FSBI 2024 Annual Symposium

ADVANCING FISH ECOLOGY, MANAGEMENT AND FORECASTING THROUGH OMICS

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ABSTRACT BOOK

FISH ECOLOGY, MANAGEMENT & FORECASTING THROUGH OMICS

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JACK JONES LECTURE

Genes, Fish and Fisheries: translating science into policy

Gary R Carvalho [1]

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Our understanding of exploited fish populations and impacts of changing environments on their spatial and temporal distribution have been informed significantly by application of genetic and genomic tools. Typically, molecular genetic markers afford two categories of utility: their use as “natural tags” to identify individuals, populations, and species, and the rather more prosaic, but fundamental role that population diversity plays in resilience and recovery of exploited populations. Among key advances have been disclosure of small-scale population structuring, rapid speed of genetic and phenotypic change, highly variable patterns of connectivity, and occasional profound impacts of isolation and reduced population size. While such findings have direct relevance to fisheries sustainability goals, there remains a relative dearth of convincing examples of how genetic and genomic data have become integrated into management and policy. Here I review briefly, salient milestones and challenges in fisheries genetics, followed by an illustration of several instances where such integration has shifted our thinking and policy in capture fisheries. I then identify common features in those cases with measurable impact, alongside those that remain constrained in application. Finally, I consider how such knowledge can inform future opportunities and challenges in our quest to promote renewable resources, where “renewable” is more than a token term.

KEYNOTE

Eco-evolutionary dynamics in managed and unmanaged systems: case studies from Pacific salmon

Kerry Naish [1]

1. University of Washington, Seattle, USA

Reciprocal interactions between ecological and evolutionary processes can influence the stability of biological systems, and impact the rate of change within these systems. Characterizing such eco-evolutionary dynamics are important to understanding how and at what pace populations may respond to influences such as habitat variation, population fragmentation and altered environments, as well as to conservation actions. Anadromous Pacific salmon along the West Coast of North America have served as models for studying eco-evolutionary dynamics because they comprise an extensive network of locally adapted metapopulations that occupy a wide range of varying environments. Population diversity in salmonids has been shown to an important component of species resilience in the face of perturbations (known as the portfolio effect), and promoting such diversity is the focus of extensive management actions. Here, we explore two types of eco-evolutionary systems in Pacific salmon using genomic approaches, with the aim of understanding how such relationships function in different selective and environmental contexts. The first system is focused on co-evolutionary predator-prey dynamics, and specifically on the disease ecology of an endemic pathogen in salmon species that are managed through a substantial part of their range. We identify host and viral evolutionary responses that influence viral transmission across the landscape, and show that heterogeneity in susceptibility to infection is a key parameter that distinguishes the ecology of viral subgroups with different infection strategies. The second system examines the ecological factors that influence the evolution of dispersal in a metapopulation of salmon from a largely undisturbed habitat. Our results identify ecological factors that influence selection on dispersal and return timing, leading to non-random gene flow and different outcomes for adaptation and population structure compared to random expectations. We end by exploring the implications of how such eco-evolutionary feedbacks can influence disease and population management of Pacific salmonids.

KEYNOTE

Vision under pressure: how deep-sea fish and cichlids see in the dark

Zuzana Musilova [1]

1. Department of Zoology, Faculty of Science, Charles University, Prague, Czech Republic

In extreme environments like the deep ocean or deep lakes, fish face significant challenges and have adapted to the harsh conditions. The absence of light and a narrower colour spectrum have shaped evolution of numerous adaptations of the visual system in the deep-water fishes. Here we focus on molecular adaptations and the (visual) ecology of different species of the deep-sea and deep-lacustrine fishes using genomics and transcriptomics to explore genes essential for vision. Some adaptations to enhance their vision in darkness are common and shared among the deep-sea and freshwater fish groups only distantly related to each other. We found loss of the genes responsible for red and UV/violet sensitivity of retina, which corresponds to the limited light spectrum in the deep. We also focus on rhodopsins, the pigments of rods sensitive in the dim light. While most fish species have one (or two) copies of the rhodopsin genes in their genome, an extreme diversity of rhodopsins has raised in several deep-sea fishes by multiple gene duplications. Spinyfins (Diretmidae; Trachichthyiformes), as an extreme example, have multiple (up to 38) rod opsins sensitive to blue-green light spectrum of 444 to 519 nm, and at the same time they have one of the shortest-sensitive rhodopsin known in vertebrates. This extraordinary set up has convergently evolved also in two other unrelated deep-sea lineages (lanternfishes; Myctophiformes and tube-eye fish; Stylephoriformes) and suggests unique mode of vision (with a potential for colour vision using rod cells), albeit its exact mechanism and function remain elusive. Interestingly, deep-sea fish larvae reside in shallow waters, so the evolved adaptations also reflect the needs of both developmental stages: the shallow-water larva and the deep-water adult.

KEYNOTE

Can environmental DNA metabarcoding really fill the marine biomonitoring gap in South Africa?

Sophie von der Heyden [1]

1. University of Stellenbosch, South Africa

South Africa hosts an incredible marine biodiversity, that includes over 2000 species of fishes. Situated across the transition between the Indian and Atlantic Oceans and being characterised by a strong environmental gradient of temperature and productivity, the coastline offers a unique ‘natural laboratory’ for studying climate change impacts on marine species. Interestingly, there are both cooling and warming scenarios for the region, complicating our understanding of marine species responses. Fishes are arguably the best studied coastal taxa in the region, given their importance for supporting artisanal and commercial fisheries, yet the extent to which fishes (and other marine fauna and flora) are shifting their ranges is poorly described. Environmental DNA metabarcoding and its application globally have revolutionised how we detect and monitor aquatic biodiversity. In this talk I examine the uptake of eDNA metabarcoding as a tool for describing marine fish communities in South Africa and provide a brief overview of the status of the field in one of the world’s marine biodiversity hotspots. Importantly, considering the scale and spatio-temporal variability of the eDNA signal, developing regional databases and testing the effectiveness of eDNA metabarcoding are crucial for building a regional standardised framework to allow for effective and consistent monitoring of marine biodiversity.

KEYNOTE

Characterization of genomic architectures, sub-populations and cryptic ecotypes within the codfishes: implications for management programmes

Sissel Jentoft [1]

1. Centre for Ecological and Evolutionary Synthesis (CEES), Department of Biosciences, University of Oslo, Oslo, Norway

The revolutionary developments within genomic and bioinformatical tools have greatly advanced our understanding of biological and evolutionary processes, as well as improved our insight into wildlife and marine population dynamics. However, integration of such genomic information into conservation and management programs is still lagging behind, especially within the complex of marine ecosystems. In this presentation I will elaborate on our findings on the iconic and economically important Atlantic cod (*Gadus morhua*) focusing on its genomic shifts throughout the past century, as well as genome-wide population structuring and discrimination of different ecotypes, including the well-known migratory Northeast Arctic cod vs. the stationary Norwegian coastal cod. Moreover, I will also present some of our recent findings on two of its close relatives: the polar cod (*Boreogadus saida*) and the Arctic cod (*Arctogadus glacialis*). For both these cold-water specialists, we detect a substantial number of larger chromosomal rearrangements, which are seemingly coupled to the genomic divergence between different of sub-populations and/or cryptic ecotypes, and thus, likely to play an important role in local adaptation to the extreme environmental conditions that these species encounter. Lastly, I will highlight the needs of taking this novel insight into account, i.e., in terms of genome-wide variation when defining the management units, their genomic composition and the dynamics between them (such as signatures of gene-flow), for future development of sustainable conservation and management programs.

KEYNOTE

From Revolutionary to Complementary: a DNA Journey through the Seafood Trade

Stefano Mariani [1]

1. School of Biological & Environmental Sciences, Liverpool John Moores University, UK

Humans have eaten fishes ever since they learnt to catch them. By progressively increasing our capturing abilities and biological knowledge, we have been able to exploit this resource in virtually every aquatic habitat on Earth, often in unsustainable fashion. The size and productivity of the oceans are such that fishes are the only class of wild vertebrates that outnumber humans, making it still possible for us to go out and literally hunt-and-gather them. Despite the extraordinary progress of aquaculture, around half the fish we trade and eat still come from entirely wild populations, fueling the most diverse and globally traded food commodity on the planet. Such complexity and diversity have two major implications: first, the journey of a fish from its natural habitat to our plate is difficult to track; second, most consumers around the world have little knowledge or understanding of the distribution, biology, population status, or even appearance of the fish species they eat. In the 21st century, the widespread application of DNA-based technologies has revolutionised the way we investigate and monitor the diversity, legality, and sustainability of global seafood supply. Increased accuracy and throughput, a rapidly expanding toolkit, progress in portability, standardization, and sharply decreasing costs have benefited researchers, government agencies, industry, and consumers. Yet, paradoxically, all this progress has taught us that, no matter how powerful and sophisticated, DNA-based approaches will always be most useful when judiciously embedded in a truly transdisciplinary, cross-sector framework.

MEDAL WINNER

The evolution of diversity of fishes and how it contributes to the understanding of biodiversity and its conservation

Skúli Skúlason [1]

1. Hólar University and the Icelandic Museum of Natural History, Iceland

Fishes are incredibly diverse group of organisms, providing unique insights into the nature and value of biological diversity. Thus, many studies have illustrated rapid diversification with species and importantly we see parallel patterns across different species and groups. I will overview these studies and discuss the significance of the underlying ecological, evolutionary and developmental processes. The relevance of comprehensive understanding of diversity for conservation and management strategies will be emphasized. This is particularly important considering the massive threats biodiversity faces, not the least in aquatic systems. To facilitate conservation and sustainable resource use, we need to apply well-developed ecosystem approach, combined with massive efforts to educate and transform our societies in order to reconnect man with nature.

MEDAL WINNER

Using fish physiology to inform management

Erika J Eliason [1]

1. Kwantlen Polytechnic University, BC, Canada; University of California, Santa Barbara, CA, USA

Natural and anthropogenic stressors are impacting fish populations across the globe, altering their abundance, distribution and behavior. In this talk, I will describe how my research group uses an integrative approach and novel techniques to assess fish performance and persistence in the face of environmental change. By collaborating closely with end users, our research is being used by managers and stakeholders to define stressor thresholds, characterize optimal habitat conditions, and improve fish outcomes.

MEDAL WINNER

The central role of time series in ecological research

Peter A. Henderson [1]

1. Pisces Conservation, UK

Long-term change in climate, habitat destruction, fisheries collapse, species diversity loss, maintenance of ecosystem services and quantification of extinction all require time series data. Addressing these concerns has major social and economic implications placing a considerable burden on the reliability of our ecological models. Effective modelling requires good quality time series extending over many generations which for fish generally indicates lengths of 40 to 100 years or more. Using long-term studies of aquatic systems we can: (1) show rates of change are not smooth: (2) demonstrate that unintended consequences from our well-intentioned actions are common: (3) place recent conditions within the wider context of past experience: (4) prove that extrapolating using time series of 5 to 15 year duration can be highly misleading and (5) identify a core of persistent species within an ecosystem under density-dependent control. Good quality time series need to be collected on a regular basis using a consistent methodology with a sampling frequency sufficient to capture change in key ecological features. Sampling regularly once a year is generally insufficient given changing seasonality. The creation of time series of sufficient length requires sustainable costs, management commitment and researchers willing participation in data collection that may not quickly enhance their careers. There are signs that techniques such as eDNA with automation may be able to generate cost-effective time series of the quality required. However, rapidly developing methodologies may, at present, be incompatible with the need for sampling consistency.

MEDAL WINNER

Diadromous life history movements of threatened non-marine elasmobranchs revealed through elemental analysis of vertebrae

Michael. I Grant* [1, 2], Peter M. Kyne [3], Julie James [4], Yi Hu [5], Sushmita Mukherji [6], Yolarnie Amepou [2], Leontine Baje [7], Andrew Chin [1], Grant Johnson [8], Tegan Lee [9], Brandon Mahan [10], Christopher Wurster [4], William T. White [11,12], Colin A. Simpfendorfer [1]

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5. Advanced Analytical Centre, James Cook University, Townsville, QLD, Australia
6. Institute for Marine and Antarctic Studies, University of Tasmania, Hobart, Tasmania, Australia
7. National Oceanic Resource Management Authority, Palikir, Pohnpei State, Federated States of Micronesia
8. Fisheries Division, Northern Territory Department of Industry, Tourism and Trade, Berrimah, NT, Australia
9. Centre for Sustainable Aquatic Ecosystems, Harry Butler Institute, Murdoch University, Perth, WA, Australia
10. IsoTropics Geochemistry Laboratory, James Cook University, Townsville, QLD, Australia
11. CSIRO Oceans and Atmosphere, Castray Esplanade, Hobart, TAS, Australia
12. Australian National Fish Collection, CSIRO National Research Collections Australia, Hobart, TAS, Australia

River sharks (*Glyphis* spp.) and some sawfishes (Pristidae) inhabit riverine environments, but their long-term habitat use patterns in rivers are poorly known. We investigated the diadromous movements of the northern river shark (*Glyphis garricki*), speartooth shark (*Glyphis glyphis*), narrow sawfish (*Anoxypristis cuspidata*), and the largetooth sawfish (*Pristis pristis*) using laser ablation inductively coupled plasma mass spectrometry (LA-ICP-MS) on vertebrae to recover elemental ratios over an individual's lifetime. We also measured elemental ratios for the bull shark (*Carcharhinus leucas*) and a range of inshore and offshore stenohaline marine species to assist in interpretation of results. Ba was found to be an effective indicator of freshwater, while Sr and Li were effective indicators of marine water. The relationship between Ba and Sr was consistently inverse. Both river shark species had prolonged use of upper estuarine environments, while adults appear to mainly use lower estuarine environments rather than marine. In comparison, a wide range of freshwater, estuarine, and marine environments were observed for *C. leucas*. For *P. pristis*, decreases in Sr:Ba at the end of the pre-natal growth zone indicated that parturition likely occurs in freshwater. There was limited evidence of prolonged riverine habitat use for *A. cuspidata*. The results of this study support elemental-environment relationships observed in teleost otoliths are also applicable to a wide range of elasmobranch species.

ORAL PRESENTATION

Demographic histories and adaptative potential in marine demersal fishes: implications for management.

Alice Manuzzi* [1], Natalia Díaz-Arce [1], Pierre-Alexandre Gagnaire [2], Kenza Mokhtar Jamai [3], Naiara Rodríguez-Ezpeleta [1]

1. AZTI, Marine Research, Basque Research and Technology Alliance (BRTA), Sukarrieta, Bizkaia, Spain
2. ISEM, Univ Montpellier, CNRS, EPHE, IRD, Montpellier, France
3. Laboratoire de Génétique des Populations Halieutiques, Institut National de Recherche H

Besides fishing pressure, commercially important marine species also face climate change-derived environmental pressures that further threaten their conservation and challenge the development of effective management plans. Understanding marine fish demographic history, which shapes population size, connectivity and distribution, as well as their adaptive potential to changes is therefore critical to ensure long-term sustainable management. Here, we tackle this by analysing genome-wide datasets in two commercially important demersal fish species: the white anglerfish (*Lophius piscatorius*) and the European hake (*Merluccius merluccius*). The white anglerfish was selected for the hybridization with the black-bellied anglerfish (*L. budegassa*), with a potential hybrid breakdown affecting both species' demographic dynamics by wasting reproductive effort. We assessed the extent and genome-wide consequences of this hybridization and estimated the timing of the event. Finally, genome-wide diversity analyses and inferences on introgression were conducted to understand the direction of hybridization, identify potential genomic incompatibilities and consequent effects for the species' assessment. The European hake was chosen for being a known case of mismatch between management and biological units. Our genetic dataset reveals a clear Isolation-By-Distance pattern, with higher genetic similarity between neighbouring populations only evident at neutral loci while adaptive markers suggest higher homogeneity along the species' range. As diversity in this species stems from demographic rather than adaptive processes, changes in connectivity may cause breaks in adjacent populations limiting a favourable genetic exchange which could lead to measurable effects (i.e. local extinctions). Decoupling adaptive and demographic processes underlying species diversity is therefore a key priority for assessing the potential impacts of future changes and the resulting management implications.

ORAL PRESENTATION

Population genomics and adaptation differences between inshore and offshore populations of Greenland halibut (GRINFISH project)

Daniel Estévez-Barcia* [1], Henrik Christiansen [1], Denis Roy [2], Adriana Nogueira [1], Rasmus Nygaard [1], Jesper Boje [1,3], Laura Wheeland [4], Kevin Hedges [4], Ingrid Spies [5], Lorenz Meire [1], Einar Egg Nielsen [6], Belén Jiménez-Mena [6]

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2. *McGill University, Montreal, Canada*
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6. *National Institute of Aquatic Resources, Silkeborg, Denmark*

Greenland halibut is a highly valuable flatfish species in the North Atlantic. In Greenland, it is exploited in both offshore and inshore fisheries, where the risk of overfishing risks and Arctic climate change may in particular impact fishing the inshore areas and thereby potentially affect the livelihoods of Greenlanders. Accordingly, Greenlandic fisheries management should be effective in terms of targeting distinct biological units and secure that the species is resilient towards environmental change. Population genomics can contribute to both aspects by delineating the biological populations from which quotas and fish stock indices are estimated, and by elucidating the genetic diversity which enables the species to respond to environmental fluctuations. The GRINFISH project combines high-throughput DNA sequencing with extensive environmental data to delineate discrete populations and to understand genotype-environment associations in Greenland halibut along the west coast of Greenland.

ORAL PRESENTATION

Evidence of genetic admixture of two exploited Mediterranean fish species in the Balearic Islands

Noemi Pasini* [1], Marta Bassitta [1], Joana F Ferragut [1], Sergio Ramírez Amaro [1,2], Antònia Picornell [1]

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Marine fishes occupy large and diverse habitats, shaping patterns of gene flow among populations across their range and driving population subdivision. The accumulation of genomic divergence due to environmental variation can modulate their underlying genomics, promoting local adaptation. In this sense, small-scale genetic differences have been commonly observed even for highly mobile species with long larval phases, which complicate population delimitation. In this case, numerous genetic markers are required to detect fine-scale population structure. The development of genomic resources has allowed the generation of techniques such as double-digest restriction-site-associated DNA sequencing (ddRAD-Seq), which has emerged as one of the preferred methods for producing a high number of Single Nucleotide Polymorphism (SNP) markers. Here, we used ddRAD-Seq to assess small-scale genetic variation in two exploited fish species in the Balearic Islands (*Mullus surmuletus* and *Serranus cabrilla*), analyzing samples of 96 individuals of each species. As preliminary results, a total of 21075 and 41982 SNPs were found for *M. surmuletus* and *S. cabrilla*, respectively. The results suggest the existence of two genetically distinct groups for both species, which apparently exhibit Mediterranean and Atlantic affinities, consistent with prior data obtained with mtDNA. According to that, the Balearic Islands would appear to be a genetically admixed group, with individuals of mixed ancestry in all sampling sites, with influence from the Spanish continental coast reaching the islands via the North Current deviation at the Ibiza Channel, while individuals from the South coast migrate across the Ibiza Channel. Further analyses will be carried out with the outlier loci to detect signals of local adaptation across environmental gradients in the study area. The study's outcomes will enhance understanding of underlying population structures essential for efficient management of marine resources.

ORAL PRESENTATION

Population genomic analysis of the European anchovy (*Engraulis encrasicolus*) in Central and Western Mediterranean

Damianos Alexandridis* [1,2,3], Tereza Manousaki [1], Rita Cannas [4,5], Antonios Magoulas [1], Maria Teresa Spedicato [6], Aglaia Antoniou [1], Marta Coll [7], Costas S. Tsigenopoulos [1]

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Genomic studies have recently become a powerful tool to gain compelling insights into species recent evolutionary history, patterns of spatial genetic structure and connectivity. The European anchovy (*Engraulis encrasicolus*), one of the most important pelagic fish in the Mediterranean Sea, constitutes a keystone species within the marine ecosystem due to its role in regulating trophic interactions, while also contributing significantly to the region's fishing industry. The aim of the study was to assess anchovy's population genetic structure in the Western and Central Mediterranean using a genomic approach. To identify a great number of polymorphic loci, we first assembled a draft reference genome of 1.69 Gb and 79.8% BUSCO completeness serving as a powerful mean for our downstream analysis. Then, we generated ddRAD-sequencing data from 398 anchovy individuals across twelve Western and Central Mediterranean sites, which led to the successful genotyping and further study based on 9,497 single nucleotide polymorphisms (SNPs). Results showed that our samples were divided into two clusters: one grouping the individuals from the Atlantic and the Alboran Sea, and the other including individuals from the Northwestern and the Central Mediterranean Seas (Fst=0.09). This differentiation highlights the presence of two distinct genetic pools, which is in alignment with prior research on European anchovy indicating once again the Almeria–Oran front as a potential dispersal barrier for gene flow in the species. Consequently, our research sets the ground for delineating distinct stocks and implementing targeted conservation strategies to safeguard the species from over-exploitation and habitat degradation.

ORAL PRESENTATION

Revisiting Stock Delimitation of European Anchovy (*Engraulis encrasicolus*) in the North-east Atlantic Using a Genomic Approach

Ane del Rio-Lavín* [1], Natalia Díaz-Arce [1], Naiara Rodriguez-Ezpeleta [1]

1. AZTI, Marine Research, Basque Research and Technology Alliance (BRTA), Sukarrieta, Bizkaia, Spain

Sustainable fisheries management relies on the appropriate delimitation of stocks, which should represent biologically significant units on which biomass estimations and other relevant assessments are performed. The European anchovy (*Engraulis encrasicolus*), an economically important species in Europe, is assessed and managed as two stocks by the International Council of the Exploration of the Sea: the Bay of Biscay stock and the Atlantic Iberian waters stock, covering the Spanish Atlantic and Portuguese coast. Previous genetic studies found inconsistent results on the population structure of this species, mostly due to ignoring two later discovered genetically distinct ecotypes: the coastal and oceanic anchovy. To unravel the genetic connectivity of anchovy, here we have assembled a dataset of 7000 Single Nucleotide Polymorphisms from 382 individuals covering the distribution range of the species from the English Channel (north) to the Canary Islands (south) plus Mediterranean waters and including coastal and oceanic locations. Our results revealed that: i) the Atlantic Iberian waters stock is composed of two genetically distinct lineages with the southern one being connected to the African coast and, to a lesser extent, the Mediterranean Sea; ii) the Bay of Biscay stock is genetically connected to northward locations not considered in the assessment; iii) the coastal and oceanic ecotypes coexist at different space-time proportions and hybridize. These discoveries challenge the current stock delimitation in European anchovy and call for future monitoring of the influence of the southern locations in the southern Portugal and Gulf of Cádiz anchovy, and that of the coastal ecotype in the oceanic one, which is the one managed and targeted by fisheries. Moreover, our study sheds light on prior conflicting results about the population structure and connectivity of European anchovy and carries significant implications for the conservation of this important species.

ORAL PRESENTATION

Delineate the population structure of a keystone marine fish species in the Northern Atlantic region using whole genome sequencing data

Siv N.K Hoff* [1], Ole Kristian Tørresen, Marius Maurstad, Mark Ravinet, Jane Aanestad Godiksen, Leif Christian Stige, Kjetill S. Jakobsen, Christophe Pampoulie, Kim Præbel, Sissel Jentoft

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Capelin (*Mallotus villosus*) — a keystone species linking lower and higher trophic levels in the food web — is a commercially important marine resource in the Northeast Pacific and Northern Atlantic Oceans. In this study, we generate and take full advantage of a chromosome-level reference genome assembly for capelin to disentangle population genomic differences and demographic history for some of the most exploited stocks in the central Northern Atlantic. At the genome-wide level, we uncover signals of genetic structure delineating three main clusters, representing Icelandic, Barents Sea, and East Greenland regions. Additionally, we detect fine-scale structuring within the Barents Sea and Iceland samples, potentially reflecting sub-population structuring and/or cohort differences. Intriguingly, we also identify several chromosomal inversions, where two are only found to be polymorphic within the East Greenland samples, while fixated in all other locations investigated, demonstrating the existence of a unique ecotype in this region. For some of the other inversions, a potential discrimination between cohorts in the Barents Sea as well as Iceland was detected. Demographic analyses uncover signals of population bottlenecks within the recent 100 years for all sub-populations identified, with indications that the Barents Sea populations have since then recovered. However, one of the Icelandic sub-populations and the East Greenland ecotype have not yet recovered. To summarize, our results demonstrate the impact of genome-wide datasets to determine stock units reflecting true biological populations, and thus, advocate for a reevaluation of how these stocks are managed.

ORAL PRESENTATION

The population structure of the small pelagic European sardine inferred from whole genome data

Rute R. da Fonseca* [1], Paula F. Campos, Alba Rey-Iglesia, Gustavo V. Barroso, Lucie A. Bergeron, Manuel Nande, Fernando Tuya, Sami Abidli, Montse Pérez, Isabel Riveiro, Pablo Carrera, Alba Jurado-Ruzafa, M. Teresa G. Santamaría, Rui Faria, André M. Machado, Miguel M. Fonseca, Elsa Froufe, L. Filipe C. Castro

1. Section for Biodiversity, University of Copenhagen, Denmark

I will present our results obtained using whole genome re-sequencing data from 108 individuals from 16 sampling areas across 5,000 Km of the European sardine distribution range (from the Eastern Mediterranean to the archipelago of Azores). The data supports at least three genetic clusters (using neutrally evolving genomic regions): i) one includes individuals from Azores and Madeira, with evidence of substructure separating these two archipelagos; ii) another cluster corresponds to the sampling sites around Iberia, in the center of the sampling range; iii) the third cluster includes all of the Mediterranean samples, except those from the Alboran Sea. Individuals from the Canary Islands appear to belong to the Mediterranean cluster. This suggests at least two important geographical barriers to gene flow, the Almeria-Oran front and one barrier within Macaronesia. These do not seem be complete barriers, with many individuals from around Iberia and the Mediterranean showing some patterns compatible with admixture with other genetic clusters. Genomic regions corresponding to the top outliers of genetic differentiation are located in areas of low recombination indicative that genetic architecture also has a role in shaping population structure. These regions include genes related to otolith formation, a calcium carbonate structure in the inner ear and other phenotypic traits previously used to distinguish *S. pilchardus* populations. This can potentially explain some of the previous conflicting results obtained using different methodological approaches. We provide a baseline for further characterization of physical and genetic barriers that divide European sardine populations.

ORAL PRESENTATION

Unravelling population structure of the European sardine (*Sardina pilchardus*) using low-coverage whole genome sequencing to inform assessment.

Marina Puebla-Aparicio* [1], Alice Manuzzi [1], Natalia Díaz-Arce [1], Naiara Rodriguez-Ezpeleta [1]

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The European sardine (*Sardina pilchardus*) is a highly valuable species in North-east Atlantic waters, where it is currently managed as three stocks: the Iberian stock, the Bay of Biscay stock, and the South Celtic Sea and English Channel stock. Despite the importance of aligning stocks with natural populations for ensuring sustainable management, there is still no clear consensus on the population boundaries of this species, especially around the Iberian Peninsula. Moreover, recent evidence forecast a northward migration for this species likely as consequence of climate change, and identify that sardines from the Mediterranean and the Atlantic respond differently to environmental pressures. To disentangle the population structure and adaptation potential of this species, here, we used low coverage whole genome sequencing (WGS) to genotype about 6 million SNP markers in 350 individuals from 44 sampling locations and different spawning groups covering the species distribution in the North-east Atlantic (from Norway to south Morocco) and the Mediterranean Sea. Our findings support genetic differentiation between the Atlantic Ocean and the Mediterranean Sea, with a transition zone in the Alborán sea, and a clinal latitudinal gradient of genetic diversity challenging current management unit delineation. Besides, we identified connectivity between northern Moroccan waters and the European Atlantic, following an isolation by distance pattern as we move south. Our research provides a wide view about connectivity patterns and genetic adaptation based on millions of markers for the European sardine in the North-east Atlantic European and North African waters, with a novel characterization of population structure in Moroccan waters, which has important implications for a more efficient fisheries assessment and management of the species in a future scenario of global change.

ORAL PRESENTATION

Integrating genomics and telemetry to unravel Northern Cod movement

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Understanding the biology of fish stocks is key to sustainable management. Recent technological advances in sequencing and telemetry equipment provide new tools that can help fill the gaps in our understanding of cod population structure and migratory behavior. Progress in genomics has facilitated the identification of genetic groups within stocks and of genetic variants associated with physiological and behavioral traits. Telemetry, instead, provides information on individual movement, which can lead to inferences regarding general migration patterns within a given stock complex. The Northern Cod (*Gadus morhua*) complex, is well known for having supported an historically important fisheries that collapsed over 30 years ago. Although sustained efforts have been made to restore the complex, it remains in a critical state. Here, we combine genomic and telemetry information to examine whether or not individual movements can be linked to variation in specific genomic region(s). Based on telemetry analyses, the Northern Cod can be divided into at least four categories: i) cod that move among multiple NAFO Divisions, ii) cod that remain mainly in 2J, iii) cod that remain mainly in 3L, and iv) cod that remain inshore year-round. Using a low-coverage whole genome sequencing approach, we obtained the genomic data of a subset of tagged cod which were released in 2019 and 2021. Preliminary results show that two regions in chromosomes 18 and 21 linked to hormone receptors are genetically different among cod that remain in the 2J and 3L NAFO Division. Any association found between the migratory behaviour and genomic regions can help inform future management of the complex.

ORAL PRESENTATION

Fine-scale genomic structuring of a freshwater apex predator

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Many top predatory fish species are declining due to overexploitation, habitat loss, and climate change. To effectively manage and preserve top predators, which often represent attractive targets for fisheries, detailed information about their movements and stock structure is needed. We applied restriction-site associated DNA sequencing (RADseq) to study the population structure and genetic diversity of an iconic freshwater apex predator, northern pike (*Esox lucius*), in the largest lake of the European Union, Lake Vänern (Sweden). Previous studies in the brackish Baltic Sea have revealed a very fine-scale population structure. Therefore, we hypothesized that strong homing behaviour combined with natural selection responsible for potential local adaptations would be the main force shaping the population structure of northern pike also within a large lake system. Altogether, we collected 129 spawning individuals and used tens of thousands of SNPs to characterize population structuring, identify individual migrants, detect putative footprints of selection, and estimate effective population sizes of pike at six breeding grounds. Our results provide, for the first time, a genome-wide perspective of the genetic divergence of pike within a large lake and have important implications for the management and conservation of an apex predator.

ORAL PRESENTATION

Comparative population genomics of *Pimelodus yuma* and *Pimelodus grosskopfii* in the Neotropical Magdalena-Cauca river basin.

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The Magdalena and Cauca are independent rivers conforming the Magdalena-Cauca Basin in Colombia, whose geological formation dates back to 33 million years ago. The total extension of this basin covers approximately ~1,600 km with sloped (Cauca) and flat (Magdalena) areas, within which 213 species of fish have been identified, of which 50% are endemic. *Pimelodus yuma* stands out as a species of great importance for artisanal fishing. This species exhibits medium and local migrations, covering distances between 50 and 100 km, being documented in the middle and upper Magdalena River but not in the Cauca River. In the case of *Pimelodus grosskopfii*, it is listed as one of the 30 most important commercially traded species within the basin. This species has been sighted in both Rivers, including the lower, middle, and upper Cauca, as well as the middle and upper Magdalena. However, *P. grosskopfii* seems to exhibit a pattern of medium migration, according to the ecological evidence. Considering the above migration patterns and the great geographical extent of the basin, we tested the hypothesis of panmixia Vs. structured patterns in these species, and evaluated their historical demography. For this, RADseq markers were analyzed from each species along the basin using coalescence-based and allele-frequency methods. Phylogeographic, structure, and Principal component analysis revealed the presence of panmixia in both species. Contrary to expectations, it was identified one individual of *P. yuma* in the Upper Cauca, and the presence of *P. grosskopfii* individuals in the lower Magdalena. A pronounced population expansion was detected for both species from 1.5 mya (*P. groskopffii*) and 1 mya (*P. yuma*), until the present. In summary, the results suggest that both *P. yuma* and *P. grosskopfi* exhibit greater mobility and geneflow than previously believed within the basin, likewise a healthy expansion of its effective size. Additionally, the presence of both species in areas that were not.

ORAL PRESENTATION

Combining population genomics with fisheries data to inform stock identification

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Fisheries scientists are increasingly turning to adaptive loci to delineate stock structures. Terms such as ‘sub-populations’ and ‘meta-populations’ attempt to capture the complexity of balancing evidence from neutral loci, suggesting significant genetic connectivity, with the evolutionary potential alluded to by adaptive loci. But how do we, as fisheries scientists, incorporate this complexity into management advice? Stock assessments providing management advice for stocks being fished at or below MSY, when neutral loci suggest panmixia (i.e. indicative of high gene flow), but adaptive loci suggest two or more sub-populations, will likely have significant gene-flow replenishing spawning stock. We show how combining population genomic analyses of adaptive loci with traditional fisheries data, can provide key information for fisheries assessments. We highlight the different contributions of gene flow from individual sub-populations to the entire meta-population. These complementary techniques provide additional information for fisheries assessments and potentially, their management.

ORAL PRESENTATION

Biology – Management Vulnerability Matrix (BMVM): a robust approach to evaluate vulnerability of fish populations to overexploitation

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Over the past decade, PSA (Productivity Susceptibility Analysis) has been the dominant approach in identifying vulnerability of different fish species to overexploitation. Along with the biological traits like fecundity and population growth rate, PSA incorporate species- specific harvest-related attributes like exploitation ratio and catchability in their assessment. Despite being comprehensive, most PSA assume a) the unit of analysis is species and not genetically- distinct individual populations and b) a uniform harvest regime along the entire geographical range. In practice, these assumptions are seldom true and thus, the resulting PSA predictions could perform poorly. We propose a heuristic combined "Biology – Management Vulnerability Matrix (BMVM) that improves PSA by incorporating information about 1) spatial distribution of genetically-distinct individual populations, 2) the possibility of multiple fisheries (management regimes) fishing same population and 3) the biological relevance of the individual management instrument to the species. As a case study, we conducted BMVM vulnerability assessment for nine fish species harvested along the west coast of India. We first used population genomic tools (ddRADseq) to identify spatial distribution of individual populations of nine species. For management analysis we then examined policies and regulations of all provinces along the study area. The BMVM matrix demonstrated that different populations of the same species differ greatly in terms of how they are managed by respective fisheries, which in turn influences their vulnerability. Moreover, the disparity between different fisheries harvesting the same population also impacts the vulnerability of that population. The matrix was also observed to be sensitive to periodic changes in the management. We argue that by addressing the key assumptions of PSA, BMVM approach enhances its applicability in predicting vulnerability of individual fish populations.

ORAL PRESENTATION

From mtDNA to genomics, the case of *Euthynnus* spp.

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Euthynnus alletteratus, a species of small tuna, is targeted for both recreational and commercial fisheries in the Atlantic and Mediterranean waters. Within the same genus, two additional species are identified: *E. affinis*, prevalent in the Indian and West Pacific Oceans, and *E. lineatus*, residing along the east coast of the Pacific Ocean. Despite the extensive geographical spread of these species, information regarding the population structure is limited. This study aims to investigate the population structure in Atlantic waters and species relationship in the global distribution of *Euthynnus* spp. To achieve this, ddRadSeq loci were sequenced paired-end for a sample of 81 individuals across 6 locations. The analysis yielded a dataset of more than 700,000 SNPs. Additionally, individuals were sequenced for the mtDNA control region and merged with the existing dataset. The results obtained from RadSeq confirm the separation of two lineages of *E. alletteratus* in the Atlantic and Mediterranean regions and also introduce new insights. Notably, segregation within the tropical group of this species is also identified. In line with earlier findings, SNPs demonstrated an inability to differentiate between *E. lineatus* and *E. affinis*. Contrary to previous information, *E. alletteratus* tropical group exhibited a lack of monophyly and was lumped within the *E. lineatus* and *E. affinis* group using SNP markers information. Moreover, further examination of mtDNA sequences revealed a third distinct population in the Northern cluster when individuals from eastern Mediterranean were segregated from western individuals, designating the Strait of Sicily as a natural barrier for this species. In summary, these findings paint an intricate picture of the genetic variability within these tuna species, emphasizing the need of management plans to address and preserve the natural diversity of *Euthynnus* spp. to prevent any loss.

ORAL PRESENTATION

Application of genetics and genomics in forecasting pink salmon catches and fisheries management in the Sea of Okhotsk basin.

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Currently, rational exploitation of fish species and sustainable fisheries management is possible only with genetics. The more pronounced the population structure of a species, the more justified is the application of genetic and genomic approaches for the prediction of catch volumes in a particular region. Due to their pronounced population structure, applying genetic and genomic approaches to solve various fisheries problems is the most reasonable for anadromous fish species. Pacific salmon of the genus *Oncorhynchus* are a group of anadromous species with a high level of homing. Predicting the approaches of the most abundant species of *Oncorhynchus*, pink salmon, into the rivers of the Sea of Okhotsk basin is one of the main challenges of Far Eastern fisheries science. Pink salmon is represented by two lineages - even years spawning and odd years spawning, that, during the long period of evolution, diverged at least to the subspecies level, and as a result, each of the lines should be assessed and predicted independently. Based on genomic data obtained at the University of Washington, we have developed two panels of SNP markers that allow us to reliably differentiate pink salmon from the Sea of Okhotsk basin at the regional level. After creating a baseline and testing the method, the approach was evaluated in practice: the data obtained were used to predict pink salmon approaches and catch volumes, and the 2022 and 2023 fishing seasons demonstrated the high accuracy of our estimates for lineages of both even and odd spawning years. Recently, we conducted genomic research focused on a massive analysis of pink salmon stocks in the Sea of Okhotsk basin that should allow us to predict the migrations of pink salmon not only at the regional level but at the population level as well.

ORAL PRESENTATION

A Machine learning best practices approach towards universal genetic stock identification of Atlantic herring, *Clupea harengus*

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Accurate stock assessment of Herring is of particular challenge, given their genetic diversity and propensity for multiple genetic populations to inhabit the same stock assessment area. Genetic stock assessment has shown some promise in the accurate separation of stocks, one example being Division 6.a, which has effectively demonstrated the ability of genetic based assessment models to differentiate a least three genetic sub-populations. However, the use of genetic stock assessments is being performed on a jurisdictional level, with different areas developing their own tailored genetic assessment models. In this analysis we conducted a genetic stock assessment of herring populations using population genetic analysis and machine learning techniques. With the collaboration of several Public and Private entities we collected baseline populations from across Europe, from 70 sampling events across 38 locations and 13 ICES statistical areas, genotyping 3464 individual herring using the MultiFishSNPChip_V1.0 genotyping array, a multi-species fisheries genotyping platform. We expanded on previous work on genetic assignment models and applied machine learning best practices, to identify a model which could accurately assign unknown stocks to one of 12 genetic populations of Herring. The work presented in this study, highlights the potential for a universal genetic assignment model for Herring, utilizing a novel array based method for fisheries genotyping.

ORAL PRESENTATION

Integrating molecular monitoring into management of salmonids in the Pacific Northwest, USA

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Genetics plays a central role in conservation of imperiled salmon in the Pacific Northwest, USA. Both genetic and genomic monitoring are integral of modern fisheries management, and provides detailed information on hatchery versus wild composition, estimation of stock abundance, as well as explaining the genetic basis for adaptive traits including run timing and age at maturity. This talk provides an overview of two primary tools used to manage hatchery (parentage-based tagging) and natural origin (genetic stock identification) returns and explains how they are used to advance conservation of imperiled stocks at the river basin scale. Additionally, we highlight recent work to identify the genetic basis for important life history traits and how those traits vary across the landscape.

ORAL PRESENTATION

Genetic based methodologies to improve bluefin tuna management and conservation

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Understanding fish distribution and dynamics as well as potential population substructure is fundamental for accurate fisheries management; however, this can be particularly challenging for migratory species with high mobility potential such as the Atlantic bluefin tuna (*Thunnus thynnus*). This species is widely distributed along the north Atlantic Ocean while mainly spawning the Mediterranean Sea and the Gulf of Mexico. Although genetic tools for stock identification have been recently developed for assigning catches to origin, recent genetic studies have also revealed that individuals from both spawning areas interbreed in a recently discovered spawning ground located in the western Atlantic, the Slope Sea. This rejects the previously assumed paradigm of two non-mixing isolated stocks and calls for a better understanding of the mixing patterns, as well as for an estimation of the degree of interbreeding occurring in the Slope Sea. With this aim, we have developed an integrated genomic monitoring tool for a comprehensive individual genetic make-up analysis consisting of ~8000 genetic markers useful for population connectivity and adaptive potential studies. The genotyping of 1920 individuals of different age classes captured at the spawning areas and feeding aggregates along the North Atlantic provides new insights into the migratory and reproductive behavior of the ABFT as well as on the adaptive capacity of this species.

ORAL PRESENTATION

Population abundance estimation with the Close Kin Mark Recapture approach: insight from research on brook trout (*Salvelinus fontinalis*) and Atlantic halibut (*Hippoglossus hippoglossus*)

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The estimation of abundance is a fundamental problem in ecology and conservation biology and in the management of wild popultions. It is a particular problem in the management of exploited marine, anadromous and freshwater populations. During this presentation I will describe progress on interdisciplinary collaborative research my lab is involved in, that is aimed at the estimation of abundance in fish populations based on genomics and the close Kin Mark Recapture approach. I will describe insight gained on potential sampling biases in the census size estimation of brook trout (*Salvelinus fontinalis*) populations based on knowledge of their effective sizes and will inform on progress in the estimation of abundance of Atlantic halibut in the Northwest Atlantic.

ORAL PRESENTATION

Close-Kin Mark-Recapture for abundance estimation of the European hake and the white anglerfish

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Close-Kin Mark-Recapture (CKMR) is a fishery-independent abundance estimation method that can also provide information on total mortality and spatial dynamics. CKMR is based on the principle that the larger a population, the smaller the probability that kins are found in a random subsample of the population, but also relies on knowledge of other demographic parameters while at the same time being able to estimate them. Applying CKMR to a given species requires gathering available knowledge on species specific characteristics such as fecundity, mortality, examining stock connectivity, developing cost-efficient methods for age, sex and kinship determination and collecting a large number of samples. Here, we present the advances made to apply CKMR to two commercially important species in the Northeast Atlantic, namely European hake and the white anglerfish. First, we have assessed stock connectivity of both species and developed a SNP array that allows to cost-effectively genotype hundreds of samples for geographic origin assignment and kin finding, and we have developed a CKMR model considering the characteristics of each species. Second, we have genotyped thousands of samples collected through an established a sampling collection network using existing scientific surveys and integrated the results into the CKMR model for estimating the abundance of the European hake and white anglerfish to inform stock assessment. Finally, we discuss how these results will contribute to set the foundations for future CKMR studies aimed at supporting the assessment and therefore the sustainability of the fish stocks worldwide.

ORAL PRESENTATION

Exploring the connection between the social network and the gut microbiome in a wild marine fish population

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The gastrointestinal tract of animals harbors diverse bacterial communities, influencing their behavior, physiology, and metabolism. However, the interplay between an individual's microbiome and its social behavior remains poorly explored in the wild. This study focuses on reconstructing the social network of a marine fish, *Xyrichtys novacula*, in its natural environment. Relying on high-resolution acoustic telemetry, we first obtained a high-quality positioning data-set comprising 7,930 one-day-long trajectories from 232 individuals (153 females and 79 males). From this data, we computed the associations between paired individuals, revealing a harem-like social structure. Territories were established by one male and several females, with males exhibiting agonistic behaviors against their neighbors to defend their territories. Subsequently, a subset of individuals of the social network was captured, and the gut microbiome diversity was quantified using operational phylogenetic units (OPUs) based on Illumina high throughput sequencing of 16S rRNA gene amplicons. The properties of the social network were intricately linked to the microbiome. Microbiome samples from individuals within the same harem, irrespective of sex, exhibited greater similarity, while distinctions with other harems were pronounced. Similar local microhabitats, encompassing food resources, and local social interactions can emerge as pivotal transmission pathways for gut symbionts. These factors have the potential to influence the shaping of the gut microbiota along social networks in aquatic animals. This study is among the first to unveil the relationship between social structure and the microbiome in wild fish. Future investigations will delve into establishing cause-and-effect relationships, exploring whether the social network shapes the microbiome or if the microbiome and resulting metabolites influence behaviors that, in turn, contribute to the structure of the social network.

ORAL PRESENTATION

Host-parasite interactions drive biodiversity in cichlid fish

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Divergent adaptation to distinct ecological niches can, over remarkably short periods of time, generate animal diversification. Some biotic features such as parasite communities are capable of driving diversification exerting strong selective pressures on their hosts. This is probably due to the ability of the host immune system to rapidly evolve in response to local parasites. There is evidence that immunity genes evolve more rapidly and are under more positive selection than the rest of the genome, and that respond to natural selection modulating defenses to parasites. These genes also play an integral role on reproductive isolation contributing to the discrimination of mating partners, and therefore to diversification. Here we explore the role of host-parasite interactions in promoting diversification and ultimately speciation in prime models for adaptive radiation, cichlid fishes in crater lakes. We studied the recent adaptive radiations of the Neotropical Midas cichlid in the Nicaraguan crater lakes and their associated parasite communities, to investigate how changes in parasite communities induce changes in the fish immune system. We discuss how these changes might start, maintain or enhance species differentiation.

ORAL PRESENTATION

Mechanisms underlying variation in sea lice resistance among salmonid species revealed by single nuclei RNA sequencing

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Sea lice parasitism poses a significant threat to both wild and farmed Atlantic salmon (*Salmo salar*). Yet some closely-related salmonid species exhibit an innate immunity to sea lice. For instance, within days of a sea louse attaching, the skin of coho salmon (*Oncorhynchus kisutch*) rapidly inflames, causing the louse to either die or detach. Pink salmon (*O. gorbuscha*) are also resistant to sea lice. However, this resistance is not uniform across all *Oncorhynchus* species, with chum salmon (*O. keta*) being highly susceptible to this parasite. The mechanisms underlying this variation in resistance among species, and whether similar strategies are employed across resistant species, remain largely unknown. This study therefore employed single-nuclei RNA sequencing to characterize the genes and cell types involved in the skin of both resistant (coho salmon, pink salmon) and susceptible (Atlantic salmon, chum salmon) species. Juvenile fish were exposed to sea lice (*Lepeophtheirus salmonis*) copepodids. Fin and skin samples where lice had attached were taken at 12h, 24h, 36h, 48h, and 60h post exposure and from unexposed fish. Nuclei isolation from each sample was followed by barcoding using Chromium (10X Genomics), Illumina sequencing, and data analysis with STAR and Seurat. We found coho and Atlantic salmon exhibited a shared wound-healing and immune response to sea lice. However, this response was attenuated in Atlantic salmon, possibly due to the lice's enhanced ability to immunomodulate this species. We identified keratinocytes as the key cell type underlying the distinct swelling observed at the site of lice attachment that is responsible for coho salmon's sea lice resistance. Multiple genes associated with variation in sea lice resistance among the studied salmonid species were identified, offering targets for gene editing to enhance the sea lice resistance of aquaculture Atlantic salmon and potentially reduce lice burdens on both farmed and wild fish populations.

ORAL PRESENTATION

Transcriptome analysis of *Flavobacterium psychrophilum* infected and proliferated in ayu *Plecoglossus altivelis*

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Flavobacterium psychrophilum is a causative agent of bacterial cold-water disease (BCWD) and make a severe loss of fish production of ayu *Plecoglossus altivelis* in Japan. For immersion challenge test, mortality rate is usually reached to 80% with 1.0 × 107 CFU/mL of the bacteria cultured in modified *Cytophaga medium* (MCY). Although the number of the bacteria is clearly lower than the immersion challenge, hanging dead fish by BCWD in a fish tank causes comparable mortality. Generally, virulence of pathogens is more virulent when they are reisolated from the host after an artificial challenge test. In this study, we compared gene expression pattern between *F. psychrophilum* proliferated in the host and those cultured in MCY broth. Ulcerative region on the skin of ayu infected with *F. psychrophilum* was collected, homogenized in MCY broth and gently centrifugated to remove the cell debris. The supernatant was serially diluted, inoculated on MCY agar to count colony forming unit (CFU), and used as bacteria derived from the host. Ayu was intraperitoneally challenged with 1.0 × 106 CFU/fish of either the bacteria derived from the host or those cultured in MCY broth. Total RNA extraction and cDNA library construction was performed using both bacteria preparation and gene expression analyses were carried out by using Illumina MiSeq. Cumulative mortalities of ayu challenged with the bacteria derived from the host and those cultured in MCY were 96% and 72%, respectively. The next generation sequencing yielded gene expression data for 2,905 genes showing more than 80% homology to genome sequence of F. psychrophilum 160401-1/5N strain. Gene expression analyses using Trinity software revealed that 68 genes significantly up-regulated in the bacteria derived from the host ($P < 0.001$, < 4-fold). Many of these genes encoded a signal peptide and were predicted to be located on the cell membrane, periplasm, or cell wall of the bacteria by GO annotation. Furthermore, genes related to type 9 secretion system, gliding motility, and protein degradation that are considered as virulence factors of F. psychrophilum were included in the up-regulated genes of the bacteria derived from the host. These genes are attractive candidates as antigens for subunit and DNA vaccines against BCWD.

ORAL PRESENTATION

Revealing the diet of small pelagic fish larvae via metabarcoding of stomach contents

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Small pelagic fish (SPF) have a key ecological role in their ecosystem and are important fisheries resources in many regions around the globe. Although the diet of SPF is known for the adult stage of most species, the same is not true for larval stages. The paucity of information on this topic is further complicated by the high vacuity rate of SPF larvae based on traditional gut content analysis. A good understanding of the trophic ecology of these important fisheries resources, and especially at the early life stages, is essential information to allow predictions of recruitment strength based on the conditions experienced at the larval stage. To this purpose, food availability must be assessed considering knowledge of diet composition and the main prey items throughout larval development. Here we study the diet of sardine and anchovy larvae collected from the Western and Southern Iberian coasts using metabarcoding of stomach contents, and compare it with results of visual inspection of prey items. Different genetic markers (18S and COI) were used to target different taxonomic groups, including prokaryotic and eukaryotic phytoplankton, and eukaryotic zooplankton. Preliminary results suggest that SPF larvae feed on a large diversity of prey spanning multiple phyla, and show high frequency of occurrence of Copepoda, Appendicularia and Hydrozoa in their stomachs. Application of metabarcoding in stomach content analysis of early life stages holds great potential to unravel the hidden prey diversity in the challenging small size scales of SPF larvae.

ORAL PRESENTATION

Catfished: how metabarcoding increases knowledge about the predation of invasive European catfish on Iberian fish communities

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Diet studies help understand the predatory pressure of invasive species on native fauna, though results may be constrained by the methods used. In this work we analysed whether metabarcoding of intestinal contents enhances to traditional stomach content analysis when evaluating the diet of the apex predator European catfish (*Silurus glanis*), which is invasive in Iberian rivers. The study focused on bony fish detection throughout seasons and predator ontogeny, by analysing 185 individuals from the Lower Tagus River. Metabarcoding detected higher taxa richness than the traditional analysis (23 vs 13, respectively), including native and endangered fish, which may partly be related to a high percentage (56%) of empty stomachs in traditional analyses. Altogether most common preys were identified by both methods, including native migratory, endangered and economically valuable *Anguilla anguilla* and *Alosa* spp., native *Chelon* spp. and *Luciobarbus* spp., and non-native *Lepomis gibbosus*. There were, however, differences in prey detection throughout the year, namely for *Alosa* spp., which was first detected in Winter, using metabarcoding, but only in Spring with traditional analysis. Additionally, seasonal variation on prey taxa richness was observed, with Autumn and Winter being the least diverse for metabarcoding and traditional analysis, respectively. Prey composition also varied with season for both methods but only with predator size for metabarcoding. Overall, metabarcoding was found important for assessing predation of *S. glanis* on fish communities and identify the full range of prey taxa and their variation patterns, which may be missed through traditional analysis due to constraints on prey ingestion, regurgitation and digestion.

ORAL PRESENTATION

Nutrigenomics in Aquaculture: A New Paradigm

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Aquaculture is one of the most important and rapidly evolving industries in terms of providing nutritious food and meeting protein demand while leaving a low carbon footprint. This is possible because of more advancement in production systems and health management practices and a better understanding of the genetic makeup of aquatic animals. To enhance aquaculture production in a sustainable manner, it is very important to have a good understanding of the growth process and the underlying mechanisms behind it. Molecular and genomic research plays a vital role in revealing a clear picture of feed utilization and metabolism in fish. Moreover, these technological tools enable us to manipulate or alter the genetic expressions through nutritional intervention, resulting in effective utilization of feed and growth performance. Nutrigenomics is a branch that links genomics with the nutritional aspect and reveals the role of nutrition on gene expression. The application of nutrigenomics in aquaculture research can aid us in developing more premium feed with better performance and functional properties, resulting in better economics and fish welfare. This article is a review, highlighting the developments in the field of nutrigenomics in aquaculture.

ORAL PRESENTATION

Beyond GWAS: Complex mechanisms underlie the simple genomic architecture of Atlantic salmon age at maturity

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A common aim in biological research, linking genotype with phenotype, has seen dramatic taxonomic diversification in recent years as new technologies have enabled genome-wide scans to be applied in almost any species. However, such diversification is not as apparent when it comes to understanding the biological processes behind identified associations, especially considering loci associated with life-history traits. Age-at-maturity is closely linked to fitness in many species, with the timing of maturation often involving trade-offs. For example, delayed maturation can lead to larger body size, higher fecundity and/or increased offspring survival, but longer generation times can carry an increased mortality risk prior to reproduction by prolonging pre-maturity life stages. Genome-wide association studies (GWAS) in Atlantic salmon earlier identified a single locus that associates strongly with age-at-maturity (sea-age), and a SNP located near the gene vgll3 explained 39 % of the phenotypic variation in maturation age. The relatively simple genetic architecture of this trait combined with the features of Atlantic salmon as a model system offer a good opportunity to better understand the ecological drivers and molecular mechanisms underlying this locally adapted life history trait. In this presentation, I will summarize my group's recent research on this topic that reveals hidden complexity along the genotype-phenotype-fitness continuum that appear to mediate the large effect of this gene on alternative life history strategies involving variation in age at maturity. If time permits, I will also present how this information can be used in salmon conservation and management.

ORAL PRESENTATION

Effect of vgll3 genotype on liver transcriptome in Atlantic salmon before and after spawning season.

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Age-at-maturity in Atlantic salmon is strongly associated with a large effect locus located in the vgll3 gene region. Thus, vgll3 genotype plays an important role in the evolutionary trade-off between smaller, early maturing individuals with reduced reproductive success, and larger, late maturing individuals with increased reproductive success but a higher risk of dying before spawning. The onset of maturation in Atlantic salmon begins during the spring before the spawning in the autumn, and lipid levels play a role in this initiation. It has previously been shown that changes in membrane and storage lipid class concentrations in the liver between seasons are associated with vgll3 genotype. To better understand the molecular mechanisms involved in the vgll3 genotype - lipid profile association, we analyzed the transcriptome of livers sampled in spring and autumn from early (vgll3*EE) and late (vgll3*LL) maturing genotype salmon. We found that 168 genes were differentially expressed between EE and LL immature males in spring, compared with only 2 genes in autumn. However, 84 genes were differentially expressed in autumn between immature and mature EE males. Functional enrichment indicated that several pathways, including lipid biosynthetic and malate metabolic processes, were enriched among the differentially expressed genes in spring. Moreover, the expression of genes involved in lipid metabolism, such as elongases of very long chain fatty acids (elovl5, elovl6), lipoprotein lipase (lpl) and fatty acyl desaturases (fads2), were associated with vgll3 genotypes in spring and/or the maturity status in autumn. Our results provide further insight into the molecular level processes contributing to the vgll3 genotype association with lipid metabolism in the liver, in particular fatty acid biosynthesis pathways and seasonal influences. Further research is needed to understand the mechanism linking vgll3 genotype and the regulation of the expression of these genes.

ORAL PRESENTATION

Will climate change impact the Baltic cod? Larvae performance under future environmental conditions

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Climate models for the Baltic Sea predict an increase in water temperature and a decrease in salinity. Marine organisms will be forced to cope with these environmental changes in the near future. During embryonic development, the Baltic subspecies of the Atlantic cod (*Gadus morhua callarias*) is sensitive to variation in salinity and temperature, and these can determine the survival of both eggs and larvae. However, how the performance of cod will be affected by the predicted temperature and salinity conditions during the early-live stages has not been investigated. In order to explore the impact of climate change on cod during early life stages, we incubated cod eggs under current and future environmental conditions and recorded hatching rate, larval survival and buoyancy. We further carried out transcriptomic analyses of these larvae to investigate the physiological responses of cod larvae to these environmental changes and a plasticity in expressed genes. Temperature increase and salinity decrease negatively affected cod egg and larval survival and influenced larval buoyancy after hatching. We found a a difference in expressed genes under different temperature but not under salinity conditions. We discuss the implications of these responses to stressful environmental conditions and conclude that future temperature and salinity conditions will negatively impact Baltic cod during early life development and that climate change will most likely become a threat to the Baltic cod in the near future.

ORAL PRESENTATION

Multi-omics refines tissues, candidate genes and putative regulatory links involved in the humic adaptation of keystone freshwater fish

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Although population genomics approaches have been successful in identifying regions of the genome shaped by natural selection, the progress in dissecting the molecular mechanisms of adaptive variants and traits has been slow. By integrating multi-tissue (gill, spleen, olfactory rosette, whole eye and liver) transcriptomes of Eurasian perch (*Perca fluviatilis*) and footprints of selection based on whole genome scan, we prioritize tissues, candidate genes and putative SNP-gene expression associations involved in humic adaptation of this keystone freshwater fish. Over 5,000 differentially expressed genes (DEGs) were discovered across the five tissues. A significant excess of outlier SNPs among DEGs found in the gill and spleen tissues indicated their involvement in humic adaptation. Further, 3,617 cis-eQTLs that associate with gene expression variation in perch were identified, with approximately 9% of genes harbouring cis-eQTLs showing differential expression between humic and clear-water habitats. Several cis-eQTLs were found in the regions showing most consistent signals of selection also harbouring DEGs (chr. 5: PLAGL2, chr. 7: PPP1R8, TCHH, chr. 8: IFITM3). Thus, our integrative analyses enabled to pinpoint specific organs that play a key role in adaptation, prioritize candidate genes under divergent selection based on their expression patterns, and identify links between SNPs and transcript abundance variation. We expect that the multi-omics strategy outlined in this work provides a practical framework for understanding the genetic basis of phenotypic diversification and adaptation for wide range of species.

ORAL PRESENTATION

Regulatory landscape of chromatin accessibility sheds light on biological processes of humic-water adaptation

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Recent studies on regulatory landscape suggest that variation in chromatin accessibility can be an important source driving phenotypic variation, adaptation, and genome evolution. In particular, Assay of Transposase Accessible Chromatin assay, generally known as ATAC-Seq, represents an efficient means obtaining insights on the evolution of open chromatin regions and regulatory landscape of an organism. Here, we aim for a first time to characterize chromatin accessibility in common freshwater fish species, Eurasian perch (*Perca fluviatilis*), across three tissues (eye, liver, and spleen) and two contrasting environments (humic and clear-water lakes). By combining ATACseq information with transcriptome data and information on footprints of selection, we hypothesized that i) open chromatin regions associate with the level of gene expression, ii) the accessibility of open chromatin regions differs between tissues, iii) the accessibility of open chromatin regions varies between habitat types, iv) open chromatin areas show enrichment in footprints of selection associated with humic adaptation. Our results show clear differences in regulatory landscape between tissues, as well as variation in the regulatory landscape between humic- and clear-water environment. Altogether, these findings illustrate the complex interactions of chromatin accessibility and gene regulation and reveal promising regulatory regions linked with humic adaptation in perch.

ORAL PRESENTATION

Maturation-related traits are mediated by vgll3 genotype, population, and diet in female Atlantic salmon

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Age at maturity is an important factor contributing to life-history diversity in many fish species, including Atlantic salmon. This trait often shows sex-specific patterns, but female Atlantic salmon are seldomly included in common-garden studies of maturation. Thus, there is a gap in our understanding of how different genetic and environmental factors shape female maturation. Using a 4-year common-garden experimental system, we assessed the influence of diet (low-fat vs. high-fat) and vgll3 – a candidate gene in the genomic region influencing age at maturity in Atlantic salmon – on maturation and related phenotypic traits of female Atlantic salmon from two Baltic salmon populations. We found the early-maturation-associated vgll3*E allele to be associated with higher probability of maturation. In addition, both body size and condition in the spring prior to spawning influenced maturation. We did not find a strong effect of population or diet on maturation probability, but these factors influenced body condition in the spring of the year of spawning. The more northern Oulu population and the low-fat diet were associated with lower body condition compared to the southern Neva population and the high-fat diet. Moreover, there was a significant interaction between population and diet on body condition suggesting that populations may respond differently to environmental conditions. These results broaden our understanding of the processes underlying maturation and demonstrate that genes and environment interact to shape age at maturity in female Atlantic salmon.

ORAL PRESENTATION

How do Atlantic salmon respond to selective pressures under various genetic architectures of life-history traits?

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The ability of species to respond to environmental change through adaptation of life history traits depends on several factors, including the rate of change, the genetic variation underlying fitness-related traits, but also the genetic architecture of these traits. In Atlantic salmon (*Salmo salar*), recent studies have shown that variation in age at maturity, a key life history trait, is strongly associated with a major effect locus. In addition, patterns of sex-dependent dominance have been shown to vary between populations. However, we lack understanding of the consequences of different genetic architectures underlying maturation on the evolution of life history traits and population dynamics of Atlantic salmon facing selective pressures such as environmental change and exploitation. We used a simulation approach, i.e. an individual-based demo-genetic model, as a virtual laboratory to simulate the life cycle of Atlantic salmon, together with the genetic basis of maturation and environmental conditions. We compared alternative scenarios of the genetic architecture of maturation (polygenic vs. major effect locus, dominance patterns) and assessed the response of population to selective pressures, both at the demographic and evolutionary level. The findings will be discussed in the light of environmental pressures affecting Atlantic salmon and ongoing research aimed at improving our understanding of the genetic basis of life-history traits.

ORAL PRESENTATION

Genome and body size diversity of the fishes using comparative phylogenetic methods:

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Genome size is one of the main factors shaping organismal traits by impacting metabolism and having a strong correlation with cell size. On the other hand, smaller or larger body sizes can affect the overall morphology and development of a species. While it is expected that body size varies depending on the number of cells and cell size, and as cell size is dependent on genome size, how body size and genome size covariate have rarely been investigated. Fishes are the largest group of vertebrates and possess a wide range of genome size and body size variation across the macroevolutionary level. Those conditions make them suitable to investigate a possible correlation between genome size and body size. We collected genome size and body size data for 1169 ray-finned species (including the commercial fishes caught around the world) and looked for a correlation between them using both phylogeny-dependent and phylogeny-independent regression analyses. Both positive and negative correlations were found at subclade levels (e.g., order). We also examined trends in genome size and body size along the phylogeny to determine, for example, how many times reduction or increase occurred. This includes modeling the rate of evolution for both body and genome size to investigate the pattern of size distribution throughout phylogeny. We argue that the biological size index, a novel size metric calculated by factoring both genome size and body size – is a more sensible metric when discussing the size of an organism.

ORAL PRESENTATION

Conservation challenges and genomic insights in salmonid populations: a study of brown trout in Northern Finland

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Brown trout (*Salmo trutta L.*) is one of the most diverse species with significant anthropogenic threats to the migratory, fast-growing life-history types. Brown trout form a continuum of migration strategies from residency to anadromy, but the genomic underpinnings of this variation have remained unresolved. Thus, tools that would efficiently produce data on single nucleotide polymorphism (SNPs) related to life-history variation, such as migration tendency, would be pivotal for monitoring and management. As a first step towards a routinely usable genomic monitoring tool, we utilized two distinct bioinformatic methods, both targeting the genetic mechanisms behind different migration tendencies and population structure in previously RADseq-genotyped brown trout from two watersheds in Finland. Originally, these data were analyzed by using the Atlantic salmon reference genome for brown trout RADseq reads, succeeded by Bayesian and Principal Component analyses to detect migration strategy-related outlier SNPs. However, as the brown trout reference genome is nowadays available, we applied a method mirroring these steps but utilizing the current brown trout reference genome for alignment and a distinct genomic pipeline for SNP identification. All these methods yielded comparable results when inferring population structure but detected distinct candidate outlier SNPs associated with varied genome regions responsible for diverse physiological functions, like growth. These outliers might not directly explain the diverse brown trout migration tendencies but might be overall related to life-history strategies. These results suggest the importance of reference genome selection in outlier marker identification and provide us with a basis to continue our project with new samples and data.

ORAL PRESENTATION

Diversity of Lake Mývatn threespine stickleback in space and time

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A major challenge facing societies is the protection of biological diversity, which is critical for ecosystem functioning and services. Biodiversity is under serious threat from human activities and we lack understanding of the processes that shape it. We used the Eco-Evo-Devo framework to guide us when studying the diverse stickleback population of Lake Mývatn, N.E. Iceland. Lake Mývatn is highly productive, spatially diverse and the animal populations in the lake show extreme temporal fluctuations. This can be clearly seen in threespine stickleback (*Gasterosteus aculeatus*) and its favorite prey, chironomidae midge larvae. We used data from our long-term monitoring of the stickleback population to explore phenotypic variation in space and time in relation to genomic variation and ecological factors, which are strong indicators of adaptive evolution. We furthermore increased our understanding of the phenotypic variation in the stickleback populations by conducting cross-generation rearing experiments where offspring of wild fish were reared at contrasting temperatures and diets. The results showed considerable phenotypic variation across the lake, with indications of both spatial and temporal adaptations. There is, however, clear evidence of the importance of transgenerational plasticity in shaping the observed diversity. Our findings will be discussed in relation to the importance of conserving intraspecific diversity.

ORAL PRESENTATION

Causal analysis of the transcriptome of the Greenland shark reveals pathways associated with ageing

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Long-lived species like the Greenland shark, boasting a lifespan exceeding 250 years, offer valuable insights into complex biological processes underlying ageing. Despite their potential, our understanding of these mechanisms in the Greenland shark remains limited. The aim of the study was to causally model ageing in the cardiac transcriptome to reveal pathways mechanistically associated with ageing. Hypergraphs present a powerful tool for causal analysis of omic data, by modelling the dynamics of the transcriptome revealing highly connected elements potentially indicative of functional relevance (Ripley et al. 2023). In this study, we utilized 28 RNA-seq ventricular samples collected over a six-year period (2017-2023) from Greenland sharks, encompassing both juvenile and adult individuals with body size ranging from 102 cm – 440 cm total length. Using hypergraph analysis of the cardiac transcriptome we identified 3,153 highly interconnected genes representing a group of genes in causally linked to the ageing process in the heart. Gene ontology (GO) and KEGG enrichment pathways analysis revealed 20 GO terms, and 142 KEGG enrichment pathways: glycophagy (cellular energy metabolism), muscle and actin filament regulation, DNA methylation (≥50-fold enrichment, adjusted p-value ≤0.05). These findings provide new insights into the ageing process in species with extended lifespan and a better analysis of complex biological processes.

ORAL PRESENTATION

Comparison of Environmental DNA metabarcoding and Underwater Visual Census for the monitoring of taxonomic and functional dimensions of fish diversity

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Fish monitoring is essential for assessing the effects of natural and anthropic stressors on marine ecosystems. In this context, environmental DNA (eDNA) metabarcoding appears to be a promising tool, due to its efficiency in species detection. Recently, several studies have sought to assess the performance of this new method compared to conventional techniques used for fish surveys, such as Underwater Visual Census (UVC). However, these analyses have mainly focused on simple diversity indices, such as species richness, without taking into account the functional dimension of biodiversity. Here we compare the ability of eDNA and UVC to assess the taxonomic and functional composition (presence/absence data) of Mediterranean fish communities. We collected eDNA samples (n=26) and performed UVC strip transects (n=246) inside and outside four Marine Protected Areas of the Mediterranean Sea encompassing a wide range of habitats. Samples for eDNA analysis were collected by filtering water simultaneously at the surface and at the bottom, and DNA was amplified using a combination of three sets of primers specific to Actinopterygian or Vertebrate taxa. Among the 60 fish taxa identified in this study, eDNA gave better results, detecting 95% of these species, whereas UVC recovered only 58% of them. 25 were unique to eDNA, 3 were unique to UVC and 32 were detected by both methods. Functional diversity was better sampled with eDNA than with UVC, with the detection of a wider breadth of functional traits. For example, cryptobenthic species as well as large mobile pelagic fishes were detected more effectively with eDNA. Unlike other studies, our results do not indicate a complementarity between the two methods (if quantitative data are not required), but rather highlight the outperformance of eDNA to investigate the taxonomic and functional diversity of fish communities.

ORAL PRESENTATION

Environmental DNA and its bycatch reveal vertebrate composition inside and outside Special Areas of Conservation in Cardigan Bay

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Two Special Areas of Conservation (SACs) have been established in the Cardigan Bay to protect various species, especially endangered fish species and Europe's largest population of bottlenose dolphins. However, the spatial usage of vertebrate in this area is not well understood. Here, we studied spatial usage of fish community inside and outside SACs using environmental DNA (eDNA) collected from 15 sites located inside Cardigan Bay SAC (CB), Pen Llŷn a'r Sarnau SAC (PLS) and the water body in between them (Outside) in June 2021. From only 45 water samples, 79 fish species were identified, including critically endangered species such as the tope shark and angelshark. Notably, a significant difference in fish composition was found between three areas (p 0.05). Common species, such as European herring, horse mackerel, sandeel, spart and pilchard were found in highest read counts, and some of them (horse mackerel and pilchard) are more abundant outside SACs. Moreover, three marine mammals: bottle-nose dolphin, common dolphin and harbour porpoise, were found in all three areas from the eDNA bycatch data, without a clear difference in spatial usage. The bottle-nose dolphin was significantly associated to flounders in network analysis, which may indicate its forging habits. Collectively, our results suggest that eDNA-based methods can be used as an efficient tool to evaluate fish spatial usage and provide a glimpse into the whole ecosystem when combined with its bycatch data. These findings also suggest that eDNA is a promising tool for evaluateing conservation efforts in marine management.

ORAL PRESENTATION

Potential and challenges of environmental DNA (eDNA) metabarcoding for assessing the ecological status of estuaries

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Estuarine ecosystems play a crucial role in supporting aquatic biodiversity, ecosystem services and human well-being. However, increasing activities and anthropogenic pressures pose threads to their sustainability. To ensure the conservation of these critical environments, the European Water Framework Directive (WFD) mandates regular assessments of estuarine ecological status. Fish are one of the biological quality elements monitored within the WFD, for which capture through trawling or other means, along with taxonomic identification are utilized. In this study, we sought to improve the assessment of estuarine ecological status by incorporating environmental DNA (eDNA) metabarcoding-based monitoring, to assess fish biodiversity and calculate the WFD-adopted AZTI's Fish Index (AFI). This study involved a comprehensive sampling strategy across 11 estuaries in the Basque Country (Spain), where eDNA samples were collected and subsequent trawling was conducted to acquire morphological data. We compared the AFI index and each of the metrics considered within based on the species detected through eDNA metabarcoding and morphological identification of trawl captured specimens. This comparison highlights advantages and limitations of each approach and provides the basics for the development of an eDNA metabarcoding based fish-quality index that could either complement or replace the traditional trawling combined with morphological identification approach. This achievement would establish the foundation for future comprehensive, non-invasive, and cost-effective estuarine ecological status assessment.

ORAL PRESENTATION

Monitoring fisheries catch and bycatch composition through on-board passive eDNA sampling

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Marine species and environments have been exploited throughout human history, leading to entire ecosystem modification, habitat degradation, and multiple species extinctions. A major direct anthropogenic pressure on the marine biome is fishing activity. Understanding catch and bycatch are crucial to enforce sustainable fisheries management, as well as improve ecosystem health. However, current methodologies to monitor fish landings are time-consuming, inconsistent, often inaccurate, and largely dependent on fishermen's good will and engagement. In this study, we deploy novel cost-effective, time-efficient passive eDNA samplers on-board Welsh fishing vessels. Methodological optimization will reveal the ideal placement of samplers aboard fishing vessels to monitor fish catch and bycatch, as well as optimal laboratory techniques and the best selection of primer sets. Comparisons with fish landing diversity, biomass, and abundance will help determine the eDNA-based passive sampler's ability to reflect catch composition and more general features of local assemblages. Upon successful implementation, we propose these novel passive eDNA samplers to be deployed on-board UK fishing vessels for routine and standardized monitoring of fish catch and bycatch, as well as to gain a better understanding of regional and temporal biodiversity patterns along the UK's coastline.

ORAL PRESENTATION

Fish and other Metazoan Biodiversity through environmental DNA

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Traditional biodiversity assessment methods often face limitations in capturing the full spectrum of species diversity in aquatic ecosystems. In response, this research harnesses the power of eDNA to provide a non-invasive, highly sensitive, and targeted approach for comprehensive biodiversity monitoring. This study focuses on elucidating biodiversity levels of fish community and other metazoans through the application of environmental DNA (eDNA) analysis in marine habitats (e.g. Celtic Sea, British Channel, North Sea). Tuna fish, as economically and ecologically vital top predator marine species, as well as other keystone metazoans species, present a compelling subject for investigation. The study employs cutting-edge molecular techniques to extract, amplify, and analyse genetic material solely from environmental samples. By utilizing eDNA markers specific to tuna fish and metazoans, this research aims to offer an understanding of their presence, distribution, and interactions within aquatic environments. The outcomes of this study contribute valuable insights into the conservation and management of tuna populations and metazoan communities, showcasing eDNA as a singularly powerful tool in marine ecological and fisheries studies.

ORAL PRESENTATION

Combining the old and the new: assessing Atlantic salmon (*Salmo salar*) abundance and habitat use in rivers using eDNA metabarcoding.

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Freshwater environments have the highest animal species richness per area, yet freshwater biodiversity has been in sharp decline during the 20th and 21st centuries due to an array of anthropogenically forced changes. Understanding how species are distributed in an environment, as well as their abundance within that environment, is vital for data driven management and conservation decisions. Therefore, effective biodiversity monitoring has never been more important. Environmental DNA (eDNA) analysis is enabling catchment and ecosystem-scale biodiversity assessment, providing data that was not possible using non-omic approaches. Yet, understanding how eDNA compares with previous non-omic methodologies of monitoring is important, not only to build trust in the insights gained, but also to explore possible limitations. Here, we focus on the Atlantic salmon (*Salmo salar*), a species that has seen decline in much of its range, despite it being a culturally, economically and ecologically important species. A previously generated 12S metabarcoding dataset from the River Conwy, Wales was utilised with samples taken longitudinally along the river at 19 timepoints between 2017-2018, in conjunction with estimated Atlantic salmon biomass modelled from rod catch records in the same period. Significant spatiotemporal relationships were identified between normalised Atlantic salmon 12S reads and estimated Atlantic salmon biomass. Significant relationships with measures of water physiochemistry were also detected. We conclude that eDNA metabarcoding can detect ecologically relevant signals of species abundance and distribution in rivers, providing powerful insights.

ORAL PRESENTATION

How far can eDNA travel into marine waters? Dynamics revealed by opportunistic water sampling

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The environmental DNA (eDNA) has been adopted as a tool for biodiversity studies in marine and fresh waters. However, to evaluate marine community composition avoiding false assignments, eDNA dynamics and transport must be considered. We investigated the level of *Salmo salar* (Atlantic salmon) DNA transport in two sites selected in a bay in the West of Ireland, and seawater was sampled in early November 2023. Site A was in an aquaculture site around a cage hosting 20000 adults of *S. salar*; site B was on a rocky beach 500 m far from the cages. 5L of surface water was filtered on 0.45 µm mixed cellulose ester (MCE) and 2 µm glass fiber (GF) filters in triplicates. At the same time, a metaprobe (Maiello et al, 2022) was deployed on both sites in duplicates to compare active and passive sampling. DNA from filters and roll-gauzes was extracted with Blood & Tissue (B&T) and Power Water (PW) kits (Qiagen). The DNA library was prepared with a two-steps PCR targeting the 12s rRNA gene. Samples were pooled after indexing, and sequenced on MiSeq Illumina (2X250PE). The demultiplexed sequences were processed with the ObiTools pipeline launched in Galaxy.eu. *S. salar* DNA was detected in site A successfully in MCE and roll-gauzes extracted with both B&T and PW kits and in GF filters extracted with B&T. The Relative Reads Abundance (RRA) of the Atlantic salmon averaged 81% due to its high abundance in the area. Conversely, only 16% RRA was observed in site B for a replicate of the MCE filter extracted with B&T, while no records were reported from other filters and roll-gauzes. Therefore, one could hypothesize that B&T extraction method is more sensitive, but further investigations are needed. This study suggests that despite the large presence of *S. salar* in the study area, the DNA decreased significantly at only 500 m from the source. Considering this, eDNA transport should be investigated further by sampling at intermediate distances from the source at different tidal conditions.

ORAL PRESENTATION

Understanding fish eDNA distribution patterns through hydrodynamic and particle tracking modelling in a dynamic estuary

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Environmental DNA (eDNA) is now a widely adopted monitoring method for biodiversity assessments, especially in aquatic habitats. One of its main limitations, however, is the knowledge gap regarding the relationship between the physical location of an animal/species (the source of eDNA) and where its DNA trace is detected (sampling location). Here, we explore these limitations, by investigating how eDNA is transported in a highly tidal estuary, the Mersey, in the Northwest of England. Periodic water sampling has been carried out across the estuary, from the mouth (marine) to the upper reaches (freshwater). Metabarcoding has been carried out using the Tele02 primers, targeting a ~167 bp fragment of the 12S gene. In parallel, we developed 2D-hydrodynamic and particle tracking models (PTM) of the estuary, which allow us to simulate how eDNA particles move in this environment due to currents and tides. This novel approach allows for spatial ranges of eDNA to be visualised, and by running the PTM backwards in time and space from a sample point, we can identify potential eDNA source locations. This multi-disciplinary approach will allow us to better understand the fate of eDNA, and therefore, design a tailored sampling approach that maximises efficiency and reduces the costs and effort of monitoring a complex estuary. This will ultimately facilitate the routine monitoring of fish biodiversity in a rapidly recovering system.

ORAL PRESENTATION

Flatfish Distributions Across the Northeast U.S. Continental Shelf: Comparing Bottom Trawl and eDNA Metabarcoding Results

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Environmental DNA holds promise for monitoring biodiversity in dynamic ecosystems and may have broad applications for resource assessments. Here, we evaluate the sufficiency of a common eDNA mitochondrial marker (i.e., the Riaz 12S primers) to match all 47 pleuronectiform species (8 families) documented from North Carolina to the Gulf of Maine. For this marker, 51% of the 47 species lack reference sequences; only 21 full and 2 partial sequences were available in GenBank (https://www.ncbi.nlm.nih.gov) as of September, 2022. We also compared flatfish taxa observed by a fishery-independent bottom trawl survey to flatfishes observed using the Riaz 12S primers across the same sampling range (35.4 – 43.0ºN) of the US east coast during Fall, 2019. The bottom trawl survey identified 12 flatfish taxa (3 identified as sp.) using morphological traits. The eDNA metabarcoding survey using filtered water samples identified 11 taxa (2 identified to family). Five common species were identified in both surveys. Much less water was strained by the eDNA method to reveal the same biodiversity: 301 20-minute trawl tows vs. a total of 346 liters of filtered seawater for eDNA metabarcoding. Additional reference sequences in GenBank are needed to improve estimates of flatfish diversity. Regarding fishery applications, 5 flatfishes with formal stock assessments are represented by sequences in GenBank, as well as an additional 2 sequences that can only be identified to family (Pleuronectidae). An initiative by NOAA Fisheries' National Systematics Laboratory, Smithsonian, will add reference sequences from vouchered specimens to GenBank. Use of multiple markers will also improve taxonomic identifications

ORAL PRESENTATION

eDNA-based assessment of highly invasive Armoured Sailfin Catfish (*Pterygoplichthys* sp.) and African sharptooth catfish (*Clarias gariepinus*) in the Water Bodies of Eastern Ghats, India

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Early detection of invasive species is crucial for effective control of the potential damage they can inflict on the ecosystems. With a lot of limitations in traditional detection methods of surveys, environmental DNA assays can offer a robust alternative. The spread of invasive *Pterygoplichthys* sp. and *Clarias gariepinus* have become a cause for concern in biodiversity-rich countries like India. Despite this, comprehensive studies on the prevalence of this invasive species are limited. The Eastern Ghats of India remain under-explored with a high potential for supporting diverse lifeforms. In this study, we have designed and optimized an eDNA-based quantitative PCR assay to map the presence and spread of the two most invasive species in selected freshwater ecosystems of the Eastern Ghats. We could assess both the species of invasive catfish in the sampled locations. Our findings revealed these species in more than 60 % of the total sampled locations. This study can be further extended to larger geographical areas, to manage invasion and conserve the diversity of the freshwater ecosystem.

ORAL PRESENTATION

Assessing the impact of genetic markers and sampled water volume in eDNA-based detection of marine fish species in a large aquarium

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Large public aquaria provide an ideal controlled environment with known resident species for testing environmental DNA (eDNA) metabarcoding procedures for fish detection. In this study, we assessed the influence of genetic markers (COI, 12S rRNA, 16S rRNA) and sampled water volume (0.5, 1.0, 2.5, 5.0, and 10L) in eDNA-based detection of 61 marine fish species (25 families) present in the Lisbon Oceanarium's 5 K million-liter tank. We filtered triplicates of each sampled water volume, and generated amplicon libraries using the following primer pairs: 2 primer cocktails (COI-A and COI-B) and the primer-pair mlCOIintF/LoboR1 for COI; the cocktail MiFish U-E for 12S; and Fish16sFD/16s2R for 16S. Illumina MiSeq reads were processed and analyzed with PIMIFISH, and taxonomically assigned to fish species. All markers combined detected 89% of the fish species present, but individually each marker did not perform better than 75% for COI, 69% for 16S and 61% for 12S. However, considering the proportion of detected species relative to the availability of reference sequences, 12S performance increased to 86%, and 16S to 77%. Also, as much as 10% of the species were detected exclusively by one of the markers. Additionally, increasing water volumes resulted in a growing number of species detected for all primers in lower water volumes, with signs of saturation observed in higher volumes. Combining all markers, it was possible to detect up to 82% of the species with a volume of 5.0 L. Our research shows the potential limitations of using a single genetic marker in eDNA-based monitoring, as it may lead to systematically missing a portion of marine fish species. Besides, achieving optimal monitoring requires a balance between maximizing the volume of sampled water while also maintaining the practical feasibility of the filtration process

ORAL PRESENTATION

Understanding the detection of fish life stages from eDNA metabarcoding across seasons

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Environmental DNA (eDNA) metabarcoding approaches are transforming the way we understand marine biodiversity. In addition to providing increasingly reliable species inventories, eDNA metabarcoding is also making it possible to study the functional diversity of an ecosystem and to evaluate conservation measures from a new angle. This macro-organism eDNA can come from multiple sources and reflect the presence of different life stages such as eggs, larvae, juveniles or adults. Studies detecting a species on the basis of its DNA implicitly interpret its presence with the adult's role in the ecosystem. However, fish may use different habitats depending on their life stage and perform different functional roles at each stage. Different life stages of the same species therefore respond differently to fishing pressure or, conversely, to protection. This study examines the extent to which the different life stages of fish can be detected by eDNA metabarcoding, and what influence these detections have on the way we interpret the presence of a species and its functional role in the ecosystem. This is done by combining complementary sampling methods targeting the detection of adult and juvenile fishes (underwater visual census) or larvae and eggs (plankton tow sorting and metabarcoding) with eDNA metabarcoding, conducted across four seasons in the Mediterranean Sea to target the same species at their different reproductive stages.

ORAL PRESENTATION

Investigating fish community composition and its seasonal changes in the Oslo fjord through eDNA metabarcoding

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In the face of global ecosystem changes driven by anthropogenic activities, effective biomonitoring strategies are crucial for mitigating impacts on vulnerable aquatic habitats. Time series analysis underscores a great significance in understanding the dynamic nature of marine ecosystems, especially amidst climate change disrupting established seasonal patterns. Focusing on Norway's Oslo fjord, our research utilizes eDNA-based monitoring for temporal analysis of aquatic biodiversity during a two year period, with bi-monthly sampling along a transect. We successfully detected 63 unique fish species, including several commercially important species. Using relative abundance through metabarcoding read counts, we found a substantial increase of species during specific migratory cycles, highlighting the efficacy of eDNA metabarcoding for fish composition characterization. Seasonal dynamics for certain species exhibit clear patterns, emphasizing the method's utility in unraveling ecological complexities. eDNA metabarcoding emerges as a cost-effective tool with significant potential for fish community monitoring for conservation purposes in dynamic marine environments like the Oslo fjord, contributing valuable insights for informed management strategies.

ORAL PRESENTATION

Characterization of the mesopelagic fish layer in Irish waters: a multidisciplinary approach integrating acoustic signatures, environmental DNA and direct catch data

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The mesopelagic fish layers are of interest due to the potential exploitability of their macrofauna, hence profiling their fish community is crucial to enable the sustainability of future fishing practices. In this context, the Multidisciplinary Mesopelagic Scouting Survey (M2S2) was carried out by the Marine Institute in September 2022 along the Irish shelf break, where it applied a multidisciplinary approach by integrating vessel-mounted acoustics, direct catch (trawl) data and environmental DNA (eDNA) analysis. Specifically, a workflow for near-real time eDNA metabarcoding analysis of fish communities was developed using a portable DNA sequencer, thus integrating omics approaches into stock assessment calibration aboard the research vessel. During M2S2, eDNA sampling and trawling were carried out when acoustic signatures (echotraces) of interest were detected. Catch data showed that the targeted layers consisted almost exclusively of the young-of-the-year cohort of a mesopelagic fish (*Maurolicus muelleri*), with little diversity in the hauls. Molecular data reflected the high prevalence of *M. muelleri*'s eDNA, while also detecting species not caught in the trawls. Catch and eDNA data were compared, showing low overlap between the species detected with each technique. However, integrating data from both methods outlined a diverse mesopelagic layer, dominated by *M. muelleri*. M2S2 showed how integrating omics methods in a multidisciplinary fisheries assessment led to a more comprehensive understanding of the upper mesopelagic layer. The comparison between trawling and eDNA data highlighted advantages and current limitations of each approach, but their integration produced ground truthing data to describe the fish community composition of target echotraces. In addition, the developed near-real time on-site eDNA metabarcoding workflow represents an accessible and valuable tool that could be integrated into future assessment and management of the mesopelagic fish layer.

ORAL PRESENTATION

Validating pelagic fish identity and abundance from acoustic backscatter using a multi-species eDNA approach

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High resolution hydroacoustic sampling paired with regular midwater trawling is a common method used to map and quantify pelagic fish. Although midwater trawling is a direct method of sampling pelagic fish, it is also expensive and does not always guarantee a representative sample of the fish schools. Using eDNA to help experts validate the identity and abundances of fish species from hydroacoustics is an enticing prospect for future fish monitoring strategies, unshackling the restrictions of current trawl-based validation methods.

Environmental DNA (eDNA) is a method of detecting marine pelagic fish species that is unburdened by the catchability bias induced by avoidance behaviours that affects pelagic fish detection from midwater trawling. In this study we combined amplicon reads from eDNA samples collected during two annual pelagic monitoring surveys around the South-West coast of the UK, with hydroacoustic data recorded across multiple transects. To ensure we use samples that have capture a majority, and least bias, aggregations of the pelagic communities the methods, times, and depth of eDNA collection were analysed. For each hydroacoustic sample point we partitioned the hydroacoustic backscatter values by the target pelagic fish species; European pilchard (*Sardina pilchardus*), European anchovy (*Engraulis encrasicolus*), Atlantic herring (Clupea harengus), Atlantic horse mackerel (*Trachurus trachurus*), boarfish (*Capros aper*) and sprat (*Sprattus sprattus*), by using the proportions of species found in the eDNA and the midwater trawl catch. When we compared the eDNA and midwater trawling backscatter values for each species we found species-specific variations in the significance of the correlations between the two methods. We also found that the variations between these two methods were consistent across the distances between the eDNA sampling location and the hydroacoustic sample locations.

ORAL PRESENTATION

Estimating small pelagic fish stock abundance using environmental DNA

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Small pelagic fishes, such as anchovies and sardines, play important ecological roles in marine ecosystems and encompass some of the economically most important fisheries worldwide. Other little-known species, such as mesopelagic fishes, have been recently proposed as potential commercial targets due to their high biomass. In both cases, accurate abundance estimates are essential either to guarantee global sustainable fisheries management or to develop strategies for emerging imminent exploitation resources. Although trawling coupled with acoustics is a widespread approach to estimate the abundance of small pelagic fish, this method is prone to potential biases derived from coverage limitations, and is invasive, as it relies on catches for species identification. Alternatively, the analysis of fish environmental DNA (eDNA) has the potential to provide information about fish distribution and abundance; yet this approach has so far not been implemented for abundance estimation in the context of fisheries stock assessment, most likely due to a lack of communication between geneticists and assessors to develop eDNA-derived abundance indices. Here, we have analysed ~300 eDNA samples collected over 6 years (2018-2023) in the Bay of Biscay to estimate the distribution and abundance of three small pelagic species: the European anchovy (*Engraulis encrasicolus*), the European sardine (*Sardina pilchardus*) and the mesopelagic Mueller's pearlside (*Maurolicus muelleri*). This work exemplifies the value of eDNA analysis as a cost-effective approach for biomass estimation and highlights the opportunity to integrate genomic methods into fisheries management.

ORAL PRESENTATION

Environmental DNA outperforms trawling in revealing fish composition in a Biosphere Reserve Lake in Mongolia

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The ecosystems in Mongolia are relatively more vulnerable under the threats of climate change because of local singular ecological structure. Hulun Lake, located at the tri-border area of three countries, is recognized as one of World Biosphere Reserves by UNESCO and Ramsar Convention. As the largest grassland lake in China, it plays a crucial role in preserving Hulunbuir grasslands' biodiversity. Despite fish occupying multiple trophic levels with essential ecological service value, their composition remains poorly explored due to underdeveloped local society. Here, we conducted a comparative study of environmental DNA (eDNA) survey with traditional trawling survey at 25 locations across Hulun Lake in June 2023. The eDNA metabarcoding reveals a total of 67 fish species, in stark contrast to the mere 13 species detected by trawling nets. Despite this disparity, the abundance of eDNA reads (log-transformed) exhibited a significant correlation with fish abundance by trawling. Notably, eDNA detected nine invasive fish species that went unnoticed by trawling, suggesting a potential early stage of invasion. In addition, eDNA detected six endangered species while traditional trawling surveys only identified two. A significant difference in fish composition from east to the west side of the lake was observed (p 0.05), but no significant difference was seen from the north to the south part of the lake, likely attributed to its main water supply coming from the southwest and southeast. Notably, the result from eDNA survey was more homogeneous, plausibly due to genomic material dispersal in the lake. In conclusion, this study suggests that eDNA metabarcoding can serve as a semi-quantitative approach for fish diversity surveys and a valuable supplement to traditional fish surveys.

ORAL PRESENTATION

Marine Biodiversity Monitoring: Insights from a 12-Year eDNA Time-Series

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Here, we present a groundbreaking 12-year project significantly advancing long-term marine biodiversity monitoring using environmental DNA (eDNA). The analysis of 460 weekly eDNA samples has unveiled unprecedented insights into UK marine biodiversity. Utilising three complementary DNA barcode markers for fishes, sharks, and marine mammals, the project achieved a remarkable 100% sample-to-result success rate for all marker genes in all 460 samples, highlighting the reliability of eDNA based methodologies. A notable innovation was the automated filtration of over 50 litres of seawater per sample over two tidal cycles. This approach not only increased DNA sample quantity but also minimised sample contamination risks compared to other DNA-based methods. Crucially, eDNA outperformed conventional trawling methods, detecting 152% more species, including 133 unique fish species. These findings hold significant value for regulatory decision-making, particularly in meeting sustainability requirements such as Biodiversity Net Gain (BNG), Environmental, Social, and Governance (ESG) criteria, and the Corporate Sustainability Reporting Directive (CSRD). This pioneering work in eDNA-based marine biodiversity monitoring has profound implications for informed decision-making in marine survey operations, offshore energy sectors, and government marine biodiversity regulation. It underscores the transformative potential of this technology in advancing our understanding of marine ecosystems and aligning with sustainability and conservation goals.

ORAL PRESENTATION

Divergent Temperature Tolerance Revealed in Atlantic Cod Ecotypes

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Climate change and environmental alterations pose significant challenges to global biodiversity. Ecotypes, representing adaptive strategies within a species, offer a mechanism for adaptation and survival. This study focuses on Atlantic cod at the southern edge of its range, particularly in the Skagerrak region, where climate change impacts are evident. Two distinct ecotypes—a fjord and more oceanic oceanic ecotype—have been identified here. Through whole-genome analysis and a 20-year genetic time series of approximately 11,000 juvenile cod, we investigate: 1) the genomic divergence between these ecotypes, and 2) the differential impact of temperature on them. 3) the correlation of frequency of specific loci with temperature tolerance. Our results show that the fjord ecotype seems more resilient to higher temperatures than the oceanic ecotype maintaining growth over the entire temperature range experienced, highlighting the importance of preserving fjord populations. As temperatures rise, the fjord ecotype could provide temperature-tolerant genes to the economically important offshore population. This long-term genetic and ecological study enhances our understanding of the interactions between genetics, ecology, and climate change. It calls for a shift in conservation and management strategies for marine populations in the face of climate change.

ORAL PRESENTATION

Whole genome analyses of archival fish specimens to understand demography and thermal adaptations

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Climate change is expected to impose strong selection pressures on ectotherm populations. Evidence shows that temperature increase induces phenotypic changes in fish, e.g. faster growth and smaller size at maturation. While foundations for fish evolution to occur in response to warming have been observed, solid cases of warming-induced genetic changes in fish and the underpinning molecular mechanisms are not well understood. Here, we use whole genome sequencing of 231 archival bone and muscle specimens of European perch (*Perca fluviatilis*) to investigate the genetic consequences of long-term warming. The perch specimens, with individual age and size measured, were collected from 1977 to 2022 in a system where one population has been subjected to substantial warming caused by nuclear power plant operation, while the other adjacent population has been experiencing natural thermal regime in parallel. There are a few unique aspects of this system: (1) the experimental set-up on an ecosystem level, naturally creating one heated and one 'control' treatment; (2) the two perch populations in question were once dwelling in one homogenous habitat before part of the coastal habitat was split into an enclosure and became the heated treatment from 1980; (3) the extent of artificial warming, with a temperature difference of 5-10 °C, enable us to strongly infer that any observed differences between populations have been caused by warming. We analyze SNPs from these perch populations of distinct thermal origins and identify selective sweeps among the populations and over time. We discuss association of SNPs to thermal adaptation, the possible causes of genetic differentiation, and potential warming-induced fish evolution. We advocate application of revolutionary genomic technologies on archived specimens to provide knowledge for better predictions of future ectotherm population dynamics amid the challenges posed by global warming.

ORAL PRESENTATION

Genomic insights into run timing in Canadian Atlantic salmon (*Salmo salar*): Assessing vulnerability to climate change

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With global environment change, mismatches between seasonally timed movements and environmental conditions are increasingly impacting species survival and persistence. Atlantic salmon (*Salmo salar*) undergo long-distance marine migrations culminating in a return to natal rivers, the timing of which varies within and among populations. Global declines of salmon suggest that phenological mismatches could be a factor contributing to these declines. The extent of which depends on the underlying genetic architecture of migration timing, as well as projected climate change impacts, both of which are poorly understood in Atlantic salmon. To address this knowledge gap, we used lc-WGS to explore the genomic basis of run timing in Atlantic salmon in eastern Canada, as well as examining maladaptation of these candidate loci through genomic offsets (a measure of climate vulnerability) to determine the extent of evolutionary change required to adapt to predicted climate change. We find strong association of individual day of return with Ppfia2 on chromosome 17, a gene previously identified as being important for long-distance migration in birds. Genomic offsets of candidate loci varied across the landscape, with the most northerly distributed population being the most maladapted to predicted climate change. These findings highlight the potential for incorporating genetic information of locally adapted phenotypes into conservation management plans to better identify those populations most susceptible to climate change.

ORAL PRESENTATION

Extrinsic and intrinsic drivers of population structure in Pacific herring

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Populations of high gene flow species may be isolated by intrinsic factors, such as chromosome inversions, or extrinsic factors, such as adaptation to different environments or barriers to gene flow. The relative importance of these factors may determine responses to global change and exploitation. Pacific herring (*Clupea pallasii*) is a culturally, ecologically, and economically important species that shows a surprising level of population and phenotypic diversity at relatively small geographic scales. In recent decades, this diversity has declined considerably. We investigated genomic differentiation among spatially and phenologically distinct spawning aggregations of Pacific herring by low-coverage whole genome sequencing yielding genotype likelihoods for over 600,000 loci. Our analyses suggested contrasting mechanisms of genetic differentiation between the three spawning groups: early spring spawners were differentiated from other spawn groups primarily at several large chromosome inversions, while winter and late-spring spawners had very similar inversion frequencies but showed selective differentiation in several narrow sections of the genome that were independent of inversions. These results indicated that structural genomic variants drive some, but not all, of the genetic differences between the different spawning phenotypes, and that both intrinsic and extrinsic drivers cause population structure. These patterns may limit an adequate response to climate change and may require a switch from spatial to temporal management.

ORAL PRESENTATION

Genclim: evolutionary and socioeconomic consequences of shifting distribution ranges in commercially exploited marine fishes

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Ongoing climate change is rapidly transforming marine ecosystems and communities throughout the world's oceans. These range shifts mean that commercially important fishery species are likely to cross geo-political boundaries, increasing the likelihood of mismatches between current fishing practices (and policies) and future distributions. Forecasting models that predict range shifts are thus essential to anticipate and mitigate potential fisheries conflicts and the subsequent socio-economic impacts of a moving resource. However, forecasting models have thus far mostly been applied at a species level. In our project, GenClim, we are employing genomic tools to assess population connectivity, levels of genomic diversity and potential local adaptation in three important commercial species across the eastern Atlantic: the European hake (*Merluccius merluccius*), the southern Africa deep-water hake (*M. paradoxus*) and anchovy (*Engraulis encrasicolus*). These data feed into both ecological forecasting models (based on a jSDM framework), and bioeconomic models, to assess if genomic information increases forecasting abilities to predict climate-mediated range shifts, as well as their evolutionary, ecological and socio-economic consequences. Our genomic results reveal different population sub-structuring patterns among the three species between the northeastern and southeastern Atlantic. Similarly, preliminary ecological forecasting models reveal different range shift patterns when considering species as a whole vs. when species are portioned into genomic-based populations. These findings suggest that genomic information should be taken into consideration in range shift predictions, as well as in bioeconomic modelling.

ORAL PRESENTATION

Potential inversions among small brook trout (*Salvelinus fontinalis*) populations of Nova Scotia, Canada

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Genomic structural variants, specifically chromosomal inversions, are an exploding area of research due to the decreased cost of next-generation sequencing methods such as low-coverage whole genome sequencing (lcWGS). The discovery of structural variants such as chromosomal inversions often allows us to better understand how species and populations are adapting to their environment. Understanding the role of inversions in adaptation among small, isolated populations is an important addition to robust conservation strategies, as many studies looking into the role of inversions in adaptations to date have been done on populations with high levels of gene flow. Brook trout (*Salvelinus fontinalis*) are economically important and one of the top sportfish in Nova Scotia, yet their limited thermal tolerance makes them vulnerable to climate change. We performed lcWGS on N=192 brook trout from nine small, isolated streams in Nova Scotia, Canada. The western streams differ from all other streams in water temperature, streamflow, and geology. We tested the indirect inversion detection framework and found evidence of four potential inversions among individuals in only western streams. We report on the evidence of four potential inversions using methods of linkage disequilibrium (LD), heterozygosity, and nucleotide diversity.

ORAL PRESENTATION

Genomic perspectives on adaptation and biological invasion: A comparative study on catfishes

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Invasive species pose significant ecological and economic threats by outcompeting native species and disrupting ecosystems. Despite extensive research on the ecological processes driving biological invasions, the role of genome evolution and natural history of invasive species in facilitating successful invasions remains poorly understood. In this study, we investigate the genomic adaptations underlying the invasive potential of catfishes (Order: Siluriformes), a highly diverse taxonomic group occupying various aquatic habitats. We de novo assembled high-quality genomes of two catfish species, *Clarias gariepinus* and *Clarias dussumieri* through a hybrid approach utilizing both Oxford Nanopore long reads and Illumina short reads. We reconstructed the phylogeny and population histories of Siluriformes taxa by incorporating publicly available genomes of other 28 catfish species, including those declared as invasive. We then performed genome wide analysis on the evolution of gene families associated with adaptation, including dispersal, reproduction, and interaction with pathogens. By comprehensively characterizing the genomic landscape of invasive catfish species, we identified numerous signatures on the evolution of genetic mechanisms facilitating adaptation to diverse environmental conditions. Furthermore, this study contributes insights into the evolutionary dynamics of catfishes as a taxonomic group. Understanding the genomic basis for adaptation in invasive species complements the knowledge from the ecological processes driving invasions which is crucial for managing invasive species.

ORAL PRESENTATION

Evidence of inbreeding depression for morphological traits in European hake

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European hake (*Merluccius merluccius*) is an economically important species that have faced an historically high fishing pressure. As a consequence of the overfishing and drastic population declines in abundance, relevant management measures were implemented to help rebuild stocks across Europe. Nonetheless, the impact of the exploitation on the genetic diversity and therefore the adaptive potential of European hake to drivers as climate change remains a concern, and continued monitoring and management efforts are necessary to ensure their sustainability. In addition, the combined effects of anthropogenic activities and environmental changes are expected to alter the phenotypic and genetic composition of the populations. Under this context, the objective of this study was to evaluate the genetic status of wild populations of European hake and to predict the expected response in body length and weight because of exploitative selection. For that, we obtained genotypes through RAD-sequencing for three populations comprising Atlantic northern and southern stocks and western Mediterranean and estimated the levels of inbreeding using different genomic coefficients. Our preliminary results suggest the occurrence of potential inbreeding depression for the traits analysed, being this effect more evident for females. Given that females typically exhibit greater size and weight, they are the main target of the size-selective fisheries exploiting hake. The results derived from this study have an important value to adjust management practices concerning fisheries, with the aim of maintaining the genetic and ecological integrity of natural populations.

ORAL PRESENTATION

Unexpected variation in genetic diversity in a small Atlantic Salmon population: the role of anthropogenic impacts

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Anthropogenic pressures can dramatically alter the demography and phenotypic composition of natural fish populations. Evolutionary dynamics can also be affected, but we currently lack understanding of patterns and drivers of contemporary evolution at a genomic genetic level (i.e., the scope for future evolutionary responses). Without these insights, we cannot accurately predict future vulnerabilities. In order to understand the complex processes of adaptation to anthropogenic impacts in Atlantic salmon (*Salmo salar*), we are using a multidisciplinary approach to identify evolutionary responses of natural populations to climate change, overfishing and introgression with cultured fish. Our specific aim is to evaluate the relative contribution of climate to historical population-level genetic and demographic changes in freshwater and marine environments. Using ecological genomics and quantitative genetics on a six-decade long sampling programme from migrating Atlantic salmon in Ireland, we work towards providing timely and critical insights into the past and future evolutionary dynamics of Atlantic salmon. Preliminary results suggest that supplementing a natural population from a local sea-ranching stock could have increased genetic diversity over time despite the reduction in the size of the natural population.

ORAL PRESENTATION

Poolseq and dynamic outlier thresholding uncover novel and confirmed targets underlying humic-driven adaptation in Eurasian perch

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Understanding the genetic mechanisms underlying adaptation is crucial in population genetics and evolutionary biology. Recent advancements in high-throughput sequencing have significantly enhanced our capacity to explore these mechanisms by enabling the detection of both neutral and adaptive regions across the whole genomes. Pooled sequencing presents a cost-effective alternative for SNP discovery and allele frequency estimation, although accurately modeling the null distribution and determining significance thresholds for outlier detection remain challenging tasks. The Eurasian perch (*Perca fluviatilis*), a keystone widely distributed mesopredator thriving in acidic, humic conditions, provides a unique opportunity to study adaptation to this extreme environment. We used pooled whole-genome sequencing to analyze 42 populations and ~900 K SNPs. Additionally, we introduced a novel dynamic outlier thresholding method to identify molecular targets and potential mechanisms behind adaptive changes. Our analysis revealed overrepresentation of SNP annotation categories such as upstream, downstream, synonymous, 5’UTR, and 3’UTR among outliers, while splice region & synonymous, non-synonymous, intergenic, and intron categories were underrepresented. Furthermore, Gene Ontology (GO) analysis showed enrichment of terms related to the nervous system, synaptic processes, cell adhesion, and channel activity among outliers. This study also confirmed several genes previously implicated in humic adaptation, including PHC1, SDK1, WDR19, CDON, CHD7, MYLIP, and OPN1LW. Furthermore, novel genes such as CLCN1, ARID3B, SYT5, PNMT, PLTP, PHACTR4, TBX2, IFT80, IFT88, and IFT172 were uncovered, shedding new light on their potential role in humic adaptation. These findings contribute to a deeper understanding of the genetic mechanisms underlying adaptation to acidic, humic environments and demonstrate the power of poolseq to screen large number of populations at whole genome level.

ORAL PRESENTATION

Genetic differentiation along an ocean/river gradient captures the signature of intragenerational selection in the European eel (*Anguilla anguilla*)

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European eel has received considerable attention in recent decades due to its significant decline. This catadromous species presents numerous estuarine migratory tactics, ranging from residency in marine water (non-migrant, NM), to various degrees of upstream colonization through estuarine and freshwater ecosystems (migrant, M). Variation in individual physiological plastic traits, such as energetic status, only partially explain the difference in M vs NM tactics. Here, we investigated the genomic divergence between M and NM glass eels. First, in a natural population along a gradient extending from the ocean to the dynamic tidal limit of the Adour River, six samples were collected, at two extreme sites (Ocean vs Upstream) and over three years (2019, 2020 & 2022). We hypothesize that upstream pools are mostly composed of M whereas ocean pools are a mixture of M and NM glass eels. Moreover, 35 M and 35 NM glass eels were identified in an experimental device that mimics alternating tidal currents. Whole genome pool sequencing of the eight pools (~35 ind. each) revealed 6.28 10^7 SNPs variants. Two different approaches, BayPass and PCAdapt, found respectively 0.02% and 0.3% of SNPs with a significantly higher genetic differentiation between Ocean vs Upstream pools (FST=0.67 on average) than the pangenomic estimate (FST=-0.006). Using a local score approach, BayPass filtered 202 outliers in 62 genomic regions of high genetic differentiation, while PCAdapt filtered 2394 outliers in 92 large genomic regions. A first functional analysis of these genomic regions shows that immune system and several cellular processes could be involved in spatial sorting along estuary gradients. Combined with studies in *A. rostrata*, our results support that variation in eel migration capacity is partly genetically determined. Thus, while panmixia maintains high level of genetic diversity, spatial sorting could promote intra-generational genetic divergence between habitats of European eels.

ORAL PRESENTATION

Whole genome resequencing reveals polygenic signatures of directional and balancing selection on alternative migratory life-histories in brown trout

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Migration in animals and associated adaptations to contrasting environments are underpinned by complex genetic architecture. Here we explore the genomic basis of facultative anadromy in brown trout (*Salmo trutta*), wherein some individuals migrate to sea whilst others remain resident in natal rivers, to better understand how alternative migratory tactics (AMTs) are maintained evolutionarily. To identify genomic variants associated with AMTs, we sequenced whole genomes for 194 individual trout from five anadromous-resident population pairs, situated above and below waterfalls, in five different Irish rivers. These waterfalls act as natural barriers to upstream migration and hence we predicted that loci underpinning AMTs should be under similar divergent selection across these replicate pairs. Our analysis revealed a highly polygenic adaptive divergence between anadromous and resident populations, encompassing 228 differentiated genomic regions (10kb windows). These regions were associated with 216 genes involved in various processes crucial for AMTs, including energy homeostasis (insig1), osmoregulation (KCNIP4), circadian rhythm (per3), thermal tolerance (CERK), neural function (grm6b) and sensory perception (ora4, cdh23). Importantly, these outlier regions exhibited higher diversity than the genomic background, particularly in the anadromous group, suggesting balancing selection may play a role in maintaining genetic variation. Further investigation pinpointed numerous regions across the genome potentially under long-term balancing selection (apparently unrelated to sexual antagonism over viability) associated with genes related to immunity, cellular homeostasis, and energy metabolism. Overall, the results from this study provide important insights into the genetic architecture of migration and the evolutionary mechanisms shaping genomic diversity within and across populations.

ORAL PRESENTATION

Next-Generation Sequencing (NGS) applications for seafood authentication and sustainability

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Processed seafood products have become particularly popular among modern consumers as a time-saving and effective alternative to enjoy the health benefits of fish in the human diet. However, the complex seafood supply chain, coupled with the lack of morphological characteristics, creates opportunities for species substitution. The application of Next Generation Sequencing tools to seafood products can play a strategic role in authentication and traceability, as well as an innovative inspection tool to ensure quality and safety. In this study, the DNA metabarcoding approach targeting 12S and COI mitochondrial gene markers was applied to assess the species composition of twelve breaded seafood products labelled as made by single species (eleven *Gadus chalcogrammus* and one *Pleuronectes platessa*). All samples were collected in Italy but sourced from a Dutch processor. Molecular results highlighted the presence of 8 marine taxa and only one sample resulted as mono-species with both primer pairs, while in 11/12 samples undeclared species were detected in addition to that declared on the label. The overall characterization highlighted untraced species as hake (*Merluccius spp*), saithe (*Pollachius virens*), haddock (*Melanogrammus aeglefinus*), Atlantic Cod (*Gadus morhua*), as well as pike perch (Sander lucioperca) and lemon sole (*Microstomus kitt*). Also, the 12S primer pair identified the presence of chicken, while the COI marker detected other non-marine taxa as fungi and mites. The study demonstrates that the combined use of molecular markers allowed a complete characterization of the processed seafood products with the possibility to identify unexpected and untraced taxa, raising concerns regarding food safety and sustainability issues. Therefore, DNA metabarcoding tests have the huge potential to enforce traceability systems of complex seafood, opening a new era of food control systems in the industry sector to combat fraud and protect consumer rights and marine ecosystems.

ORAL PRESENTATION

DNA barcoding for identification of freshwater fish species in the River Beas, India

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One of the major rivers of the Indus River system, the Beas River is situated in Himachal Pradesh, India, and is home to a wide variety of freshwater fish species. In order to raise awareness of the critical need to maintain fish populations and their resources, we employed DNA barcoding to create the first freshwater fish species inventory for the river Beas. We discovered 43 species, grouped into 31 genera, 16 families, and 10 orders, based on the sequencing of 203 specimens from Beas River. 485 sequences of Indian origin were taken from BOLD, generating a dataset of 688 sequences, which was then used to examine the genetic divergence and phylogeny of the identified species. Our findings consistently revealed a hierarchical increase in the mean K2P genetic divergence within species (0.80%), genus (9.06%), and families (15.35%). The proposed species and their phylogeny were identified using Automated Barcode Gap discovery, Neighbour Joining, and Bayesian inference consensus tree methodologies. With just a few exceptions, most of the taxa were effectively delimited. Six species were found to have considerable intra-specific divergence (>2%) in the results, which may indicate the existence of sister species and incorrectly recognized sequences in online databases. The current DNA barcoding-based inventory of the Beas River's freshwater fish species offers thorough insights into vulnerable and economically exploited species. We advocate the implementation of specific measures to safeguard genetic resources and biodiversity to ensure the sustainable use of aquatic resources in the Beas River.

ORAL PRESENTATION

Molecular Barcoding of Fish Larvae Reveals Intergenerational Connectivity Across a Seascape

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Fish larvae possess few morphological diagnostic characters that hinder precise species discrimination via morphology alone. Fortunately, high-throughput DNA barcoding has become more accessible through advancements in technology—including the improvements in PCR technology, sequencing speed and chemistry (e.g. MinION, Oxford Nanopore Technology), as well as data analysis (e.g. ONTbarcoder2.0). The associated use of a “reverse-workflow”—where samples are barcoded prior to morphological species sorting and taxonomic validation—for specimen processing is straightforward, inexpensive and can be conducted for a large number of samples easily, which is especially useful for plankton tow sampling of fish larvae. By expediting the taxonomic identification process, the distribution and movement of fish species can be estimated more effectively. Here, a total of 3022 fish larval specimens from plankton tows across four sites in Singapore were DNA barcoded and sorted into 343 molecular operational taxonomic units (mOTU). The diversity of fish larvae across sites are discussed in relation to the diverse habitats that their respective adults are found to better understand the migration of marine fishes. We show that accurate taxonomic identification of fish larvae allows for a more precise sampling of the species diversity across a seascape and leads to better understanding of fish connectivity.

ORAL PRESENTATION

Unveiling diversity and seasonal variations in ichthyoplankton communities using DNA metabarcoding

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Ichthyoplankton monitoring plays a pivotal role in fish stock assessments by presenting crucial insights into spawning grounds, seasonal patterns, recruitment dynamics, spawning stock size, and regional ichthyofauna dynamics. Traditionally, taxonomic experts identify fish eggs and larvae through morphological examination in a challenging task due to the similarities between species' characteristics. To address these limitations, DNA metabarcoding is emerging as an efficient and cost-effective complement, capable of improving species identification accuracy. To evaluate the effectiveness of DNA metabarcoding in identifying fish species and its capability to discern seasonal variations in regional ichthyofauna, monthly samplings were carried out over 13 months in three points of the Guadiana River estuary, located in the southeastern part of Portugal. Each sample was subdivided and specifically preserved for molecular and morphological species identification, allowing the comparison of diversity identified between both approaches. 98 fish species were successfully identified from the analysis of 39 ichthyoplankton samples. DNA metabarcoding overperformed the traditional method in terms of taxa detected (92 vs 28) and provided solutions for certain identifications made through morphology at higher taxonomic levels (family or genus). Employing a multi-molecular marker approach (COI, 12S, and 16S) was crucial for uncovering the maximum possible diversity, as 21 species were exclusively identified by a specific marker. Furthermore, DNA metabarcoding successfully exposed temporal variations in species richness and ichthyofauna composition across different seasons, revealing higher diversity during summer compared to other seasons. In summary, the results were highly promising, confirming the potential of DNA metabarcoding for high-throughput accurate identifications of fish species in ichthyoplankton thereby supporting fish stock assessment and management decisions.

ORAL PRESENTATION

Phreatic puzzles: remarkable patterns of cryptic diversity and distribution in fossorial and aquifer-dwelling fishes of southern India

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The lateritic aquifers of southern peninsular India harbour a unique assemblage of enigmatic stygobitic fishes which are encountered very rarely, either when they surface during the digging and cleaning of homestead wells, or when they accidentally find their way into household water distribution systems. Here, we focus on two of the most unusual members of this assemblage: *Horaglanis* – a genus of tiny, blind, pigment-less catfish, and *Rakthamichthys* – a genus of whiplike, blind eels. A six-year exploratory and citizen-science backed survey supported by molecular phylogenetic analysis and species-delimitation approaches using the mitochondrial cox1 gene, have revealed novel insights into the diversity, distribution and population structure of both these genera. *Horaglanis* is characterized by high levels of intra-specific and inter-specific genetic divergence, with phylogenetically distinct species recovered >7.0% genetic-distance threshold. In contrast, a phylogenetic analysis and multiple species delimitation approaches revealed the presence of 11 distinct genetic 'lineages' within *Rakthamichthys*, separated by an intra-lineage genetic divergence between 5.8–20.3%, and inter-lineage genetic divergence between 0–4.5%. Contrasting with this deep genetic divergence, however, is an exceptional morphological stasis within species of *Horaglanis* and *Rakthamichthys*. An interesting and complex pattern of distribution (a combination of point endemics, restricted-range, and widely occurring species) was also revealed in members of both the genera, which may be linked to patterns of isolation and reconnection in the subterranean systems.

ORAL PRESENTATION

Benchmarking the species discriminatory power of commonly used markers and amplicons in marine fish (e)DNA metabarcoding

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Environmental DNA (eDNA) metabarcoding is revolutionizing the study of aquatic ecosystems, enabling high-throughput biodiversity analysis with minimal disturbance. As an emerging tool for assessing marine species, it has the potential to greatly support fisheries management. However, the choice of DNA fragments can vastly influence the accuracy of species identification. This study compared the discriminatory power of three markers commonly used in marine fish (e)DNA metabarcoding – 12S rRNA, 16S rRNA and cytochrome oxidase subunit I (COI) – including their respective amplicons. Mitochondrial genome sequences were mined from NCBI GenBank for five groups of fishes, each comprising a pair of closely related orders. Marine species were retained, and taxonomy standardized using WoRMS. From a total of 771 species and 2094 mitogenomes, nine genomic regions were extracted using Python and MAFFT. A Neighbour-joining tree was constructed for each of the resulting 45 data sets. Resorting to R, the percentage of monophyletic species in each tree was determined as a metric for species discrimination, and average congeneric pairwise distances were calculated. Our findings suggest that species discrimination is influenced by the chosen marker, substitution rate, fragment length, and target fish order. The COI and 16S full regions showed the highest discriminatory power (90.3% and 90.4%, respectively). Amongst metabarcoding amplicons, the COI Leray-Lobo region exhibited the highest discriminatory capability (87.0%) while the 12S Teleo region performed the poorest (71.6%). This study emphasizes the importance of marker and amplicon selection in marine fish (e)DNA metabarcoding research. While shorter amplicons offer technical advantages, they may lack sufficient resolution to discriminate closely related species. In the context of (e)DNA metabarcoding for ichthyofauna surveys, different fragments should be employed to resolve potential ambiguities for species-level identifications.

POSTER PRESENTATION

Environmental DNA (eDNA) as a non-invasive genetic tool for monitoring Antarctic fish community

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Antarctic fish are already experiencing the selective pressure of human-driven climate change and thus require non-invasive monitoring approaches. The aim of this research project is therefore to identify effective genetic tools for monitoring the Antarctic fish community, which minimize the impact of sampling compared to traditional methods. To this end, this project is aimed at developing non-invasive biomonitoring approaches based on the analysis of environmental DNA (eDNA). Among the Antarctic fish fauna, the suborder Notothenioidei is dominant in terms of biomass and species richness. Antarctic notothenioids therefore represent a key group of indicators of environmental shifts and changes in connectivity in the Southern Ocean. To record spatial and temporal variations in notothenioid fish communities, we will develop mitochondrial eDNA-based species detection methods, involving the analysis of water samples collected in the Weddell Sea (Southern Ocean). By testing the efficacy of this targeted approach, we will optimize species-specific markers for detecting presence-absence of target species directly in the field. Two notothenioid species will be considered as priority research targets, namely *Neopagetopsis ionah* and *Aetothaxis mitopteryx*. The results of this analysis will be compared with a classical metabarcoding approach for assessing the overall notothenioid biodiversity. This project integrates with international efforts to design a scientifically robust observation strategy, prioritizing areas according to their ecological relevance and susceptibility to environmental change. The Weddell Sea has been recognized as a potential refugium for cold-adapted organisms and thus non-invasive monitoring methods, such as those applying eDNA, should be favoured over traditional approaches (e.g. trawling) to monitor Antarctic notothenioids facing climatic shifts.

POSTER PRESENTATION

Does mercury biomagnification in a boreal lake food web vary year-round? – assessing patterns with bulk δ15N and compound-specific δ15N of amino acids

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Seasonality plays a characterizing role in northern latitude lakes, which may influence variation in food web biomagnification of contaminants. While biomagnification of neurotoxic mercury (Hg) has been documented in numerous and diverse aquatic food webs, limited knowledge exists regarding how this process fluctuates seasonally. This study tested potential fluctuations in year-round Hg biomagnification using trophic magnification slopes in the food web of boreal humic Lake Pääjärvi, in southern Finland. A representative sample of the food web was collected in three open-water seasons and one ice-covered season. Trophic level (TL) was calculated from δ15N measured using two methods: bulk stable isotopes of δ15N (SIA) and compound specific isotope δ15N analysis of amino acids (CSIA). Although biomagnification of total Hg (THg) was detected in all seasons using both methods, significant differences in seasonal trophic magnification slopes in- and between each isotope method were not detected. Trophic magnification slope was highest during winter and spring, and the lowest in summer and autumn in both of these methods, while the reverse relationship was found for basal THg concentrations, i.e. regression intercepts. However, basal THg estimates were significantly different in spring, summer, and autumn between isotope methods. Overall, TMS and basal THg values were higher in SIA than CSIA. SIA estimated TLs of primary producers and pelagic primary consumers as higher than those derived from CSIA, whereas the opposite was observed in many fish species. By using a calibrated TL 1 for primary producers in both methods, CSIA food chain lengths were approximately one TL longer than those from SIA. These results highlight an urgent need to calculate trophic magnification slopes using system-specific TLs and to effectively calibrate TL calculations derived from SIA and CSIA, especially in different spatial and temporal settings.

POSTER PRESENTATION

Assessing past fish distribution throughout collagen fingerprint: a study on archaeological remains of Salmonids

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Paleoecological studies provide critical evidence for understanding aquatic ecosystem functions and their responses to climate change. Fish remains are often abundant in prehistoric and historical archaeological sites. They are increasingly used to explore past human subsistence activities and diet, but they are also an invaluable record of past distributions and evolution of particular fish species. Vertebrae are usually the most frequent osseous fish components retrieved during excavations and are suitable for various analyses, from morphological to biomolecular. A key prerequisite to fully exploit this resource is species identification, a task that is difficult in the cases of phenotypically close sister species living in sympatry, as is true for brown trout (*Salmo trutta*) and Atlantic salmon (*Salmo salar*) along the European Atlantic coast. For salmonids, some criteria for morphological species identification do exist, but their accuracy is limited. Moreover, although genetic identification is an alternative, its cost prohibits the screening of large archaeological samples. We decided to tackle the issue by leveraging the collagen peptide signature through a technique known as Zooarchaeology by Mass Spectrometry (ZooMS), a biomolecular method used in archaeozoology for taxon identification up to the species level, including for fish. In our work, we applied ZooMS on more than 130 salmonid samples from northern Atlantic Spain dated to the Upper Palaeolithic. In this presentation, we report the results of our work that we believe important for assessing the potential and sensibility of the ZooMS method for accurately identifying prehistoric fish remains.

POSTER PRESENTATION

Using the microbiome to discriminate production method in turbot (*Scophthalmus maximus*): wild versus farmed.

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Turbot (*Scophthalmus maximus*) is a flatfish with a high economic value. The largest production of turbot is obtained from aquaculture (the largest production of turbot is obtained from aquaculture, which is 10 times higher than that obtained by catch). Nevertheless, wild turbot is more appreciated by the consumers. Since 2013, in the European Union, it has been mandatory to indicate the production method on the labelling of fishery products [Regulation (UE) Nº 1379/2013]. Hence, it becomes necessary to use traceability methods, as molecular traceability techniques, that allow the production method verification of fish labelling. Currently, high-throughput sequencing (HTS) technologies have been applied in host-associated microbiome studies to establish geographical patterns since microbiota is affected by numerous factors as: environment variables, human manipulation, or geographical origin. In this study, we used metabarcoding of the 16S rRNA gene to analyse gill, mucus, and gut microbiomes from 20 specimens of each wild and farmed turbot, sampled seasonally, to evaluate their ability to discriminate the production method. After the analyses of the mucus dataset we found that in both, wild and farmed turbot, the microbiome was dominated by Proteobacteria phylo. However, a highest percentage of Photobacterium genus was observed in wild specimens while the Acinobacter genus was present mainly in farmed specimens. Based on the β-diversity of the samples, they group together according to the production method explaining the 30% of the microbiome composition diversity found among the turbot specimens. The preliminary results in gills and gut show similar results, with a clustering of the samples according to the production methods when we select some bacterial groups. Therefore, the data show that microbiome analysis by metabarcoding approach can be a useful tool for fish products traceability, and specifically to identify the production method.

POSTER PRESENTATION

Mitogenome-based phylogenetics and molecular evolution in Travancoria elongata, an endangered mountain loach from the Western Ghats Biodiversity Hotspot

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We decoded the complete mitogenome (16,543 bp) of *Travancoria elongata*, an endangered mountain loach (family Balitoridae), endemic to the Western Ghats (WG) Hotspot (WG) in peninsular India and use this information to determine its phylogenetic relationships and molecular selection pressures on protein coding genes. The phylogeny based on balitorid mitogenomes recovered *T. elongata* into a well-resolved clade, with another WG endemic species, *Bhavania australis* as its sister taxon. The branch of the two WG endemics, *T. elongata* and *B. australis* were under episodic diversifying selection (optimized branch length = 0.0157, Likelihood ratio test = 6.8117, $P = 0.0118$, $\omega1 = 0.0297$ (99%), $\omega2 = 100000$ (0.64%)). Further, the test for selection relaxation on the branch of WG endemic balitorids ($K = 0.61$) was significant ($p = 0.007$, $LR = 7.38$). Site-wise selection analysis using FEL revealed that on the branch of WG endemic lineages, 136 sites were under purifying selection ($p \leq 0.1$), while 22 sites were under diversifying positive selection ($p \leq 0.1$). Members of Balitoridae can withstand extreme water turbulence in torrential streams through their adhesion devices. As a result, we hypothesize that genes involved in energy production will be under selection based on unique habitats of the species. Since the mitochondrial protein-coding genes are responsible for oxidative phosphorylation, it is not surprising that our analyses indicate various selection pressures acting on them. While the purifying selection is important for purging deleterious and potentially harmful mutations, the overall relaxation on the purifying selection on the branch leading to WG endemic lineages could be a result of the unique mountainous habitats of the species. The relaxation in selection can possibly explain the episodic diversifying selection in mitochondrial genes, which might have helped the species in occupying high elevation, cold-water habitats in the Western Ghats Hotspot.

POSTER PRESENTATION

Untangling the diets of gelatinous zooplankton using DNA metabarcoding

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Gelatinous zooplankton populations bloom and oscillate throughout the year, leading to large variations in their biomass and diversity within marine environments. Such alterations may have significant ecological impacts leading to shifts in community structure and energy transfer. However, their diets are hard to study using traditional methods, and this limits our understanding of their ecological role. In this study, we applied DNA metabarcoding using primers to amplify the V9 region of the 18S rRNA gene to study the diet composition of whole gelatinous zooplankton caught using plankton nets in the Western English Channel between April and August 2015. Environmental samples surveying community structure were also taken to enable assessment of feeding specificity. We found that the diet composition of various gelatinous zooplankton species did not strongly resemble that of the environmental samples, suggesting selective feeding of prey items. Diets of the genera *Beroe*, *Cyanea*, *Leuckartiara*, *Pleurobrachia*, *Cosmetira* and *Chrysaora* each featured strong representation of gelatinous zooplankton species indicating a large component of their diet is formed by predation between different gelatinous zooplankton within the Western English Channel. Our study demonstrates the use of molecular approaches to provide novel information on the diet of gelatinous zooplankton. In the present talk, these novel findings will be discussed further to enable us to begin to decipher the trophic niche occupied by gelatinous zooplankton in the marine environment.

POSTER PRESENTATION

Developmental plasticity within and among populations of Icelandic Arctic charr

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A major challenge of evolutionary biology is to understand how biological diversity is generated, maintained, and altered. Recent literature outlines the importance of integrating the fields of ecology, evolution and development to grasp a better understanding of how phenotypic variation is formed within and among species. Using young of the year Icelandic Arctic charr (*Salvelinus alpinus*) from different populations, we show how egg size can shape early phenotypes differently. In a second experiment, we show that brain size and brain shape differ among populations occupying different habitats (benthic vs pelagic), and having different reproductive strategies (migratory/stream versus lake). Our results highlights how various factors can shape early phenotypes with potential consequences for life histories of fish. We discuss the needs of -omics approaches to complement our understanding of adaptation and phenotypic plasticity in a polymorphic species like Arctic charr. Such integrated approach may be necessary to make effective restoration and conservation plans for fish populations.

POSTER PRESENTATION

Problem Polymers in Aquaculture: Proteomic Insights into PVP Exposure

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The synthetic polymer, polyvinylpyrrolidone or povidone (PVP) poses a dual threat as an emerging freshwater pollutant and an inhibitory pollutant within aquaculture systems. It is a common surfactant additive in biosecurity products used to prevent and treat disease outbreaks in the aquaculture industry. However, recent studies have linked PVP exposure to behavioural and physiological toxicity within commercial fish species. Our project delves into the proteomic mechanisms underlying these toxicities in a commercially important aquatic vertebrate model, Poecilia reticulata. Applying nano LC-MS, this work unravels the intricate protein expression pathways affected by low-dose PVP exposure, comparing this directly with a biodegradable alternative surfactant polymer; polyvinyl alcohol (PVA). Our findings not only shed light on the molecular intricacies of PVP toxicity but also investigate potential chemical substitution of PVP within aquaculture biosecurity products, where chemical sustainability and pollution mitigation is vital for preserving aquatic ecosystems and the future of aquaculture.

POSTER PRESENTATION

Ecological consequences of single base pair variation in rhodopsin

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Visual sensory systems of many animals are vital for perceiving their environment and in aquatic environments, light intensity and frequency spectrum change along a depth gradient because of the properties of water and suspended particles. Rhodopsin (RH1), a protein in the retina, is responsible for gathering achromatic visual information and detecting light spectra around the λmax-value of 500nm (the blue-green part of the spectrum). In this study we examine the role of a single base pair mutation (A292S) in RH1 that leads to a shift in light spectrum sensitivity and which has been hypothesised to play a role in ecological divergence during the early part of speciation in a number of species pairs. We tested this hypothesis using polymorphic populations of *Astatotilapia calliptera*, a generalist cichlid fish species found in different depth and turbidity environments in and around Lake Malawi. We set up feeding trials in aquaria under reciprocally optimal light conditions, to test for differences in feeding efficiency of alternative genotypes, to test for a selective advantage of one genotype over another, in different light environments. The Lake Malawi cichlid fish radiation is known for gene exchange via hybridization and ultimately, any selective advantage we can demonstrate for specific polymorphisms allows us to better understand the ecological pressures which can lead to evolutionary change, and eventually spread across radiations.

POSTER PRESENTATION

Regional environmental genetic adaptation leads to differential climate vulnerability of two ecologically important copepods in the Northwest Atlantic

Danielle Davenport* [1,2], Claudio DiBacco [1], Stephane Plourde [3], Pierre Pepin [4], Catherine Johnson [1], Tony Kess [4], Meghan C. McBride [1], Ian Bradbury [4,5,6,7]

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With climate change altering all aspects of marine ecosystems, actionable management strategies to preserve marine ecosystem functioning, commercial fisheries and species at risk require knowledge of how and why species may be vulnerable to future climate change. From an evolutionary perspective, populations evolve differences that provide a fitness advantage under local environmental conditions. Predictions of expected evolutionary responses to future climates via evolutionary pathways can be achieved by studying the environmental drivers of genomic variation and then incorporating genomic information into climate change impact assessments to determine genomic vulnerability. In this study, we present evidence of environmentally mediated intraspecific genetic diversity in two species of *Calanus* copepod; *C. finmarchicus* (N=458) and *C. hyperboreus* (N = 233), both dominant zooplankton species of the North West Atlantic (NWA), and important prey for endangered whales and commercial fish species alike. Using RADseq genotyping and population genomic analysis across a strong environmental gradient, we identify local genetic adaptation, population structure (Atlantic, Arctic and Gulf of Saint Lawrence) and predict spatiotemporal shifts in genomic vulnerability under future climate scenarios with important implications for environmentally associated ecosystem change in the NWA. (Words = 176).

POSTER PRESENTATION

Unveiling the nightlife of coral reef fish in our changing world

Emma Weschke* [1], Evie Croxford [1], Jules Schligler [2], Ben Williams [3], Bartosz Dworzanski [1], Suzanne Mills [2,4], Ricardo Beldade [5], Steve Simpson [1], Andrew Radford [1]

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The field of nighttime ecology is substantially outpaced by diurnal studies, this research bias was coined the "nocturnal problem" over 80 years ago by ecologist Orlando Park which has persisted to this day. This bias undoubtedly stems from ecologists' innate diurnality coupled with the logistical and technological challenges associated with nighttime observation and experimentation, which is further exacerbated in aquatic systems. For my FSBI PhD Studentship we developed remote underwater infrared cameras to unobtrusively unveil the secret nightlife of coral reef fishes. We used this technology in aquaria and field investigations to unveil the baseline nighttime behavioural ecology of coral reef fishes and to assess species-level and community-wide responses to sensory pollutants of global concern. We found that nocturnal reef fish communities fluctuate across the lunar cycle, with elevated fish activity and diversity during a full moon compared to the new moon. We also found that motorboat noise, dominant during daylight hours, can have latent implications on the nighttime activity and behaviour of nocturnal fishes. And finally, we found that artificial light alters the nighttime composition of fish communities by attracting nocturnal and diurnal predators to artificially illuminated reefs and causes diurnal fishes to exhibit daytime behaviours at night. With the plethora of anthropogenetic stressors threatening coral reefs today, it has become essential to consider beyond just daylit hours if we are to obtain a temporally holistic understanding of the functioning and resilience of these ecosystems in our changing world.

POSTER PRESENTATION

Nocturnal predators drive community composition of acoustically enriched restoration reefs

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Miles Parsons [3], Andrew Radford [1], Steve Simpson [1]

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Coral reef restoration is increasing in scale and ambition in response to current negative trends in reef health around the world. To date, studies investigating the interaction between coral reef restoration and coral reef fish have generally focused on changes in diurnal reef fish communities. However, the activity of nocturnal coral reef fish is crucial for ecosystem functioning, including predation and nutrient cycling, so could influence outcomes of restoration techniques. We have developed infrared cameras to monitor nocturnal fish communities with minimal disturbance and provide insight into nocturnal predation. Working with the ‘Reef Song Project’, which is experimentally investigating methods to enhance coral reef recovery in Australia, we investigated the influence of acoustic-enrichment and fish restocking restoration techniques on nocturnal fish communities at Lizard Island (Great Barrier Reef). Treatment differences in community composition were driven by predatory genera that occurred more frequently in nocturnal video surveys on the acoustically enriched patch reefs compared to those on control patch reefs. Our work using this new monitoring technology has important implications for this restoration technique as the activity of nocturnal predators could influence net gains in fish abundance, and in restoration more widely. Moreover, we demonstrate the importance of varied monitoring techniques that investigate functionally important species to ensure that current restoration techniques are not hindered by the cloak of darkness.

POSTER PRESENTATION

Can telomere length be estimated from fish scales to inform on individual stress?

Gaëlle Brahy* [1], Aurélie Manicki [1], Maika Minjou [1], François Gueraud [1], Sylvie Muratorio [1], Jacques Labonne [1]

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Telomeres, which are protective, non-coding sequences at the end of chromosomes, are known to shorten as a result of aging processes in various taxa. Moreover, previous studies showed that telomere attrition is faster following exposure to harsh environmental conditions, suggesting that relative telomere length (RTL) can be a proxy of stress and therefore of major interest in ecological analyses. While RTL can be routinely characterized in fishes for multiple individuals at low cost using qPCR after DNA extraction from fresh fin, blood, muscle or liver material, no study up to now attempted to evaluate the potential for such an approach on fish scales. Scale material is indeed easily sampled and conserved, and ample collections are available for many species over decades. To test this potential, we used a fish scale collection spanning over 50 years from a well-documented case study of brown trout colonization in the subantarctic Kerguelen Islands. We estimated RTLs in 182 individuals from scales sampled between 2011 and 2018, and in 254 individuals from scales sampled between 1973 and 2003. In order to assess variation in RTL, our sampling includes individuals of various age from six different populations presenting contrasted environments with regard to density. This new methodological development could provide a cost-effective, non-invasive approach to estimate a proxy of stress, either using scale sampling in the field or capitalizing on existing scale samples collections.

POSTER PRESENTATION

Validation of a pipeline for eDNA analysis by mock communities: evaluation of variables influencing mitochondrial DNA abundance

Giulia Mariani* [1,2], Luana Fiorella Mincarelli [1], Bogna Griffin [3], Barbara Secondini [1], Marco Di Domenico [1], Pierluigi Castelli [1], Andrea Bucciacchio [1], Ludovica Di Renzo [1], Nicola Ferri [1], Cesare Cammà [1]

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Environmental DNA (eDNA) has acquired importance over the last decade growing quickly along with laboratory and sequencing techniques. Despite eDNA analysis is a cost-effective non-invasive method for monitoring biodiversity, there's still a need to investigate factors affecting final outputs. We explored protocols for each step of the eDNA analysis, and mock communities were created to delve deeper into the variables influencing results. 13 DNA fish extracts were used to compose non-normalized (MC1) and normalized (MC2) mock communities. To investigate the mitochondrial DNA (mtDNA) proportion in fish extracts, MC1 and MC2 were created with pre-PCR extracts (before the 1st step PCR of the library preparation) and amplified extracts (post-PCR) by using tele02 primers targeting the 12S ribosomal RNA (rRNA) gene. The DNA library was prepared with a two-step approach, samples were pooled after indexing and sequenced on MiSeq Illumina (2X250PE). Demultiplexed sequences were processed with the ObiTools pipeline launched in Galaxy.eu. The parameters were set based on known species composition. We reported a significant and positive correlation (Pearson=0.9, p 0.05) between the number of reads and concentration only when the target gene is available in a high number of copies (MC1 post-PCR). Additionally, as expected, the Relative Read Abundance (RRA) pointed out an even proportion among species in MC2 (E=0.91) and MC1 (E=0.90) post-PCR, in contrast with a lack of evenness in MC2 (E=0.68) and MC1 (E=0.49) pre-PCR. We also highlighted that primer efficiency may vary among fish extracts and depending on starting concentrations, as no reads were assigned to Mullus barbatus in MC1 pre-PCR regardless of the starting concentration (13 ng/µl). Conversely, M. barbatus showed 10% RRA in MC1 post-PCR (averaged RRA/species was 7.86%). These results suggest that in real communities some species are less likely to be detected due to mtDNA starting concentration and primer efficiency.

POSTER PRESENTATION

Using genomic tools to monitor skate and ray communities in Irish Atlantic coastal waters

Rachel Coleman Horgan [1], Ilaria Coscia* [2], Maurice Clarke [2], Luca Mirimin [1], Allan Mc Devitt [1]

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Irish coastal waters are home to at least 18 species of skates and rays, ranging from the relatively abundant cuckoo (*Leucoraja naevus*) and thornback rays (*Raja clavata*) to critically endangered flapper (*Dipturus intermedius*) and white skates (*Rostroraja alba*). Areas along the west coast, particularly Tralee, Dingle, and Galway bays, have emerged as potentially critical refuges for these species, although detailed distribution and population data are lacking. This project aims to address these issues by characterising the distribution, abundance and connectivity of skates and rays in Irish waters using both environmental DNA (eDNA) and genomic techniques, thus creating permanent genetic resources that could prove crucial for the future management of these species. The key components of this project include an eDNA metabarcoding survey to assess multi-species distribution across temporal scales, a targeted, species-specific eDNA survey to detect the critically endangered white skate, and a population genomics study of cuckoo rays to explore stock structure, abundance and genetic adaptation to the environment.

POSTER PRESENTATION

Omics and experimental needs to advance with ecosystem models under management and climate scenarios

Jose A Fernandes-Salvador* [1]

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There is a large range of research on the last decade aiming provide forecasting of changes in species distribution, abundance and sizes by using ecosystem models. These models range from habitat suitability statistical based models to complex mechanistic models that add ecophysiology, dispersal, growth, population dynamics and other mechanisms. While these models have been able to forecast some of the trends we are already observing with empirical data, the species capacity to adapt to climate change and fisheries pressures has been sparsely addressed. This talk firstly revises current status of ecosystem models at global, regional and local level based on experience within FISH-MIP global initiative and European projects EURO-BASIN, CERES and FutureMARES. Secondly, the needs of parameters that could be addressed with omics and/or experimental work are highlighted. Moreover, advantages, limitations, and complementarity of both approaches is presented. The talk ends by presenting how ecosystem models can be improved to incorporate the results from omic and experimental research.

POSTER PRESENTATION

Influence of a hydroelectric dam on the selection and local adaptation of the Amazonian fish Cichla temensis

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The Balbina hydroelectric dam was built in the 1970s in the headwaters of the Uatumã River to supply electricity for Manaus, the capital of the Amazonas State, Brazil. The construction of the dam dramatically changed the landscape into a large, lentic, artificial reservoir as opposed to a previously dynamic riverine system. These changes affected and continue to affect the microevolutionary processes acting on aquatic organisms including non-migratory fish species. In this study, we evaluated the effects of this ecological transformation on genomic diversity and differentiation of the peacock bass (*Cichla temensis*), an iconic non-migratory fish from the Amazon. We collected ddRAD-seq data and extracted SNPs, dividing the SNPs into neutral and non-neutral loci. The neutral SNPs showed a population structure of two genetic groups, upstream and downstream of the dam with low gene flow between them. Level of structuring increased when non-neutral data were included in the analyses, indicating that isolation accelerated as a consequence of an adaptation to the lentic environment of the Balbina retention dam. Differences in genetic diversity between the two groups were also detected. This study provides the first evidence of hydroelectric dams promoting local adaptation in populations of a non-migratory fish species in the Amazon.

POSTER PRESENTATION

eDNA metabarcoding, a promising tool for monitoring aquatic biodiversity in the estuaries of Reunion Island (South-West Indian Ocean)

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Reunion Island is a remote oceanic island located in the South-West Indian Ocean (SWIO), where all freshwater fish species are diadromous. The ecological status assessments of freshwater in watersheds have revealed a continuing deterioration in these fish populations due to anthropic pressures. In this context, monitoring the fish biological sustainability is crucial to ensure health of theses estuarine ecosystems. The aim of this study is to compare the efficacy of conventional electrofishing monitoring (EF) with the environmental DNA metabarcoding tool to evaluate fish biodiversity in the estuaries of Reunion Island. We measured the diversity and structure of the fish community in three estuaries with various geographical, hydrological, and anthropogenic conditions over different seasons. To this end, fish were captured by EF, and we then isolated DNA from the water samples to perform bioinformatic analyses derived from eDNA, using the 12S marker to target fish. Statistical analyses were carried out to compare the results of these two methods. For all watersheds combined, a comparison of the results for measuring fish richness showed that eDNA performed significantly better than EF. Indeed, the eDNA detected 31 species, whereas the EF detected only 12 species. For both methods, we observed significant differences in community structure between watersheds. Moreover, compared to EF, eDNA enabled the detection of endemic to the Mascarene region species and introduced exotic species. Furthermore, eDNA analysis has unveiled the presence of species that are challenging to capture through EF and has enabled the identification of species captured using EF but that are morphologically unidentifiable due to their juvenile life stage. At the end, in comparison to EF, our data confirm the strength of eDNA to detect fish species in Reunion Island, both taxonomically and in terms of species richness.Thus, eDNA proves to be an effective tool to be developed for monitoring fish.

POSTER PRESENTATION

Genetic connectivity in a key nesting icefish in the Weddell Sea, a candidate area for protection in the Southern Ocean

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

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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. Preliminary results from genetic data (RAD sequencing) indicate the presence of very low differentiation between the Antarctic Peninsula and the Weddell Sea. However, genome scan indicates that differentiation is particularly high in and almost limited to two specific chromosomes. This suggests that, despite high gene flow, probably by larval dispersal, the two populations might be locally adapted. Otolith analysis will confirm if individuals sampled in different areas were born and reared in the same area or may have migrated long distances. Studying species connectivity can provide valuable insight into the number and distribution of *N. ionah* spawning sites. This could have far-reaching implications for conservation and could further promote the urgent need to protect key benthic habitats in the Southern Ocean.

POSTER PRESENTATION

Performance of environmental DNA metabarcoding for long-term integrated fish monitoring around marine infrastructure

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Accurate and cost-effective approaches are desired for efficient and sustained long-term biodiversity monitoring. Environmental DNA (eDNA) metabarcoding is a relatively recent genetic method that is becoming a species-monitoring tool. Still, its ability to reveal key aspects of biodiversity beyond richness and to elucidate species' spatial dynamics, especially across depth in coastal ecosystems, remains poorly assessed. One critical aspect is the performance and reliability of eDNA metabarcoding, which requires testing against high-effort traditional survey methods in relevant ecological and geographical environments. We evaluated the performance of eDNA metabarcoding for monitoring the fish community associated with a port terminal on the central coast of Peru. At the terminal, a long-term monitoring program (BMAP) has gathered 12 years of continuous fish data using fisheries gears (nets and hooks) coupled with visual identification and barcoding. Water samples were collected and filtered in two seasons of 2023 from the infrastructure and adjacent areas, and eDNA metabarcoding was performed using MiFish-U/E primers, which target a region of the 12S rRNA gene. We compared taxonomic, functional, and phylogenetic diversity estimates and the spatial distribution (horizontal and vertical) obtained from BMAP surveys and eDNA metabarcoding. Preliminary data shows a positive correlation between estimates of the species richness and relative abundance (proportion of reads) obtained with each approach. Together, both approaches detected more species than individually; nevertheless, each captured species that remained undetected by the other. Notably, eDNA metabarcoding proved to be significantly cheaper than the BMAP surveys. We will discuss eDNA metabarcoding performance and considerations as an integrated long-term tool for fish monitoring.

POSTER PRESENTATION

Fish-DNA-Monitor: Supporting management of fisheries resources in Guinea-Bissau through eDNA metabarcoding

Luis Machado* [1,2], Ignacio Ribera [3], Iça Barri [4], João Meira [1,2], João T Fontes [1,2], André Ferreira [1,2], Claúdia Machado [1,2], Josepha Gomes [4], Amadeu Almeida [4], Raul Jumpe [4], Candelaria Burgos [4], Sofia Duarte [1,2], Pedro Soares [1,2], Filipe O Costa [1,2]

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Guinea-Bissau (GB) has one of the wealthiest marine biodiversity zones of West Africa and, in relation to fish communities, is estimated to harvest one million tons of fisheries resources. In this country, the fisheries sector contributes substantially to the economy and food security of its population, with 700k people living in coastal areas and 225k employed by small fishing sector. Notwithstanding, high quality monitoring data for fish stock assessment, which is critical for the management of fisheries resources, is still deficient. The Fish-DNA-Monitor is a project funded by the Aga Khan Development Network that aims to provide training and carrying-capacity for application of DNA-based approaches to fisheries resources monitoring and management in Guinea-Bissau. Molecular tools have been increasingly used in complement to traditional methods, providing accurate and faster species identifications from unknown specimens at any life stage, or even damaged specimens, therefore increasing efficiency of monitoring strategies. In a collaborative effort between the Center of Molecular and Environmental Biology (CBMA/University of Minho), INIPO (GB's national institute for fisheries research) and Instituto Español de Oceanografía (IEO), we aim to: i) implement a DNA barcode reference library for GB's fisheries resources together with tissue and DNA vouchers, available for the international community; ii) develop a protocol for implementation of DNA metabarcoding in zooplankton surveys. Additionally, we have a training program for technical capacitation of GB's INIPO staff, with a laboratory internship already executed. It is expected that these capacity-building on cutting-edge DNA-based approaches will bring economic benefits to the country and therefore improving the quality of life of its people. This project integrates an action endorsed by the UN Ocean Decade that aims to extend these approaches to other countries along the west Africa coast.

POSTER PRESENTATION

A tale of clones, robots, and agents: the role of behavioural individuality in the schooling dynamics of the Amazon molly

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Grouping is vital for many fish species, and whilst we can explain the reasons for social behaviour across different contexts (e.g., foraging or predator avoidance), the behavioural mechanisms underlying collective behaviour are not fully understood. Computer simulations are vital for disentangling these mechanisms, but most models assume that individuals are identical in the behaviour rules they follow, something not supported by empirical findings. Individuals in a fish school may differ not only in their physical characteristics but also in their behavioural traits (‘personalities’). This heterogeneity is especially interesting when individuals are genetically identical, as in the case of the Amazon molly (*Poecilia formosa*): a unique clonal fish that even when individuals are reared under near identical conditions, they still develop behavioural individuality. In this project, we investigate how the personality composition of a genetically identical group affects its collective motion dynamics and decision-making properties by combining lab experiments, bio-mimetic robotics, and computer simulations. By first identifying the social tendency of individual mollies to approach and follow a robotic conspecific (the Robofish), we track groups of varying sizes and social tendencies of their members. Using our empirical data, we develop an agent-based model in which agents resemble our fish in individual behaviour and simulate heterogeneous groups to understand how the collective patterns we observe emerge through self-organization. Overall, our findings can have a great impact on predicting the effect of changing environmental conditions on fish populations, especially with changes affecting individual sociality, as well as support biohybrid solutions that can resolve human-wildlife conflicts (e.g., using a robotic fish to navigate schools through fragmented environments). This project is funded by an FSBI Postdoctoral International Travelling Fellowship (PITF).

POSTER PRESENTATION

Quantification of Atlantic bluefin tuna environmental DNA in the Mediterranean Sea

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Estimating the abundance of the economical and ecologically important Atlantic bluefin tuna (ABFT; *Thunnus thynnus*) is key for establishing effective management and conservation measures for this species. ABFT abundance indices can be inferred from fishery-dependent data such as catch per unit effort (CPUE) or fishery-independent data such as tagging, aerial imaging and larval counts at spawning sites. However, CPUE-based estimates can be biased and dedicated aerial, tagging and larval surveys are costly and logistically complex. In a quest for an alternative approach for ABFT abundance estimation, we have developed an ABFT-specific digital PCR assay and applied it to environmental DNA extracted from water samples collected around the Balearic Islands, in the Mediterranean Sea. The assay, targeting the mitochondrial control region, has shown high specificity to the ABFT, over other tuna species found in the Mediterranean Sea, when tested in DNA extracted from tissue samples. The assay was performed on approximately 150 samples gathered at various depths (0 - 2500m) and in various seasons, across 12 distinct stations. Of the samples, 38 were collected at stations in ABFT spawning regions during the spawning season. This provided associated larval counts. For each sample, we have estimated the number of ABFT eDNA copies per litre of water and interpreted the outcomes considering sample depth, location, month and available larval count data. Our results demonstrate annually recurring patterns and confirm the presence of ABFT eDNA at stations where larvae had been detected. However, we found no direct correlation between estimated eDNA copies per litre and larval counts. Finally, we elaborated on different hypotheses to explain this lack of direct correlation, such as stochastic DNA dispersal patterns or lower eDNA input from larvae compared to adult ABFT and propose future steps to improve estimates of ABFT abundance based on eDNA read count.

POSTER PRESENTATION

Unravelling Ballast Water Biodiversity: A Genomic Approach to Non-Native Species Management

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Anthropogenic factors, such as introducing non-native species via ballast water, perturb native biodiversity. Identifying metazoan diversity in the ballast water of international cargo ships can yield valuable insights into the biodiversity transported through this medium. This study aims to characterize metazoan diversity in the ballast water of ships arriving at V.O. Chidambaram Port in Thoothukudi, Tamil Nadu, India. Environmental DNA (eDNA) was isolated from both ships' ballast and port water to compare biodiversity and identify non-native species. The V7 region of the 18S rDNA was amplified and sequenced using the Illumina MiSeq NGS platform. Sequence analysis revealed a total of 2025 operational taxonomic units (OTUs) across harbor and ballast waters. Of these, 767 OTUs were exclusive to ballast water, while approximately 1100 OTUs were shared between ballast and harbor waters. The analysis also detected the presence of non-native species in ballast water, including *Calanus finmarchicus* (Copepod), *Siokunichthys nigrolineatus* (Mushroom coral pipefish), *Vetulina stalactites*, *Cacospongia mycofijiensis* (Sea sponge), Red algae (*Bulboplastis* sp.), and other diatoms. These species likely entered the ballast water as eggs, cysts, traces of biological material, or dead cells. Maritime regulations require ships to treat ballast water before releasing it into non-native waters. However, some hardy species may withstand treatment measures and survive in non-native ecosystems. This study provides essential baseline information on the biodiversity composition of ballast water and harbor water in the Gulf of Mannar region

POSTER PRESENTATION

Abandoned, Lost, or Discarded Fishing Gears (ALDFG) in the Arabian Gulf

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Abandoned, lost, or discarded fishing gear (ALDFG) represents a significant percentage of global plastic pollution and is currently considered one of the major environmental threats. ALDFG is more harmful than marine litter, as it has the potential to continue catching marine fauna through 'ghost fishing'. Introduced into the marine environment from fisheries-related activities, ALDFG contributes substantially to adverse environmental and socioeconomic effects. Despite being a major global concern, adequate data are still limited regarding the quantities of ALDFG present on the sea bottom and their wide range of impacts on the environment. This pilot study focuses on data gathered from an underwater survey conducted along the reef flats of Jana Island in the Arabian Gulf. Most ALDFG items observed during the survey were related to the local fishery operating in the region, such as gill nets, pieces of trawl nets, anchors (manshal) commonly used for gargoor (traps), weights, cables, plastic ropes, and buoys. Jana Island is one of the potential fishing areas, and all the items reported here are directly related to fisheries activities. Entanglement of a juvenile green turtle (*Chelonia mydas*) in an abandoned gill net was also observed. The Gulf region's economic landscape is significantly influenced by the fisheries sector, making it crucial to assess the effects of ALDFG. Given the urgency of the situation, it is essential to prioritize the adoption of robust mitigation strategies.

POSTER PRESENTATION

Mitogenome organization and evolution in a living fossil, *Aenigmachanna gollum*

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More than 400 species of teleost fishes are known have the capability to breathe air, including members of order Labyrinthici, a group of freshwater fishes comprising three suborders, Channoidei, Anabantoidei and Nandoidei. The living fossil, *Aenigmachanna gollum*, an ancient relic lineage within Labyrinthici (suborder Channoidei) was discovered from the subterranean habitats in southern peninsular India, and subsequently assigned to an entirely new family of teleost fishes – Aenigmachannidae. The general arrangement of mitochondrial genome of *Aenigmachanna* is similar to other members of Labyrinthici. Though phylogenetically related to members of Channoidei, *Aenigmachanna* has relatively less GC and higher AT content in its genome similar to members of Anabantoidei and Nandoidei – reflected in the relative synonymous codon usage, where A and T containing codons have a higher preference than G and C containing codons. Molecular evolutionary analysis revealed that nine of 13 protein coding genes of Labyrinthici mitochondrion have sites under positive selection. In *Aenigmachanna*, several genes are subjected to episodic positive selection where the selection pressure is either relaxed or intensified. We hypothesize that the low GC content in *Aenigmachanna* mitogenome compared to members of Channoidei is due to the ancestral character state in Labyrinthicini, also reflected in members of Anabantoidei and Nandoidei. Further, the episodic selection in protein coding genes of *Aenigmachanna* could be an artefact of its subterranean lifestyle.

POSTER PRESENTATION

Invasion genomics of a non-indigenous salmonid in Norway: local lessons, global challenges

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Biological invasions are a significant catalyst for environmental change, impacting conservation efforts, agriculture, and human health. To effectively reduce the impact of non-indigenous species, it is essential to thoroughly understand their invasion history, including their origin, how they spread, their ability to invade, and any genetic adaptations they may have developed to cope with new environmental challenges in the regions they have invaded. Our objective is to determine the primary environmental factors that promote dispersal events along the invasion gradient and to analyse the spatial distribution of genetic diversity in feral populations of the non-native pink salmon in Northern Norway. We initially employed four ecological niche models utilizing diverse modelling techniques of varying complexity, including both regression-based and tree-based machine-learning algorithms. Subsequently, we used the triple-enzyme restriction-site associated DNA sequencing (3RADseq) method to obtain genome-wide single-nucleotide polymorphisms to investigate genetic diversity and gene flow patterns within the pink salmon's putative invasion hotspot. Our research indicates that the variations in extreme weather events caused by climate change will probably continue to create favourable conditions for the pink salmon outside of its original or introduced habitats. Rivers that have been invaded locally have the potential to become source populations of invaders in the ongoing secondary spread of pink salmon in Northern Norway. Our study demonstrates that the use of species distribution models (SDMs) and genomic data can uncover the factors that determine the distribution of species. This information can be used to guide post-control measures and potentially make inferences about their effectiveness.

POSTER PRESENTATION

The Rapid Historic Extirpation of *Dipturus batis*, *Dipturus intermedius* and Other British Elasmobranchs Based off Notes Made by W. C. MacIntosh in 1884

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Apex predators such as the common skate complex, *Dipturus batis* and *Dipturus intermedius*, have suffered local extirpations from much of their former habitat. Due to taxonomic confusion from the tendency to group historic landings into 'skates and rays', the historic distribution of many British elasmobranchs is not well understood. However, despite these challenges, historical fishing surveys provides a unique opportunity to reconnect missing baseline data for these critically endangered species. The archived notes of William C. MacIntosh from an 1884 fishing survey were examined. This trawl caught nine key predatory elasmobranch species off Scotland's east coast including *D. batis* and *D. intermedius* as well as *Raja clavata*, *Amblyraja radiata*, *Leucoraja circularis*, *Rostroraja alba*, *Dipturus oxyrinchus*, *Dipturus nidarosiensis* and *Squalus acanacanthias*. This trawl catch was compared with the Scottish Groundfish Survey from 1925 to 1928. Dipturs batis was the most abundant elasmobranch caught in MacIntosh's 1884 trawl. However, during the Groundfish Survey, *R. calvata* catches surpassed Common Skate catches both by numbers and catch per unit effort. *Squalus acnathis* dominated the elasmobranch makeup of the catch in the 1920's though it was noted just nine times in the 1880's. MacIntosh also caught two large predatory skates *D. oxyrinchus* and *R. alba* which have not been observed on Scotland's east coast since 1884. The results of this comparative historical study raise the issue that our understanding of British elasmobranch composition may be profoundly distorted by time and local extinctions

POSTER PRESENTATION

Larval length per developmental stage decreases during spawning season of Atlantic herring

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For many fish species, the interactions between environmental factors such as salinity, temperature, food availability and larval characteristics (size, developmental stage, age, and growth) have been studied in different constellations. Most of these studies were conducted under controlled laboratory environments, however, corresponding studies in the field are more challenging and require a close-knit survey and sampling design. In this study, we analyzed herring larvae during their spawning season of two years with regards to the length per stage relationship. Atlantic herring spawn in multiple cohorts over a period of two months, at the Western Baltic coast generally between March and May. Therefore, larvae hatching earlier in the season experience different conditions, such as lower temperatures and different food quality and quantity than larvae hatching later in the season. Over the course of the spawning season, we sampled larvae each week from March to Juli within a major nursery ground of the Western Baltic herring. The larvae were staged and measured to examine seasonal and interannual differences in the observed length per stage. The length within a developmental stage generally decreases over the course of the spawning season and sampling time thus later hatching larvae are smaller during their development than larvae hatching earlier in the year. The data also show that the size difference between the cohorts is especially significant in the stages after 7 (end of dorsal fin development). Several mechanisms could be underlying our observations, and we can only discuss them accordingly. Nevertheless, our results have implications for individual larvae, as differences in larval size per stage affect their probability of survival. Larval size could e.g., influence other parameters such as ability for food intake and swimming speed and can therefore cause or worsen mortality bottlenecks during the larval development.