5th ANNUAL MEETING of the GDR MarCo "Marine Connectivity"

Montpellier - Aquarium Mare Nostrum
16-18 September 2015

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Programme & list of abstracts
## Programme

**Wednesday 16/09/2015**

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Adams TP (SAMS, Oban, UK), Burrows MT & KD Black.
E-mail: Thomas Adams <Thomas.Adams@sams.ac.uk>

Many marine plants and animals spend their adult lives living on submerged surfaces, moving only during their juvenile larval stage. Dispersal and recruitment of such organisms is therefore governed by hydrodynamic processes. In coastal environments such as the West coast of Scotland, understanding such processes is particularly complicated. This area contains a broad range of topographic features and resulting environmental conditions and biological habitats. As a result, marine flora and fauna varies dramatically over small spatial scales, as does the suitability of particular sites for aquaculture, fishing and marine renewable energy devices. We used the latest developments in hydrodynamic modelling (FVCOM) in conjunction with biological particle tracking, population models and network analysis to tackle several management challenges facing the region. Implementation of biological particle tracking alone can provide useful insights into how marine metapopulations operate and sustain themselves; population models can provide additional detail. This is illustrated using examples from two recent case studies: i) understanding the threat posed by invasive species, and the potential implications of altering habitat structure via addition of “stepping stones” in the form of renewable energy devices; and ii) the management and control of sea lice, a parasite affecting farmed and wild salmonid fish.

Porro Barbara (ISEM, CNRS, Station Biologique –OREME-, Sète, France), Alloncle N (Agence des aires marines protégées, Brest, France), Arnould-Haond S (Ifremer, UMR MARBEC, Sète, France).

E-mail: Neil Alloncle <neil.alloncle@aires-marines.fr>

A collaboration has been kicked off between the French Agency for Marine Protected Areas and the GDR MarCo with the main goal of better accounting for connectivity in the evaluation and design of networks of MPAs. In this framework a synthesis is being drafted involving the Agency and researchers from the GDR, to reach managers and stakeholders and improve their understanding of connectivity issues (and non-issues) related to MPAs. Here we aim at detailing the challenges related to connectivity in performances of MPAs depending on their variety of objectives, and the way this should be integrated in the creation and management of networks of MPAs. The usefulness and accuracy of the priority criteria that will be retained are explored using a case study, focusing bioregions of the Mediterranean Sea and the way they fit present day MPAs and knowledge about species connectivity.
QTL mapping of stress related traits in the model brown alga *Ectocarpus siliculosus*.

**Avia K** (Algal Genetics Group, LBI2M/UMR 8227/UMI EBEA 3614, Station Biologique de Roscoff, France). E-mail: Komlan Avia <Komlan.avia@sb-roscoff.fr>

Brown algae are complex photosynthetic organisms with a very different evolutionary history to green plants. They are dominant species in rocky coastal ecosystems. They are economically important as food products, animal feed, fertilizer, source of polysaccharides or other important extracts, or even biofuel resources. Despite their importance, many aspects of these organisms are still poorly understood. The filamentous brown alga *Ectocarpus siliculosus* has been proposed as a general model for the brown algae and its genome has been sequenced. As sessile organisms, brown algae require high levels of tolerance to various abiotic stressors (osmotic pressure, temperature, salinity, light) and previous studies showed that an important proportion of the expressed genes are regulated in response to hyposaline, hypersaline or oxidative stresses. Using double digest RAD sequencing method, a denser genetic map has been constructed and QTL for two stress-related phenotypes (tolerance to high temperature and low salinity) have been mapped. These first results of QTL mapping in Ectocarpales are discussed in the light of the peculiar as well as common characteristics of these species relative to other algae and land plants.
Boundaries in the sea: using connectivity to define regions.

Berline L (MIO, Mediterranean Institute of Oceanography, Marseille, France).
E-mail: Leo Berline <leo.berline@univ-amu.fr>

Regionalization of the ocean is a necessary step towards spatial management of marine resources. Classical regionalization efforts are based either on the distribution of species or on the distribution of physical and biogeochemical properties. These approaches ignore the dispersal of species by oceanic circulation that can connect regions and isolates others. This dispersal effect can be quantified through connectivity defined as the probability, or time of transport between distinct regions. Here, in the framework of the Coconet project, a new regionalization method based on a connectivity approach is described and applied to the Mediterranean Sea. This method is based on ensemble Lagrangian particle simulations using ocean model outputs at 1/12° resolution. The domain is divided into square cells of 50km size. Particle trajectories are used to quantify the oceanographic distance between each pair of cells, here defined as the mean connection time. Finally the distance matrix based on connection time is used to cluster hierarchically the domain. By construction, one region is formed by cells that are closer in connection time than they are from other regions cells. 22 regions are retained and discussed with regard to general circulation. Other connectivity metrics and diagnostics are also discussed. This partition of the domain now has to be tested with genetic and diversity data.

What can Tara Ocean tell us about connectivity?

Bowler C (Ecology and Evolutionary Biology Section, IBENS-, Paris, FRANCE) and the Tara Oceans Consortium
E-mail: Christopher Bowler <cbowler@biologie.ens.fr>

The Agulhas choke point is a barrier to plankton dispersal

Agulhas rings provide the principal route for ocean waters to circulate from the Indo-Pacific to the Atlantic basin. Well known for their influence in global ocean circulation, their role in plankton transport is largely unknown. During the Tara Oceans expedition we combined hydrographic, optical and genetic sampling to show that the overall structure of plankton communities was continuous across the Agulhas choke point. However, intraspecific genetic diversity was extensively reshaped between Indian and Atlantic plankton populations. Direct in situ sampling of a young Agulhas ring indicated that strong vertical mixing within the rings drove complex nitrogen cycling, shaping community metabolism and biogeochemical signatures as plankton transited westwards. The special local environment observed inside a young Agulhas ring provides a selective mechanism explaining the limited dispersal of Indian Ocean plankton populations into the Atlantic. We conclude that the distinct plankton diversity in Indian and Atlantic Oceans implies that the Agulhas choke point constitutes a barrier to plankton dispersal.
C.

Comparative patterns of connectivity in the northwest Mediterranean: a multispecies approach.

Cahill A (IMBE, Aix-Marseille University, Marseille, France).
E-mail: Abigail Cahill <abigail.cahill@imbe.fr>

In marine invertebrate species, adults are often sessile and populations exchange individuals via dispersal of gametes and larvae. This leads to a general pattern where species that have a long larval period are expected to be more connected than those without larval dispersal. However, in the northwestern Mediterranean Sea (Marseilles, France), even species with relatively long-lived larvae and correspondingly high dispersal potential show a surprising number of genetic breaks over a small spatial scale (approx. 250 km). We compiled data on genetic patterns, habitat, and life history traits in nine species spanning five phyla. We hoped to understand what factors (life history, habitat, environment, etc.) best explain the number and placement of these genetic breaks. By using data from a single area, we minimized the effects of sampling at different sites and instead focused on traits that may influence connectivity.

Microsatellite-based monitoring of hatchey-born cohorts in natural stocks of great scallop (Pecten maximus).

Charrier G (UMR 6539 LEMAR, Brest, France), Morvezen R, Borcier E, Le Duff N, Coheleach M, Boudry P & J Laroche.
E-mail: Grégory Charrier <gregory.charrier@univ-brest.fr>

The great scallop (Pecten maximus) is a European bivalve with a high commercial interest. In order to ensure the sustainability of some local fisheries, natural stocks are seeded with hatchery-reared spat in some regions. In particular, in the Bay of Brest (France), a hatchery-based stock enhancement program has been developed since 1983, after a drastic demographic collapse due to an extremely cold winter in 1962-1963. Thanks to the annual release of hatchery-born cohorts, a small scallop fishery has been maintained in the Bay of Brest. Therefore, hatchery-based stock enhancement programs have started in other regions along the French coast, such as the Pertuis Charentais. However, this practice may strongly impact the genetic variability of local scallop populations. In particular, the possible erosion of the genetic diversity in hatchery propagated stocks might compromise the capacity of natural populations to adapt to future environmental changes. In the present study, microsatellite markers have been applied to monitor the genetic variability of hatchery-born and naturally recruited cohorts in seeded populations in the Bay of Brest and the Pertuis Charentais. Furthermore, hatchery-born scallops have been tracked after their release in local stocks, by the mean of microsatellite-based pedigrees. Such an approach, which can be assimilated to parentage-based tagging, appears as a promising tool, which could be further developed to efficiently (1) control the success of stock enhancement programs, and (2) ensure the traceability of hatchery-born scallops.
Elemental fingerprinting as a tool to study connectivity in the invasive gastropod *Crepidula fornicata*.

**Comtet T** (UMR 7144, Station Biologique de Roscoff, Roscoff, France), **Doré J, Pécheyran C & J Thébault**.
E-mail: Thierry Comtet <comtet@sb-roscoff.fr>

In marine ecosystems, dispersal through a pelagic free-swimming larval phase is a key process of population and community dynamics and a major component of communities’ response to environmental changes. Quantifying larval dispersal and connectivity among marine populations however remains a major challenge, and typically requires integrated interdisciplinary approaches. If genetic tools and larval transport modelling are powerful approaches, they may fail to infer connectivity or lead to some discrepancies in some cases. In the last two decades, elemental fingerprinting has been proposed as an alternative method to study connectivity, through the identification of the natal origin of larvae and recruits, based on the elemental composition of their calcified structures. We investigated the relevance of this method to assess connectivity between populations of the invasive species *C. fornicata*. We here present preliminary results on the spatial variations in the elemental composition of shells of encapsulated embryos, at two spatial scales, i.e. within and among three coastal bays of the Western English Channel. Linear discriminant analysis based on elemental ratios of Ba, La, Ce, Mn, Cr, Pb, Fe and Sr, to Ca, followed by a prediction of the geographic origin of the embryos, allowed to obtain assignment success of 53% to the bay of origin and 27% to the site of origin. Embryonic shells from the bay of Brest, further analyzed by laser ablation coupled with ICP-MS, were successfully assigned to their native bay. These preliminary data are encouraging but need further investigations before this approach could be used to estimate the connectivity between populations of *C. fornicata*.

Marine connectivity in temperate biogenic reefs and implication for their conservation: a Mediterranean meta-analysis.

**Costantini F** (University of Bologna, Bologna, Italy).
E-mail: Federica Costantini <federica.costantini@unibo.it>

Temperate subtidal biogenic reefs are structured in geographical isolated patches distributed along the coastline below 30-40 meters in depth. Along with tropical coral reefs, they are considered hot spots of marine biodiversity, due to the high species diversity and richness. Moreover, they are probably among the most threatened habitats globally due to a variety of human activities. The need for conservation of these reefs has been set as a priority by several international bodies, and a bulk of scientific literatures analysing ecological processes and stressing their relevance has been recently published. Despite the key role that connectivity plays in effective conservation strategies of marine habitats (e.g. planning networks of MPA, managing harvest of marine invertebrates), a comprehensive view of genetic diversity and structuring among populations of species inhabiting temperate reefs is lacking. Here, we summarized the outcome of the literature on genetic structuring in species of the Mediterranean coralligenous reefs to identify generalities and/or patterns in population structure and to understand the processes causing subdivision at different spatial scales (e.g. bio-ecological features of the species, abiotic characteristics). A meta-analytic approach was used to investigate how population genetic structure (Fst) is affected by geographical distance, genetic markers and pelagic larval duration. Moreover, we reveal gaps in the data and suggest how to address these gaps. We discuss the implications of these findings for sustainable management and conservation of temperate biogenic reefs assemblages, providing general recommendations for a broadly assessment and monitoring of marine biodiversity.
A model-based evaluation of reef fish connectivity - Implications for future marine spatial planning policies in the Mozambique Channel.

Crochelet E (UMR Entropie, La Réunion, France).
E-mail: Estelle Crochelet <Estelle.crochelet@yahoo.fr>

Marine resources are under increasing pressure from a wide variety of threats such as overfishing, offshore energy development, and climate change. As marine ecosystems degrade, so do the well-being and livelihoods of humans that depend directly on the ecosystem goods and services they provide. Marine protected areas have been proposed to protect biodiversity, restore damaged ecosystems, sustain fisheries, and rebuild overexploited stocks. The effectiveness of marine protected areas depends in part on their effectiveness as connected networks, linked over large areas by ecological processes such as larval dispersal. Here, we applied a biophysical model driven by ocean currents derived from satellite altimetry to evaluate connectivity between Mozambique Channel reefs. We applied graph-theoretic analysis, including clustering and a betweenness centrality metric. Our results show high interconnectivity within several regions and lower connectivity across the Western Indian Ocean region. We compared the results with the current MPA network, and proposed sites/reefs that should be considered priority sites for MPA implementation. Our results are timely, considering the oil and gas exploration that is ongoing in the region. We discuss implications for transboundary marine policies and regional cooperation in the Mozambique Channel, and advocate the creation of a regional-scale organization to structure interactions among the different actors.
Marine ecosystems are threatened by multiple stressors such as fishing, pollution and climate change, which affect the functioning of ecosystems and their capacity to provide services to society. In that context, Marine Protected Areas (MPAs) have been promoted as a powerful tool to mitigate threats to oceans. Population dynamics in marine environment is related to landscape connectivity, a landscape feature measuring the movement capacity of species between different habitats. Connectivity between populations allows the recovery of declining populations, larvae and adults export from protected to unprotected areas, and it also maintains genetic diversity, which is fundamental for species’ evolutionary potential. Quantifying connectivity in marine environment is thus essential for the conservation of populations and for a sustainable management of fishery stocks. My PhD fits in the SEACONNECT project (2014-2017), which aims to optimize future network of MPAs in response to global change by combining genetic connectivity and biophysical models. My PhD focuses on estimating genetic connectivity of fishes from a large spatial sampling at the scale of the Mediterranean Sea using “Next Generation Sequencing” technology. I will describe gene flow patterns and estimate genetic connectivity in the Mediterranean Sea for two highly commercial fish species: the stripped red mullet (Mullus surmuletus) and the white seabream (Diplodus sargus) using genomic data (SNPs). Then, I will look at the connectivity and export potential of some Mediterranean MPAs using genomic data of D. sargus. Finally, these estimations of connectivity will be included in a multi-species and multi-criteria approach of reserve design in the Mediterranean Sea.

Flatfish have a complex life cycle. They undergo a strong change in living environment from the water column (pelagic stages) to the bottom of the Ocean (benthic stages). The benthic phase after metamorphosis is organized on three different grounds that are spatially separated: the nursery ground, the feeding ground and the spawning ground. Effective fishery management requires good understanding of connectivity between spawning grounds and nurseries as well as the processes driving larval retention and dispersal. For marine organisms, planktonic larval stages often determine population connectivity. Sole (Solea solea) is among the most valuable fish species in the Belgian fishery, yet little is known about its early life stage dynamics. In the present study, we investigate the geographical origin of Young Of the Year (YOY) sole living in the Belgian nursery. Previous studies have shown that powerful tools such as genomic approaches can reveal fine scale population structure. A total of 1400 larvae and 700 juveniles of sole were sampled monthly in 2013 and 2014 at 13 sites and genotyped using the double digest Restriction Site-Associated sequencing (ddRADseq) technique. One thousand Single Nucleotide Polymorphic sites (SNPs) were identified and used initially to identify population structuring at a fine geographical (<150 km) and temporal scale on 140 juveniles. Outlier tests were run in order to identify markers that could be used for traceability and show signature of local adaptation. We also compared early-life and adult connectivity patterns at the European scale. Central Northeastern Atlantic populations seem to be highly connected. Sole off the Belgian coast are closely related to the eastern English Channel and the Thames estuary. Results confirm the high auto-recruitment predictions of hydrodynamic and individual based models previously applied.
Do metal elements incorporated in otoliths allow to study estuarine fish connectivity? Experimental and in situ approaches.

Echard A (IRSTEA, Bordeaux, France), Selleslagh J, Pecheyran C, Baudrimont M & F Daverat.
E-mail: Aurélie Echard <aurelie.echard@irstea.fr>

Estuaries consist of mosaic of habitats interconnected. They are natural sinks for a wide range of contaminants that accumulate and hence could affect fish recruitment and stocks, despite recent management efforts and decreasing efforts. The focus of this study was to demonstrate the potential use of otoliths as natural tracer of metal contamination and habitats connectivity for fish. Thus, bioaccumulation of metal (cocktail of Cd, Pb and Ni) in otolith of juvenile flounder (*Platichthys flesus*) was analysed after increasing levels (natural, 5-time, 10-time and null) along a 3-months direct exposure period under controlled conditions. Chemical analyses were carried out by ICP-OES and GTA-AAS for water while otolith microchemistry analyses were performed with a femtosecond laser ablation – high resolution inductively coupled plasma mass spectrometry (fsLA-ICPMS-HR). Significant increases of Pb (only) were detected between contaminated and control fish from the end of the first exposure level. Juvenile fish progressively exposed to higher concentrations of Pb showed increasing levels in their otoliths. Although the relationships between exposure level and the Pb concentration in otolith were sometimes complex, concentrations in otolith were related to this in water in general. Analyses of a fish collection from the Gironde estuary showed different Pb signatures in fish otolith from different habitats of the estuary. Thus, the present study suggests the possibility to use otolith microchemistry as powerful bioassessment tool to retrace fish movements in estuarine environment.
Complex evolutionary processes in seaweeds along the latitudinal gradient of the Chilean coast.

Faugeron S (UMI 3614, Department of Ecology, Universidad Catolica de Chile, Chile).
E-mail: Sylvain Faugeron <sfaugeron@bio.puc.cl>

The coast of Chile presents a simple linear topography with a north-south orientation spanning more than 4,600km. Yet, environmental heterogeneity associated with two major biogeographic boundaries has been described along the SEP (30°-33°S and 42°S). Recent phylogeographic studies of seaweeds revealed strong genetic discontinuities broadly congruent with the biogeographic boundaries, and strongly suggesting budding speciation occurrences. Two major structuring patterns are observed. First, endemic species living north of 42°S show complex haplotype networks and an almost complete genetic isolation among populations located even a few kilometers away. The existence of this extreme genetic patchiness has been related to the combined effects of limited dispersal, reduced population size and high population turnover due to stochastic effects of climatic and tectonic catastrophes. Additionally, evidences of local adaptation seem to reinforce population/species divergence and geographic delimitation. On the other hand, species distributed south of 42°S, an area highly affected by the coastal ice cap during the Last Glacial Maximum (LGM), show typical signatures of post-glacial demographic expansion. At last, molecular studies reveal that several species are recent immigrant from New Zealand, demonstrating the importance of oceanic dispersal in shaping species diversity in Chile. This presentation will provide a broad overview of the model species and approaches developed along the Chilean coast.
Making inferences about the structuring of genetic diversity in marine species.

**Gaggiotti O** (Scottish Oceans Institute, University of St Andrews, East Sands, St Andrews, KY16 8LE).
E-mail: Oscar Gaggiotti <oeg@st-andrews.ac.uk>

The spatial structuring of the genetic diversity of species has many impacts on a species’ demography and evolution. Several genetic, ecological, and physical factors drive the observed spatial genetic diversity patterns and much effort has been devoted to their identification. In marine sciences much emphasis has been put on ocean currents as drivers of demographic connectivity and, therefore, of the spatial genetic patterns exhibited by a species. However, studies comparing genetic structuring of several species belonging to a single marine community have failed to uncover strong correlations across species. In fact, marine systems harbour diverse and often surprising spatial genetic structuring patterns and there is great interest in understanding how interactions between different factors influence such patterns. Achieving this goal requires interdisciplinary approaches that include measurements of genetic and species diversity as well as biophysical modelling and development of sophisticated statistical methods capable of integrating different types of information. In my talk I will provide an overview of the state of the art in this research area.

Polygenic adaptation to variable coastal environments in the gilthead sea bream (*Sparus aurata*), linking selected variants with adaptive phenotypes and fitness.

**Gagnaire PA** (CNRS, UMR 5554 ISEM, Station Biologique – OREME, Sète, France) & AM Darnaude.
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Understanding the genetic underpinnings of adaptation to ecologically contrasted habitats remains a major challenge in evolutionary biology. In the Mediterranean gilthead sea bream (*Sparus aurata*), juveniles use various marine and lagoonal nursery habitats characterized by a trade-off between food availability and stress linked to environmental instability. Phenotypic differences between habitats are observed at the end of the first year, but the extent to which differential survival among genotypes shape these phenotypic differences remains unclear. We screened genetic polymorphism genome-wide using RAD-sequencing in three samples from the same cohort, consisting of pre-settlement larvae and young juveniles that lived in two different habitats. Population genomic analyses provided evidence for divergent selection operating at multiple loci that have antagonistic additive effects on two fitness-related traits (growth and condition factor) across environments. We measured the adaptive landscape in each environment using pre-selection and post-selection samples, and found evidence for genotype-by-environment interaction for fitness, and a positive relationship between individual growth and fitness. Altogether, these results close the genotype-phenotype-fitness loop in a natural panmictic population, and provide an empirical estimate of the genetic load due to the segregation of locally adaptive polymorphisms underlying complex traits.
Population structure and Heterozygosity Fitness Correlations of a highly mobile delphinid species (*Stenella coeruleoalba*) in European waters.

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The population structure and Heterozygosity Fitness Correlations (HFCs) of the striped dolphin (*Stenella coeruleoalba*) were investigated in the Mediterranean Sea and Atlantic Ocean. A total panel of 20 microsatellite loci were used in conjunction with recent coalescent based approaches in order to investigate the genetic structure. Present results illustrate a potentially important structure of the species in question in the given area and Bayesian computations through different demographic scenarios suggest that the eastern North Atlantic and Mediterranean clusters may have reached different levels of migration-drift equilibrium. The fitness trait measure was comprised of the parasite burden of highly pathogenic lung nematodes, and the genetic diversity using neutral (microsatellites) and non-neutral (exon-2 MHC Class II DQB1) markers was measured to evaluate associations on the matter. Analyses suggest evidence for a stronger HFCs for individuals in non-epizootic period, and this was true both for the correlation with genomic diversity as assessed using neutral markers, and for the functional immune system gene. Results illustrate potentially important interactions between genetic drift and selection, and provide specific information that will be valuable towards the conservation and management of diversity in the species in question.

Influence of demography and spatial structure of migration on the effective connectivity of sedentary benthic species.

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Understanding the patterns and maintenance of connectivity is essential in marine spatial planning and the proper design of Marine Protected Areas (MPAs). We present a spatially explicit coupled metapopulation-gene flow model that simulates the effect of demographic fluctuations and connectivity structure on the allele frequencies of sedentary benthic species. Seascape genetic models enable to test the relative importance of the processes leading to genetic structuration at a regional scale when compared with observed patterns. Genetic structure patterns were simulated at the metapopulation scale, and compared to empirical analysis of genetic population structure of the gorgonian species, *Eunicella singularis*, in the Gulf of Lions, France. The modeled pattern of genetic structure of *E. singularis* in the Gulf of Lions agreed with the observed, and demonstrates that both genetic and demographic differentiation among populations can arise from the spatial structure of migration alone. The model provides a tool for evaluating different scenarios of conservation spatial planning and highlights the need of finding a compromise between the requirements for species demographic persistence and conservation of genetic diversity.
Connecting time and plaice: spatial, temporal and decadal movements defined using natural and artificial tags.

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Although “connectivity” is a relatively recent addition to the lexicon of fisheries science, observations of migrations, population structure and spatial dynamics and associated predictions of how phenology and dynamics combine to influence stock sustainability have been established subjects of scrutiny and speculation now for many decades. From inception in 1902, Cefas have collected fisheries data and otoliths for age determination, both from market sampling and from surveys, while large-scale mark and recapture experiments were conducted to provide information about the movements and growth rates of fish, stock structure and mixing, and how these might affect fishery management. Although incomplete, these data represent a significant component of Cefas historical data archive, which in recent years has received high priority for cataloguing and digitising, and for developing permanent data storage solutions to better understand the past of our marine environment. Within this context, I will present an overview of current knowledge for the flatfish, plaice Pleuronectes platessa, in the North Sea. Using the framework of what is arguably the world’s longest fish size distribution time-series, collated using material archived at Cefas (UK, 1902–present) and data from ICES (1966–present), I will explore how our archive of natural and artificial tags can provide significant behavioural insights beyond the marked decadal changes in fish size observed, including plaice sub-stocks and the connectivity among them. By cross-referencing with what the fish were eating (from the DAPSTOM fish stomach content records database), with growth and survival estimates (through otolith analysis and age readings), the aim has been to discriminate whether observed changes relate to changes in bottom fauna (e.g. disappearance of bivalve beds with onset of extensive beam trawling), climate change, changes in fishing pressure (including times of reduced pressure during wars, reduction in current EU fleet capacity), and eutrophication, and whether these changes were systematic across all sub-stocks. Ultimately, these data provide a model that will benefit our understanding of decadal changes in spatial movements and connectivity between populations and areas, and are a powerful illustration of the relevance of legacy data in strengthening the advice provided towards current and ongoing marine policy questions.
Contrasting patterns of genetic connectivity and demographic history for two demersal sharks (*Scyliorhinus canicula* and *Squalus blainville*) in the Mediterranean Sea.

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Coastal and demersal chondrichthyans are expected to exhibit genetic differentiation in areas of complex geomorphology like the Mediterranean Basin, due to their limited dispersal ability. To test this hypothesis, we used a fragment of the mitochondrial COI gene and nuclear microsatellite loci in order to investigate the genetic connectivity and historical demography of two demersal sharks with similar life history traits, the small-spotted catshark (*Scylhiorhinus canicula*) and the longnose spurdog (*Squallus blainville*). For *S. canicula*, both mitochondrial and nuclear microsatellite DNA data revealed a strong genetic subdivision, mainly between the western and eastern Mediterranean, while the Levantine Basin shared haplotypes with both areas. The geographic isolation of the Mediterranean basins seems to enforce the population genetic differentiation of the species, with the deep sea acting as a strong barrier to its dispersal. Contrasting historical demographic patterns were also observed in different parts of the species’ distribution, most notably a population growth trend in the western Mediterranean/Atlantic area and a slight decreasing one in the Aegean Sea. The different effects of the Pleistocene glacial periods on the habitat availability may explain the contrasting demographic patterns observed. On the contrary, *S. blainville* (samples collected only from eastern Mediterranean), exhibited high connectivity between Aegean and Ionian Seas and a pattern of recent historical demographic expansion. These differences in genetic structure between species with similar geographic distribution and life history traits could be attributed to small differences in certain traits (e.g. body size and mobility), but also to the stochastic nature of the historical events.

Genetic diversity of *Cymodocea nodosa* in the Aegean Sea, Eastern Mediterranean.

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Genetic diversity and structure of the marine angiosperm *Cymodocea nodosa* were investigated in the Aegean Sea, eastern Mediterranean basin with extra meadows at the marginal range of species distribution. A relative sub-structuring was revealed, suggesting a barrier to gene flow possibly due to the significant factor of the cyclonic system within the studied area a presence of sub-populations overall in the studied area. The observed barriers maybe related to angiosperms re-colonization from warmer parts of the eastern Mediterranean, after the last glacial maximum as a potential consideration for unidentified limited dispersal and demographic habits of the species in question. On the other hand, sexual reproduction events may contribute to the maintenance of genetic diversity of *C. nodosa* structuring in the Aegean Sea, where the species is also exhibiting extensive morphological plasticity and reduced sexual capacity at the marginal range of their distribution.
What do otolith microchemical signatures tell us about sardines' stock structure and movements along the Atlantic coast of Morocco (NW Africa).

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In the Eastern Atlantic, the European sardine (Sardina pilchardus) is found from the Celtic Sea and the North Sea down to Mauritania. However, several studies have shown a sharp change in both the species' genetic structure and its morphology along the Atlantic coast of Morocco, from the area of the Bay of Agadir and southward. In this study, we characterize the chemical signatures of the otoliths of sardines caught at different locations spread along the Moroccan Atlantic coast to get additional information on their movements, in particular by comparing them to otolith chemical signatures from other exploited fish species with different trophic levels but sedentary. Indeed, the Moroccan coast is characterized by the presence of an important upwelling, permanent in the south and intermittent in the center but absent in the north. When reaching the surface, the deep and cold oceanic waters, rich in nutrients, enhance the coastal biological productivity, from lower to higher trophic levels. The Atlantic Moroccan coast is also under the direct influence of several anthropogenic activities such as phosphates industries in the North. All these variations in environmental conditions can generate differences in the chemical signatures of fish otoliths, which might therefore be usable as geographical tracers. Fishes for this work were collected from local fish markets in June and November 2012, at 7 locations spread along the Moroccan Atlantic coast. Otolith elemental concentrations (for 10-15 individuals of each species per location) were measured by ICP-MS on whole otoliths to characterize spatial variations in otolith signatures. Then, the otoliths from sardines collected at sea in June 2013 during a sampling campaign along the Moroccan coast were analyzed, using LA-ICP-MS to make transects from their nucleus to their edges and thereby investigate differences in individual lifetime movements in the area.

Estimation de la connectivité larvaire dans le lagon Sud de la Nouvelle-Calédonie – Bilan du projet COMPO

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Habitat-driven population structure of bottlenose dolphins in the North East Atlantic.


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Despite no obvious barrier to gene flow, environmental variation and ecological specializations can lead to genetic differentiation in the marine environment. Bottlenose dolphins are highly mobile social marine mammals. In the North-East Atlantic, they are found both in coastal waters where they form either discrete sedentary populations of tens to hundreds of individuals or mobile groups and in pelagic waters with abundance estimates of thousands of individuals. We investigated bottlenose dolphin genetic structure from Scotland to the Azores through analyses of biopsy samples (n=162) and samples from stranded animals (n=242) using 25 microsatellite markers and a portion of the mitochondrial control region. Clustering analyses based on multilocus genotypes and mitochondrial sequences showed a clear separation between coastal and pelagic dolphins, suggesting the existence of two genetically distinct ecotypes. A second approach of landscape genetics combined multilocus genotypes and the location of individuals to infer population structure. For stranded individuals, the most likely location of death was inferred using a drift prediction model (Peltier et al. 2012). This approach confirmed the differentiation between pelagic and coastal individuals. Moreover, the pelagic population was divided in two clusters with individuals sampled in Gibraltar, Cadiz and the Mediterranean Sea forming a separate cluster from individuals sampled in pelagic waters of the North East Atlantic. Likewise, coastal dolphins were divided in two clusters: a cluster composed of individuals sampled in the United Kingdom and Ireland and a cluster composed of individuals sampled in France and south Galician waters. Our results suggest that connectivity may be limited by ecological specializations and behavioral differences.
Cryptic species, ecomorphs and GFP/GFP-like profiles in the cnidarian *Anemonia viridis*.

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Cryptic species have recently been identified in many cnidarians despite a lack of morphological variation. Only the use of molecular markers allowed the detection of these taxonomic entities. Contrastingly, 5 clearly different morphs have been described in the sea anemone *Anemonia viridis*, based on the expression profiles of GFP-like proteins. However, no clear genetic differences had been found so far among these morphs. In this study, we tested if these morphs belong to the same species or to independent gene pools, using a set of 8 genes whose expression patterns are modified by environmental factors. For each of these genes, an EPIC marker has been developed (by comparison with published cnidarian genomes) and was sequenced on 38 individuals of the three most common morphs from 6 populations in the Mediterranean Sea and 2 in the English Channel. No clear genetic differentiation between the morphs of *A. viridis* was revealed on any gene or when using spedeSTEM, which evaluates the most probable species tree from the EPIC gene trees by a coalescent approach. Also, we surprisingly found a high degree of introgression with the species used as an outgroup, *Paranemona cinerea*. These results have to be confirmed with more EPICs.
Genetics and genomics in the service of elasmobranch marine spatial planning

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The role of elasmobranchs as apex predators is fundamental to ecosystem health. Yet because of their low fecundity and slow life history traits many are considered highly vulnerable to both over exploitation (impacting food security), and habitat disturbance from offshore renewables. In European waters several species, including some listed as marine search features, are critically endangered, and others are considered vulnerable. Although the ‘Community Plan of Action for Sharks’, and ‘Common Fisheries Policy’ aim to maintain and restore marine biodiversity and stock health there remains little substantive data on elasmobranch population structure, movement and population connectivity, or identification of critical habitat (for mating, pupping, nursery and feeding grounds). We have established the use of high resolution cutting edge genetic and genomic tools in several elasmobranchs. Integrated with novel approaches to tracking and behavioural observations, these approaches promise a step change in understanding elasmobranch spatial ecology, supplying the necessary high resolution spatial data to allow proper evaluation of population connectivity, management plans and identification of critical habitats for Marine Protected Area (MPA) designation.

Seascape genomics and isolation by habitat in the birdsnest coral.

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Genetic approaches have yielded important insights regarding connectivity in marine systems. Increasingly, many empirical studies attempt to quantify effects of multiple “seascape” attributes such as environmental or oceanographic factors alongside more static physical factors such as distance or habitat disjunctions. Now, population genomics offers the potential to reveal how different parts of a genome respond to various spatial factors and thus, combined with spatially explicit analyses, can shed light on the geographic dynamics of adaptation and speciation. First, the emerging fields of seascape genetics and genomics will be discussed, especially considering how spatially explicit analyses can augment other approaches and the specific challenges to undertaking spatially explicit analyses in the marine context. Second, the genomic patterns of differentiation in the birdnest coral, *Seriatopora hystrix*, will be presented. Previously considered a habitat generalist, we find strong and replicated differentiation by depth in both the cnidarian host and algal symbionts. Coral ecotypes are differentiated across much of their genomes yet some gene flow is apparent. Additionally divergence between hosts and symbionts is correlated, both between and within ecotypes, indicative of tight co-evolution between symbiotic partners that could contribute to *S. hystrix*'s divergence in sympatry.
Parallel patterns of genetic differentiation between cryptic lineages in Atlantic and Mediterranean populations of the long-snouted seahorse *Hippocampus guttulatus*.

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Many CITES-protected marine species suffer from few or no data, as direct studies in the field is difficult in the sea. Population genetics offers a straightforward approach to help in a better understanding of connectivity and demography of populations of these species. We here examined the genetic connectivity at a large spatial scale and the demographic history dynamics of the CITES-protected seahorse, *Hippocampus guttulatus*, by genotyping 318 SNPs on a non-invasive sampling of 461 individuals along its distribution range (from the English Channel to the Black Sea). While *H. guttulatus* displays poor dispersal abilities and is difficult to observe in the wild, large-scale panmixia was often observed, suggesting gene flow (Nm) to be larger than thought. However, a mosaic of four strongly differentiated genetic clusters separated by abrupt discontinuities was also observed. The spatial distribution of lineages and the genome-wide heterogeneity of the differentiation suggest partial reproductive isolation is maintaining the divergence. In the Atlantic Ocean a northern and a southern lineage meet in a hybrid zone in the southwest of France. In the Mediterranean Sea two lineages are also found, one that tends to inhabit lagoon-like habitats while the other has been sampled in the sea. Surprisingly, the lagoon lineage of the Mediterranean Sea is sharing a similar genetic composition with the northern Atlantic lineage at the most differentiated loci. Although convergent adaptation is difficult to refute, the alternative spatial distribution and an absence of differentiation between lagoon and sea samples in the Atlantic Ocean suggest the genetic parallelism is likely due to a shared ancestry. Population genetics proved efficient in unraveling parallel speciation and cryptic biodiversity in seahorses with strong conservation issue.


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Assessing the impact of connectivity on the spatial structures and dynamics of marine populations is still a major challenge for ecologists. In addition, the need to manage marine resources from a large-scale perspective and considering the whole ecosystem is recognized but the absence of appropriate tools to address these objectives limits the implementation of globally pertinent strategies. For instance, an important question poorly explored from the fisheries assessment perspective is which harvested species and which management units’ boundaries are sensitive to connectivity processes. We focus on the European hake in the Western Mediterranean to investigate the links between two distinct management units, the mainland spawning areas (Iberian and French continental shelves) and the recruited stock around the Balearic Islands. We combine larval dispersion experiments using the recently developed Lagrangian Flow Networks and information on young recruits from trawl surveys to test if inter-annual variations of hake recruitment in the Balearic archipelago is related to changing patterns of connectivity. We evaluate larval connectivity at different depths and from all identified spawning areas over multiple years. The Lagrangian Flow Network methodology also allows the identification of hydrodynamical provinces and the computation of various connectivity proxies measuring retention and exchange of larvae. Moreover, thanks to our spatial discretization and
Lagrangian approach, further methodological improvements (e.g. parametrization of habitat patchiness and of the effects of abiotic variables...) are handily accessible. This systematic characterization of multi-scale dispersal and connectivity of hake's larvae is compared against long-term observations to permit a better characterization of population connectivity at multiple scales and to inform its ecological and managerial interpretations. We finally discuss similar management implications of connectivity processes in other areas of the Mediterranean Sea.

S.

Coral reef fish populations can persist without immigration.

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Determining the conditions under which populations may persist requires accurate estimates of demographic parameters, including immigration, fecundity, and mortality rates. In marine populations, empirical estimates of these parameters are rare, due at least in part to the pelagic dispersal stage common to most marine organisms. Here, we evaluate population persistence and turnover for a population of orange clownfish, *Amphiprion percula*, at Kimbe Island in Papua New Guinea. All fish in the population were sampled and genotyped on 5 occasions at two-year intervals spanning 8 years. The genetic data enabled estimates of fecundity retained in the same population (fecundity to self-recruitment), fecundity exported to other subpopulation (fecundity to local connectivity) and immigration and mortality rates of sub-adults and adults. Approximately 50% of the recruits were assigned to parents from the Kimbe Island population and this was stable through the sampling period. Stability in the proportion of local and immigrant settlers is likely due to: low annual mortality rates and stable egg production rates, the short larval stages and sensory capacities of reef fish larvae. Biannual mortality rates ranged from 0.09 to 0.55 and varied significantly spatially. We used these data to parameterize a model that estimated the probability of the Kimbe Island population persisting in the absence of immigration. The Kimbe Island population was found to persist without significant immigration. Model results suggest the Island population persists because the largest of the sub-populations are maintained due to having low mortality and high self-recruitment rates. Our results enable managers to appropriately target and scale actions to maximize persistence likelihood as disturbance frequencies increase.

Connectivity of estuarine habitats and origin of OM supporting fish communities: a stable isotope analysis in the Gironde.

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Estuaries consist of a mosaic of different types of habitats, often interconnected. Knowledge of juvenile fish movements within estuarine habitats is crucial and constitutes a prerequisite for effective conservation and management. Stable isotopes ($\delta^{13}C$ and $\delta^{15}N$) were used to analyse food web in the downstream area of the Gironde estuary. The different sources of organic matter supporting the most abundant fish species were determined, as well as habitat connectivity for fish. Different producers
(marine, freshwater and local sources), primary consumers (zooplankton and macrozoobenthos) and nine fish were collected in June-July 2012 in three estuarine habitats. All sources and invertebrates had significant different isotopic signatures between habitats. On the contrary, fish species showed no significant difference in isotopic signature with the exception of sole *S. solea*. This overlap was interpreted as evidence that fish had not been feeding exclusively in the habitat where they were collected, reflecting high habitat connectivity for fish. As the base of the fish food web significantly differed between habitats, the present study indicated the suitability of stable isotopes in tracing fish movements between habitats distant from less than 10 km, particularly between estuarine habitats without salinity difference but located in opposite banks. The SIAR mixing model estimations of each organic matter source contribution to fish diet in the Gironde estuary were quite similar for the fish species investigated. The major source contributing to fish species was marine-derived POM, with contribution >75% for each species. Freshwater and local POM surprisingly contributed little to the overall fish food webs in the Gironde estuary. Only flounder *P. flesus* and shad *A. alosa*, diadromous species, utilised freshwater POM in greater proportion. The observed low freshwater POM - high marine POM contribution in fish food web seems to be explained by the reduced intertidal surface of the system. The characterization of the trophic base and habitat connectivity for the most important fish provides a novel insight for future management of the Gironde estuary in the actual global change context.

Genetic exchange after secondary contact between two parapatric species of soles reveal within-species connectivity patterns.

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Hybrid zones provide natural areas where collisions among genomes from divergent species produce recombinant genotypes which are useful to our understanding of reproductive isolation. Genetic introgression usually has highly heterogeneous impact across the genome. While neutral genomic regions can easily homogenize, regions involved in reproductive isolation remain resistant to gene flow. These variations in the rate of gene flow between species provide original tools to investigate within-species connectivity patterns revealed by introgression. In order to understand how genetic exchange between two parapatric species of soles (*Solea senegalensis* and *Solea aegytiaca*) has shaped spatial genetic diversity patterns outside the hybrid zone, we genotyped 178 specimens taken along a Senegal-Egypt transect using RAD-sequencing. We then infer the demographic history of speciation using different models of divergence-with-gene-flow that take into account variation in the rate of introgression. The best scenario appeared to be a recent secondary contact in which only a small proportion of the genome has been exchanged since the onset of secondary gene flow. We show that freely introgressing markers display spatial gradients in allele frequency that extend far away from the hybrid zone within the *S. senegalensis* distribution range. These tails of introgression reveal within-species connectivity patterns where neutral markers are generally uninformative.
Connecting gametes in the intertidal: Restricted fertilization distance and clumped spore dispersal in a natural population of the haploid-diploid red seaweed *Chondrus crispus*.

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Intertidal seaweeds are excellent models with which to study the links between life history traits and landscape dynamics with the population genetic structure. Members of the Rhodophyta combine several unique features: (1) three types of macroscopic individuals coexist, (2) three types of propagules are released and (3) each fertilization event is followed by the mitotic amplification of the zygote (cystocarp) resulting in thousands of identical diploid spores. The objective of this study was to understand the impacts of haploid-diploidy, male gamete dispersal and the intertidal landscape on fine-scale genetic structure. Individual fronds of the red alga *Chondrus crispus*, were sampled every 25 cm in two 5 m x 5 m grids located in the upper and lower edge of the species intertidal range. Fronds and cystocarps (excised from female haploid gametophytes) were genotyped using polymorphic microsatellite loci. Very large levels of inbreeding were detected within populations using analyses of population structure. This was supported by paternity analyses revealing larger kinship coefficients between males siring cystocarps on the same female in comparison to males in the entire population. However, only one putative father was identified in the sampled population, the remaining 424 sires were not sampled. Restricted fertilization distance and clumped spore dispersal likely generates the high levels of intergametophytic selfing detected in these populations. Such dispersal mechanisms may be a mode of reproductive assurance due to non-motile gametes associated with putatively reduced effects of inbreeding depression due to the free-living haploid stage in *C. crispus*.

Understanding winter distribution and transport pathways of the invasive ctenophore *Mnemiopsis leidyi* in the North Sea: coupling habitat and dispersal modelling approaches.

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The invasive ctenophore *Mnemiopsis leidyi* has been reported in various coastal locations in the southern North Sea in the past years. Since 2009, International Bottom Trawl Surveys have recorded this species each winter in open waters. As this species, well-known for its dramatic disturbance of ecosystems, was expected not to be able to overwinter offshore it is crucial to understand its distribution dynamics. Two modelling methods, a quantile regression and a particle tracking model, were used (1) to identify habitats where the invasive ctenophore *M. leidyi* could survive the North Sea cold winters and (2) to investigate the dispersal of individuals between these different habitats, emphasizing favorable areas where sustainable populations could have been established. Temperature was found to be the crucial factor controlling the winter distribution of *M. leidyi* in the North Sea. High abundance predictions in winter were associated with low values of temperature, which characterise south-eastern coastal areas and estuaries influenced by riverine runoff. A retention-based *M. leidyi* population was indicated along the northern Dutch coast and German Bight and a transport-based
population offshore from the western Danish coast. Individuals found in the open waters were transported from southern coasts of the North Sea, thus the open water population densities depend on the flux of offspring from these areas. This study provides the first estimates of the overwinter areas of this invasive species over the cold winters in the North Sea. Based on the agreement of habitat and dispersal model results, we conclude that *M. leidyi* has become established along south-eastern coasts of the North Sea where the environment conditions allows overwintering and it can be retained for later blooms.

**From population genetics to population genomics to investigate connectivity at a worldwide scale: a case study with the invasive alga *Sargassum muticum.***

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Many species ranges go nowadays beyond natural barriers because human activities promoted their transport and successful settlement far from their native range: human-mediated dispersal is enhancing connectivity at global scale. In this context, the brown seaweed *Sargassum muticum* is particularly emblematic. Native to Asia, it has successfully invaded the North-Eastern Pacific coasts since the 1940s and the North-Eastern Atlantic since the 1970s. We first examined the introduction history and expansion patterns in these two areas using a set of 14 microsatellite markers (polymorphic in the native range). Conversely to what have been documented in most marine introduced species, European and American introduced populations were found to be genetically monomorphic. This unexpected result is balancing the popular paradigm of introduction without founder events in marine systems. To better understand the observed patterns, and attempt to elucidate the invasion history of *S. muticum*, we developed a genotyping-by-sequencing method (ddRadseq), a first in an invasive seaweed. Large scale libraries were successfully sequenced for 303 individuals from 21 populations (Europe: 9, North-West America: 7 and Japan: 5). Conversely to the previous studies, genetic polymorphism was detected in the introduced populations with 2026 SNPs (He = 0.15 and 0.12 in American and European areas respectively). Nevertheless much larger diversity was found in the native range and, as expected, severe founder events were evidenced in the introduction ranges. A decreasing number of polymorphic loci was observed between the native range, NW America and Europe (1259, 455 and 232 respectively) as well as strong genetic similarities between America and Europe only; this supports predictions of a secondary introduction in Europe from America where *S. muticum* was introduced earlier. Our results confirm the relevance of genome-wide strategies to investigate the genetic diversity of weakly polymorphic algal species. In addition, while the link between genetic diversity and invasion success has often been highlighted in marine systems, we here document a success story of a global invasion with limited genetic polymorphism.
W.

Modelling marine species dispersal in the Great Barrier Reef.

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The aim of our project is to acquire a better understanding of the current driven connectivity of marine populations in the Great Barrier Reef. We use the multi-scale hydrodynamical model (SLIM) in order to predict the evolution of seagrass, coral and fish species in a coral reef ecosystem. The methodology developed is general and could be applied to various marine ecosystems but the project is primarily focused on the Great Barrier Reef (Australia). The hydrodynamical model is used to assess the spatial evolution of populations driven by larvae transport and dispersion. These results are summarized in connectivity matrixes which enable us to apprehend the exchanges between the sub-populations. This connectivity information will be integrated into an ecosystem model which will provide the temporal evolution of these interacting populations. Different scenarios will then be used to evaluate the resilience of the ecosystem under several disturbances like storms, coral bleaching or crown-of-thorn starfish outbreaks.

The importance of understanding population structure to North Sea fishery management advice.

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The need to match fishery management units to the scale of population structuring is increasingly being recognised. Failure to account for multiple populations within a management unit can lead to false perceptions about productivity and resilience. Conversely, when only a portion of a population is contained within a managed unit it can be difficult to understand stock – recruitment dynamics. In this talk I will briefly describe how genetic, otolith microchemistry, tagging studies and models of early passive transport have been used to improve our understanding of the scale of population structuring in sandeel, cod and haddock before considering how this has affected perceptions of stock productivity. In sandeel and cod there is now recognition that the scale of population processes is at a sub-stock level and there are important differences in local life history characteristics and productivity. In haddock, two previously managed units have been merged following evidence for high levels of connectivity between them. This has helped explain the large changes in recruitment within the smaller of the two stocks.
Dispersal, connectivity, and genetic structure of the California sea cucumber (*Parastichopus californicus*) in the Northwest Pacific Ocean: implications for marine management.

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Ocean circulation plays a critical role in determining connectivity pathways among populations of many marine organisms, particularly of those that undergo a passively dispersing larval stage. As a result, spatial patterns of genetic variation often do not conform to traditional models, such as isolation by distance. In my thesis, I integrate biophysical oceanographic models and genetic data to determine the influence of ocean circulation on larval dispersal and gene flow in the California sea cucumber (*Parastichopus californicus*) in the northeastern Pacific Ocean. Additionally, I examine the effect of environmental features (e.g. temperature, salinity, habitat structure) and geography on the frequency of potentially adaptive genetic markers. Based on these findings I will investigate the effectiveness of marine protected areas to maintain genetic connectivity. Overall, I propose to address four primary objectives: (1) provide a conceptual framework for designing effective marine protected areas while accounting for variability due to climate change; (2) determine predicted patterns of population genetic structure using simulations of larval dispersal and gene flow based on a biophysical model developed for the Pacific coast of Canada; (3) assess actual spatial patterns of neutral and adaptive genetic variation using single nucleotide polymorphisms identified from DNA samples collected from 18 sites in the coastal waters of British Columbia; (4) compare designs of marine protected area networks using genetic distance as a proxy for functional connectivity. This work will have important applications for the sustainability of a commercially valuable species as well as for the management of marine resources in the face of global climate change.