOR THE INTEGRATION OF MFC IN MARINE PLANNING, POLICY, AND CONSERVATION

Teff-Seker Y. *[1], Mackelworth P.M. [2], Darnaude A. [3], Goldsborough D. [4], Hunter Ewan [5], Kot C. Y. [6]
1. University of California, Davis, CA
2. Blue World Institute, Croatia
3. MARBEC, Monpellier, France
4. Van Hall Larenstein University, Leewarden, NL
5. Agri -Food and Biosciences Institute (AFBI), NI
6. Duke University, Beaufort, NC

A deeper and more comprehensive understanding of the functional connectivity of marine populations and habitats (MFC) is essential for conservation and sustainable development efforts, as it is fundamental for ensuring long-term ecosystem and species resilience, and for controlling the spread of invasive species. Following a 2023-2024 two-phase qualitative Delphi survey of 71 experts belonging to the European COST Action “Unifying Approaches to Marine Connectivity for Improved Resource Management for the Seas” (aka SEA-UNICORN), we gained expert insights into the recommended next steps for integrating MFC into decision-making processes, and for transforming MFC science into actionable policies and strategies. Insights from this survey include the need for collaborative science-stakeholder platforms, including data sharing, and data integration; encouraging inter-disciplinary approaches to MFC and providing MFC training for marine scientists; a clear, unified, and practical definition of MFC; creating better spatial MFC visualization maps; “translating” MFC science to non-scientists (e.g., via policy briefs), including collecting case studies of MFC-integration success and failure cases, providing easy-to-apply MFC-informed measurement methods for monitoring, and providing clear and straightforward mitigation strategies and guidelines for marine area management and MSP. Addressing future challenges, MFC experts emphasized the difficulty - and yet the necessity - of predicting and adapting to climate change through comprehensive MFC-informed models. Another future challenge is the predicted intensification of marine uses and therefore added cumulative pressure on marine resources, creating a need for species-specific, and use-specific planning, as well as the development and integration of emerging monitoring and mitigation technologies and practices.

TRACING A VISION FOR CHALLENGE 2 OF THE UN DECADE OF OCEAN SCIENCE FOR SUSTAINABLE DEVELOPMENT: CO-DESIGN TO SUPPORT CONSERVATION, RESTORATION, AND EQUITABLE DEVELOPMENT

Frank Muller-Karger [1], Aileen Tan Shau Hwai [2], and Working Group for Ocean Decade Challenge 2 [3]
1. College of Marine Science, University of South Florida, Florida, USA
2. Universiti Sains Malaysia, Malaysia
3. Ocean Decade Vision 2030 WG2 (https://oceandecade.org/vision-2030/)

The UN Decade of Ocean Science for Sustainable Development (the Ocean Decade) has launched a strategic ambition-setting process to identify common measures of success for the 10 Ocean Decade Challenges on the road to 2030. The process seeks to answer the question: What does success look like for these Challenges at the end of the Decade? Each of the 10 Challenges is led by a Working Group that includes representatives from Decade Actions, government, intergovernmental organizations, private sector, Indigenous and local communities, early career ocean professionals, non-governmental organizations, academia, and philanthropic foundations. Members represent diverse demographics, genders, and age groups, and are led by two Co-Chairs. Each Working Group is developing a White Paper to present a draft strategic ambition at the Ocean Decade Conference planned for Barcelona (10-12 April, 2024). The process is managed by IOC/UNESCO in its role as coordinator of the Ocean Decade. Working Group 2 addresses Challenge 2, namely to “Protect and restore ecosystems and biodiversity. Understand the effects of multiple stressors on ocean ecosystems, and develop solutions to monitor, protect, manage and restore ecosystems and their biodiversity under changing environmental, social and climate conditions.” We present the status of the White Paper on Challenge 2 and invite participants to contribute to shaping the implementation of a vision that goes beyond 2030. Achieving this vision requires specific actions that use co-design and partnerships between social and natural scientists, engineers, and stakeholders to find solutions.

THE INTERFACE OF MARINE CONNECTIVITY RESEARCH AND THE LEGALISATION OF CONNECTIVITY FOR ITS PROTECTION

L.B.L. Lyons Youna*[1], Huang Danwei [2]
1. National University of Singapore, Singapore and Advisory Committee on Protection of the Sea, UK
2. National University of Singapore, Singapore

As is highlighted by the Sea-Unicorn project, marine connectivity has multiple facets that underpin ecosystem functionalities and their overall resilience. The critical features uncovered by scientific research undertaken on this topic therefore need considering in the context of the design of adequate protection and preservation measures under international and global instruments. However the latter functions with its own legal and institutional systemic constraints. Concepts of marine connectivity have progressively entered a large number of global and regional instruments and mechanisms that provide for rules, standards and guidance to protect and preserve the marine environment, as a criterion to identify a marine area as sensitive and consider its eligibility to different protective measures (or a stronger duty). This paper examines first the concept of connectivity adopted in the context of developments under more than 15 international and regional instruments. Second, broad features of this 'legalised' scientific connectivity are categorised according to substantive types of application (e.g. genetic connectivity or migratory species' critical habitat connectivity) and purpose (identification for further monitoring or protection), as well as geographic applicability. Third, these are compared with broad types and purposes of marine connectivity concepts in marine scientific research, including processes of structural and biophysical connectivity, timescale considerations and their relationship to elements of functional connectivity. Fourth, the significance of 'legalised' connectivity concepts and their value to MFC research is discussed, including their limitations. The conclusion proposes an overarching taxonomy of connectivity designed to connect the scientific understanding of MFC to the global legal architecture.

CO-DESIGNING ECOLOGICAL CONNECTIVITY RESEARCH IN THE SOUTHWEST INDIAN OCEAN

Baronce Roseline *[1], Bailly Denis [1]
1. UMR AMURE, UBO, Brest and Reunion Island, France

Since 2022, the project CAFRINE ((Connectivity at lArge scale FoR local management in the INdian ocEan) has set up a research-action project in close collaboration with the French maritime affairs and the south Indian ocean overseas maritime council, focusing on ecological connectivity at the level of French overseas territories. With the objective of co-designing a research that would inform environmental policy in the coastal zones, water quality, conservation or resources management, the proposal was to consider simultaneously land to sea continuum and highseas to coastal seas ecological connectivity. The initial consultation process shows that the research community has focused on levers for action based on the study of connectivity in support of marine protected areas and on a decade of research programmes aimed at consolidating scientific measurement tools and understanding and identifying levers for transforming socio-systems. But knowledge of functional marine connectivity is addressed mainly within the concept of the land-sea continuum, with little interest if any for marine ecological connectivity. Furthermore, this research is not integrated in causal diagnosis of DPSIR or D(A)PSI(W) type as recommended when it comes to integrating knowledge into public policy. The multi-stakeholder group in the CAFRINE workshops highlighted the importance of scientific issues surrounding marine biological connectivity. Finally, although the ecosystem networks of connectivity science and research players are complex to maintain, networking remains the most integrative research approach to use and build the knowledge of marine ecological connectivity needed at all the scales in the Indian Ocean.

CONTRIBUTION TO IMPROVING KNOWLEDGE AND MANAGEMENT ON THE CONNECTIVITY OF MIGRATORY CATADROMOUS SPECIES, *ANGUILLA MOSSAMBICA*, IN THE SOUTH WEST OF INDIAN OCEAN

O'Brien Gordon *[1], Bailly Deny [2], Kihia Charles M. [3], Mbaru Emmanuel [4], Gitonga Lena M. [5], Gaspare Lydia [6], Nehama Fialho P.J. [7], Willows-Munro Sandi [8], Lavitra Thierry [9], Vaitilingon Devarajen [10], Baronce Roseline [2]
1. University of Mpumalanga, South Africa
2. UMR AMURE - Université de Bretagne Occidentale (UBO), Brest, Reunion, France
3. Egerton University, Kenya
4. Kenya Marine and Fisheries Research Institute, Kenya
5. Kenya Fisheries Service (KeFS), Kenya
6. University of Dar es Salaam, Tanzania
7. School of Marine and Coastal Sciences - Eduardo Mondlane University, Mozambique
8. University of KwaZulu-Natal, South Africa
9. Institut Halieutique et des Sciences Marines (IH.SM) - University of Toliara (UTUL), Madagascar
10. Bluquest Consulting, Mauritius

In the south-west Indian Ocean, catadromous fish are known to migrate to the spawning area in the open sea and return to the rivers to grow into their adult phase for many years. Thus, their life strategy raises the question of how to define and consider marine ecological connectivity in a sustainable management plan at a regional scale. Therefore, the Western Indian Ocean Anguillidae Eels project has been designed to contribute to the knowledge of the connectivity of eel species which one of the 4 species presents in the region, *Anguilla Mossambica*, has a conservation status near threatened and declared critical in one of the island of the Mascarene archipelago. Consequently, will local communities take into account marine functional connectivity for the sustainable management and restoration of WIO Anguillidae eels in their management or future management? The socio-ecological systems of the SWIO include unique connected biodiversity and vulnerable human communities, both of which need to be carefully managed to ensure their sustainability. Eels are indicators of the well-being of social-ecological systems that can demonstrate their sustainable use and protection of these connected habitats, including marine ecosystem through marine protected areas. One of the expected outcomes is to describe the population dynamics and connectivity of SWIO eel populations and also determine the risk of multiple anthropogenic stressors affecting the Anguillid eels with different representatives from nations of the SWIO region including Kenya, Tanzania, Mozambique, South Africa, Madagascar, Reunion and Mauritius Islands.

LARVAL DISPERSAL AND CONNECTIVITY OF PHERONEMA CARPENTERI POPULATIONS IN THE AZORES

Viegas Cláudia N. [1], Juliano Manuela [2], Colaço Ana [1]
1. OKEANOS Institute of Marine Sciences, Portugal
2. University of the Azores, Portugal

The study of larval dispersal and connectivity between deep-sea populations is an important factor for effectively conserving and managing deep-sea environments and designing and implementing Marine Protected Areas. Dense sponge aggregations, known as “sponge grounds”, are a key component of marine benthic ecosystems, and characteristic organisms of the Azores deep-sea environment. These sessile organisms rely mostly on larval dispersal for their reproduction. Connectivity between specific Pheronema carpenteri sponge aggregations in the Azores archipelago was studied using biophysical dispersal model driven by 3-D hydrodynamic model. Different scenarios and biological traits were studied considering spawning seasonality and pelagic larval duration. Model results show how the regional circulation patterns drive larval dispersion, shaping population connectivity, and reveal the existence of connectivity between Pheronema carpenteri sponge aggregations in the Azores, Some areas present high retention rates, receiving larvae from several sponge aggregations. Those are also important source populations. In contrast, other populations are isolated from the others. Larval dispersal and connectivity patterns were used to assess the effectiveness of current Marine Protected Areas (MPA) in the Azores. Results reinforced the importance of maintaining the protection efforts in the existing MPAs, and new areas are proposed to maintain populations’ connectivity.

POPULATION GENETIC CONNECTIVITY OF THE ENDEMIC NEW ZEALAND GREENSHELL MUSSEL: APPLICATIONS TO AQUACULTURE, CONSERVATION AND PHYLOGEOGRAPHY

Gardner Jonathan P. A. *[1], Parada Roberto [1], Mendiola Mikel [1], Quigley Calvin N. [1,3], Chaput Romain [1,4], Toone Trevyn [2], Jeffs Andrew G. [2]
1. School of Biological Sciences, Victoria University of Wellington, New Zealand
2. School of Biological Sciences, University of Auckland, New Zealand
3. Present address, Woods Hole Institute of Oceanography, Woods Hole, Massachusetts, USA
4. Present address, Cawthron Institute, Nelson, New Zealand

New Zealand's endemic greenshell mussel, *Perna canaliculus*, is widely distributed on intertidal and shallow subtidal rocky reefs across the whole country, spanning approximately 12 degrees of latitude. It is an economically important aquaculture species and an ecologically important ecosystem engineer. This mussel is also a culturally important species to Māori, and is collected as food from many coastal locations, where its abundance is now often reported to be declining. Using genotyping-by-sequencing we developed a panel of neutral and non-neutral SNP loci to assess regional and national-scale genetic connectivity of this important species. We also employed particle tracking approaches to test connectivity in physical oceanographic models. Our results confirm previous findings of a pronounced north-south genetic discontinuity but for the first time we were able to identify between-regional differences within the northern group, and also within-region differences in one location and within-region homogeneity within another region. These results are relevant to, and will be discussed in the context of aquaculture and the movement of stocks around New Zealand, to ongoing conservation efforts to restore wild beds, and to our understanding of the evolutionary origin of the northern and southern mussel lineages.

POPULATION GENOMICS RESOLVES STOCK CONNECTIVITY OF EUROPEAN ANCHOVY (*ENGRAULIS ENCRASICOLUS*)

del Rio-Lavín Ane *[1], Díaz-Arce Natalia [1], Rodríguez-Ezpeleta Naiara [1]
1. AZTI, Marine Research, Basque Research and Technology Alliance (BRTA), Sukarrieta, Spain

Mismatches between management units (stocks) and biologically significant units might result in inappropriate assessment of fisheries resources and lead to overfishing or under exploitation. This could be the case of the commercially important European anchovy (*Engraulis encrasicolus*), assessed and managed as two stocks in southern Europe: the Bay of Biscay stock and the Atlantic Iberian waters stock, with a break point in Galicia. Studies performed so far have reported discrepant results regarding the stock connectivity of this species, partly due to ignoring the presence of the two genetically distinct ecotypes. To disentangle the connectivity patterns of European anchovy, we have assembled a dataset with thousands of single nucleotide polymorphisms (SNPs) from 382 individuals along the North-east Atlantic coast, from the English Channel (north) to the Canary Islands (south), including the Mediterranean Sea. Our population structure analyses reveal three genetically distinct groups: a southern lineage ranging from the Canary Islands to southern Portugal, a coastal lineage, present mostly in Atlantic and Mediterranean estuarine locations, and a third lineage present mostly in northern Atlantic and Mediterranean oceanic locations. Moreover, the Alboran is a transition zone, and the English Chanel is genetically distinct from the other northern Atlantic locations. These results have important management and conservation implications, supporting a redefinition of the stock delimitation in European anchovy, proposed south of Lisbon, and calling for a continuous monitoring in European anchovy to determine the role of the southern and estuarine lineages in shaping the genetic diversity the species.

CHALLENGING COMMON PARADIGMS IN MARINE CONSERVATION AND FISHERIES SCIENCES

Harrison Hugo B *[1], Jones Geoffrey P [2]
1. University of Bristol, UK
2. James Cook University, Australia

Marine conservation and fisheries management practices are often data-poor, resulting in decision frameworks that may be either ineffective or even counterproductive to their intended goals. Given the uncertainties in reproductive success, larval dispersal, and recruitment dynamics – processes that regulate fisheries stocks – sustainable fisheries and effective conservation measures must also incorporate hedging strategies to buffer against volatility in stock sizes and environmental disturbances. Here we show how empirical studies using genetic parentage analysis can inform management practices for an exploited species of coral reef fish: the bar-cheek coral grouper (Plectropomus maculatus) in the Keppel Islands, Great Barrier Reef – Australia. We combined the results of parentage analysis with in-water surveys of adults and ageing of juvenile fish to provide empirical data on the recruitment contribution of no-take marine reserves, size-based reproductive success of adult fish, and the likely timing of spawning activity. Our findings challenge common paradigms in the use of no-take marine reserves, size limits, and spawning closures in fisheries management and identify management strategies that can effectively buffer against the volatility of dispersal patterns to ensure a consistent replenishment of exploited fish stocks. The findings are broadly applicable to coral reef fisheries globally and highlight the value of parentage studies in ecology and fisheries sciences.

LONG-TERM MARK-RECAPTURE AND ACOUSTIC TELEMETRY REVEAL SIZE-SPECIFIC MOVEMENTS OF THE EUROPEAN SPINY LOBSTER, PALINURUS ELEPHAS

Gonse Marine *[1], Woillez Mathieu [1], Quémeneur Erwan [2], Buanic Mickaël [3], and Laurans Martial [1]
1. DECOD (Ecosystem Dynamics and Sustainability), IFREMER, INRAE, Institut Agro, Brest, France
2. Comité Départementale des Pêches Maritimes et des Elevages Marins du Finistère, France
3. Parc Naturel Marin d'Iroise, France

Understanding the spatial behaviour of exploited marine species is essential for effective management strategies. The European spiny lobster, *Palinurus elephas*, has experienced a significant decline in catches since the 1960s in the Bay of Biscay and the Channel. In response, a series of management measures have been implemented in France. Fishers established a strict protected area for spiny lobsters in the Iroise Sea in 2007. Starting from 2009, an annual mark-recapture survey using conventional tags has tracked over 1622 individuals, providing abundance estimates and multiple recaptures. In 2015 and 2016, as part of the LR2 project, fishers tagged 6000 immature spiny lobsters along the French Atlantic and Channel coasts. By September 2023, 427 individuals have been recaptured either by professional fishers or during annual surveys conducted within the protected area. Immature spiny lobsters exhibited extensive movements, traveling up to 800 km from their release sites, while mature ones displayed a more sedentary behaviour, indicating size-specific movements. In 2022, four acoustic receivers were deployed in the protected area as part of the Fish Intel project. Twenty spiny lobsters were equipped with acoustic transmitters, capturing their presence and depth data. Initial findings showed strong residency of individuals in the protected area. Immature spiny lobsters spent longer durations outside the network compared to mature ones, suggesting size-specific residency behaviours. As more data accumulates, integrating various tracking methods will better characterize the functional connectivity of the European spiny lobster, facilitating the implementation of tailored spatial management strategies for its sustainable exploitation.

RANGE-WIDE GENETIC DIVERSITY INDICATES EXTENSIVE CONNECTIVITY IN CARIBBEAN SPINY LOBSTERS

Ellis Charlie D. [1], King R. Andrew [1], Ellis Robert P. [1], Stevens Jamie R. *[1]
1. University of Exeter, UK

The use of genetic data to designate populations within frameworks relevant to shared evolutionary histories, environmental adaptations and demographic independence is a critical step towards enacting effective conservation management. Using RAD-sequencing, we genotyped thousands of SNPs across hundreds of individuals from 14 sites encompassing near range-wide coverage of the Caribbean spiny lobster, *Panulirus argus*, to investigate population genetic diversity, structure and adaptation. We evidence high genetic diversity and little population structuring across extensive spatial scales, indicative of panmixia and high demographic connectivity. We also determine that outlying individuals are not explained via interspecific introgression with four other Panulirus species of potentially overlapping distributions. In order to provide a tool relevant to future molecular research, we identify a subset of hypervariable loci linked to inter- and intra-specific variation in P. argus, and use these to develop SNP assays compatible with high-throughput applications. We affirm their effectiveness to provide robust and rapid genotyping, even of poor quality samples, to characterise genetic diversity and variation. The relevance of these developments and our findings are explored with reference to conservation management of *P. argus* populations, along with consideration of the importance of quality RAD-seq data and bioinformatic filtering processes to SNP discovery and downstream impacts to population genetic analyses.

SETTING THE MULTIDISCIPLINARY BASIS TO INTEGRATE FUNCTIONAL CONNECTIVITY INTO SPATIAL STOCK ASSESSMENT MODELS: THE CASE OF RED MULLET IN THE NORTHWESTERN MEDITERRANEAN SEA

Kerametsidis Georgios [1,2], Rossi Vincent [3], Goethel Daniel [4], Álvarez-Berastegui Diego [1], Barnes Cheryl [5], Certain Gregoire [6], Esteban Antonio [7], García Encarnación [7], Jadaud Angelique [6], López-López Lucía [8], Morales-Nin Beatriz [9], Mourre Baptiste [10], Pérez-Mayol Sílvia [9], Piñeiro Safo [1], Reglero Patricia [1], Ser-Giacomi Enrico [11], Thorson James [12], Vivas Miguel [7], Hidalgo Manuel *[1]
1. Oceanographic Centre of the Balearic Islands (IEO-CSIC), Spain
2. University of the Balearic Islands, Spain
3. Mediterranean Institute of Oceanography, France
4. NOAA, Alaska Fisheries Science Center, Juneau, USA
5. Oregon State University, USA
6. MARBEC Montpellier, France
7. Oceanographic Centre of Murcia (IEO-CSIC), Spain
8. Oceanographic Centre of Santander (IEO-CSIC), Spain
9. IMEDEA, Spain
10. SOCIB, Spain
11. IFISC, Spain
12. NOAA, Alaska Fisheries Science Center, Seattle, USA

Achieving sustainable management of marine resources and implementing biologically realistic assessment depend on accurate identification of stock structure. Most harvested marine species are currently assessed under the broad and long-standing assumption of “unit stock” within designated spatially and temporally invariant polygons known as assessment units, despite evidence of passive and/or active dispersal across multiple scales. Presumably, the main challenges moving toward spatially explicit stock assessment models are to obtain adequate connectivity information and to incorporate it into the models. Here, we combined spatiotemporal modelling, fisheries-dependent and -independent data, simulated larval dispersion and chemical markers to investigate the connectivity and structure of the red mullet (*Mullus barbatus*) populations in the Northwestern Mediterranean Sea, the third most important demersal fish species of the Mediterranean Sea. We observe discrepancies between the actual biological subpopulations and the presently recognised "closed" assessment units, thus documenting a metapopulation system. When evaluating each subpopulation, we find that their demographic roles are dissimilar, and we show that a high proportion of individuals born in a given unit may settle and recruit in distant areas within and outside the boundaries of the assessment unit. This transport is of elevated importance for species that do not migrate during their adult phase, as red mullet. We then attempt to incorporate this information into a spatially explicit assessment model, and we finally compare conventional (i.e., “closed”) and connectivity-integrated stock structures. Our research emphasizes the value of spatial stock assessment frameworks that would include a range of important, yet still largely disregarded, ecological information.

DEVELOPING A SPATIAL STOCK ASSESSMENT MODEL TO ACCOUNT FOR THE COMPLEX SEA BASS POPULATION STRUCTURE AND CONNECTIVITY

Woillez Mathieu *[1], Drogou Mickael [1], Gonse Marine [1], Goossens Jolien [2, 3], Reubens Jan [3], Wright Serena [4], Hunter Ewan [4, 5], Lambert Gwladys [4], Hyder Kieran [4], Bertignac Michel [1]
1. DECOD (Ecosystem Dynamics and Sustainability), IFREMER, INRAE, Institut Agro, Brest, France
2. Marine Biology Research Group, Ghent University, 9000 Ghent, Belgium
3. Marine Observation Centre, Flanders Marine Institute, 8400 Ostend, Belgium
4. Centre for Environment, Fisheries and Aquaculture Science, Lowestoft, Suffolk, UK
5. Agri-Food and BioSciences Institute, Belfast, United Kingdom

Because animal movements and migrations shape internal dynamics and population structure, the choice of inappropriate spatial and/or temporal scales for assessing wild populations can have disastrous effects on their exploitation and conservation. In the case of the Northeast Atlantic sea bass population, ICES currently considers four assessment stock units. Two of those are assessed analytically with one covering the North Sea, Channel, Celtic Sea and Irish Sea and the other the Bay of Biscay. However, the last ICES stock identification workshop has reviewed new evidence regarding biologically relevant stock boundaries of sea bass using tagging data, genetic analyses, scientific surveys, and egg and larvae drift connectivity modelling. Experts have proposed new plausible stock structure hypotheses for the assessment of the seabass stocks based on three meta-populations located in the Irish Sea, the North Sea and the Bay of Biscay with some mixing occurring in a central area, whose limits vary between hypotheses. Mixing is seasonally dependant with more mixing occurring during summer compared to winter. Here we present the data requirements and key elements that need to be accounted for to test those population structure hypotheses and help develop a spatial stock assessment model in Stock Synthesis. More specifically, large-scale conventional and electronic tagging data have been collected on both side of the English Channel and along the French coast. They allowed the description of seasonal migration, site fidelity and sea bass behaviour. They can also be used to estimate movement rates between meta-population or stock areas, some of the fundamental parameters required to account for mixing, a key modelling challenge in a spatial stock assessment model.

USING THE POWER OF COMMUNITY DETECTION IN MARINE ECOLOGICAL NETWORKS

Pastor Ane *[1], Treml Eric A. [1]
1. Australian Institute of Marine Science (AIMS) and UWA Oceans Institute, The University of Western Australia, Crawley, WA, Australia

Habitat loss, fragmentation, and degradation primarily resulting from human activities pose a significant threat to global biodiversity. Due to these pressures, the management and monitoring of populations within complex habitat mosaics becomes exceptionally challenging, necessitating proper zonation and bioregionalization. Over the past few decades, efforts have been made to delineate terrestrial and marine systems into management zones, and in the last 20 years these systems have been treated as networks. The application of network theory has become integral to understanding ecological landscapes. Here, networks consist of a set of nodes (e.g., habitat patches, islands or populations) connected by edges or links (e.g., movement, dispersal probability). In network terms, tightly grouped nodes are considered communities that exhibit a higher likelihood of connecting to each other than with nodes from other communities. Applying these network-based community detection algorithms to terrestrial landscapes and the marine seascape can help identify effective management and conservation units. This novel network perspective is particularly relevant in the marine environment, where applications range from selecting marine protected areas and delineating fisheries zones to managing and monitoring marine invasive species. Despite these advantages, there is no consensus on the application of these algorithms, and a clear application to ecology has not been well-documented. This study reviews the science of community detection in ecological networks, identifying common algorithms, and evaluating their effectiveness and appropriate use through several marine connectivity case studies. This research demonstrates how one must appropriately select community detection algorithms to achieve a desirable conservation and management impact.

GENETIC CONNECTIVITY ASSESSMENT TO INFORM MARINE PROTECTED AREAS ESTABLISHMENT: A CASE STUDY OF AN ISOLATED FISH POPULATION IN THE SOUTHWESTERN ATLANTIC

Julia Tovar Verba *[1,2,3,4], Linda Hagberg [4], Maria Grazia Pennino [3,5], Carlos E. L. Ferreira [6], Priscila F. M. Lopes [1,3], Beatrice Padovani Ferreira [7] , Sergio Maia Queiroz Lima [8], Adam Stow [2]
1. Programa de Pós-Graduação em Ecologia, Universidade Federal do Rio Grande do Norte, Natal RN 59078-970, Brazil;
2. Conservation Genetics Lab Macquarie University, Sydney NSW 2109, Australia;
3. Fishing Ecology, Management and Economics, Department of Ecology, Universidade Federal do Rio Grande do Norte, Natal RN 59078-970, Brazil
4. Division of Evolutionary Biology, Faculty of Biology II, Ludwig-Maximilians-Universität München, Planegg-Martinsried 82152, Germany
5. Instituto Español de Oceanografía/Consejo Superior de Investigaciones Cientificas, Vigo 36390, Spain
6. Reef Systems Ecology and Conservation Lab, Marine Biology Department, Universidade Federal Fluminense, Niterói RJ 24220-900, Brazil
7. Department of Oceanography, Universidade Federal de Pernambuco, Recife PE 50740-540, Brazil
8. Laboratório de Ictiologia Sistemática e Evolutiva, Universidade Federal do Rio Grande do Norte, Natal RN 59078-970, Brazil

Despite the lack of obvious barriers, marine populations can present different levels of connectivity throughout their distribution. The degree of population connectivity of exploited species should be considered when defining conservation measures. We investigated the genetic connectivity of the endemic and exploited Gray Parrotfish, *Sparisoma axillare*. This vulnerable species is exploited and there is a dearth of ecological data needed to support sustainable management actions. Nine locations were sampled in coastal to oceanic environments with varying levels of protection. The combination of depth, ocean currents, and distance were the major drivers explaining patterns of genetic divergence between *S. axillare* populations. Samples from six coastal sites and from two off-coast sites showed high levels of connectivity. An isolated and genetically distinct population was revealed in the waters surrounding Trindade Island, located 1000km off-coast. Despite the Seamounts of Vitoria-Trindade Chain connect coastal and Trindade Island populations for several species, including from other parrotfishes, it does not seem to be for *S. axillare*. This indicates that, even species with shared life and evolutionary histories, levels of genetic connectivity can strongly vary. Our results have important management implications: a large no-take area has recently been established in part of Trindade Island, increasing country’s marine protection. However, this loosely regulated area is located in the open ocean, leaving out shallow areas. Despite bans to fisheries, these areas are still exploited. Granting Trindade full protection would provide a response to criticisms and give some respite to a unique and isolated *S. axillare* lineage.

SPATIAL PRIORITIZATION FOR MARINE FUNCTIONAL CONNECTIVITY IN THE MEDITERRANEAN

Çiçek Burak A. *[1], Türkmen Ant [2], Soğancı Mustafa [1], Akbora Hasan D. [1], Snape Robin T.E. [3], Beton Damla [3], Demirel Nazlı [4], Ulman Aylin [5], Candan Onur [6], Başkele Eyüp [7], Canpolat Ali F. [8], Broderick Annette [3], Godley Brendan [3], Beger Maria [9]
1. EKAD, Turkey
2. LifeWatch ERIC, Italy
3. University of Exeter, UK
4. Istanbul University, Turkey
5. Mersea, Turkey
6. Ordu University, Turkey
7. Pamukkale University Turkey
8. Hacettepe University, Turkey
9. University of Leeds, UK

Spatial prioritization at the Mediterranean level involves a comprehensive approach to conservation planning in one of the world's most biologically diverse and culturally rich regions. The Mediterranean Basin is characterized by its unique biodiversity, significant number of endemic species, and a long history of human habitation and use, which presents unique challenges and opportunities for conservation. Spatial prioritization in the context of conservation planning is a strategic approach to identify and prioritize areas for conservation action considering ecological, economical and social factors. The goal is to optimize conservation outcomes while considering the diverse needs and constraints of different stakeholders/sectors. This process is essential in managing and allocating limited resources efficiently to areas that will yield the highest conservation benefits. In this study, to optimize Marine Protected Area (MPA) planning, the process begun with creating planning units tailored to the movement of highly mobile marine species like whales and sea turtles. This involves transforming their movement tracks into GIS shapefiles for overlay with planning units, followed by the generation of a file outlining track-to-planning unit relationships. Connectivity matrices are then produced, encompassing all species tracks, and integrated into MarxanConnect, where specialized layers such as habitats, invasive species, and socio-economic costs like fishing and boat traffic are added. Through Marxan with Connectivity, various scenarios are analyzed to ensure robust MPA networks that foster good connectivity for conservation purposes while avoiding pathways that exacerbate the spread of invasive species, ultimately aiming for a balanced approach that upholds ecological integrity and considers human impact.

Speed Talks

Session 1

Multi-disciplinary approaches in Marine Functional Connectivity research

I-MarCo
2024

Conveners

Katell Guizien (France)
Cécile Fauvelot (France)
Anna Sturrock (UK)
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ONTOGENETIC CONNECTIVITY AND LIFETIME ESTUARY USE BY THE EUROPEAN ANCHOVY IN THE GULF OF CADIZ

Miró Juan M.* [1], Megina César [1], Donázar-Aramendía Iñigo [1], García-Gómez Jose C. [1], Tanner Susanne [2], Cameron Thomas [3], Trueman Clive [4], Sturrock Anna M. [3]
1. University of Seville , Spain
2. MARE - Marine and Environmental Sciences Centre/ARNET - Aquatic Research Network Associated Laboratory, Department of Animal Biology, Faculty of Sciences, University of Lisbon, Lisbon, Portugal
3. University of Essex, UK
4. University of Southampton, UK

The European anchovy *(Engraulis encrasicolus*) spawns in offshore marine waters and opportunistically uses estuaries as nursery grounds, with the warmer, shallower waters thought to enhance growth while providing refuge from large predators. To better understand this ontogenetic connectivity and to determine the importance of these ecosystems to the valuable anchovy fishery in the Gulf of Cadiz, we reconstructed lifetime habitat use using otolith element concentrations in juvenile and adult fish. Juvenile anchovies were sampled in inner and outer parts of the main four estuaries in the region for three consecutive years (2016-18) to generate a chemical atlas of coastal and estuarine nursery areas. Random forest classification models assigned known-origin juveniles correctly to their capture site with 84% accuracy (95% CI: 70-92%) using out-of-sample prediction. Application of these models to the juvenile region of adult otoliths suggested that 35% of adults had used estuaries as nursery areas, particularly the Guadiana estuary. While using known-origin juveniles from all years combined resulted in high classification success, individual elements often varied significantly among years, suggesting that cohort-matched samples should be used where possible. In a separate analysis, using otolith Ba/Ca as a proxy for estuary entry, otolith barium profiles suggested that 72% of adults had used an estuary at some point in their lifetime demonstrating the importance of these habitats across all life stages. These results demonstrate the importance of protecting and restoring estuary habitats, and maintaining functional connectivity across the salinity gradient, for supporting one of the most valuable fisheries in the region.

DEVELOPMENT OF PASSIVE ENVIRONMENTAL DNA SAMPLERS FOR THE DETECTION OF RARE AND ELUSIVE MARINE MEGAFAUNA

Medetian Dimitri *[1], Rolland Jean-Luc [2], Felix Christine [2], Cornu David [3], Bechelany Mikhael [3], Cambedouzou Julien [3], Arnal Véronique [1], Miaud Claude [1]
1. CEFE Montpellier, France
2. MARBEC Montpellier, France
3. IEM, Univ. Montpellier, Montpellier, France

Our team is currently developing a set of passive sampler that can effectively trap environmental DNA (thereafter eDNA ie DNA naturally released by organisms) in marine ecosystems to detect low density and mobile megafauna through time and space. Classical eDNA inventories are based on boat transects and water pumping and have proven to be highly effective in marine waters to describe the local aquatic communities. However, mobile taxa and taxa with low abundance are prone to be underestimated or missed with this method. Thus, an innovative interdisciplinary approach is conducted (molecular biology, physical oceanography, materials science, ecology) to tackle this challenge. We are optimising this passive sampler to trap and preserve from degradation the highest quantity of eDNA in order to maximise chances of detection of rare and mobile megafauna. With previous laboratory tests, mesocosm experiments and in natura studies, the goal is to propose an adapted sampling plan (number of samplers, localisation, depth, exposition time) in accordance with eDNA dispersion modeling in open sea. The space-time aspects of samplers immersion will be conditioned to targeted species and both biotic (biofouling) and abiotic constraints (temperature, dissolved oxygen…). This study can therefore provide new insights to evaluate the movements and the distribution of marine megafauna. In this short presentation we will present the global project and the on-going results, especially concerning the sampling prototype validation.

TIDES OF GENETIC EXCHANGE: EXPLORING THE IMPACT OF REPRODUCTIVE STRATEGIES AND OCEAN CURRENTS ON SCLERACTINIAN CORAL CONNECTIVITY IN THE DUTCH CARIBBEAN

López-Márquez V.*[1,2], Scherpereel C.[3], HellemansB. [2], Mijts E.N.[1], Hanert E.[3],. Volckaert F.P.[2]
1. SISSTEM programme, University of Aruba, Oranjestad, Aruba
2. Laboratory of Biodiversity and Evolutionary Genomics, KU Leuven, B-3000 Leuven, Belgium
3. Earth and Life Institute & Institute of Mechanics, UC Louvain, B-1348 Louvain-la-Neuve, Belgium

Dispersal dynamics shape the (meta)population dynamics of marine organisms. This study explores (i) the interplay between ocean circulation and two reproductive strategies of scleractinian corals, and (ii) their collective impact on genetic connectivity off the islands of Aruba, Bonaire and Curaçao. The reproductive mode of corals, specifically in the case of brooders and broadcast spawners, significantly influences the genetic structuring of their populations. We hypothesize that local brooding corals are more genetically structured compared to species with external gamete broadcasting, where the planula larvae reside longer in the water column. 3D hydrodynamic simulations replicating ocean circulation of the Caribbean Current off the islands coupled to an individual based model simulating the biological traits of the brooding corals *Favia fragum* and *Porites astreoides*, and the broadcast corals *Diploria labyrinthiformis* and *D. strigosa*, provide a first assessment of the complex abiotic connectivity. As expected, the potential of broadcast spawners to disperse proves much higher. Genotyping of all four species with about 15 microsatellite markers each reveals high genetic differentiation of brooding corals, and comparatively lower levels of broadcast spawners. We also observe occasional dispersive events of brooding corals that contribute to the considerable genetic diversity, and evidence of source-sink dynamics. Our thorough analysis of population connectivity and genetic structure in scleractinian corals enhances our understanding of reef ecosystems and establishes a basis for well-informed conservation decision-making. This research plays an important role in advancing the long-term sustainability efforts of these crucial reef-building species.

PARALLEL PATTERNS OF DIFFERENTIATION AT CHROMOSOMAL INVERSIONS AND OTHER GENOMIC REGIONS IN THE EUROPEAN FLAT OYSTER

Colston-Nepali L.*[1,2], Doniol-Valcroze P.[3], Reisser C [1], Fraisse C.[4], Cornette F.[1], Bierne N.[2], Lapègue S.[1]
1. MARBEC, Montpellier, France
2. ISEM, Montpellier, France
3. CEFE, Montpellier, France
4. EEP, Lille, France

Chromosomal inversions can contribute to local adaptation by reducing recombination between co-adapted alleles. However, the importance of inversions in parallel evolution is not well understood. In this study, we investigate the contribution of chromosomal inversions to parallel evolution in the European flat oyster, *Ostrea edulis*. Previous work identified parallel evolution between geographically distant populations at putative chromosomal inversions. However, marker density was too low to identify smaller genomic regions reflecting parallel signals of evolution. To further investigate this pattern, we used whole genome sequencing to analyze 35 individuals throughout the range of the flat oyster. We confirmed the presence of three polymorphic chromosomal inversions, two of which demonstrated a parallel pattern of differentiation. In addition, we identified narrower signals of parallelism between genetic lineages throughout the genome, not just within inverted regions. Demographic history analyses revealed a signal of secondary contact, suggesting that chromosomal inversions as well as the non-inverted islands of genetic parallelism retain a shared evolutionary history that has been erased by recent gene flow in the majority of the genome. Our findings indicate that while chromosomal inversions may play an important role in parallel evolution, other genomic regions may also be involved. Finally, these results may have implications for conservation management. The flat oyster is an economically important species that has experienced a large decline in population size due to overexploitation. Understanding the contrasting patterns of population structure in this species may be an important step to informing translocations and other management actions.

EVOLUTIONARY HISTORIES OF THE NATIVE AND NON-INDIGENOUS CLAMS, *RUDITAPES DECUSSATUS* AND *R. PHILIPPINARUM*

Riquet Florentine *[1], Painblanc Solène [1], Heurtebise Serge [1], Le Clanche Ulysse [2], Cormier Alexandre [2]
1. ASIM, La Tremblade, France
2. SeBiMer, Brest, France

Along the French coast, two clam species live in sympatry: the grooved carpet shell clam, *Ruditapes decussatus,* endemic to European coasts, and the Manila clam, *R. philippinarum*, introduced to European coasts in the 1970s. This introduction has led to evolutionary changes in both species: (i) a strong foundation effect (i.e. loss of genetic diversity linked to the introduction of a small number of individuals into a new environment) has been observed in the Manila clam in Spain and (ii) a loss of genetic diversity expected in the grooved carpet shell clam following the significant reduction in populations throughout its distribution ranges. However, the evolutionary history of these two species is relatively poorly described. Based on 78 whole genome sequencing, we inferred the evolutionary history of these two clam species by analyzing genetic structure on a large scale, by delineating genetic lineages in each species and by studying the co-introduced pathogen *Perkinsus olseni* spillover in *R. decussatus*.

TROPHIC CONNECTIVITY: UNDERSTANDING SPATIAL FORAGING BASED ON COMMUNITY ISOTOPIC SIGNATURES

Ortiz Juan J. *[1], Preciado Izaskun [1], Hidalgo Manuel [2], Vivas Miguel [3], Rabanal Irene M. [1], García-Rodríguez Encarnación [3], Esteban Antonio [3], López-López Lucía [1]
1. Spanish Institute of Oceanography (IEO-CSIC), C.O. Santander, Santander, Spain
2. Spanish Institute of Oceanography (IEO-CSIC), C.O. Baleares, Palma, Spain
3. Spanish Institute of Oceanography (IEO-CSIC), C.O. Murcia, San Pedro del Pinatar, Spain

Trophic connectivity accounts for species connecting different habitats, food-webs and ecosystems while performing foraging movements, being one of the least studied components of marine functional connectivity. Here, we propose, for the first time, the use of bulk stable isotope signatures at the community level to quantify species foraging patterns, employing two complementary approaches. Firstly, we estimated the residuals from a demersal community isotopic signatures, eliminating the effect of species and individual length from the raw data. Based on these residuals, this approach represents an approximation to baseline isoscapes of nitrogen (δ15N) and carbon (δ13C), using mean spatial patterns in isotopic residuals of the demersal community. This approach allowed us to estimate the baseline as an anomaly, and integrating the contribution of benthic and pelagic resources in demersal predators' diet. Results were particularly promising for δ13C, explaining 30.2% of the baseline variability associated to environmental factors such as Chlorophyll-a (pelagic source) and sediment type (benthic source). Secondly, we addressed the variability of the community residuals to investigate the spatial scale at which habitat diversity could leave an imprint on isotopic signatures. To achieve this, we linked the spatial variance of isotopic residuals with habitat diversity at different spatial scales. Our results identified an effect of habitat diversity in δ15N at small scales for some of the species closely associated to the bottom, suggesting that habitat diversity could be predictor for trophic diversity in benthic-feeding species, being critical to protect this habitat heterogeneity given their crucial role in terms promoting trophic connectivity.

ASSESSING THE POTENTIAL OF GENOMIC CONNECTIVITY FOR THE RESTORATION OF CORAL FORESTS IN THE TWILIGHT ZONE

Costantini Federica *[1,2], Terzin Marko [1], Poliseno Angelo [3], Giordano Bruna [4,5], LA Torre Martina [2], Bramanti Lorenzo [5], Darnaude Audrey M. [6], Rossi Sergio [7,8]
1. Dipartimento di Scienze Biologiche, Geologiche e Ambientali, Università di Bologna, Ravenna, Italy
2. Consorzio Nazionale Interuniversitario per le Scienze del Mare, Roma, Italy
3. Molecular Invertebrate Systematics and Ecology Laboratory, University of the Ryukyus, Nishihara, Japan
4. Dipartimento della vita e delle Scienze Ambientali, Università di Cagliari, Cagliari, Italy
5. Laboratoire d'Ecogéochimie des Environments Bentiques, LECOB, Observatoire Océanologique de Banyuls sur mer, Centre National de la Recherche Scientifique (CNRS), Sorbonne Université, Bnayuls sur Mer, France
6. MARBEC Montpellier, France
7. Dipartimento di Scienze e Tecnologie Biologiche e Ambientali (DISTEBA), Università del Salento, Lecce, Italy
8. Universidade Federal do Ceara, Instituto de Ciencias do Mar (Labomar), Fortaleza, Ceara, Brazil

In the last years, the marine exploration of mesophotic environments, revealed complex and diverse animal forests in the so-called twilight zone. These structures are essential for maintaining the overall functionality of the ecosystem, but, despite their ecological importance, they face numerous threats due to human-related activities. To ensure the preservation of these invaluable habitats, genetic connectivity can provide valuable insight, allowing us to understand the processes of population maintenance and replenishment following disturbances. Information on genetic connectivity can be used to shape conservation and restoration strategies enhancing population resilience and establishing new ecological corridors that may strengthen the recovery of neighboring populations. However, genetic connectivity is not always included in the recent restoration activity plans. Here, we present how genetic connectivity data were used in three Mediterranean anthozoan species to increase our knowledge on their reproductive behavior, to resolve phylogenomic disparities within taxonomically problematic groups, and to understand which populations could serve as a potential source of genetic diversity for adjacent populations. Then, we present a roadmap in which this information establishes the basis for the development of innovative and sustainable protocols for the monitoring, restoration, and conservation of corals dwelling in the mesophotic zone.

MOVEMENT ECOLOGY AND THERMAL TOLERANCE OF THREE SYMPATRIC MULLET SPECIES IN A MODIFIED WARM TEMPERATE ESTUARY

Ziko Bantony A.*[1,2], Murray Taryn S[1], Childs Amber A. [2]
1. South African Institute for Aquatic Biodiversity, South Africa
2. Rhodes University, South Africa

Mugilids are a diverse group of fishes inhabiting a wide range of habitats, globally being utilised for various socio-economic purposes. These fishes often occur in high biomass and are abundant in many parts of their ranges, making them ideal environmental indicators of climate change. Despite their socio-economic and ecological significance, information on the movement ecology of these estuarine associated mugilids is largely lacking. As such, the movements of three co-occurring estuary-dependant mullet species were monitored using acoustic telemetry in the Kowie Estuary, Port Alfred, South Africa. A total of 31 mullets (13 striped mullet *Chelon tricuspidens* (234 – 330 mm fork length (FL)), 12 grooved mullet *C. dumerili* (190 – 303 mm FL) and six southern mullet *C. richardsonii* (223 – 303 FL)) were caught in the Kowie Estuary, and were surgically equipped with acoustic transmitters (V9, Innovasea). Movements of these three species are currently being monitored by a linear array of 23 acoustic receivers deployed from the estuary mouth to approximately 21 km upstream near the riverine-estuarine interface. Data from a 8-month monitoring period (March to October) have indicated high estuary use for all species. In addition, there is also evidence of interspecific habitat partitioning by the three species where *C. tricuspidens* generally use the lower reaches of the estuary, *C. dumerili* tend to occupy more of the middle reaches, and *C. richardsonii* utilise the middle to upper reaches. This information is essential in understanding the ecology of these species, information which is pivotal for habitat and fisheries management and conservation.

MAPPING THE INVASION POTENTIAL OF THE PACIFIC OYSTER IN THE BALTIC SEA THROUGH QUANTITATIVE GENETICS, ADAPTATION GENOMICS AND DISPERSAL MODELLING

Kinnby Alexandra [1,2], Robert Chloé [2], Havenhand Jonathan N. [2], Broström Göran [2], Bussière Luc [3], De Wit Pierre R. *[2,3]
1. Nofima AS, Tromsø, Norway
2. Department of Marine Sciences, University of Gothenburg, Sweden
3. Department of Biological and Environmental Sciences, University of Gothenburg, Sweden

Pacific oysters (*Magallana gigas*) originate in the northeastern Pacific Ocean, but have spread throughout the world in the past half-century due to human-mediated transport for aquaculture purposes. When introduced, they have the ability to rapidly transform the intertidal environment and form reef structures with large numbers of individuals clumping together, thus reshaping local ecosystems. Pacific oysters were introduced in Europe in the 1970s as a replacement for the dwindling local flat oyster stocks in aquaculture production, but rapidly spread all along the European coastline. They first arrived in Scandinavia in 2006, likely by larval dispersal from the west coast of Denmark, and since then they have spread also along the Scandinavian west coast. However, they have to date not colonized the brackish waters of the Baltic Sea, and it has been generally assumed that the entrance of the Baltic acts as a barrier due to the presumed inability of Pacific oyster eggs to be fertilized in low salinities. To test the above assumption, we have studied differences in fertilization rates among oysters along the invasion range, and examined the trait heritability through controlled crosses. We find that low-salinity fertilization rates are much higher near the range front, due to both plastic and genetic components. We also use whole genome sequence data to identify genomic regions associated with embryonal low salinity tolerance. Further, we biophysically model the dispersal potential of larvae at the current invasion front, and find that there is potential for the future spread of oysters into the Baltic.

THE IMPORTANCE OF ESTUARINE-RIVERINE AND ESTUARINE-MARINE CONNECTIVITY FOR FLATHEAD MULLET, *MUGIL CEPHALUS* IN A WARM-TEMPEARTRE ESTUARY

Mukhari Dinah L. *[1,2], Murray Taryn S. [1], Pegg Josephine [1], Childs, Amber-Robyn [2]
1. South African Institute for Aquatic Biodiversity, South Africa
2. Department of Ichthyology and Fisheries Science, Rhodes University, South Africa

Estuaries are transition zones connecting both freshwater and marine environments. These valuable environments, through their fish resources, provide high protein food, income generation and recreational activities for people living near their vicinities. Many fish species occupying estuaries, especially smaller-bodied species such as mullet, use estuaries as nursery habitats, but also use the neighbouring freshwater and marine environments to varying degrees. Global studies on flathead mullet *Mugil cephalus* show evidence of partial facultative migration, estuarine residency and sometimes extensive use of the freshwater environment. However, information regarding the timing, frequency and extent of dependency on these environments is lacking in South Africa. Here, we used acoustic telemetry to determine the importance of estuarine-riverine and estuarine-marine connectivity of *M. cephalus* in a warm temperate permanently open South African estuary by tagging 21 individuals and monitoring their movements for a period of one year. Results revealed the use of the entire estuary, with periods of high connectivity with the freshwater environment, particularly during spring high tides of warmer summer months, and the mouth region/marine environment throughout the year. Understanding this functional connectivity, through identification of seasonal movements, migration routes, and areas of high use, is crucial for the conservation and management of this species and the ecosystems in which they inhabit.

LONG DISTANCE GENETIC CONNECTIVITY OF *EUNICE NORVEGICA* WORMS LIVING IN ASSOCIATION WITH DEEP-WATER CORALS FROM THE NE ATLANTIC

Gracia-Sancha Carlota *[1], Ruíz Sofía [3], Roterman Nicolai [2],Taboada Sergi [1]
1. Museo Nacional de Ciencias Naturales (MNCN), Spain
2. University of Portsmouth, United Kingdom
3. Universidad Complutense de Madrid (UCM), Spain

Deep-sea corals such as *Lophelia pertusa* play a crucial role in the ecosystems where they occur, providing shelter for a plethora of marine organisms. Despite several studies having focusing on the genetic connectivity of this coral across the North Atlantic, little is known about the associated fauna. One such organism is the annelid *Eunice norvegica*, which inhabits the coral skeleton as an obligate symbiote. Here we present a genetic connectivity analyses of *E. norvegica* populations across the NE Atlantic at depths ranging 200-1,200 m using a combined 16S and ddRADseq (1067 SNPs) approach. Our results are consistent with a single panmictic genetic population across ca. 2000 km, which suggests that predominant oceanographic currents, such as the southward slope current, are able to connect distant locations through the passive transport of the planktotrophic larvae of *E. norvegica*. Genetic connectivity patterns have also been investigated in the NE Atlantic for L. pertusa, confirming the high degree of gene flow between coral habitats in the study area, which aligns with the conclusions presented in our study. This contrasts with *Phakellia ventilabrum*, a sponge-ground forming species with lecithotrophic larvae where recently published results indicate clear genetic structure between the Cantabrian and northernmost areas. Our study highlights the importance of using species with different dispersal potential to establish genetic connectivity patterns in order to provide proper recommendations for conservation purposes.

INFLUENCE OF LARVAL CONNECTIVITY ON THE POPULATION GENETIC STRUCTURE OF THE GREAT SCALLOP POPULATIONS IN THE IROISE SEA

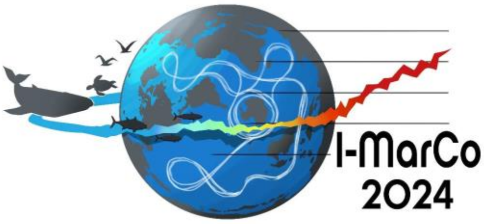
Charrier G.* [1], Bechennec N. [1], Le Gall R. [1], Handal W. [1], Marzloff M. [2], Cugier P. [2], Viricel A. [1] , Pante E. [1]
1. Univ Brest, CNRS, IRD, Ifremer, LEMAR, F-29280 Plouzané, France
2. Ifremer, DYNECO, LEBCO, F-29280 Plouzané, France

The Iroise Sea is a highly dynamic region, where larval dispersal is strongly influenced by particular hydrodynamic features such as the Ushant Front. This seasonal front separates from May to October stratified offshore waters from mixed coastal waters. Such a potential barrier to larval dispersal may play a significant role on the population genetic structure of bentho-pelagic species like the great scallop, *Pecten maximus*. This species of high economical value is largely distributed in the Iroise Sea and surrounding waters, like the Bay of Brest and the western English Channel. To explore how larval connectivity could shape the population structure of the great scallop in the Iroise Sea, 175 individuals sampled across seven sites were sequenced using a genotype by sequencing approach. In addition, larval dispersal modelling was realized using a high-resolution hydrodynamic model (MARS3D) to explore connectivity among fishing grounds from the Iroise Sea to the Western English Channel. Population genetics and modelling underlined a barrier to larval dispersal induced by the Ushant Front between the southern and the northern samples. In addition a northward dispersal pattern, from the Bay of Douarnenez to the Bay of Brest, emerged from the modelling. Thus, the lack of genetic differentiation found between the Iroise Sea and the Bay of Brest is likely induced by gene flow. Finally, a potential selective divergence between the Bay of Brest (including its outer entrance) and samples from the Iroise Sea, the Bay of Douarnenez and Western English Channel was emphasized, underlining fine-scale outlier genetic differentiation among great scallop fishing grounds.

Speed Talks

Session 2

Marine Functional Connectivity research and the global functioning and health of the Ocean



<u>Conveners</u>

Stéphanie D'Agata (France)
Amber Childs (South Africa)
Manuel Hidalgo (Spain)
Thomas Lamy (France)
Fabien Leprieur (France)
Lucía López López (Spain)

CRYPTIC SPECIES IN MARINE ANIMALS: WHERE DO WE FIND THEM AND WHY DOES IT MATTER?

Cahill Abigail E. *[1], Meglecz Emese [2], Tran Bach V. [1], Chenuil Anne [2]
1. Biology Department, Albion College, USA
2. IMBE, Aix Marseille University, France

Cryptic species (CS) are reproductively isolated units that are morphologically indistinguishable, and have been increasingly identified in the marine environment with the rise of molecular markers. Overlooking or ignoring CS can mean misestimating ecological parameters, including estimates of biodiversity or connectivity. We conducted a literature review and identified over 900 CS complexes in free-living marine animal species. Comparing these CS cases to data on all free-living marine animal species, we found that scientific history and biogeographical factors both contribute to the likelihood that a taxon contains CS: earlier-described species and species in the polar zones were more likely to contain CS. Species containing CS had larger ranges than those without. Biological factors also played a role, with hard skeletons, internal fertilization, and image-forming vision leading to fewer CS than expected within a taxonomic class. We then used this information to predict which taxonomic groups and oceans are more likely to contain missed CS complexes (e.g. where is overlooking CS more likely to lead to errors in parameter estimates). For example, although many CS have been identified in fish, a larger portion of CS are yet to be identified in other groups such as annelids or sponges. This information can be used to identify places or taxa in which connectivity may be misestimated due to the presence of CS.

THE EFFECTS OF EXPLOITATION ON THE ACTIVITY OF RED ROMAN (*CHRYSOBLEPHUS LATICEP*S) IN A THERMALLY VARIABLE ENVIRONMENT

Mlotshwa Nonhle T. *[1], Skeels Michael R. [1], Childs Amber-Robyn [1], Potts Warren [1], Winkler Alex [1], Muller Cuen [1], Duncan Murray M. [2]
1. Rhodes University, South Africa
2. Stanford University, California, United States of America

South Africa’s coastal environments are changing rapidly with some parts displaying extensive thermal variability. These rapid changes in temperature may push marine fish beyond their thermal tolerance threshold. Exacerbating the effects of climate variability is exploitation. Recent evidence has shown that exploitation reduces the population’s resilience to environmental stressors by reducing physiological diversity within populations through removing physically fit individuals. A recent study compared the relationship between field metabolic rate (FMR) and in-situ temperature of an exploited and unexploited population of a reef-associated commercial fishery species, Chrysoblephus laticeps, and found that the FMR and activity of fish in the exploited population was lower than that of the unexploited population, particularly at thermal extremes. The aim of this study was to augment our understanding of the impact of exploitation on the activity of C. laticeps across a thermal gradient by assessing a different exploited and unexploited population of C. laticeps in South Africa. To do this, *C. laticeps* were tagged with accelerometer transmitters in both sites. We found that temperature had a significant effect on the activity of fish in both populations ($p < 0.05$). Fish from the exploited population were less active than those from the unexploited population at warmer temperatures. These findings highlight how exploitation removes high thermal performance phenotypes, compromising the resilience of exploited populations against thermal variability. Our findings highlight the importance of marine protected areas for the promotion of fish populations’ resilience in the Anthropocene.

CONNECTIVITY VS. CONFINEMENT: THE STRUCTURING AXIS OF COMPLEXITY AND RESILIENCE IN COASTAL LAGOONS

Pérez-Ruzafa Angel *[1], Fernández-Alías Alfredo [1], Pérez-Marcos María [2], Marcos Concepción [1]
1. Department of Ecology and Hydrology, Campus of International Excellence “Mare Nostrum”, University of Murcia, 30100 Murcia, Spain.
2. Laboratory of Biological Control and Ecosystem Services, Institute for Agricultural and Environmental Research and Development of Murcia (IMIDA), La Alberca 30150, Spain

Confinement is one of the main parameters proposed to explain gradients of biological richness, abundance and productivity in coastal lagoons. Since its original proposal at the end of the 20th century, this concept, initially formulated as a turnover rate or gradient of influence of trace elements of marine origin, has evolved towards colonisation rates of individuals and species from the open sea and their role in the functioning of lagoon communities. This links this concept to that of functional connectivity, which is playing an increasingly important role in considerations of conservation measures and the design of marine protected area networks. The two concepts could be seen as two opposing forces in ecosystem structuring. Coastal lagoons are therefore a good example to understand the true extent of both vectors in the generation of biodiversity and complexity in marine ecosystems and the emergent properties such as resilience and homeostatic capacities that arise from the combination of both, which are essential for the adaptation of species and ecosystems to human pressures and climate change. In this work we review the mechanisms of action of both processes and their effects on the genetic structure of populations, community structuring and ecosystem responses to pressures such as eutrophication.

INTEGRATION OF GENETIC CONNECTIVITY AND LOCAL ADAPTATION IN THE DESIGN OF MARINE PROTECTED AREAS IN THE SOUTHERN OCEAN: A CASE STUDY OF TREMATOMUS FISHES

Verheye Marie L. *[1]#, Christiansen Henrik [1,2]#, Aerts Dorien [1,3], Van de Putte Anton [3,4], Schön Isa [3], Geslain Enora [1], Hellemans Bart [1], Volckaert Filip. A.M. [1]
#co-first authors
1. Laboratory of Biodiversity and Evolutionary Genomics, KU Leuven, Leuven, Belgium
2. Greenland Institute of Natural Resources, Nuuk, Greenland
3. Directorate Natural Environment, Royal Belgian Institute of Natural Sciences, Brussels, Belgium
4. Marine Biology Lab, Université Libre de Bruxelles, Brussels, Belgium

Polar ecosystems harbour a unique cold-adapted biodiversity that is threatened by rapid environmental change and increasing anthropogenic impact. In this context, multi-scale data on connectivity and adaptation are essential for supporting exploitation and conservation management of living resources and ecosystems. Marine protected areas are most effective if implemented as a network that considers functional diversity and connectivity within and between species. In the present study, 607 individuals of ten Trematomus species were sequenced using ddRAD sequencing techniques. Thousands of genomic single nucleotide polymorphisms (SNPs) were used to investigate inter- and intraspecific patterns of divergence and connectivity across the Southern Ocean shelf. Moreover, SNPs that showed evidence of selection (“outlier loci”) were used to explore potential local adaptation of the populations to different environmental conditions. Population structure analyses of four species (*Trematomus loennbergii*, *T. eulepidotus*, *T. scotti* and *T. newnesi*) suggest long- range dispersal across the Weddell Sea and even along the entire West Antarctic coast. We hypothesize that connectivity might be facilitated by the Weddell Sea Gyre and Antarctic Coastal current. A genetic break at the level of the Filchner Trough was observed in several species. The strong outflow from the Filchner-Ronne ice shelf may separate the trough area from the remaining Weddell Sea habitat. Finally, results suggest that previously undetected cryptic diversity may be present within *T. eulepidotus* and *T. loennbergii*. Altogether, the present results contribute to the assessment of diversity, connectivity and adaptation in the Southern Ocean, which is imperative in view of unprecedented global change.

ANTHROPOGENIC HYBRIDIZATION LED TO A DOCK MUSSEL ECOTYPE WITH A FULLY ADMIXED GENOME

Touchard F.[1], SimonA. [1,2], Nascimento SchulzeJ. [3], Hori T.[4], Coolen J.[5], Cerqueira F. [1], Pezy JP.[6], Bouchoucha M.[7], Comtet T.[8], Ellis R.[3], Viard F.[1], Bierne N.*[1]
1. ISEM, Université de Montpellier, CNRS, IRD, Montpellier 34095, France
2. Center of Population Biology and Department of Evolution and Ecology, University of California Davis, Davis, California, USA
3. Biosciences, Faculty of Health and Life Sciences, University of Exeter, Exeter, UK
4. Atlantic Aqua Farms, Borden, PE, Canada
5. Wageningen Marine Research, Den Helder, the Netherlands
6. Laboratoire Morphodynamique Continentale et Côtière, CNRS UMR 6143 M2C, Normandie Univ, UNICAEN, UNIROUEN, Caen, France
7. Ifremer, Laboratoire Environnement Ressources Provence Azur Corse, La Seyne Sur Mer, France
8. Sorbonne Universite, CNRS, Adaptation et Diversité en Milieu Marin, AD2M, Station Biologique de Roscoff, Roscoff 29680, France

Humans transport species across oceans, fostering increased anthropogenic hybridization in altered habitats. One such case is the hybridization between the native *Mytilus edulis* mussel and its non-native congener, the Mediterranean lineage of *Mytilus galloprovincialis*, facilitated by maritime traffic. It resulted in the emergence of a distinct dock mussel ecotype that is now prevalent in French commercial ports. Prior investigations have revealed that this dock mussel lineage exhibits remarkably consistent ancestry proportions across populations, with an approximate genetic makeup of 70% Mediterranean *M. galloprovincialis* and 30% *M. edulis*. Furthermore, these dock mussels are enclosed within ports forming genetic breaks with native populations at their entrances. In the present study, we conducted genotyping on a substantial sample of ~2,000 mussels using a KASP multiplex genotyping approach. Our objective was to assess the spatial distribution of the dock mussel lineage and to inspect the ancestry proportions within each sampled port. Additionally, leveraging a medium density 60K SNP array, we inferred local ancestry patterns across the genomes of 320 dock mussels. Our findings reveal the presence of dock mussels in newly studied ports, with differences in ancestry proportions between the northernmost and southernmost populations. Notably, the dock mussel genome is found fully admixed, with no fixation of ancestry toward either of its parent lineages. Selective pressures appear to favor higher proportions of the major parent ancestry and increased genome-wide heterozygosity. We nonetheless detected two islands of high *edulis* ancestry suggesting adaptive introgression for locally selected genes. Overall the landscape of ancestry detected within this dock mussel ecotype genome was likely shaped by intricate mechanisms involving polygenic selective processes in interaction with recombination and demography.

LINKING MARINE FUNCTIONAL CONNECTIVITY TO ECOSYSTEM FUNCTIONING AND SERVICE PROVISION

López-López Lucía *[1], Agiadi Konstantina [2], Barboza Francisco R. [3], Blanco Andreu [4], Costantini Federica [5], Di Franco Antonio [6], Giraldo Carolina [7], Guizien Katell [8], Guy-Haim Tamar [9], Quintana Cintia [10], Darnaude Audrey [11], Cabanellas Miguel [12], Campos-Candela Andrea [13], Mariani Stefano [14], Perez-Ruzafa Ángel [15], Reul Andreas [16], Rilov Gil [17], Rossi Vincent [18], Ser-Giacomi Enrico [19], Serrao Ester [20], Sturrock Anna [21], Tanner Susanne [22], Türkmen Ant [23], Hidalgo Manuel [12]
1. Oceanographic Centre of Santander. Spanish Institute of Oceanography (CSIC), Santander, Spain.
2. University of Vienna, Austria.
3.Estonian Marine Institute, University of Tartu, Mäealuse 14, 12618 Tallinn, Estonia.
4.Centro de Investigación Mariña, Universidade de Vigo, Future Oceans Lab, 36310 Vigo, Spain.
5. Department of Biological, Geological and Environmental Sciences, University of Bologna, UOS Ravenna, Italy.
6. Stazione Zoologica Anton Dohrn, Palermo, Italia.
7. IFREMER, HMMN – Unité halieutique Manche-Mer du Nord, 62200 Boulogne sur mer, France.
8. Laboratoire d'écogéochimie des environnements benthiques (LECOB/CNRS-Sorbonne Université) Observatoire Océanologique de Banyuls, France.
9. National Institute of Oceanography, Israel Oceanographic & Limnological Research, Tel-Shikmona, PO Box 2336, 3109701, Haifa,
10. Department of Biology, University of Southern Denmark, Campusvej 55, Odense M, 5230
11. MARBEC, Univ Montpellier, CNRS, Ifremer, IRD, Montpellier, France.
12. Oceanographic Center of the Balearic Islands, Ecosystem Oceanography Group (GRECO), Spanish Institute of Oceanography (IEO, CSIC), 07015 Palma, Spain.
13. Department of Biological Sciences, University of Bergen (BIO-UiB), P.O. Box 7800, N-5020 Bergen, Norway.
14. School of Biological and Environmental Sciences. Liverpool John Moores University, UK.
15.Department of Ecology and Hydrology, and Regional Campus of International Excellence “Mare Nostrum”, University of Murcia, 30100 Murcia, Spain.
16. Departamento de Ecología y Geología, Facultad de Ciencias, Universidad de Málaga, Campus Universitario de Teatinos, s/n, 29071 Málaga, Spain.
17. National Institute of Oceanography, Israel Oceanographic & Limnological Research, (IOLR) Tel-Shikmona, PO Box 2336, 3109701, Haifa, Israel.
18. Mediterranean Institute of Oceanography (MIO) , CNRS, Marseille, France.
19. Department of Earth, Atmospheric and Planetary Sciences, Massachusetts Institute of Technology, 54-1514 MIT, Cambridge, MA, 02139, USA.
20. CCMAR, University of Algarve, Gambelas, 8005-139 Faro, Portugal.
21. School of Life Sciences, University of Essex, Wivenhoe Park, Colchester, UK.
22. MARE, ARNET, Department of Animal Biology, Faculdade de Ciências, Universidade de Lisboa, Lisbon, Portugal.
23. LifeWatch ERIC, Lecce, Italy.

Fluxes caused by organisms' movements can have a similar order of magnitude to passive subsidies and yet their role in ecosystem functioning has not been comprehensively assessed to-date. The timing, magnitude and duration of these fluxes across scales have ecosystem implications that can only be understood through several ecosystem processes, in which one or more species might be involved. For example, animal migrations would have a limited contribution to ecosystem functioning without animals feeding and excreting, or even being fed upon and/or dying during their journeys. These processes collectively contribute to particular ecosystem functions, with potential implications for ecosystem services. This interdependence acquires a unique dimension in the 3D and apparently borderless marine environment, where connectivity processes are commonly wider- reaching than in terrestrial environments. We identified different areas in which marine functional connectivity becomes an essential feature of marine ecosystems, creating dynamic patterns of energy, matter and gene flow that shape five of the most relevant functions within these ecosystems: (1) biological production, (2) energy transfer, (3) nutrient recycling, (4) carbon export and sequestration, and (5) habitat formation. Based on expert knowledge, we evaluated the associations between connectivity, these functions and Nature's Contributions to People, finding particularly strong support for the importance of connectivity as a driver of food and feed provision, maintenance of options, and habitat creation and maintenance. Our work evidences the cross-scale nature of marine functional connectivity processes on ecosystem functioning, highlighting the need to identify key connectivity features to design effective conservation and management measures.

SYMPATRIC SPECIES OF CORAL TROUT (*PLECTROPOMUS*) SHOW CONTRASTING PATTERNS OF GENOMIC STRUCTURE ACROSS ISOLATED ATOLL REEFS

Payet S.*[1], DiBattista J.D.[2,3], Newman S.J.[1], Rushworth K.J.[1], Wakefield C.B.[1], Evans R.D.[4,5], Travers M.J.[1]
1. Western Australian Fisheries and Marine Research Laboratories, Department of Primary Industries and Regional Development, Government of Western Australia, P.O. Box 20, North Beach 6920, Western Australia, Australia.
2. Trace and Environmental DNA (TrEnD) Laboratory, School of Molecular and Life Sciences, Curtin University, Perth, WA, 6102, Australia
3. Australian Museum Research Institute, Australian Museum, 1 William St, Sydney, NSW, 2010, Australia
4. Department of Biodiversity Conservation and Attractions, 17 Dick Perry Ave, Kensington, 6151, Australia.
5. Oceans Institute, The University of Western Australia, Crawley, WA 6009, Australia

Understanding patterns of connectivity across remote atoll reefs is important for managing fishery target species, as they often have small population sizes and limited options for replenishment in the event of localised decline. In this study, we used a comprehensive hierarchical sampling design combined with reduced representation genotyping to compare the population genomics of two sympatric species of coral trout (*Plectropomus*) within and between three isolated offshore atoll reef systems in north-western Australia. The blue spot coral trout, *Plectropomus laevis* (8,979 single nucleotide polymorphisms - SNPs, 223 individuals, 25 sites) and the passionfruit coral trout, *P. areolatus* (3,702 SNPs, 452 individuals, 20 sites) showed high levels of connectivity within reef systems and restricted connectivity between reef systems, indicating that biological stocks primarily occur at the scale of each reef system. Despite being closely related and co-managed species, inter-specific variation in the magnitude of genetic structure was notable. *Plectropomus areolatus* at the southern-most reef system display modest genetic structure with populations ~450 km to the north, whilst *P. laevis* at the same location show a level of genetic divergence that reflects deep historical isolation. Our results provide the most comprehensive assessment of genetic connectivity across these remote atoll reefs, facilitating management advice that reflect empirically determined population dynamics for these species. We identify contrasting patterns of genetic connectivity among closely related sympatric species, and highlight the role of extrinsic (e.g., geography/environment) and intrinsic (e.g., life history) factors in shaping population dynamics.

ASSESSING CORAL HOLOBIONT CONNECTIVITY ON URBANISED REEFS

Ong Jing Hui *[1], Ling Min Kang [1], Chang Jia Jin Marc [1], Wainwright Benjamin J. [1,2], Huang Danwei [1,3,4,5]
1. Department of Biological Sciences, National University of Singapore, Singapore
2. Yale-NUS College, National University of Singapore, Singapore
3. Lee Kong Chian Natural History Museum, National University of Singapore, Singapore
4. Tropical Marine Science Institute, National University of Singapore, Singapore
5. Centre for Nature-based Climate Solutions, National University of Singapore, Singapore

Coral connectivity is essential for resilient and healthy reefs while the association between corals and the microorganisms they host is vital to the coral's health. Understanding the interactions within this dynamic system is crucial for predicting adaptive responses to disturbances and planning reef management strategies. Many studies have established how the assemblage of microorganisms in the coral holobiont varies across a myriad of factors including biogeography, depth, coral species and health, as well as environmental parameters. However, the influence of host coral population structure on its symbiont community remains poorly understood. In this study, we characterised the bacterial and Symbiodiniaceae communities hosted by three cryptic lineages of the broadcast spawning coral, Porites lutea, in the urban reefs of Singapore. Genome-wide single-nucleotide polymorphisms were used to estimate Porites lutea population structure, from which genetic connectivity was inferred. We tested the relationship between host coral connectivity and symbiont community connectivity as well as the effects of geographic distance on holobiont connectivity. We also examined the interactions between host coral lineage and symbiont communities through a network analysis. Our findings reveal the intricate relationships between symbiont community structure through space and host population structure and provide insights into the community dynamics of the coral holobiont.

MATING DISTANCE FIELD EXPERIMENTS TO OPTIMIZE RESTORATION ACTIONS FOR THE CONSERVATION OF THE MEDITERRANEAN RED CORAL (*CORALLIUM RUBRUM*)

Giordano Bruna *[1,2], Cannas Rita [1], Cau Alessandro [1,4], Costantini Federica [3,4], Guizien Katell [2], Bramanti Lorenzo [2]
1. Department of Life and Environmental Sciences, University of Cagliari, Cagliari, Italy
2. Laboratoire d’Ecogéochimie des Environnements Benthiques, LECOB, Observatoire Océanologique de Banyuls sur Mer Centre, France
3. Department of Biological, Geological and Environmental Sciences, University of Bologna, UOS Ravenna, Ravenna, Italy
4. National Interuniversity Consortium for Marine Sciences (CoNISMa), Rome, Italy

Corallium rubrum is an octocoral endemic of the Mediterranean Sea, which suffers from population decline due to overfishing and warming-driven mass mortality events. For several years, scientists and managers have been interested in fostering the persistence of this resource, promoting conservation and restoration actions. Understanding how the mating system influences the spatial distribution of a species and knowing the parameters affecting its reproductive success is crucial to planning efficient restoration initiatives. In this study, we will untangle some of the processes underlying the strong genetic structure of *C. rubrum*. Through two breeding seasons (summer 2022 and 2023), we analyzed 1) the males' maximum fertilization distance and 2) the effect of sperm dilution on female fecundity by studying a population in a semi-controlled environment (i.e., submerged artificial caves) where the genotype, sex, and morphology of all individuals, as well as the population density, are known. Parentage analysis was performed through SNPs data, assigning each released larvae to its respective parents. Results show that polyandry is likely the norm in *C. rubrum* and that the species' potential fertilization distance can reach tens of meters. In addition, we observed a significant effect of sperm dilution on the fecundity of female colonies, recording significantly higher larval release from females placed close to male (cm scale) individuals than from those isolated (meters to tens of meters scale). Results suggest that male gamete dispersal capacity could buffer the genetic drift expected in a declining population affected by disturbances, offering an excellent recovery potential for the species.

Speed Talks

Session 3

Marine Functional Connectivity knowledge use for improved environmental policies and sustainable development

Conveners

Maria Beger (UK)
Andreu Blanco (Spain)
David Goldsborough (the Netherlands)
Ewan Hunter (UK)
Yael Teff-Seker (USA)
Ant Türkmen (Italy)

IMPACT OF OFFSHORE WIND FARMS ON MARINE BENTHIC CONNECTIVITY

Boutin K.*[1], Alekseenko E. [1], Ben Rais Lasram F.[1], Gaudron S.M.[1,2]
1. Univ. Littoral Côte d'Opale, Univ. Lille, CNRS, IRD, UMR 8187, LOG, Laboratoire d'Océanologie et de Géosciences, F 62930 Wimereux, France
2. Sorbonne Univ., UFR 927, 75005 Paris, France

Offshore wind farms (OWFs) are known to be potentially responsible to facilitate the dispersal of benthic species whether of commercial/ecological interests or non-indigenous, due to the stepping stone effect. Six OWFs are planned in the Eastern English Channel (EEC) in the next years and, to anticipate their impacts the connectivity of five targeted marine species was studied: *Asterias rubens*, *Lanice conchilega*, *Magallana gigas*, *Mytilus edulis* and *Necora puber*. A Lagrangian model (ICHTHYOP) was employed to investigate the larval dispersal. Several biological parameters were implemented into the model for each species, including Pelagic Larval Duration (PLD), spawning periods and larval physical density. Each year, between 32,000 and 58,000 particles were released from rocky areas and, between 144,000 and 260,000 particles were released from wind turbine (every 5 meters until the seafloor). Depending on the spawning period of the species, between 5 to 9 spawning events were modelled. The model demonstrated sensitivity to the physical density of the larvae, influencing their dispersal trajectory and retention rate within the EEC. The less dense larvae are Asterias larvae (1025.25 kg/m3) and the denser larvae are Lanice larvae (1026.50 kg/m3). Denser larvae exhibit a higher retention rate throughout the entire EEC, with 97.4% for Lanice conchilega, in comparison to less dense larvae (75.3% for Asterias rubens). The corresponding connectivity matrices identified two primary connectivity zones among 26 rocky areas and wind farm zones in the EEC: the Calais Strait and the Bay of Seine. The denser larvae demonstrated a better self-recruitment than the less dense larvae.

WHERE DO THEY COME FROM? A KAITAIA SPAT STORY

Parada Roberto *[1], Chaput Romain [1,2], Mendiola Michael [1] and Gardner Jonathan P.A. [1]
1. School of Biological Sciences, Victoria University of Wellington, Wellington, New Zealand
2. Cawthron Institute, Nelson, New Zealand

Studying larval dispersal and connectivity is relevant for conservation, restoration, and management decisions in marine species. The endemic green-lipped mussel aquaculture industry is highly profitable in New Zealand, reporting earnings of NZ$300 million per year. About 80% of the spat used by this industry comes from Ninety Mile Beach, at the north-west of the North Island. The importance of this resource has prompted attempts to identify its source, with no conclusive results in the past. In this study, we use RAD-seq derived SNPs to associate a sample of spat, coming from Ninety Mile Beach, to specific regions in the North Island. Using a neutral panel of 185 SNPs and an adaptive panel of 28 SNPs, we were able to find genetic signals enabling us to infer that the spat sample is sourced from a set of locations comprising mussel beds from Ninety Mile Beach down to Maunganui Bluff. We contrasted our results with outputs of Lagrangian models tracking larval dispersal, discarding Raglan as immediate source, even though high genetic connectivity was found. Our results will help establish management initiatives securing the protection of this vital resource for the aquaculture sector in New Zealand.

POPULATION GENOMICS OF THE EUROPEAN SARDINE (*SARDINA PILCHARDUS*) CHALLENGE CURRENT MANAGEMENT UNITS AND INFORM ABOUT RESILIENCE OF THIS SPECIES TO GLOBAL CHANGE

Puebla-Aparicio Marina *[1], Manuzzi Alice [1], Díaz-Arce Natalia [1], Mokhtar-Jamaï Kenza [2], Gagnaire Pierre Alexandre[3], Rodriguez-Ezpeleta Naiara [1]
1. AZTI, Marine Research, Basque Research and Technology Alliance (BRTA), Sukarrieta, Bizkaia, Spain
2. Institut de Recherche Halieutique, Morrocco
3. ISEM, University of Montpellier, France

Emerging population genomic techniques offer insights into the diversity and connectivity of fish populations, contributing to better delineating management units and understanding their resilience to environmental changes and anthropogenic impacts. The European sardine (*Sardina pilchardus*) is a highly valuable species in North-east Atlantic waters, where it is managed as three stocks. Nevertheless, studies based on regional differences in morphology, maturity, growth, spawning seasonality and, lately, genetic markers suggest a mismatch between natural populations and management units. Additionally, recent evidence points out a northward migration of this species most likely as consequence of climate change. In this study, we used low coverage whole genome sequencing of 355 individuals from 44 sampling locations and different spawning groups covering the species distribution in the North-east Atlantic, including the Mediterranean Sea, to disentangle the population structure and adaptation potential of this species. Using genotype likelihoods estimated for variant sites at almost 2 million genome-wide loci, our findings support genetic differentiation between the Atlantic Ocean and the Mediterranean Sea, with a transition zone in the Alboran sea, and a clinal latitudinal gradient of genetic diversity within the North Atlantic, challenging current management unit delineation. Moreover, our data allowed to identify genetic traits associated to spawning components as well as genomic signs of adaptation that are key to understand the impact of climate change in this highly commercial species. Our research provides a novel and wide view about connectivity patterns and genetic adaptation for the European sardine in the North-east Atlantic, which has important implications for a more efficient fisheries assessment and management of the species in a global change scenario.

UNDERSTANDING THE POPULATION STRUCTURE OF ATRINA VEXILLUM, GIANT BIVALVES, IN FRENCH POLYNESIA

Guttierez Thomas *[1], Planes Serge [1]
1. CRIOBE Perpignan, France

Atrina vexillum is a native bivalve in French Polynesia. Limited knowledge exists in the scientific literature, especially regarding the connectivity of its populations. The insular context of Polynesia poses an additional barrier to larval dissemination and, consequently, the resilience of local populations. My PhD aims to provide the first data on the demography, connectivity and habitat of these populations. Initially, different populations were identified and then characterized in terms of size, age, and proximity to each other over a year on five islands, revealing over 2600 individuals. Ecosystems specific to their development were also identified. These initial findings highlight the geographical proximity of the species to certain pressures, particularly anthropogenic, emphasizing the importance of effective species protection, considering its decline described by the local population. A study using the analysis of 30 microsatellite markers is underway to examine the population structure across the Society Islands through genetic connectivity and the building of a pedigree. These data could be used for environmental management. A preliminary study indicates very low connectivity between two islands separated by only 50 km. This work aligns with the Polynesian government's initiative to protect its biodiversity.

CROSS-CHANNEL STRAYING FACILITATES CONNECTIVITY IN A UNIQUE CHALK-STREAM VARIANT OF ATLANTIC SALMON (*SALMO SALAR* L.) IN THE RIVERS OF SOUTHERN ENGLAND AND NORTHERN FRANCE

Stevens Jamie R.*[1], King R. Andrew [1], Evanno Guillaume [2]
1. Department of Biosciences, University of Exeter, UK
2. INRAE, Rennes, France

Atlantic salmon (*Salmo salar* L.) in rivers flowing over chalk in the Hampshire basin of southern England are recognised as a unique genetic variant of the species, as different, for example, as are Atlantic salmon from rivers entering the Baltic Sea. This study expands previous molecular work to include analysis of Atlantic salmon from the chalk rivers of Upper Normandy in northeast France. Assignment analysis of SNP profiles provides evidence of cross-Channel straying of a small number of adult salmon, which appears sufficient to maintain the integrity of the genetic signatures of 'chalk' salmon on both sides of the Channel. As a result, salmon inhabiting rivers flowing over chalk form a cohesive genetic entity and are more similar to each other than they are to fish inhabiting geographically closer rivers flowing off granite and other non-chalk landscapes. Results reinforce the importance of designating marine protected areas for anadromous species during their at-sea migrations, and the importance of conservation actions that transcend international borders.

SOLE FACING BREXIT AND CLIMATE CHANGE

Barbut L.*[1], Depestele J.[2], Lam S.[1], Van Moorleghem C.[2], Lacroix G.[1]
1. RBINS, Brussels, Belgium
2. ILVO, Ostend, Belgium

Following the European Union's Common Fisheries Policy, the Exclusive Economic Zones (EEZs) of member states are collectively managed, the recent Brexit necessitates a re-evaluation of fisheries management strategies in areas where waters are shared among EU and UK, such as the North Sea. Common sole (*Solea solea*) is one of the most valuable fish in the North Sea. Understanding connectivity between UK and EU waters is a key factor for fisheries management. Furthermore, the North Sea is one of the most rapidly warming regional seas in the NE Atlantic (0.45°C per decade as estimated from the 1984-2014 period (Hughes et al 2017)). During the last decade, change in distribution and spawning period of sole has been observed. This warming trend may also affect larval transport and temperature-dependent growth, which may affect survival of early life stages and the number of fish recruited. Employing a Lagrangian larval transport model, which coupled a 3D hydrodynamic model and a particle-tracking model (LARVAE&CO), enables the assessment of environmental impacts on larval settlement pattern and the disparity between dispersal during early life stage in EU and UK waters. This approach offers crucial insights supporting adaptive fisheries management strategies in response to changing environmental conditions and management policies.

MARINE ECOLOGICAL CORRIDORS: AN INNOVATIVE APPROACH TO IDENTIFY ECOLOGICAL CONNECTIVITY AMONG PROTECTED AREAS

Podda Cinzia *[1], Baroli Maura [1], Grech Daniele [1], Serra Elisa [1], Porporato Erika M.D. [1]
1. IMC, International Marine Centre, Oristano, Italy
2. NBFC, National Biodiversity Future Center, Palermo, Italy

The incorporation of ecological connectivity into marine and coastal Protected Areas (PAs) design and management is critical to achieving conservation outcomes. However, the understanding and implementation of ecological connectivity among PAs in marine environments lag compared to their terrestrial counterparts. Here, we studied the structural ecological connectivity by using Ecological Corridors (ECs) among PAs in Sardinia (Central-Western Mediterranean, Italy). The target species identified is the endemic seagrass *Posidonia oceanica*, selected for its pivotal ecological role and crucial ecosystem servicesprovider. Despite *P. oceanica* is the most widespread seagrass in the Mediterranean Sea, it has been sharply declining. Existing data on *P. oceanica* occurrence were collected to generate a resistance map starting from the habitat suitability obtained by an ensemble modelling approach. ECs were identified using a Least cost path analysis on the resistance map. As final output, 9 ECs were obtained for P. oceanica in Sardinia, covering a surface of about 400 km2. By using the innovative approach of ECs, although only structural attributes were considered, this study represents the first attempt to analyse marine ecological connectivity among PAs in Sardinia. These results will lay new basis to support the identification, in the next future, of new marine and coastal areas to be protected in Sardinian territorial waters according to 30x30 target of the EU Biodiversity Strategy.

Managing transboundary turtles in a dynamic ocean

Shillinger George*[1]
1. Upwell turtles, Monterey, USA

Here we present a case study about the importance and applicability of transboundary management strategies for the conservation of sea turtles and other highly migratory marine species. The case study will focus on critically endangered Pacific leatherback turtles, and will highlight the subpopulation of East Pacific (EP) turtles nesting at Playa Grande, Costa Rica, Central America’s most important index nesting beach. EP leatherbacks have declined by over 95% during the past three decades and their extirpation from the EP appears imminent within the next 20-40 years, barring major reductions in bycatch across an extensive transboundary region spanning their entire home range, from coastal nesting beaches and foraging habits to the high seas. Management and conservation measures aimed at ensuring the continued persistence of leatherback turtles must be transboundary and collaborative, designed to mitigate bycatch impacts, wherever and whenever turtles are must vulnerable to anthropogenic threats. They must also be dynamic in their nature and design, recognizing ever-changing oceanic environmental conditions and their influences on sea turtle movement and behavior. Here we examine a suite of different and evolving modeling efforts with varying utilities, all aimed at providing predictive outputs to inform managers and stakeholders about ways to potentially mitigate sea-turtle-fisheries interactions and bycatch impacts to leatherback turtles in the Pacific Ocean.

FISH TALES UNLEASHED: IDENTIFYING EUROPEAN HAKE POPULATION CONNECTIVITY THROUGH OTOLITH SHAPE AND CHEMICAL COMPOSITION

Martinho Filipe *[1], Vaz Ana [1], Guerreiro Milene A. [1], Tanner Susanne E. [2], Reis-Santos Patrick [3], Stransky Christoph [4], Pardal Miguel A. [1]
1. Centre for Functional Ecology - Science for People & the Planet, Associate Laboratory TERRA, Department of Life Sciences, University of Coimbra, Portugal
2. MARE – Marine and Environmental Sciences Centre/ARNET – Aquatic Research Network Associated Laboratory, Department of Animal Biology, Faculty of Sciences, University of Lisbon, Portugal
3. Southern Seas Ecology Laboratories, School of Biological Sciences, The University of Adelaide, Australia
4. Thünen Institute of Sea Fisheries, Bremerhaven, Germany

Identifying the structure of fish stocks is key to understanding population connectivity over large geographical areas, thus contributing to efficient fisheries management. The European hake, *Merluccius merluccius*, is one of the most commercially important marine fishes in Europe, yet gaps still persist in our knowledge of its stock structure. Our aim was to combine two natural markers - otolith shape and chemical composition to improve the delineation of stock structure along the NE Atlantic Ocean and the Mediterranean Sea for this species. Otolith shape was analysed through wavelet analysis, and a subsequent canonical analysis of principal coordinates and random forest procedures provided evidence for different population units with a clear separation between the NE Atlantic and the Mediterranean, but with limited resolution for the NE Atlantic. Based on otolith core chemical composition (indicative of spawning area), an unsupervised random forest followed by K-means cluster analyses identified two clusters in the Atlantic region and two others in the Mediterranean Sea, suggesting different origins of European hake. Otolith edge chemical composition (indicative of capture area) was also effective in classifying the individuals back to their sampling locations but suggested a higher mixing of individuals in the NE Atlantic compared with core chemical composition, consistent with otolith shape descriptors. Overall, our results suggest a potential difference in spatial habitat use between European hake early life stages and adults, and provide support for a multidisciplinary approach to fish stock identification for management purposes.

ASSESS OF NON-INDIGENOUS ROUND GOBY (*NEOGOBIUS MELANOSTOMUS*) DISTRIBUTION RANGE USING TAGGING METHODS FOR THE SPATIAL MANAGEMENT OF FISHERIES IN LATVIAN COASTAL AREAS OF BALTIC SEA

Rozenfelde Loreta *[1], Putnis Ivars [1], Heimrats Karlis [1], Tetere Rebeka [1]
1. Institute for Food Safety, Animal Health and Environment "BIOR", Latvia

Round goby is one of the main invasive species of the Baltic Sea and has become the predominant fish species in several coastal areas, caused habitat shifts of competing fish species. However, in some areas round goby became an important subject for the coastal fishery and one of the highest round goby commercial landings are observed in Latvian coastal waters. The problem of invasive species are targeted by implementation of the new new fishery management methods that allows to minimize the bycatch of non-target species. To efficiently utilize the abundant source and to minimize the invasion rate based on Latvian coastal habitats and round goby distribution range are developed spatial management for coastal fishery. This will help to identify the most effective fishing areas and serve as a basis to efficiently distribute round goby fishing pressure. 8,000 round gobies was tagged with T-tags on the Latvian coast, after receiving 245 posts about catching and releasing concluded that the round goby exhibits pronounced territorial behavior. In particular, 66% of all the designated round gobies were still within a radius of nearly two kilometers of the initial release points within two weeks of their release into the sea. Due to the territorial behavior and the low migration speed, it is expected that in places where populations have already been detected, they will continue to be preserved. The highest catches and populations of round sea bream were found in habitats with rocky bottoms, indicating that these areas may experience higher fishing pressure.

GENETIC STRUCTURE OF OCTOPUS VULGARIS POPULATIONS IN THE ATLANTIC-MEDITERRANEAN REGIONS

Blanco Andreu [1,2], Roura Álvaro [3], Beger Maria [4,5], Franco João N. [6], Lemo, Marco F.L. [6], Albo Marta [7], Arechavala-López Pablo [8], Ben Souissi Jamila [9], Bernal-Ibáñez Alejandro [10], Domenichetti Filippo [11], Faria João [12], Fernández-Álvarez Fernando Á. [13], Grech Daniele [14], Guy-Haim Tamar [15], Hüseyinoglu Mehmet Fatih [16], Izquierdo-Gómez David [17], Jimenez Carlos [18], Kousteni Vasiliki [19], Koutrakis Manos [19], Lefkaditou Evgenia [20], Naasan Aga - Spyridopoulou Roxani [21], Ponte Giovanna [22], Rotllant Guiomar [13], Tiralongo Francesco [11,23,24], Zacchetti Lorenzo [11,25], Mouronvalle Clara [26], Planes Serge [26]

1. Centro de Investigación Mariña, Universidade de Vigo, Future Oceans Lab, Torre CACTI, Campus de Vigo, As Lagoas, Marcosende 36310 Vigo, Spain
2. Departamento de Ecoloxía e Bioloxía Animal, Universidade de Vigo, Campus As Lagoas-Marcosende, 36310 Vigo, Spain
3. Instituto de Investigaciones Marinas (IIM-CSIC), Eduardo Cabello 6, 36208 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 / ARNET − Aquatic Research Network, ESTM, Instituto Politécnico de Leiria, Peniche, Portugal
7. Ecosystems Oceanography Group (GRECO), Centre Oceanogràfic de Balears (COB-IEO, CSIC), Moll de Ponent sn, 07015 Palma, Spain
8. Mediterranean Institute of Advanced Studies (IMEDEA-CSIC), 07190, Esporles, Spain.
9. Tunis El Manar University (LR11ES09), National Institute of Agronomy of Tunisia, Tunis, Tunisia.
10. MARE − Marine and Environmental Sciences Centre / ARNET − Aquatic Research Network, Agência Regional para o Desenvolvimento da Investigação Tecnologia e Inovação (ARDITI) Funchal, 9020-105 Madeira, Portugal
11. Institute for Biological Resources and Marine Biotechnology, National Research Council, Ancona, 60125, Italy
12. CIBIO - Research Centre in Biodiversity and Genetic Resources, InBIO Associate Laboratory, Pólo dos Açores – Department of Biology, University of Azores, Ponta Delgada 9501-801, Portugal
13. Institut de Ciències del Mar (CSIC) - Passeig Marítim de la Barceloneta, 37, 08003 Barcelona, Spain
14. IMC - International Marine Centre, Loc. Sa Mardini, 09170 Torregrande, Oristano, Italy
15. National Institute of Oceanography, Israel Oceanographic and Limnological Research, Tel-Shikmona, Haifa, Israel
16. Faculty of Maritime Studies, University of Kyrenia, Kyrenia, Cyprus
17. The Norwegian Institute of Food, Fisheries and Aquaculture Research (NOFIMA), Muninbakken 9-13, Breivika, 9291, Tromsø, Norway
18. Enalia Physis Environmental Research Centre, Cyprus

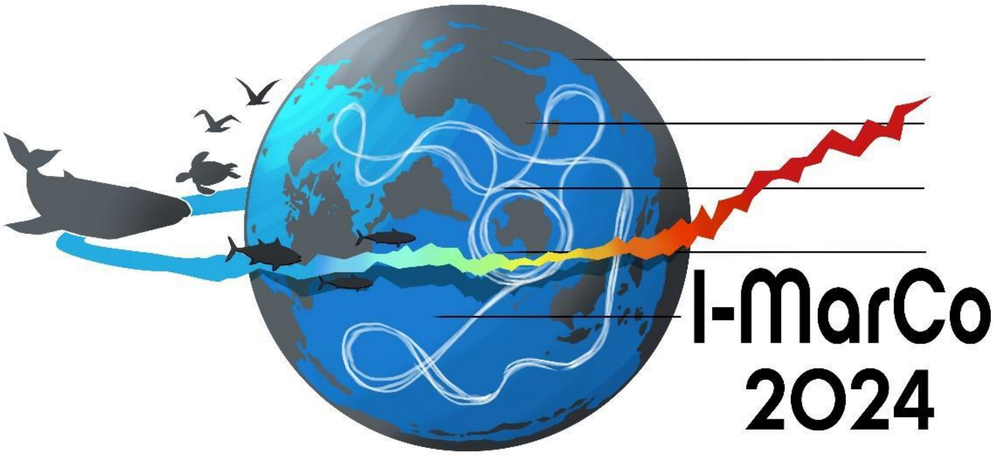
19. Fisheries Research Institute, Hellenic Agricultural Organization, 640 07, Nea Peramos, Kavala, Greece
20. Institute of Marine Biological Resources & Inland Waters, Hellenic Centre for Marine Research, 576 Side RD, Vouliagmenis Ave, Argyroupolis , GR-16452, Athens
21. iSea, Environmental Organisation for the Preservation of the Aquatic Ecosystems, 12 Kritis, 54645, Thessaloniki, Greece
22. Department of Biology and Evolution of Marine Organisms, Stazione Zoologica Anton Dohrn, villa Comunale, 80121, Napoli, Italy
23. Department of Biological, Geological and Environmental Science, University of Catania, Catania, Italy
24. Ente Fauna Marina Mediterranean, Scientific Organization for Research and Conservation of Marine Biodiversity, Avola, Italy
25. Department of Biological, Geological, and Environmental Sciences (BiGeA), Alma Mater Studiorum - University of Bologna, Bologna, 40126, Italy
26. CRIOBE-USR 3278, CNRS-EPHE-UPVD, Laboratoire d'Excellence 'CORAIL', 58 Avenue Paul Alduy, 66860, Perpignan, France

The common octopus, *Octopus vulgaris*, is the most studied cephalopod species and one of the most important fisheries in the EU (mean total income of 118.2 ± 29.9 M €/year) with a high interannual variability in landings (20967 ± 3432 Tn/year). Such variability is associated with its inherent population dynamic traits and strong influence of environmental conditions. Still, *O. vulgaris* is excluded from EU fishing regulations and quotas, rendering its management to the Member States who evaluate and manage fishing stocks locally (at different administrative levels) rather than on the true biological borders (i.e. genetic stocks). Thus, this study aims to shed light on *O. vulgaris* genetic population structure across its distribution range in Southern Europe (Atlantic Ocean and Mediterranean Sea) to help develop science-based fishing policies. To do so, a total of 1016 samples collected in 44 locations along eight countries in the NE Atlantic and Mediterranean (from Azores to Cyprus and from the Gulf of Biscay to the Canary Islands) were analysed using a set of 14 de novo developed species-specific microsatellite loci. A clear genetic distinction was found between Atlantic and Mediterranean populations. Within the Mediterranean, further segregation occurred between western and eastern basins. In the Atlantic, a latitudinal gradient was observed, with the Canary Islands population genetically isolated from the other locations sampled. These findings provide valuable insights for developing science-based fisheries policies, promoting sustainable management of *O. vulgaris* genetic stocks across its Atlantic-Mediterranean distribution range.

Posters

Session 1

Multi-disciplinary approaches in Marine Functional Connectivity research



FACTORS LIMITING RANGE EDGE POPULATIONS OF THE PINK SEA FAN (*EUNICELLA VERRUCOSA*)

Wheatley Kornblum Kaila* [1], Brodrick Emelie [1], Robins Peter [2], Lock Kate [3], Craggs Jamie [4], Highfield James [5], Stevens Jamie R. [1]
1. Department of Health and Life Science, University of Exeter, UK
2. School of Ocean Science, Bangor University, Wales, UK
3. Natural Resources of Wales, UK
4. Horniman Museum & Gardens, UK
5. Natural England, UK

The pink sea fan (*Eunicella verrucosa*) is a cold-water gorgonian octocoral with a distribution ranging from northwest Ireland to the Mediterranean. Recognised as a priority species in Great Britain under the UK Wildlife and Countryside Act 1981, many marine protected areas (MPAs) have been designated to safeguard priority species like the pink sea fan. However, for MPAs to achieve their goal of protecting marine biodiversity, a comprehensive understanding of population connectivity and limiting factors at range edges is critical. Our aim is to address the knowledge gaps in pink sea fan life history and connectivity using a multidisciplinary approach that harnesses molecular ecology, life history aquaria experiments and histology, as well as ocean dynamic modelling. Whole genome sequencing captures genetic variation across the species' range; preliminary analysis has revealed fine-scale patterns of connectivity and potential evidence of adaptation at range edges. Life history analyses are ongoing to understand gonadal development timing and elucidating reproductive processes, growth rates, and temperature-related pelagic larval duration. These novel data will allow us to build species-specific particle tracking models to simulate connectivity across the species' range, which will offer insights into settlement locations and population dynamics within and between MPAs and non-MPA populations, as well as how the species' range may shift under climate change. In summary, by integrating genomics, biological and life history data, and ocean dynamic modelling, we aim to evaluate the current effectiveness of MPA networks in preserving connectivity among populations of the pink sea fan in the UK and beyond.

GENETIC DIVERSITY AND POPULATION STRUCTURE OF *EPINEPHELUS MARGINATUS*, *EPINEPHELUS AENEUS* AND *EPINEPHELUS COSTAE* IN THE CENTRAL MEDITERRANEAN SEA: GULF OF GABES

Elglid Aziza* [1], Crouau-Roy Brigitte [2], Bradai Mohamed Nejmeddine [1]
1. National Institute of Marine Sciences and Technology (INSTM), Tunisia
2. EDB UMR 5174, CNRS-Univ. P. Sabatier, Toulouse, France

Groupers are among the most highly priced and appreciated fish in the Mediterranean Sea. However, species of this genus have been found to be at risk, especially for *E. marginatus* which is endangered (IUCN EN A2d) because of their long life, slow reproduction and overfishing. The objective of this study was to describe the genetic population structure of three species of groupers in Central Mediterranean Sea (Gulf of Gabès): *Epinephelus mraginatus*, *Epinephelus aeneus* and *Epinephelus costae* using cytochrome b (cytb) gene and seven nuclear microsatellites. Based on 940 base pairs of the cytochrome b segment, we found low levels of genetic variability for the two samples analyzed (h=0.395 and h=0.294 respectively for *E. aeneus* and *E. marginatus*) and high level (h=0.833) for *E. costae*. In addition, a low rate of heterozygosity (Ho=0.4, Ho=0.57, Ho=0.55), and a high inbreeding coefficient (Fis = 0.218, Fis = 0.232, Fis=0.231) respectively for *E. marginatus*, *E. aeneus* and *E. costae* makes these species susceptible to exploitation specifically for *E.marginatus* and *E.aeneus*.

POPULATION GENETIC STRUCTURE OF NATURAL AND HATCHERY RAISED POPULATIONS OF EUROPEAN ABALONE *HALIOTIS TUBERCULATA TUBERCULATA*: LESSONS FOR FUTURE RESTOCKING AND STOCK ENHANCEMENT

Le Gall Ronan* [1], Chauvaud Pierre [1], Roussel Sabine [1], Pante Eric [2], Viricel Amélia [1], Charrier Grégory [1]
1. University of Brest, Laboratory of Environmental Marine Sciences, CNRS-UBO-IRD-Ifremer, European Institute for Marine Studies, Plouzané, France
2. Centre national de la recherche scientifique, Laboratory of Environmental Marine Sciences, CNRS-UBO-IRD-Ifremer, European Institute for Marine Studies, Plouzané, France

Up to 80% of European abalone (*Haliotis tuberculata tuberculata*) populations have declined sharply along North-western French coasts (Brittany and Normandy) over the last two decades, mainly due to a pathogenic bacterium (*Vibrio harveyi*). Restocking or stock-enhancement operations based on hatchery-reared juveniles might be efficient to restore collapsed populations and preserve fishing activities. Assessing the genetic composition of wild populations and hatchery-reared individuals is a primary concern in supplementation programs, to preserve the genetic diversity and adaptive potential of wild populations. The genetic diversity of ten wild abalone populations was assessed along the coasts of Brittany and Normandy, as well as 14 hatchery-reared samples, using 157 SNPs. Similar levels of genetic variability were found between wild and hatchery samples. However, those samples were strongly differentiated, thus reflecting strong genetic drift in the hatchery. Thus, despite hatchery practices ensured a high level of genetic diversity in hatchery-raised cohorts, the seeds released in natural populations should be composed of several cohorts and/or generations to buffer the genetic heterogeneity between cultured individuals and wild populations. In addition, a clear genetic structure was observed between wild populations from Normandy and northern Brittany and those from western and southern Brittany. This spatial structuring of wild abalone populations suggested that the farm broodstock should be chosen depending on the locality where the produced seeds would be released. Overall, the guidelines depicted here should strongly reduce the risk of altering the genetic diversity of natural populations, and thus maintain their adaptive potential to environmental variability.

IDENTIFYING CRITICAL NURSERIES AND ONOTGENETIC CONNECTIVITY OF A VALUABLE MARINE FISH USING NATURAL TAGS IN ARCHIVAL STRUCTURES

Lefebvre du Prey Marion* [1], Ciotti Benjamin J. [1], Sheehan Emma V. [1], Stewart James [2], Sturrock Anna M. [3]
1. University of Plymouth, UK
2. Severn and Devon IFCA (Inshore Fisheries and Conservation Agency), UK
3. University of Essex, UK

Inshore habitats play an essential role in the growth and survival of juvenile fish, fundamentally supporting recruitment into adult populations. Identifying important fish nurseries is critical for species conservation and fisheries management. In this work we use chemical markers to investigate within-estuary connectivity and reconstruct the main nursery areas used by surviving adults. We focus on juvenile sole (*Solea solea*) in the Severn estuary (UK), a management-relevant yet data-scarce system. We aim to build a chemical map using juvenile otolith elemental chemistry and eye lens isotopic signatures, and validating our proxies for diet, salinity, and hypoxia through a combination of fieldwork and controlled experiments. Otolith and eye lenses grow incrementally through the fish's life, allowing us to reconstruct the conditions experienced by individuals over time. Subsequently, by sampling adult soles in the Bristol Channel and interrogating the juvenile tissue layers we will estimate the contribution rates of different estuarine. Contribution rates will be linked to variation in abundance, feeding and growth of juveniles to understand processes determining juvenile habitat quality. Our findings will offer crucial information for managers and help to inform conservation priorities in this region. Furthermore, our efforts to validate chemical proxies in both field and laboratory settings will enhance the reliability and applicability of these tools for a robust understanding of ontogenetic connectivity patterns in commercially valuable fish populations.

UNRAVELING SPATIO-TEMPORAL GENETIC CONNECTIVITY OF LOGGERHEAD SEA TURTLES IN THE NORTH ATLANTIC

Lima Françoise D.* [1], Monzón-Argüello Catalina [2], Parra Hugo [1], Santos Marco A. [3], Herguedas Andrea [1], Lagoa João [4], Varo Nuria [5], Dellinger Thomas [6], Shamblin Brian [7], Bjorndal Karen [8], Vandeperre Frederic [1]
1. Universidade dos Açores, Portugal
2. Universidade de Las Palmas de Gran Canaria, Spain
3. Direção Regional do Ordenamento do Território e dos Recursos Hídricos, Portugal
4. Direção Regional de Políticas Marítimas, Portugal
5. Instituto Canario de Ciencias Marinas, Spain
6. Universidade da Madeira, Portugal
7. University of Georgia, USA
8. Archie Carr Center for Sea Turtle Research and Department of Biology, University of Florida, USA

The North Atlantic islands in Macaronesia (Azores, Madeira, Canaries, and Cape Verde) play a crucial role as foraging grounds (FG) for juvenile loggerhead sea turtles (*Caretta caretta*). In order to identify the origins of sea turtles in these areas and evaluate changes in genetic composition along time, we collected tissue samples from individuals in Azores (n = 40), Canaries (n = 20), Madeira (n = 63), and areas beyond national jurisdiction in the Eastern Atlantic (ABNJ-EA: n = 29) from 2010 to 2018. Furthermore, we obtained additional current and historical sequences (1987-2004) from literature. Fragments of mtDNA control region were employed to perform Bayesian Mixed Stock Analysis. Additionally, temporal genetic diversity and the fixation index (FST) were estimated. The majority of sea turtles in Macaronesia originate from rookeries in East Florida. The time comparison showed the Cape Verde rookery contribution increased for all FG and was significantly higher for Canaries (from 6% to 49%). This result suggests a potential recovery in the Cape Verde nesting population. The haplotype diversity decreased over time for all sites and the pairwise FST comparisons indicated significant genetic variation within the same sites over time. The genetic structure between sampling timeframes and the decreasing of genetic diversity over time can indicate fluctuations in rookeries sizes due to anthropogenic threats or conservation efforts. Therefore, genetic studies are essential for monitoring this highly migratory species and identifying changes in the FG composition over the years, which is important for detecting population recovery or early signs of recruitment decline.

UNCOVERING THE GENETIC STRUCTURE OF EUROPEAN ANCHOVY POPULATIONS IN NORTHWESTERN AND CENTRAL MEDITERRANEAN

Alexandridis Damianos [1,2], Manousaki Tereza [1], Magoulas Antonios [1], Cannas Rita [3,4], Spedicato Maria T. [5], Coll Marta [6], Tsigenopoulos Costas S.* [1]
1. IMBBC, HCMR, Heraklion, Greece
2. University of Crete, Heraklion, Greece
3. University of Cagliari, Cagliari, Italy
4. CoNISMa, Rome, Italy
5. COISPA, Bari, Italy
6. ICM-CSIC, Barcelona, Spain

The European anchovy (*Engraulis encrasicolus*) is a long-studied small pelagic fish species, attracting massive attention due to its role in regulating trophic interactions in marine ecosystems, as well as to its significant socio-economic impact on the regional fishing industry. Genomic studies constitute a powerful tool for uncovering the evolutionary history, patterns of spatial genetic structure and connectivity of a species. We used advanced genomic techniques and the double-digest random amplified DNA (ddRAD) sequencing approach to study the population structure of European anchovies. In order to increase the number of polymorphic loci, we first assembled a draft reference genome for the species (1.69 Gb assembly size and 79.8% BUSCO completeness) which facilitated to map ddRAD-seq data from 398 anchovy individuals across one Atlantic and eleven sites in Western and Central Mediterranean. The dataset consisted of 9,497 single nucleotide polymorphism (SNP) markers and clustering analyses revealed that the anchovy populations could be divided into two main groups: one group found in the Atlantic and Alboran Sea, and another group found in the Northwestern and Central Mediterranean Seas (FST=0.09). These groups showed some genetic differences, suggesting that there are distinct genetic pools among anchovy populations. This finding confirms previous studies and suggests that the area of the Almeria–Oran front may act as a barrier to gene flow between anchovy populations. Overall, our research sheds light on how anchovy populations are connected genetically. This information is crucial for developing conservation strategies to protect anchovies from threats like overfishing and habitat loss.

GENETIC CONNECTIVITY OF STRIPPED VENUS CLAM (*CHAMELEA GALLINA*) ACROSS ITS DISTRIBUTION RANGE

Ozturk Rafet C.* [1], Altinok Ilhan [1]
1. Karadenız Technical University, Türkiye

Chamelea gallina, is an economically important clam species inhabiting coastal waters of the Mediterranean Sea and the Eastern Atlantic Ocean coasts of Europe. Despite the economic value of the species, there is limited information about genetic connectivity on a geographical scale. In this study, the population genetic structure of *C. gallina* sampled from the Black Sea, the Levantine Sea, the Adriatic Sea, and the Atlantic Ocean was assessed by using microsatellites, mtDNA and nuclear markers. No significant genetic difference was found between sampling sites and geographic regions based on the microsatellite analysis, leading to the inference that gene flow was sufficient across sampling sites. Positive and significant spatial autocorrelation of microsatellite genotypes was detected among *C. gallina* sampled within the geographic range of 100− 300 km. The structure analysis did not reveal population sub-structuring. High level of genetic homogeneity in the Black Sea indicates that *C. gallina* could be managed at the regional level. COI appeared to be comparatively more polymorphic than 16S rRNA and ITS2. Based on COI and 16S rRNA sequence analysis, the Black Sea specimens were identified and separated from the Levantine Sea, the Adriatic Sea, and the Atlantic Ocean specimens. Both mtDNA and nuclear markers were able to discriminate *C. gallina* and *C. striatula*. Meanwhile, microsatellite loci were successfully cross amplified in *C. striatula* specimens but did not discriminate taxa. Our study revealed the extant population genetic structure of *C. gallina* and explained the weak population structure of a species with a long planktonic larval stage.

INSIGHTS ON THE POTENTIAL ROLE OF DOUBLY UNIPARENTAL INHERITANCE OF MITOCHONDRIA IN GENETIC STRUCTURE AND FITNESS OF THE MARINE BIVALVE *MACOMA BALTHICA*

Pante Eric* [1], Le Cam Sabrina [2], Viricel Amélia [1], Bidault Adeline [1], Salin Karine [1], Breton Sophie [3], Blier Pierre [2]
1. University of Brest, CNRS, IRD, Ifremer, LEMAR, IUEM, Plouzane, France
2. Département de biologie, chimie et géographie, Université du Québec à Rimouski, Rimouski, Canada
3. Département de sciences biologiques, Université de Montréal, Montréal, Canada

Mito-nuclear genetic incompatibilities (MNI) can contribute to reproductive isolation. The remarkable system of doubly uniparental inheritance (DUI) of bivalves is an attractive model to study the role of MNI in maintaining reproductive isolation because males carry two highly divergent mitochondrial genomes. We look for MNIs in populations of *Macoma balthica*, a littoral species characterized by DUI and hybrid zones that may be conducive to MNIs. We inventoried interacting mitochondrial and nuclear genes using reference transcriptomes and used these data to build a custom capture bait set. We applied the latter to 254 male individuals (bearing both male and female mitotypes) across the hybrid zone spanning from Finistère to Cotentin along the seashore of Western France. We will look for statistical signatures of MNIs for male- and female-specific mitochondrial function pathways. Genomic data will be coupled to an ecophysiological assessment of mitochondrial function across the hybrid zone. Enzyme activities involved in bioenergetics (Citrate synthase and ATPase) will be assessed in and out of the hybrid zone to investigate the effect of MNI on individual energetic metabolism. We hope these data will help shed light on the potential interaction between DUI and MNIs in shaping patterns of genetic structure and local adaptation of the baltic tellin.

WEDDELL SEA KEY? POPULATION GENOMICS AND CONNECTIVITY IN A KEY NESTING ICEFISH IN AN ANTARCTIC CANDIDATE AREA FOR PROTECTION

Marino Ilaria A.M. [1], Schiavon Luca [1], Hughes Laura M. [1], Prestanti Alessia [1], Mark Felix C. [2], Lucassen Magnus [2], Hanel Reinhold [3], Chakrabarti Lisa [4], Held Christoph [2], Jones Christopher [5], La Mesa Mario [6], Di Franco Antonio [7], Matschiner Michael [8], Ceballos Santiago G. [9], Purser Autun [2], Papetti Chiara* [1]

1. University of Padova, Italy
2. Alfred Wegener Institute Helmholtz-Centre for Polar and Marine Research (AWI), Germany
3. Thünen Institute of Fisheries Ecology, Germany
4. University of Nottingham, UK
5. NOAA Fisheries, USA
6. Istituto Scienze Polari, Italy
7. Zoological Station Anton Dohrn, Italy
8. University of Oslo, Norway
9. Universidad Nacional de Tierra del Fuego, Argentina

A recent, breakthrough discovery from seabed imaging provides the opportunity to test connectivity hypotheses in an iconic Antarctic species. A vast breeding ground (45,000 km2) of the Antarctic icefish *Neopagetopsis ionah* was found in the Weddell Sea (Southern Ocean), which is currently under consideration as a Marine Protected Area. This is the first evidence that Antarctic icefish perform large spawning aggregations and raises the question of whether *N. ionah* migrates to this single nesting site or if there are other circum-Antarctic nesting sites. In this study, we aim to answer this question by applying a multidisciplinary approach that includes population genomics, otolith ageing, and microchemistry analyses on *N. ionah* samples (fin clips and otoliths) collected from the Weddell Sea spawning aggregation as well as the Antarctic Peninsula. Studying species connectivity can provide valuable insight into the number and distribution of *N. ionah* spawning sites. Understanding the nesting site distribution of *N. ionah* could have far-reaching implications for conservation and could further promote the urgent need to protect key benthic habitats in the Southern Ocean.

DISPERSAL CAPABILITY OF AN INVASIVE MUSSEL IN THE NW COAST OF THE IBERIAN PENINSULA

Peteiro Laura G.* [1], Olabarria Celia. [2], Babarro Jose M.F. [1], Vázquez Elsa [2]
1. Institute of Marine Research, Spanish National Research Council (IIM-CSIC), Spain
2. University of Vigo (UVigo), Spain

The invasive mussel *Xenostrobus securis*, native of New Zealand, has been first documented in the NW coast of the Iberian Peninsula in the 2000's. This species coexists with the native mussel, *Mytilus galloprovincialis*, although it is limited to areas of intermediate-low salinity. Nonetheless, this invasive species seems to be spreading, and there are already new records in Galicia in nearby estuaries.

Dispersal pathways of this species are unknown, rising concerns not just around the colonization capability of the initial population, but also about the existence of new accidental anthropogenic introductions. To try to understand the dispersal capability of *X. securis* and the degree of connectivity between the initially detected population and the new populations, we employed a combined approach. First, a comparative study was carried out on larval settlement patterns between the native mussel and the invader. Artificial collectors were used to obtain high-frequency (every other day) settlement time series during the reproductive peak of the species along a saline gradient. Then the degree of larval interchange between both estuaries was evaluated using natural tagging techniques based on the geochemical composition of the shells. Our results showed a much greater settlement of the invasive mussel in the more estuarine locations. Nonetheless, sporadic presence was detected in the outermost areas of the estuary where oceanic conditions are dominant. These results indicate that *X. securis* larvae can survive in oceanic environments even if they are not optimal, which would favour the invasion of other estuaries.

SPINELESS AND OVERLOOKED: DNA METABARCODING OF AUTONOMOUS REEF MONITORING STRUCTURES REVEALS INTRA- AND INTERSPECIFIC GENETIC DIVERSITY IN MEDITERRANEAN INVERTEBRATES

Thomasdotter Anna [1], Shum Peter [2], Mugnai Francesco [3], Vingiani Marina [4], Dubut Vincent [5], Marschal Florent [5], Abbiati Marco [6], Chenuil Anne [5], Costantini Federica* [3]
1. County Administrative Board of Västerbotten, Umeå, Sweden
2. School of Biological and Environmental Sciences, Liverpool John Moores University, Liverpool, UK
3. Department of Biological, Geological and Environmental Sciences, University of Bologna, Ravenna, Italy
4. National Research Council, Institute of Marine Sciences, CNR-ISMAR, Venice, Italy
5. Aix Marseille Université, Avignon Université, CNRS, IRD, IMBE, Marseille, France
6. Department of Cultural Heritage, University of Bologna, Ravenna, Italy

The ability to gather genetic information using DNA metabarcoding of bulk samples obtained directly from the environment is crucial to determine biodiversity baselines and understand population dynamics in the marine realm. While DNA metabarcoding is effective in evaluating biodiversity at community level, genetic patterns within species are often concealed in metabarcoding studies and overlooked for marine invertebrates. In the present study, we implement recently developed bioinformatics tools to investigate intraspecific genetic variability for invertebrate taxa in the Mediterranean Sea. Using metabarcoding samples from Autonomous Reef Monitoring Structures (ARMS) deployed in three locations, we present haplotypes and diversity estimates for 145 unique species. While overall genetic diversity was low, we identified several species with high diversity records and potential cryptic lineages. Further, we emphasize the spatial scale of genetic variability, which was observed from locations to individual sampling units (ARMS). We carried out a population genetic analysis of several important yet understudied species, which highlights the current knowledge gap concerning intraspecific genetic patterns for the target taxa in the Mediterranean basin. Our approach considerably enhances biodiversity monitoring of charismatic and understudied Mediterranean species, which can be incorporated into ARMS surveys.

EVALUATION OF LOCAL AND REGIONAL CONNECTIVITY USING HYDRODYNAMIC MODEL IN SOUTH TYRRHENIAN SEA

Saviano S.* [1], Kokoszka F. [2], Botte V. [3], Iudicone D. [3], Cianelli D. [1]
1. Stazione Zoologica di Napoli Anton Dohrn, Department of Research Infrastructures for Marine Research, Naples, Italy
2. Consiglio Nazionale delle Ricerche, Istituto di Scienze Marine, Naples, Italy
3. Stazione Zoologica di Napoli Anton Dohrn, Department of Integrative Marine Ecology, Naples, Italy

Coastal connectivity in densely urbanized areas becomes of crucial interest for service management and ecosystem protection in coastal areas, such as the Campania Region (Southern Italy) where highly polluted rivers flow and several marine protected areas and sites of cultural interest are present. The purpose of this work is to obtain a representation of connectivity patterns through the estimation of ocean currents in the region of interest and for a period sufficient to represent the greatest variability of the system. The numerical simulations have been performed using a regional ocean modeling system (ROMS) developed for the Tyrrhenian Sea and downscaled for the Campania coastal area to cover temporal scale at high resolution (from January 2013 to December 2017). The transport package is forced with the ROMS velocity fields to track trajectories of virtual particles, released into the model domain from coastal waters, to estimate nearshore sites connectivity. The simulations highlight the role of local current in affecting particle destinations and the relevant effect of the seasonal variability of the area. As a regional and mid-term investigation, this study provides results, consistent with the literature and the observed data, and useful for diverse group of end-users. Application to specific process studies will contribute to clarify the relationship between the physical forcings occurring in the upper layers of the water column and the spatial distribution of the different particles (i.e., plankton, larvae or microplastics).

FACTORS INFLUENCING SALMON SURVIVAL AND MARINE MIGRATORY PATHWAYS IN A CHANGING WORLD

Smith Lucy R.* [1], Hanson Nora [2], Bull Collin [3], O'Gorman Eoin [1], Sturrock Anna M. [1]
1. University of Essex, UK
2. Marine Directorate, Scottish Government, UK
3. University of Stirling, UK

Over the last few decades, Atlantic salmon (*Salmo salar*) in the North Atlantic have experienced synchronous and widespread declines in abundance, concurrent with increasing mortality at sea. Atlantic salmon survival is threatened throughout their complex life histories, but large-scale oceanographic shifts in the North Atlantic are thought to be a key driver of the decline in return rates. In order to understand selective pressures across their life cycle, it is critical to quantify the influence of outmigration size on marine survival (carryover effects) and how subsequent migratory routes at sea are influenced by changing ocean conditions. While tagging technology has become more sophisticated, it is difficult and expensive to track the smallest and earliest life stages using traditional tagging techniques. We used otolith microchemistry and eye lens isotopes to reconstruct freshwater-marine transition in post-spawned adults from 14 populations, comparing the outmigration sizes among four years (2020-2023). Specifically, we tested the hypothesis that unfavourable ocean conditions are associated with increased mortality among smaller outmigrants (less body reserves), resulting in larger and less variable outmigrant sizes observed among the surviving adults. We also describe the methods by which we will reconstruct marine migration pathways using otolith δ18O values within a state-space model framework. The results of this work can be used to inform salmon population dynamics models, and improve our understanding of the their response to climate change and vulnerability to marine stressors such as offshore wind developments and salmon farms.

NEW ECOLOGICAL INSIGHTS USING SIZE-SPECIFIC SPECIES DISTRIBUTION MODELS

Smoliński Szymon* [1], Radtke Krzysztof [1], Lindmark Max [2], Orio Alessandro [2], Tanaka Kisei [3]
1. Department of Fisheries Resources, National Marine Fisheries Research Institute, Gdynia, Poland
2. Department of Aquatic Resources, Swedish University of Agricultural Sciences, Institute of Marine Research, Lysekil, Sweden
3. Pacific Islands Fisheries Science Center, National Marine Fisheries Service, National Oceanic and Atmospheric Administration, Honolulu, USA

Spatial distribution models (SDMs) are valuable tools for predicting the distribution of marine resources and for marine spatial planning. Fish populations exhibit a size-structured organization, with individuals of different sizes displaying distinct habitat preferences. In this study, we investigated how changes in habitat preferences of the fish species during lifetime growth can result in differences in the distribution and its driving factors between size classes. We tested 1) the differences in the importance of the predictors of fish spatial distribution between different size classes within species and 2) the differences in the distribution-environment relationships between size classes. Additionally, we investigated how the application of size-specific models affects the accuracy of prediction. To test our hypotheses, we used Baltic International Trawl Surveys (BITS) data collected from 1993 to 2021. We selected Atlantic cod (*Gadus morhua*) and modeled its density (individuals/km2) distribution as a function of selected environmental variables using random forest models fitted separately to the different size classes. Our results showed that size-specific SDMs offer a valuable alternative to models based on overall species abundance when predicting spatial distribution. Such an approach can be helpful in a more in-depth investigation of the relationships between species and the environment, and provide information on size-specific habitat preferences, which can further serve as a baseline for studies on functional connectivity. This framework is a generic and robust tool and has the potential to be applied to a broad range of species, not limited to marine ecosystems.

THE CONNECTIVITY OF PATHOGENS AND ANTIBIOTIC RESISTANCE GENES (ARGs) BETWEEN HUMANS, LIVESTOCKS AND THE ENVIRONMENT IN NHA TRANG BAY, VIETNAM

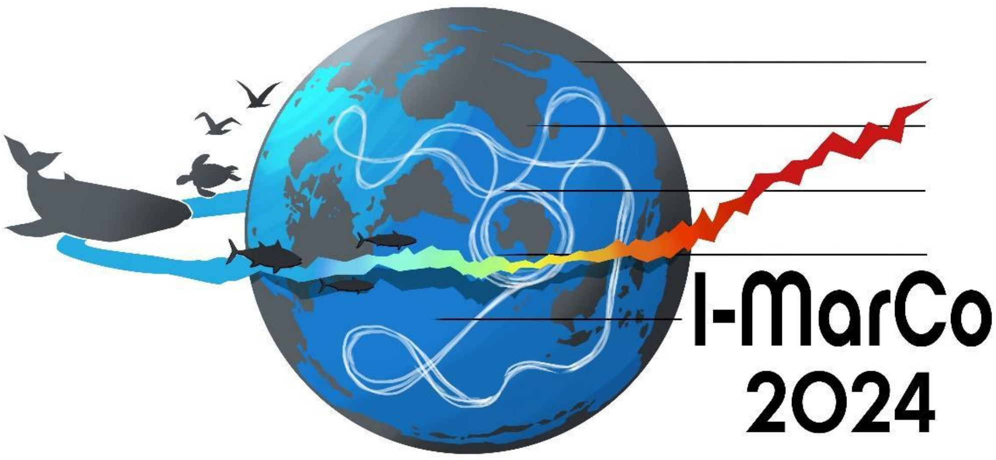
Tran Son-Hoang* [1,2], Auguet Jean-Christophe [1], Claudia Restrepo-Ortiz [1]
1. MARBEC, Montpellier, France
2. University of Science and Technology of Hanoi, Hanoi, Vietnam

The connectivity of pathogens and antibiotic resistance genes (ARGs) in the marine environment introduces a unique dimension to the complex interaction between humans, animals, and ecosystems. Marine and particularly coastal environments can function as transmission foci for PPB (potentially pathogenic bacteria) and/or ARGs because of the concentrated aggregations of bacteria from different sources, both marine and terrestrial, where environmental, human, and/or animal-related bacteria can coexist, at least temporally. With half a million inhabitants and more than 200 aquaculture farms distributed along the coast, the waters of Nha Trang Bay are heavily impacted by anthropogenic inputs (of urban and/or aquaculture origins), making this an ideal location for sampling. Here, we collected fecal and skin samples from 25 sea-cage workers and gut samples from livestocks. Environmental samples as water and sediment around the Nha Trang Bay were also collected in parallel with humans and animals. Analysis of the microbiome from all compartments revealed differences in bacterial diversity and abundance. PPB has shown more abundance, up to 45% of total bacteria when isolated and analyzed from Urban transect where anthropogenic activities are intensive and distance to the coast was a driver for the abundance of pathogens. There was also a number of PHPB (potentially human pathogenic bacteria) that shared between compartments indicating a circulation of PPB. Metagenomic analysis also detected 565 ARGs encompassing 62 classes of antibiotics where Rifampicin, Quinolones, and Resistance to multiple antibiotics (“multidrug”) were dominating the resistome. This study represents a valuable effort towards surveillance and control programs, and limiting the socioeconomic impact of pathogen contaminations and ARGs.

Posters

Session 2

Marine Functional Connectivity research and the global functioning and health of the Ocean



MODELING LARVAL DISPERSAL AND CONNECTIVITY: A COMPARATIVE ANALYSIS OF ECHINODERMS, CRUSTACEANS, AND OSTEICHTHYANS IN THE MEDITERRANEAN SEA

Barrier Céline* [1], Beneteau Thomas [1], Ternengo Sonia [1,2], Lett Christophe [3], Lenfant Philippe [4], Pasqualini Vanina [1,2], Durieux Eric D.H. [1,2]

1. Université de Corse, UMR CNRS 6134 Sciences pour l'Environnement, Corte, France
2. Université de Corse, UAR CNRS 3514 Stella Mare, Biguglia, France
3. MARBEC, Université de Montpellier, CNRS, Ifremer, IRD, Sète, France
4. Université de Perpignan Via Domitia, Centre de Formation et de Recherche sur les environnements Méditerranéens, UMR 5110, Perpignan, France

Our study employs a modeling approach using Ichthyop software to investigate larval dispersal and connectivity in the Mediterranean Sea over a decade. We focus on two distinct spatial scales: the entire Mediterranean Sea, using the Mediterranean Sea Physics Reanalysis model, and the Northwestern Mediterranean Sea, specifically with the MARS3D model. It addresses three coastal fishery-exploited taxonomic groups with model species: an echinoderm (*Paracentrotus lividus*), a crustacean (*Maja squinado*), and a fish (*Diplodus sargus*). These species display diverse larval characteristics, including pelagic larval duration (PLD) and more or less complex behaviors such as vertical migration and oriented swimming. The research highlights the diversity and spatio-temporal variability of larval dispersal processes, emphasizing the importance of considering species-specific traits in fisheries management. Through comparative analysis of model simulations, this study aims to generate spatially relevant indicators for fisheries management (receiving zones, emitting zones, larval flows, connectivity, self-recruitment, local retention, connectivity distances, orientation of flows), thereby facilitating sustainable exploitation. These findings seek to enhance our understanding of the larval dynamics and connectivity of exploited species, offering a nuanced view of marine ecology crucial for the effective spatial management of fisheries in the Mediterranean Sea and the broader relevance of marine spatial planning.

EXPLORING HABITAT CONNECTIVITY BETWEEN ANTHROPOGENICALLY MANAGED AND NATURAL SEAWEED HABITATS FOR EPIPHYTIC PARTLY PARASITIC COMMUNITIES ASSOCIATED TO DOMESTICATED TROPICAL RED ALGAE

Brakel Janina* [1,2,3], Ruiz Gonzalez Carla [1], O'Connell Callum [1], Zhang Qian Yi [1], Matoju Ivy [4], Rusekwa Sadock [4], Ndawala Msafiri [4], Msuya Flower E. [4], Faisan Joseph Jr. [5], Robinson, Georgina [1], Pascal Fred [6], Joanne Paul [6], Brodie Juliet [7], Lim Phaik E. [8], Poong Sze-Wan [8], Díaz-Tapia Pilar [9], Gachon Claire M.M. [1,10]
1. Scottish Association for Marine Science, United Kingdom
2. Helmholtz Institute for Functional Marine Biodiversity at the University of Oldenburg, Germany
3. Alfred Wegener Institute Helmholtz Center for Polar and Marine Research, Germany
4. University of Dar es Salaam, Tanzania
5. Aquaculture Department, Southeast Asian Fisheries Development Centre, Philippines
6. Ocean Farmers, Madagascar
7. Natural History Museum, Science, United Kingdom
8. University of Malaya, Malaysia
9. Universidade de Santiago de Compostela, Spain
10. Muséum National d'Histoire Naturelle, CNRS, Paris, France

Seaweed aquaculture is an increasing activity in coastal regions globally. The open-water cultivation of seaweeds may lead to changes in seascapes, including habitat connectivity. One of the largest seaweed cultivation sectors globally is the cultivation of the red algae *Kappaphycus* and *Eucheuma*, which are cultivated in the tropics for their carrageenan content and reach an annual production of 9.9 million tonnes in 2020. However, an increasing challenge in the cultivation of *Kappaphycus* and *Eucheuma* in this region is the occurrence of epiphytic filamentous red algae of which some species are parasitic and lead to decreases in farming yields. Here, we present research investigating these cryptic epiphytical communities and their connectivity across anthropogenically managed habitats (open-water seaweed farm) and natural habitat (seaweeds or seagrasses) in the surrounding of seaweed farms. In a replicated, hierarchical structured sampling design, we collected epiphytical communities across habitats in two regions in the Western Indian Ocean (Unguja, Zanzibar, Tanzania and Atsimo-Andrefana, Madagascar). We assess through a highly multiplexed barcoding approach the community composition and compare amplicon sequence variant (ASV) composition between different habitats (seaweed farms and natural seaweed or seagrass populations). Our aim is to better understand connectivity in these anthropogenically managed habitats and thereby identify pathways of introduction into farming systems and into natural ecosystem. We hope gained insights will be of support for a sustainable seaweed farming sector.

POTENTIAL LARVAL MIXING OF NORWAY LOBSTER POPULATIONS AMONG NO-TAKE RESERVES IN THE NW MEDITERRANEAN SEA

Clavel-Henry Morane* [1], Bahamon Nixon [1], López Miguel [1], Aguzzi Jacopo [1], Navarro Joan [1], Company Joan B. [1,2]
1. ICM-CSIC, Barcelona, Spain
2. ICatMar, Barcelona, Spain

Early life stages of demersal species may inhabit in pelagic waters, are dispersed by ocean currents, and can mix, establishing assemblages. To protect fishery resources such as *Nephrops norvegicus* and contribute to ecosystem recovery, a network of no-take reserves (NTRs) has recently been implemented in the northwestern (NW) Mediterranean. However, little is known about larval dispersal and mixing among the NTRs. We coupled a particle transport model to a 3D hydrodynamic model of the NW Mediterranean to simulate the trajectories of pelagic early life stages (larvae and postlarvae) of *N. norvegicus* from four NW Mediterranean NTRs targeting its recovery. We investigated the mixing of postlarval stages (i.e. presumably individuals settling on the seafloor) from these reserves, the effect of larval release timing on mixing, and the locations of mixing. Mixing metrics revealed diverse combinations and strengths of mixing depending on release timing of larvae and surface ocean circulation. Most of the postlarval assemblages settled away from the existing NTRs, i.e. with relatively low postlarval abundances settling inside the NTRs. These abundances in the assemblages were uneven, with a prevalence of individuals from specific NTRs. These mixing metrics allowed a better understanding of oceanographic connectivity processes in the NTR network, regardless of the larval destination. Furthermore, they suggested potential settlement areas of larval assemblages outside the NTR network, thereby increasing awareness of the network design effectiveness in optimising connectivity.

MED-TROPH: A COMPREHENSIVE TROPHIC ECOLOGY DATABASE OF MARINE ORGANISMS IN THE MEDITERRANEAN SEA

Coll M.* [1], Pastor-Prieto M. [1], Ferández-Corredor E. [1], Ouled-Cheikh Bonan J. [1,2], Giménez J. [1,3], Navarro J. [1], Ramírez, F. [1]
1. Institute of Marine Science (ICM- CSIC), Barcelona, Spain
2. University of Barcelona (UB), Barcelona, Spain
3. Centro Oceanográfico Malaga (IEO-CSIC), Malaga, Malaga, Spain

Feeding behavior and ecology of organisms intervene importantly in marine connectivity as species move towards or prey upon organisms that belong to different habitats. While doing so, they establish ecological linkages that substantially contribute to the structure and functioning of marine ecosystems. Describing and understanding these linkages is essential to manage ecosystems with an integrative perspective. Here, we present a large trophic database that details trophic interactions among marine organisms from the Mediterranean Sea (MED-TROPH), including more than 34000 records and more than 2400 entities (bacteria, chromists, protozoans, plants and animals). Most of the data is sourced from stomach content analysis, followed by stable isotopes analysis and DNA metabarcoding registries. From a spatial perspective, the Western Mediterranean region clearly dominates in terms of available studies and, from the temporal side, an increasing number of studies published per year can be observed. We use the Mediterranean Sea trophic database to (1) characterize the knowledge available about trophic ecology in the region, (2) quantify the relationship between main species trophic linkages and their traits (e.g. habitat, taxa), (3) assess marine food-web network structure, and (4) simulate potential effects of changes in trophic interlinkages caused by depletion of commercial and vulnerable species groups.

TEMPERATURE ALTERS THE SIZE SELECTIVITY OF SOUTHERN OCEAN FISH

Eskuche-Keith Patrick* [1,2], Hill Simeon L. [2], López-López Lucía [3], Rosenbaum Benjamin [4,5], Saunders Ryan A. [2], Tarling Geraint A. [2], O’Gorman Eoin J. [1]
1. School of Life Sciences, University of Essex, UK
2. British Antarctic Survey, Cambridge, UK
3. Ecosystem Oceanography Group GRECO, Oceanographic Centre of Santander (CN IEO, CSIC), Spain
4. EcoNetLab, German Centre for Integrative Biodiversity Research (iDiv), Germany
5. Institute of Biodiversity, Friedrich Schiller University Jena, Germany

A primary response of many marine ectotherms to warming is a reduction in body size, to lower the metabolic costs associated with higher temperatures. The impact of such changes on ecosystem dynamics and stability will depend on the resulting changes to community size-structure, but few studies have investigated how temperature affects the relative size of predators and their prey in natural systems. We analysed predator-prey mass ratios using >3,700 prey size measurements from ten mesopelagic myctophid fish species sampled across a temperature gradient in the Scotia Sea, Antarctica. We also used data on the size-distribution of zooplankton in the environment, taken from the same cruises as the fish samples, to investigate how temperature influences size-selective feeding. As temperature increased, predators became closer in size to their prey, driven primarily by a decline in predator size and an increase in the relative abundance of intermediate-sized prey. The potential implications of these changes include reduced top-down control of prey populations and a reduction in the diversity of predator-prey interactions. Both of these factors will likely reduce the stability of community dynamics and ecosystem resistance to perturbations.

UNVEILING A CORAL DISEASE DYNAMICS: SCTLD'S REACH INTO THE US VIRGIN ISLANDS MESOPHOTIC REEFS

Scherpereel Colin *[1], Holstein Daniel M. [2], Lambrechts Jonathan [3], Hanert Emmanuel [1,3]
1. Earth and Life Institute, UCLouvain, Louvain-la-Neuve, Belgium
2. Department of Oceanography and Coastal Sciences, Louisiana State University, Baton Rouge, USA
3. Institute of Mechanics, Materials and Civil Engineering, UCLouvain, Louvain-la-Neuve, Belgium

In the Caribbean, coral reefs face unprecedented challenges, with the stony coral tissue loss disease (SCTLD) emerging as a predominant threat since 2014. This disease, exacerbated by factors such as extreme bleaching events, hurricane-induced physical damage, and coastal pollution, has led to substantial declines in Caribbean coral populations. Despite extensive conservation efforts, SCTLD has become endemic to the region. Our research delves into the impact of SCTLD on mesophotic coral ecosystems (MCEs), situated at depths exceeding 30m and abundant in the Caribbean. Unlike shallow reefs, the extent of SCTLD's reach into MCEs remains uncertain. Employing a 3D multi-scale high-resolution biophysical model coupled with an SIR epidemic model, we assess the potential transmission of SCTLD to MCEs following the contamination of shallow coral populations in the United States Virgin Islands (USVI). By replicating the observed propagation pattern in the Northern USVI from early 2019 to mid-2020, our study sheds light on the dynamics of the disease at a regional scale. Furthermore, we identify key reefs that likely acted as super spreaders in the coral connectivity network during the outbreak. This comprehensive modeling approach enhances our understanding of SCTLD dynamics and aids in pinpointing reefs where protection efforts should be concentrated to effectively mitigate the emergence of future outbreaks. Given the looming threat of SCTLD spreading to the Pacific, our findings could guide strategic monitoring/treatment planning and prioritize reef protection initiatives.

INDIVIDUAL VARIATION IN PHILOPATRY AND SPATIAL BEHAVIOURS IN *RAJA UNDULATA* AND POTENTIAL IMPLICATIONS ON CONSERVATION AND CONNECTIVITY

Hillinger Alina* [1], Villegas-Ríos David [1], Monk Christopher [2], Mucientes Gonzalo [1], Papadopoulo Kenn [1], Alonso-Fernández Alexandre [1]
1. Department of Ecology and Marine Resources, Instituto de Investigaciones Marinas (IIM-CSIC), Spain
2. Research Division 3: Marine Ecology, GEOMAR, Germany

Individual variation in almost any trait is a common feature of aquatic species. Despite being crucial to understand ecological and evolutionary processes (demography, habitat use, distribution/migrations/connectivity and fisheries-induced evolution), individual variation often remains overlooked in conservation and ecology studies. We investigated whether 1) individuals vary in the large-scaled movements they perform in and out of our study area (philopatry), and 2) whether these large-scaled movements co-vary with fine-scaled movements (activity, activity space) in a population of the endangered undulate skate, *Raja undulata*, within a small marine protected area in NW Spain. We tracked ~200 individuals across four years to explore long-term philopatry strategies based on presence/absence patterns in the study area and fine-scaled behaviours based on high-resolution positions. Then, we used Bayesian multivariate mixed-effects models to investigate behavioural consistency at the individual level, and co-variation between broad-scaled movement strategies and fine-scaled behaviours. We illustrate that individual variation of philopatry strategies exist in our population, which together with recapture data suggests that the study site may act as a node in a connectivity network, impacting the connectivity with other sites and efficiency of conservation measures. Furthermore, we found consistent individual variation in fine-scaled spatial behaviours, reinforcing the idea that individual variation in behaviour is common in aquatic species, while we detected no co-variation between large- and fine-scaled behaviours. Our results suggest that in order to enhance resilience and ensure protection of different behavioural types and thus connectivity, individual variation should be taken into account when designing and managing spatial protective measures.

REGIME SHIFTS IN ADRIATIC FISHERIES

Kamberi Elvis* [1,2], Hala Edmond [1], Kule Marco [3], Möllmann Christian [2]
1. Department of Aquaculture and Fishery, Agricultural University of Tirana, Albania
2. Institute of Marine Ecosystem and Fisheries Science (IFM), Center for Earth System Research and Sustainability (CEN), University of Hamburg, Germany
3. Directory of Aquaculture and Fisheries Services, Ministry of Agriculture and Rural Development, Albania

The Adriatic Sea is changing rapidly due to the impact of anthropogenic and climatic pressures. Fishing and climate change are recognized as two of the main drivers affecting the ecosystem structure, functioning and the services they provide to humans. The impact of these external drivers may lead to a change of the equilibrium state of the ecosystem. This can induce a non-linear response, forcing the system to move to another state, recognized as a regime shift. The occurrence of these regime shifts can have significant implications in the effectiveness of the management measures, potentially influencing their success. Here we analysed landings of the main commercially targeted species (27 taxa) for the period 1970 - 2020 and found a significant correlation with variations in sea surface temperature. In our study, we furthermore implemented Rodionov's Regime Shift Index to investigate whether the fishing community experienced a discontinuous change. We found that the Adriatic Sea fish community displays a discontinuous dynamic as a consequence of its eroded resilience by external drivers. Our results support the current body of knowledge regarding the dynamics of the fish community evolution in the Adriatic and indicate the importance of considering such dynamics in the decision-making process to preserve its ecological integrity and economic viability.

LARVAL CONNECTIVITY TRAILS OF NORWAY LOBSTER IN THE FISHERIES-CONSERVATION-OFFSHORE RENEWABLES NEXUS

Kruse Maren* [1], Bockelmann Frank [2], Neumann Hermann [1], Probst Wolfgang N. [1], Stelzenmüller Vanessa [1]
1. Thünen Institute for Sea Fisheries, DE
2. Helmholtz Zentrum Hereon, DE

The Norway lobster (*Nephrops norvegicus*) plays a pivotal role in marine food web dynamics and is a valuable target in European fisheries. Despite its ecological and economic significance, populations are declining, primarily due to increasing habitat fragmentation and climate change. Preserving local populations requires a deeper understanding of the processes governing species survival. As a non-migratory megafauna dwelling in muddy sediment burrows in deep waters, its persistence relies extensively on larval connectivity, facilitating the exchange between suitable habitat patches and existing populations. Our study focuses specifically on larval drift as the primary mechanism driving this exchange using the North Sea as an illustrative example. Offshore renewables sites in this region significantly overlap with areas of high Norway lobster density, posing a threat to resident individuals and population persistence. Employing ensemble learning and Lagrangian methods we demonstrate how long-range transport maintains connectivity between distant habitat patches, serving as potential sources or sinks for larval dispersal. Our findings contribute to the broader context of current conservation efforts and fisheries management, emphasizing the necessity to consider functional connectivity in ecosystem-based marine spatial planning.

GENOMIC POPULATION STRUCTURE OF THE COMMON DOLPHIN (DELPHINUS DELPHIS) IN THE NORTH-EAST ATLANTIC OCEAN

Malkocs Tamas* [1,2], Méndez-Fernandez Paula [3], Kiszka Jeremy [4], Murphy Sinead [5], Covelo Pablo [6], Torres-Pereira Andreia [7], Alves Filipe [8], Lapègue Sylvie [9], Viricel Amelia [1]
1. LEMAR, Plouzané, France
2. LIENSs, La Rochelle, France
3. PELAGIS ,La Rochelle, France
4. Florida International University, North Miami, USA
5. MFRC, Atlantic Technological University Galway, Ireland
6. CEMMA Gondomar (Pontevedra), Spain
7. CESAM & DBio, Universidade de Aveiro, Spain
8. MARE Funchal, Portugal

Population structure plays a vital role in the management of marine species, guiding conservation efforts and mitigating threats such as bycatch.Since the 1990s, significant dolphin mortality events have occurred during the winter along the French Atlantic coast of the Bay of Biscay resulting in stranding peaks. Most stranded dolphins are common dolphins (*Delphinus delphis*) exhibiting lesions associated with bycatch. Our understanding of how bycatch impacts common dolphins in the Bay of Biscay and the North-east Atlantic is constrained by our knowledge of their population structure. Previous studies using mitochondrial genetic markers or nuclear microsatellites found no population structure in this species on the scale of the North-east Atlantic Ocean, in contrast with studies using ecological tracers, which identified differences between oceanic and neritic populations. The present study uses population genomics to investigate the existence of distinct common dolphin populations in neritic versus oceanic zones in the Bay of Biscay, along with trying to uncover any population genomic structure in the North-East Atlantic Ocean. We are using biopsy samples from common dolphins collected in the Bay of Biscay in 2022 and 2023, as well as tissue samples collected from stranded dolphins, covering most of their distribution area in the North-east Atlantic Ocean, including the coasts of Spain, Portugal (mainland and Madeira islands), Ireland and the English Channel. Our study includes 288 individuals analyzed using a ddRAD sequencing approach. With this dataset, we will assess which populations are most affected by bycatch so that appropriate management measures can be undertaken.

SPATIAL DISTRIBUTION OF THE BLUE SHARK (*PRIONACE GLAUCA*) IN THE GALAPAGOS MARINE RESERVE AND IN SURROUNDING WATERS

Palomino Ángela P.* [1], Hearn Alex [1,2], Hammerschlag Neil [3]
1. Colegio de Ciencias Biólogicas y Aplicadas and Galápagos Academic Institute for the Arts and Sciences, Universidad San Francisco de Quito-USFQ, Ecuador
2. Galapagos Science Center, Universidad San Francisco de Quito – University of North Carolina at Chapell Hill, Ecuador
3. Rosenstiel School of Marine and Atmospheric Science, Department of Marine ecosystems and Society, USA

In recent years, several attempts have been made to understand how a marine reserve that is fixed in space helps protect species that are highly mobile. Previous studies of elasmobranchs in the Galapagos Marine Reserve (GMR) have focused on species such as the scalloped hammerhead (*Sphyrna lewini*) or the Galapagos shark (*Carcharhinus falciformis*). Although these species can move long distances depending on the season, their behavior tends to be more associated with coastal areas compared to pelagic species such as the blue shark (*Prionace glauca*). The blue shark is one of the most abundant and cosmopolitan species, with a wide distribution, being one of the species with the widest distribution range. However, in recent decades its population has decreased because it is one of the most exploited species in the world by pelagic longline fisheries. Fishing projects carried out in the Eastern Tropical Pacific (ETP) region show that the blue shark is one of the most common bycatch species, after the thresher shark (*Alopias pelagicus*). This study analyses the spatial distribution of *P. glauca* in the waters surrounding the GMR, evaluating the fidelity around the archipelago, the connectivity with other MPAs of the ETP and including this information in the evaluation of Ecosystem-Based Management models of the region. To achieve this goal, a pilot project began in 2019, which has made it possible to obtain data from 9 blue sharks, through satellite biotelemetry, to determine the level of protection provided by the GMR and other reserves in the ETP in a highly migratory species.

TRACK CHANGES IN STABILITY OF ATLANTIC COD (*GADUS MORHUA*) IN THE NORTH SEA OVER TIME AND ACROSS SPACE

Tao Hsiao-Hang* [1], Hsieh Chih-hao [2], Hidalgo Manuel [3], Dakos Vasilis [1]
1. Institute des Sciences de l'Evolution de Montpellier (ISEM), France
2. National Taiwan University, Taiwan
3. Spanish Institute of Oceanography (CSIC), Spain

Marine ecosystems provide key functions and services including nutrient cycling, biodiversity, and food resources. Disturbances, such as climate change and overfishing, are seriously threatening the future provision of these services, raising an urgent need for undertaking management actions that promote marine ecosystem stability. The stability of a marine ecosystem is defined as the capacity to persist or maintain its present state in the face of disturbances. When a marine ecosystem is vulnerable, disturbances may destabilize marine populations and the services they provide. In this work, we tracked the evolution of population stability over time and across space for an important fish population: Atlantic cod (*Gadus morhua*) in the North Sea. We did so by using empirical dynamic modelling (EDM), an equation-free, mechanic model based on reconstructing the underlying dynamical system from observed time series. We examined whether and how interactions between age groups and age structure of the population contributed to its stability. This work further aims at producing an online interactive stability map for fisheries managers to visualize yearly population stability at the subarea level of the North Sea between 1977 and 2023.

GENETIC STRUCTURE OF THE COMMON CUTTLEFISH IN THE BAY OF BISCAY AND ADJACENT WATERS

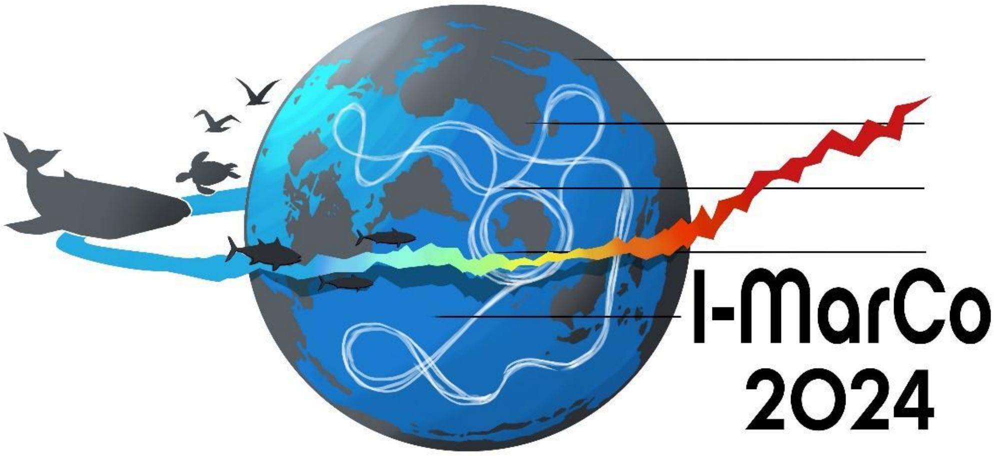
Viricel Amelia* [1], Malkocs Tamas [1][2], Perennou Morgan [1], Lacoue-Labarthe Thomas [2], Jozet-Alves Christelle [3], Leleu Kévin [4], Madeira Lopes Vanessa [5], Rosa Rui [5,6], Weiller Yohan [7], Réveillac Elodie [2]
1. LEMAR Plouzané, France
2. LIENSs La Rochelle, France
3. ETHOS Caen, France
4. Marine natural park of Arcachon Bay, French Office of Biodiversity, France
5. MARE Cascais, Portugal
6. DBA FCUL Lisboa, Portugal
7. PNM de la Mer des Pertuis, France

The common cuttlefish, *Sepia officinalis*, is the most exploited cephalopod species in the French Atlantic coast. Despite its economic importance, knowledge on its population structure and dynamics is still scarce. The cuttlefish migrates offshore in autumn and inshore in spring for reproduction. Sexual maturation occurs during their final inshore migration, culminating in adult spawning and subsequent death in the coastal area. This semelparous life cycle of the cuttlefish is completed predominantly within one year in the southern regions and extending to two years in the northern part of its distribution range. This implies a rapid turnover of these short-lived populations, renewing entirely every 1 or 2 years, with potential variations in the overlap of generations along different latitudes. Due to the absence of a pelagic larval phase in this benthic species' life cycle and its limited latitudinal dispersal during the longitudinal offshore-inshore migrations, we anticipate significant genetic differentiation across its distribution range. The aim of the present study is to investigate the cuttlefish genetic structure i) between life cycle strategies, ii) along the Atlantic Arc (Iberian Peninsula, Bay of Biscay and English Channel) and iii) among major breeding areas of the Bay of Biscay. Our investigation also includes a thorough examination of fine-scale genetic structure both inside and outside the two semi-enclosed Bays of Pertuis and Arcachon. Our study primarily concentrates on sexually mature individuals collected in 2021 and 2022, with a total of 125 individuals genotyped using an sdRAD approach sequenced on a Novaseq X Plus platform.

Posters

Session 3

Marine Functional Connectivity knowledge use for improved environmental policies and sustainable development



MPA EUROPE: DESIGNING REPRESENTATIVE AND ECOLOGICAL COHERENT MPA NETWORKS

Addamo Anna M.* [1], MPA Europe Team [2], Costello Mark J. [1]
1. Nord University, Norway
2. CCMAR, Portugal; IOC-UNESCO, Belgium; Aarhus University, Denmark; SAMS, United Kingdom; JNCC, United Kingdom; CLIMAZUL, Greece; Ocean University of China, China; University of the Ryukyus, Japan; Science Crunchers, Portugal

Recently, both European and global initiatives targets call for protecting at least 30% of marine ecosystems by 2030 through the establishment of marine protected areas (MPA) and other area-based conservation measures (OECM) to safeguard the most important areas for biodiversity. In addition to previous targets, partially achieved in number but less in quality, we should reach ecologically coherent, equitably and effectively managed MPA networks. The Horizon Europe "MPA Europe" project is using systematic conservation planning to map a network of MPA which are representative of species, habitats and ecosystems. This enables alternative weighting of variables and multiple scenarios and thus support wider marine spatial planning. Because of climate change driven shifts in species distributions, including habitat forming species, it is of interest to know how well places in this network are connected by oceanographic currents which may aid species dispersal. We will present the first-year results of the project, including new data-driven maps of marine ecosystems, species range maps, blue carbon and discuss the key role that marine functional connectivity will play in the future analysis of the MPA Europe.

CONSERVATION MANAGEMENT OF POLAR ECOSYSTEMS (COPE PROJECT): USING GENOMIC APPROACHES TO STUDY CONNECTIVITY IN ANTARCTIC FISHES AND AMPHIPODS, ACROSS SPATIAL AND FUNCTIONAL SCALES

Verheye, Marie L.* [1], Aerts Dorien* [1,2], Christiansen Henrik [1,3], Van de Putte Anton [2,4], Geslain Enora [1], Hellemans Bart [1], Schön Isa [2], Volckaert Filip. A.M. [1]
1. Laboratory of Biodiversity and Evolutionary Genomics, Leuven, Belgium
2. Directorate Natural Environment, Royal Belgian Institute of Natural Sciences, Brussels, Belgium
3. Greenland Institute of Natural Resources, Nuuk, Greenland
4. Marine Biology Lab, Université Libre de Bruxelles, Brussels, Belgium

The unique cold-adapted ecosystems of the Southern Ocean are threatened by rapid environmental change and increasing anthropogenic impact. Marine protected areas (MPAs), areas of ocean where human activities are limited or prohibited, have been increasingly promoted as a tool for mitigating ocean threats and conserving biodiversity. National governments and the Commission for the Conservation of Antarctic Marine Living Resources (CCAMLR) is progressing towards establishing a representative network of MPAs in the Southern Ocean. Connectivity is now widely recognized to be a crucial variable for the design and management of MPA networks through the effects that movements of individuals, biomass, energy and genes have on population viability, metapopulation persistence, and resilience to disturbance. The understanding of connectivity patterns is required to prioritize the allocation of conservation effort towards, for instance, areas acting as central connection nodes in a network of MPAs. The COPE project aims to advance the understanding of genetic connectivity and adaptation in key benthic and pelagic Antarctic organisms (crustaceans and actinopterygian fishes) using population genomic approaches (ddRAD sequencing). Thousands of genomic variants were used in two model genera, the *Charcotia* amphipod and the *Trematomus* fishes, to provide estimates of neutral and adaptive genetic variation and structure at different trophic levels and at a circumpolar scale. The results of the COPE project will contribute to our understanding of the spatial and functional distribution of biological variation in the Southern Ocean, required to develop suitable management and conservation strategies through CCAMLR.

SOLE (*SOLEA SOLEA*) NURSERY GROUND QUALITY ACROSS THE NORTHEAST ATLANTIC OCEAN

Van Moorleghem Charlotte [1], Allison Chyanna [2], Barbut Leo* [3], Burt Gary [2], Clare David [2], Couce Elena[2], Thompson Murray [2], Lacroix Geneviève [3], Depestele Jochen[1]
1. Flanders research institute for Agriculture, Fisheries and Food (ILVO), Belgium
2. Centre for Environment Fisheries and Aquaculture Science (CEFAS), UK
3. Royal Belgian Institute of Natural Sciences (RBINS), Belgium

Common sole (*Solea solea*) in the northeast Atlantic migrates extensively during its lifetime. Whether it is while residing in spatially distinct spawning grounds, within nurseries or on feeding grounds, sole individuals deal with a specific set of location and stage specific stressors. Although information on the nature and influence of these stressors is crucial in estimating future population trends, spatial and temporal knowledge remains scarce. This stands in contrast to the importance of the high commercial value of the species. In this study, we focused on the pre-recruitment life stages of sole in the eastern English Channel and Greater North Sea. Across this spatial range, nurseries may receive larvae from fish that spawned in waters with different environmental backgrounds. Some nurseries may receive settling larvae from both Western and Eastern North Sea waters, while others only receive larvae from one side. Does this variance in connectivity affect the settlements of recruits? And how do prevailing human stressors in spatially distinct nurseries affect nursery ground quality and subsequent recruit production? Through spatial and temporal modelling of historical survey data we aim to answer these questions. In our analyses we focus on the origin of the settling larvae, as well as linking the observed variance in nursery ground quality to external stressors, such as eutrophication and offshore windfarm development and operation. With these analyses, and a background of environmental mediating drivers, we expect to better inform current management strategies and fisheries policies about the impact of local stressors and spatial connectivity patterns.

INTEGRATING MARINE CONNECTIVITY IN THE MARITIME SPATIAL PLANNING OF ITALIAN SEAS

Raschetti Sofia * [1,2], Barbanti Andrea [2], Andrello Marco [1]
1.Institute for the study of anthropic impacts and sustainability in the marine environment, National Research Council (IAS CNR), Rome, Italy
2. Institute of marine sciences, National Research Council (ISMAR CNR), Venice, Italy

MSP4BIODIVERSITY is the Italian National Biodiversity Future Center (NBFC)'s activity dedicated to biodiversity mainstreaming in maritime spatial planning. One of the tasks of MSP4BIODIVERSITY is building and analyzing scenarios of possible and desirable future uses of marine and coastal areas in three pilot areas in Italy: the Northern Adriatic Sea, the Strait of Sicily, and the Northern Tyrrhenian Sea. Three scenarios have been built by considering the main drivers and boundary conditions (climate, policy targets, socio-economic trends…): 1) Slow pace (following the current trends of economic development and environmental regulations); 2) Blue development (promotion of fast grow and innovations using a “build-with-nature” vision); and 3) Nature@Work (reducing negative effects by adopting strict measures for protecting valuable and vulnerable marine ecosystems). We formulate strategic objectives for functional connectivity for each of the three scenarios, considering the different roles of marine connectivity for species viability, fisheries, and protected area planning and how these aspects can be weighted in light of the higher goal of each scenario. We then use ‘prioritizr’ to formulate and solve mathematical problems of spatial conservation planning that integrate different objectives for marine connectivity, possibly integrating different data sources (structural habitat connectivity, biophysical models, genetic connectivity) at different spatial scales (subnational and national scale). The results of this systematic conservation planning approach (e.g. maps of priority areas) will then be used to inform the analysis and evaluation of the three scenarios.

USING BIOPHYSICAL MODELLING AND MARINE CONNECTIVITY TO ASSESS THE RISK OF NATURAL DISPERSAL OF NON-INDIGENIOUS SPECIES TO COMPLY WITH THE BALLAST WATER MANAGEMENT CONVENTION

Flemming Thorbjørn Hansen[1,2], Ane Pastor[3], Asbjørn Christensen[1], Frank Stuer-Lauridsen[4]
1. DTU AQUA, National Institute of Aquatic Resources, Kemitorvet 1, 2800 Kgs. Lyngby, Denmark
2. present address: DHI A/S, Agern Alle 5, 2970 Hørsholm, Denmark
3. School of Life and Environmental Sciences, Centre for Marine Science, Deakin University, Queenscliff, Victoria, 3220, Australia
4. Litehauz Aps, 2800 Kgs. Lyngby, Denmark

The introduction of Marine Non-Indigenous Species (NIS) poses a significant threat to global marine biodiversity and ecosystems. To mitigate this risk, the Ballast Water Management Convention (BWMC) was adopted by the UN International Maritime Organisation (IMO), setting strict criteria for discharges of ballast water. However, the BWMC permits exemptions for shipping routes operating within a geographical area, known as a Same-Risk-Area (SRA). An SRA can be established in areas where a risk assessment (RA) can conclude that the spread of NIS via ballast water is low relative to the predicted natural dispersal. Despite the BWMC's requirement for RAs to be based on modelling of the natural dispersal of NIS, no standard procedures have been established. This paper presents a methodology utilizing biophysical modelling and marine connectivity analyses to conduct SRA RA and delineation. Focusing on the Kattegat and Øresund connecting the North Sea and Baltic Sea, we examine two SRA candidates spanning Danish and Swedish waters. We provide an example on how to conduct an RA including an RA summary, and addressing findings, challenges, and prospects. Our study aims to advance the development and adoption of consistent, transparent, and scientifically robust SRA assessments for effective ballast water management.

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INFORMING THE RECOVERY AND RESTORATION OF TROPICAL SEAGRASSES USING A BIOPHYSICAL MODELLING APPROACH

Hanuise Douchan* [1,3], Rasheed Michael [1], York Paul H. [1], Smith Thimothy M. [1], Choukroun Severine [1], Lambrechts Jonathan [2], Grech Alana [1], Hanert Emmanuel [2,3]
1. James Cook University, Centre for Tropical Water and Aquatic Ecosystem Research, Cairns and Townsville, Queensland, Australia
2. Université Catholique de Louvain, Institute of Mechanics, Materials and Civil Engineering, Louvain-la-Neuve, Belgium
3. Université Catholique de Louvain, Earth and Life Institute, Louvain-la-Neuve, Belgium

Seagrasses provide essential services for human well-being, including fisheries habitat, water filtration, coastal protection and carbon sequestration. Globally, these coastal ecosystems have been declining at an alarming rate due to the cumulative and interactive effects of coastal development, pollution and climate change. Coastal and catchment management and restoration projects have been implemented to mitigate the impacts of human stressors on seagrasses. However, their success rate is highly variable. A comprehensive understanding of seagrass dynamics, especially in tropical regions like the Great Barrier Reef (GBR) in Australia, is critical to inform effective mitigation and management approaches. This study focuses on assessing seagrass dispersal and connectivity over the entire GBR, using a high-resolution biophysical modeling approach. A sensitivity analysis will be performed to refine input parameters of GBR biophysical models, such as the impact of vegetation drag coefficient on tropical seagrass dispersal. This refined model will identify metapopulations and source-sink dynamics over decadal time scales. The outputs of this study will inform the evidence base for seagrass management and restoration in the GBR and tropical ecosystems globally by producing new information on dispersal and connectivity processes that influence natural recovery. This information includes identification of suitable meadows for natural recovery, assess isolated and at-risk areas, and identify key contributors to the seagrass network.

BEST MANAGEMENT POLICY FOR MARINE PROTECTED AREAS IN ISRAEL

Lachyani N. [1]*, Portman M.E. [1]
1. MarCoast Ecosystems Integration Lab, Faculty of Architecture and Town Planning, Technion, Israel and Institute of Technology, Haifa, Israel

Maintaining marine natural values is necessary for ensuring the continued existence of ecosystems. At sea, this includes protection from stressors such as pollution, overfishing, extinction of marine animal and plant species, and general protection from damage to marine ecosystem services. Protecting marine ecology also protects humans; in recent years, marine protected areas (MPAs) have been considered an important tool almost globally. In Israel there is currently no official governance policy for MPAs. There are indeed several policy documents and guidelines for some of the older marine reserves – one of Israel's most extraordinary MPAs had existed in the Red Sea since 1964 – but there is no central policy authority that stipulates different levels of conservation or how to address connectivity. Specifically, there are no instructions regarding what is permitted and what is prohibited in terms of human activities within Israel's MPAs. Additionally, co-management that involves the public or stakeholders in any way is not addressed. This study will analyze and examine plans and tools for the management of MPAs from the world over that might be suited to the Israeli context. It will begin with a characterization according to the accepted levels of protection, the types of enforcement, and the methods of community involvement existing worldwide. These parameters will be matched with the current Israeli situation with regard to the types of MPAs that exist, their physical and legal characteristics, including their current regulatory state, and profiles of stakeholders that could potentially be involved in their management.

A STUDY OF THE CONSTRUCTION OF THE MARINE PROTECTED AREAS IN THE SOUTH CHINA SEA UNDER THE BACKGROUND OF CLIMATE CHANGE

Liu Yuxiao* [1,2]
1. University College Cork, Ireland
2. Hainan University, China

The Azores have been recognised as a marine biodiversity hotspot due to the uniqueness of its marine biota, being a melting pot where northern species co-occur with subtropical and Mediterranean ones. This biogeographic character also results from the west maritime currents and prevailing winds that provide not only a pathway for natural dispersal but also a convenient route for sailing boats coming from America, Africa and going to Europe. These can speed up the natural colonization and impact marine Atlantic ecosystems. From ship cargo to nautical tourism, increasing maritime traffic seems to be the main human-mediated species introduction vector, either by fouling or ballast water. Species can, by this means, overcome distance and oceanographic barriers, modifying benthic communities and shortening the distance of once isolated archipelago, leading to a tendency of biota homogenisation throughout the Atlantic. The official shipping data on the number of calls in port, the last port call, the number of available berths, and the number of NIS reported in the archipelago's marinas can be used to assess this pressure. The most common international origin of marine traffic arriving in the Azores is from the Caribbean, which used to be called the westernmost Flores Island, which displayed a high percentage of international arrivals, later called other archipelagos' harbours, some of which with much higher traffic intensity. A detailed analysis of prevailing shipping routes between the Azores and both sides of the Atlantic is paramount to evaluating the magnitude of this human-mediated connectivity and identifying invading corridors.

ASSESSING HABITAT SUITABILITY AND OCEANOGRAPHIC CONNECTIVITY OF DEMERSAL SPECIES TO IMPROVE A MARINE PROTECTED AREA NETWORK IN THE NW MEDITERRANEAN SEA

López Miguel* [1], Clavel-Henry Morane [1], Company Joan B. [1,2], Bahamón Nixon [1]
1. Instituto de Ciencias del Mar (ICM-CSIC), Barcelona, Spain
2. Institut Català de Recerca per a la Governança del Mar (ICATMAR), Barcelona, Spain

Marine Protected Area (MPA) networks are an important tool for conserving and recovering demersal habitats and fishery resources that have been under human exploitation for long periods of time. Assessing the effectiveness of MPAs within a network in terms of oceanographic connectivity requires an understanding of the oceanographic conditions. However, the habitat suitability of the protected areas also needs to be estimated in order to evaluate the potential settlement success of larvae, and their successive development into adults. We used a joint species distribution modelling (JSDM) approach to determine the habitat suitability of several demersal species in the NW Mediterranean Sea, where a 35-MPA network was recently established. We then identified potential sources and destination areas of eggs and larvae, and applied a lagrangian transport model under average oceanographic conditions to determine connectivity patterns among suitable areas. Due to the no-take fishing nature of MPAs, we used the JSDM to identify areas of high predicted abundance of individuals as egss and larvae release locations from within the MPAs. Only areas suitable for larval settlement that fell under MPA domains and their surrounding areas were considered as possible destinations. Our results highlighted optimal and suboptimal areas to be delimited as MPAs in the context of larval connectivity and MPA networks. Based on these results, we propose modifications of the current network for improved efficiency in protecting target species. The sustainability of fishery resources may benefit from optimal MPA network design approaches that maximize connecting subpopulations over suitable habitats of the species.

OCEAN LITERACY FOR THE MARGINALISED ECOSYSTEM DEPENDENTS IN THE PERI-URBAN SETUP: IMPLICATIONS FOR CONNECTED SPECIES.

Oteke Risper A.* [1]
1. She-Nature, Kenya

Tudor Creek is among critical marine ecosystems supporting biodiversity of fish species, marine birds, crustaceans, mollusks and other unidentified marine vertebrates and invertebrates. The area is uniquely located at 4°2’4”S 39°40’27”E. The wetland, which is key in providing environmental, social and economic benefits to communities living close by has been subjected to increasing threats from both anthropogenic and natural factors. A mosaic of pristine, degraded and restored mangrove sites is seen from higher elevations around the creek. Pronounced within are mangrove ecosystems of varied species. Out of the 10 true species of the Western Indian Ocean (WIO) region, four species support a haven of ecological goods and services within. Urban green spaces capture and sequester tonnes of carbon emissions generated from various sources. Kenya’s mangroves sequester about 3% of carbon emissions each year. With two seasonal rivers and numerous streams draining in the creek, it has always been a great point for seasonal species such as prawns and also offering recharge and flow of essential nutrients into the creek. This flow however has been accompanied by untreated sewage. Pollution Menace in cities spills into ecosystems within. Raw sewage finds its way to mangrove waters affecting the establishment of mangrove seedlings, and the quality and safety of fish consumed by the community. Besides human influence, the decline in some species within has been attributed to factors such as El Niño rains that silted habitats of some grouper species. Enhancing capacities of local fishers and providing enabling conditions that promote sustainable ecosystems.