EuroMarine Foresight Workshop

# GENOMICS & FISHERIES

Faro, Portugal
2017

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# Contents

# Welcome to Faro

Faro is the administrative centre for the whole of the Algarve region with a population of approximately 60,000 inhabitants spreading over 210 km2, of which 30% are integrated in the Ria Formosa Nature Reserve. The Ria Formosa lagoon, a 19 km long system of barrier islands that communicates with the sea through six inlets, five of which are natural and have mobility characteristics, and one is an artificial inlet that was opened with the purpose of allowing easier access to the port of Faro. This system forms three main islands, which can be reached by boat, and are excellent places to enjoy pleasant days in contact with nature, enjoying boating, biking or walking.

To discover the city and its essence, a walk through the streets of Faro is recommended. The garden Jardim Manuel Bívar, an ex-libris of the city, is a mandatory passage point for anyone wishing to know the city, with a pleasant sidewalk and several esplanades where you can enjoy the mild climate.

The city also has an attractive marina, well-maintained parks and plazas and an old town full of outdoor cafés and pedestrian lanes.

Vila Adentro is the primitive nucleus of the city of Faro, formerly called Ossónoba and fully enclosed by walls. The oldest building in the city, the Igreja da Sé (the Cathedral) is located here, built in 1251, with its marvellous altarpieces and the impressive 18th century organ with chinoiserie motifs. From its bell tower, you can enjoy a breath-taking view over the city and the Ria Formosa. Adjacent to the building is the Capela dos Ossos (Chapel of Bones).

The Paço Episcopal and the Seminário Episcopal, respectively the residence and place of training for the Clergy, surround the stately Largo da Sé. Their “scissor roofs” (shaped like open scissors) and whitewashed façades, associated with the orange trees that adorn the public space, transport us to the urban landscapes of a Mediterranean paradise.

By walking through the irregular streets of Vila Adentro you will find the Faro Municipal Museum in the old convent of Nossa Senhora da Assunção (Lady of Assumption), one of the first examples of a type of Portuguese proto-Renaissance cloisters.

Right in the centre of Vila Adentro is the Câmara Municipal de Faro building (the City Hall), housing the administrative power of the city.

Faro has a diversified architectural heritage with a natural backdrop for providing excellence, and the necessary requirements for the practice of nautical tourism and for nature-lovers. The unique characteristics of the Ria Formosa, one of the national Seven Wonders, allow for the practice of several activities, such as kite-surfing, canoeing, windsurfing, rowing, boating and bird-watching, granting the visitor unique moments in contact with nature. Ria Formosa environmental and landscape features are opportunities to develop scientific, cultural, social and economic added value which has been preserved over time. Artisanal fishing, salt production, aquaculture, and shellfish farms are examples of local relevant economic and social activities.

# Welcome from the workshop convenor

Dear Friends and Colleagues,

It is our great pleasure to warmly welcome you to "The application of population genomics to fisheries management" workshop organised by the Centre of Marine Sciences (CCMAR). We have among us geneticists not working on fisheries related problems, fisheries researchers which do not use genetics as a tool, and people who combine both.
We were privileged in attracting some of the world leaders as keynote speakers, and the programme was designed to offer plenty opportunities for discussions in and off working sessions. We will search for a synthesis on the current status of the use of population genomics in fisheries management and ideally will be able to provide a set of guidelines of best practice for obtaining fisheries-relevant data together with its correct interpretation and application in management plans.

At CCMAR we do hope that you will join us in what promises to be a fruitful workshop!

Rita Castilho,
on behalf of the Scientific and Organising Committees
Workshop Convenor
CCMAR
University of Algarve, Faro, Portugal

# Scientific Committee

Rita Castilho (Convener)
Naiara Rodriguez-Ezpeleta
Cymon Cox

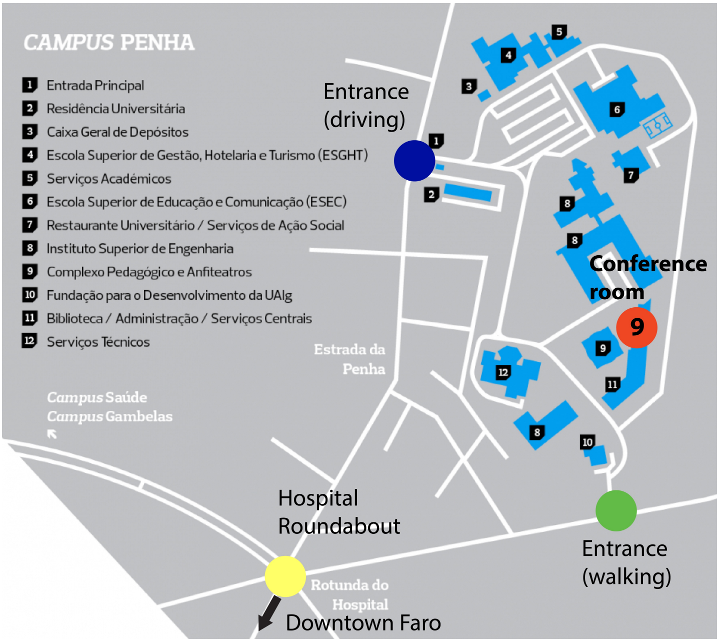
# Organising Committee

Rita Castilho (Convener)
Tiago Magalhães
Bruno Louro

# Conference information

## Finding the conference venue

University of Algarve, Penha Campus, Complexo Pedagógico,
**Building 9, Room 1.4**
GPS: 37°01'42.4"N  7°55’28.4"W



## Registration and Helpdesk

The registration and helpdesk are located in the open area adjacent to the lecture theatre (see map on the next page) at the entrance of Building 9. The registration desk will be open from Monday 8th of May to Wednesday 10th of May from 9.30 until the end of sessions in the evening.

## WiFi

All delegates will be registered in advance for access to University WiFi. Those delegates who have access to Eduroam may have automatic access to the University WiFi with their own credentials.

## Use of Social Media

This workshop organization support the communication and discussion of science. Information presented at the meeting (in oral or poster format) may be reported and discussed by attendees and science writers via blogs, Twitter, or other formats. If presenters **do not wish** to give their consent, they **must** inform delegates at the start of their presentation or on their poster.

## Archiving and sharing your poster

We encourage you to consider archiving your poster. Doing so makes it publicly available and citable by yourself and others. In addition, those interested can easily download it for later reference and it may provide increased visibility for your work (e.g. to those not attending the conference or who were there but missed it among the hundreds of others).

We suggest figshare (https://figshare.com/about) as a platform to do this. Research deposited on figshare is stored under Creative Commons licenses that allow you to retain ownership and get credit for your work.

## Refreshments and Lunch

Daily refreshments (including tea, coffee and water) will be provided adjacent to the workshop lecture theatre and lunch in the University canteen.

## Charging stations

Charging stations will be available at the Registration & Helpdesk.

## Message board

A message board will be located near the Registration & Helpdesk. Registrants are welcome to post notices about events, jobs, announcements, and messages for other attendees.

# The application of population genomics to fisheries management

## Workshop Programme

### Monday 8th May 2017

| | |
|---|---|
| 09:30 – 10:00 | Registration and Reception of participants |
| 10:00 – 10:15 | Welcome address and housekeeping |
| 10:15 – 11:00 | **STEFANO MARIANI.** Stock identification in the genomic era: paradigm shift or missed opportunity? |
| 11:00 – 11:30 | Coffee-break |
| 11:30 – 12:15 | **SHAWN NARUM.** Integrating Genomics with Fisheries Conservation and Management in the Columbia River, USA. |
| 12:15 – 12:35 | **TORILD JOHANSEN.** Real time regulation of coastal fisheries in a protected fjord based on genetic monitoring. |
| 12:35 – 14:00 | Lunch |
| 14:00 – 14.15 | Point of order |
| 14:15 – 15.00 | **NAIARA RODRIGUEZ-EZPELETA.** Connectivity and traceability in mackerel and bluefin tuna: providing advice and tools for management. |
| 15:00 – 15:20 | **SAMANTHA A. HOOK.** One fin too many; using DNA barcoding to identify illegal, unreported and unregulated chondrichthyan fishing in Morocco. |
| 15:20 – 15.40 | **RITA CASTILHO.** Expected benefits of population genomics of European anchovies. |
| 15:40 – 16.15 | Coffee-break |
| 16:15 – 17.15 | Open floor discussion |
| 17:15 – 17:45 | Poster session |

## Tuesday 9th May 2017

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|---|---|
| 09:40 – 09:50 | House keeping |
| 09:50 – 10:00 | Rapporteur summary |
| 10:00 – 10:45 | **IAN R. BRADBURY.** Promises, promises: The emerging field of fisheries genomics. |
| 10:45 – 11:05 | **SABRINA LE CAM.** RAD genotyping to investigate fine scale population structure delineation of the Thornback ray (*Raja clavata*) in the North East. |
| 11:05 – 11:30 | Coffee-break |
| 11:30 – 12:15 | **CINDY LAWLEY.** Applications for genetic tools in Aquagenomics: Fisheries, Aquaculture and Water sampling. |
| 12:15 – 12:35 | **TOM JENKINS.** Exploring the population structure of European lobster: the utility of SNPs in lobster fisheries management. |
| 12:35 – 14:00 | Lunch |
| 14:00 – 14.15 | Point of order |
| 14:15 – 14.50 | **FLORIAN GRAEDLER.** From microarrays to Next Generation Sequencing: Genomics tools revolutionize science. |
| 14:50 – 15:20 | **MARK COULSON.** Development of optimal molecular markers of domestication in Atlantic salmon for assessing introgression in wild populations. |
| 15:20 – 15.40 | **PIERRE-ALEXANDRE GAGNAIRE**. Revealing fine-scale population structure using introgression signals in the European sea bass. |
| 15:40 – 16.20 | Coffee-break |

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|---|---|
| 16:20 – 16.40 | **STEPHEN SABATINO**. Conservation genomics of the Eurasian shad (*Alosa*). |
| 16:40 – 17:00 | **PANAGIOTIS KASAPIDIS**. Global genetic structure of the swordifish (*Xiphias gladius*, L.) as revealed by microsatellite DNA and ddRAD analyses. |
| 17:00 – 17:50 | Open floor discussion |

## Wednesday 10th May 2017

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|---|---|
| 09:00 – 09:10 | House keeping |
| 09:10 – 09:20 | Rapporteur summary |
| 09:20 – 10:05 | **GARY CARVALHO.** Genomics and the fishing industry: translating advances into action. |
| 10:05 – 10:25 | **CLAUDIA JUNGE.** Towards synthesized knowledge management and transfer for 'omics' data to better advise fisheries management. |
| 10:25 – 11:10 | **JANN THORSTEN MARTINSOHN**. Fisheries Genomics and the Common Fisheries Policy: A square peg in a round hole? |
| 11:10 – 11:35 | Coffee-break |
| 11:35 – 12:30 | Final discussion. Closing. |
| 12:30 – 14:00 | Lunch |
| 14:00 | Bus to downtown Faro. Boat excursion. |

# Abstract of keynote presentations

# Stock identification in the genomic era: paradigm shift or missed opportunity?

**Stefano Mariani**, University of Salford, UK
s.mariani@salford.ac.uk

The last decade has seen the advent of next-generation sequencing technologies in the realm of fisheries genetics, which enabled marine population biologists to rapidly access much wider segments of genomic variation, and even sequence whole genomes at staggeringly reduced costs. This 'sea change' has been hailed as the most significant technological advancement since the development of polymerase chain reaction, and is revolutionising the toolkit of fisheries and conservation biology. By analysing nearly 5,000 studies published since 2008, I show that the use of genomic SNPs has gradually increased from <10% to nearly 50% of the published literature in fish population genetics, with a particularly sharp increase over the last two years. However, a closer analysis of the >800 articles using SNPs, reveals that 338 of them (40%) focus specifically on salmonid species, and 71 on Atlantic cod. The vast majority of the remainder are centred on functional genomics of farmed animals, with only a tiny minority of studies that actually employ these novel techniques for the purpose of stock identification, dispersal, biogeography, etc. Thus far, only 17 marine fish species have been investigated using high through-put genomic approaches, the majority of which only by a single study, and with only a handful that examined genomic SNPs and earlier-generation methods on the same populations and individuals. Here I examine the reasons for this trend and the potential disadvantages for resource management; I also discuss possible mitigating strategies that may promote a more significant spillage of genomic approaches into the environmental and ecological arenas.

# Integrating genomics with fisheries Conservation and management in the Columbia River, USA

**Shawn Narum**, CRITFC, USA

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As abundance and diversity of native fishes have declined throughout the Columbia River in the last century, there is high conservation priority for several species in this system. Conservation management of distinct stocks requires understanding of not only neutral genetic structure, but also the genomic basis for functional traits that contribute to complex life histories. A combination of neutral and adaptive genetic markers can be critical tools for genetic monitoring and tracking of specific stocks so that managers can adjust harvest to focus on healthy stocks and reduce impact on endangered stocks. It is also necessary to evaluate various hatchery release strategies used to supplement natural stocks in order to determine the most effective manner to increase abundance without reducing fitness of wild stocks. I will demonstrate how these different concepts are being incorporated into fisheries management in the Columbia River with a combination of genomic approaches such as RAD-seq, Pool-seq, and GTseq that utilize NextGen sequencing.

## Connectivity and traceability in mackerel and bluefin tuna: providing advice and tools for management

**Naiara Rodriguez-Ezpeleta**, Natalia Díaz-Arce, Paula Álvarez and Haritz Arrizabalaga, AZTI, Spain

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Atlantic mackerel (*Scomber scombrus* L.) and Atlantic bluefin tuna (*Thunnus thynnus*) are widely distributed fish that perform extensive migrations between spawning and feeding grounds. Within the western and eastern Atlantic Ocean, mackerel include two or three spawning components respectively, though, it is not clear if components within each side are genetically differentiated and if, consequently, this species exhibits a natal homing behavior. On the other hand, this species has expanded its northern limit, with new feeding areas found in Icelandic and Greenlandic waters in recent years; yet, the origin (western or eastern Atlantic) of individuals caught in the northern limit of the species is unclear. A correct management of this species requires determining connectivity among spawning components within each side of the Atlantic and developing a traceability tool to assign origin of individuals caught in feeding grounds. The Atlantic bluefin tuna spawns in two main areas (the Gulf of Mexico and the Mediterranean Sea), but individuals mix extensively in the Atlantic Ocean and can even cross from the west to the east coast. Yet, management of this species assumes two stocks, one at each side of the 45°W meridian. A correct management of this species requires a traceability tool that can assign individuals caught in the mixing areas to their birth place. Here, we have assessed homing behavior in Atlantic mackerel and Atlantic Bluefin tuna through population structure analyses of reference samples (larvae, young of the year and spawning adults) using Single Nucleotide Polymorphisms (SNPs) discovered and genotyped through restriction site associated DNA sequencing (RAD-seq). For Bluefin tuna, we have derived a panel of 96 SNPs that has been, after technical and biological validation, applied to assign origin of one thousand Bluefin tuna individuals captured throughout the Atlantic Ocean. Overall, our study provides critical advice on connectivity among spawning areas and supply valuable traceability tools for effective management of these two species.

# Promises, promises: The emerging field of fisheries genomics

**Ian R. Bradbury**, DFO, Canada
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Advances in DNA sequencing technology have fundamentally changed the field of population genetics, allowing genome-wide patterns of spatial divergence and linkage disequilibrium to be examined on scales previous impossible. This presents huge potential for application to marine conservation and fisheries management, but also brings challenges both logistical and theoretical. Here I explore potential advances that the emerging field of population genomics may hold for fisheries management, focusing on the benefits, limitations, and the challenges that remain. Specifically, I will examine how a high resolution genome-wide perspective can alter our interpretation of marine population structure, contributes to our understanding of fishery associated exploitation, and enhances predictions of future stock productivity and distribution patterns. Genomic studies increasingly report cryptic diversity in exploited marine species, which is revealing a need for changes in the geographic scales of management, but also complicated by substantial variation in differentiation across the genome and among methods. Using new genomics-based descriptions of stock structure, stock specific exploitation can be resolved at spatial scales previously not possible. However, logistical challenges such as the design and assessment of informative panels of loci from huge datasets remains a source of significant bias and error. Similarly, marine genomic data integration with high resolution environmental and habitat data are allowing the prediction of future distribution patterns under marine climate change scenarios. In the near future, environmental DNA (eDNA) may enable monitoring of species distribution and abundance changes as they occur. Genomic applications in fisheries science offer the potential for significant advances to the management of marine resources, yet will undoubtedly require continued consideration of the logistical and theoretical limitations if potential gains are to be fully realized.

# Advances in DNA sequencing technology have fundamentally change

**Cindy Lawley**, Illumina, USA

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Join Illumina for a lively discussion around how our customers are using molecular methods including genotyping and next generation sequencing (NGS) as tools to address challenges in important areas of fisheries, aquaculture and water sampling. These include fisheries applications of species ID, characterizing species stock structure, mixed stock analysis, estimating abundance, genetic consequences of stock enhancement and ecosystem monitoring through metagenome analyses. In aquaculture, we can share methods for genome based breeding, genomic selection (broodstock selection on multiple traits), pathogen detection, and haplotype characterization. Freshwater sampling and oceanography applications primarily revolve around diversity analysis and environmental DNA applications through micro and metagenome methodologies.

# From microarrays to Next Generation Sequencing: Genomics tools revolutionize science

**Florian Graedler**, Illumina, USA

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Using Bead Array technology and the Infinium assay, Illumina took the leadership in SNP genotyping with microarrays before it became the market leader of next generation sequencing (NGS). This presentation will give an insight into the principles of Illumina microarray and NGS technology and how these techniques can be easily implemented for applications like sequencing by synthesis or 16S rRNA metagenomics profiling. While the analysis of large NGS data sets seemed for many labs the bottleneck that prevented them from using this technology in their projects, Illumina's cloud-based BaseSpace now offers a user-friendly platform with many software applications for data analysis, data management, sharing and interpretation.

## Genomics and the fishing industry: translating advances into action

Gary Carvalho, University of Bangor, UK

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It is well recognised that fisheries resources are a major contributor to human well-being across the globe, providing a range of social and economic benefits. Moreover, exploited species typically comprise important components of aquatic ecosystems across trophic levels, and thus underpin aspects of ecosystem diversity and function. Such contributions are, however, increasingly under threat. Despite the long-held aim of sustainable yields, numerous wild fisheries either are over-exploited or are in precipitous decline. While the global view is not universally pessimistic, we need to recognise fisheries as natural resources that are not necessarily renewable. Moreover, the time-scale for management should be extended to incorporate effectively the implications of biological integrity (species and population-level), genetic change and evolutionary response. Such ideas are, however, not new. Since the turn of the 20th century, emphasis was placed on the local self-sustaining population or stock, and not the typological species, as the unit of study for fisheries management. Correspondingly, there has been significant investment in identifying and monitoring the dynamics of such population-level integrity. Nevertheless, it is the usual lack of recognition that stock integrity is influenced by genetic processes that renders it vulnerable to environmental change and that jeopardises sustainability. Here, I consider the underlying rationale for sustainable exploitation within an evolutionary context: why it is necessary, and how it can facilitate recovery and conservation of natural fisheries resources. A brief historical narrative and critique of genetic and genomic approaches will be presented, with an emphasis on the role that fisheries geneticists and managers can play in developing programmes towards sustainable exploitation. There remains a need to focus efforts that integrate a quantitative (numerical change in fish abundance) with a qualitative (changes in genetic composition) approach. New techniques such as the application of genome-wide sequencing technologies will be considered, with applications ranging from traceability to conservation of adaptive diversity. Challenges such as climate change, fisheries-induced evolution, overexploitation, stock recovery and resilience, and the devastating impact of illegal, unreported and unregulated fishing (IUU) will be highlighted.

# Fisheries Genomics and the Common Fisheries Policy: A square peg in a round hole?

**Jann Martinsohn**, JRC, Italy

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The Common Fisheries Policy (CFP) is a major policy framework, under which 28 European Union (EU) Member States (MS) share the management of the common natural renewable resource fish and shellfish. The CFP aims to ensure that fishing and aquaculture are environmentally, economically and socially sustainable and that they provide a source of healthy food for EU citizens. To that end it insists on the provision of "best available scientific advice", that should underpin major goals such as moving towards maximum sustainable yield as well the implementation of an ecosystem-based approach to fisheries management. Paving the way for sustainable and profitable wild capture marine fisheries and aquaculture is a challenging policy endeavour. Both activities rely on the health of complex and vulnerable ecosystems that are hardly understood. Also fisheries and aquaculture are embedded in a complex social and economic environment, compete with other activities and depend highly on global trade patterns. It is now generally accepted that a shift towards a sustainable and profitable exploitation of marine natural resources requires the integration of knowledge derived from various sources. Here, the rapid progress in the field of genetics and genomics offers major opportunities to strongly support marine resource management, particularly when integrated with other approaches. And yet, while the CFP provides a fertile environment to integrate scientific advice into its policy cycle, the incorporation of genetic and genomic information under its scientific advice mechanisms remains surprisingly marginal. This presentation will discuss the current status of the application of genetic and genomic approaches for fisheries and aquaculture management with emphasis on the CFP. Needs emerging from this major EU policy that might be addressed with genomic approaches will be depicted. Moreover, a selection of examples will illustrate value and successes, but also specific challenges and pitfalls.

# OTHER ORAL PRESENTATIONS

# Real time regulation of coastal fisheries in a protected fjord based on genetic monitoring

**Torild Johansen,** Jon-Ivar Westgaard, Bjørghild Seliussen, Kjell Nedreaas, Geir Dahle, Roger Kvalsund, Aglen Asge
Institute of Marine Research Norwegian, Tromsø, Norway

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Evaluating the effectiveness of fishery closures of mixed stock fishing grounds for protection of vulnerable stock components is challenging. Since 2007, the Institute of Marine Research, Norway, has monitored cod (*Gadus morhua* L) in a mixed stock fishery of Northeast Arctic cod (NEAC) and Norwegian coastal cod (NCC) based on genetic sampling. The NCC is more vulnerable and in need of protection to rebuild the spawning stock. We monitored a fjord system in Northwest Norway. Sampling of cod entering the protected fjord was conducted three times a week throughout the spawning season to assess the fraction of NEAC in the catches. Some samples were also collected from within the protected fjord to compare the stock composition within the protected area to sampling sites outside the area. Samples of mature adults and fertilized eggs were analyzed for microsatellites and single nucleotide polymorphism (SNP) markers. Results show that although NEAC enter the fjord, they do not seem to spawn in any large quantities. This new information of the cod stock dynamic within a fjord system may have a relevance to similar ecosystems.

# One fin too many; using DNA barcoding to identify illegal, unreported and unregulated chondrichthyan fishing in Morocco

[1]**Samantha A Hook**, [2]Louise Ruddell, [1]Michael Buckley, [3]Andrew Griffiths
[1]University of Manchester, [2]Fin Fighters.org, Bristol, [3]University of Exeter

samantha.hook@manchester.ac.uk

The world is rife with illegal, unreported and unregulated (IUU) fishing. It is estimated that up to 40% of the fish caught in West Africa is from an IUU source, with sharks, rays and chimaeras (chondrichthyans) at most risk due to the demand for fin trade and increasing number of regulations put in place. The country of Morocco (located geographically in North West Africa) is one of the least researched countries for chondrichthyan landings and IUU fishing, despite internationally recognised trade and fisheries partnership agreements of around €30 million per year with the European Union. Morocco is also a part of the Conservation for Migratory Species (CMS) and Convention on International Trade in Endangered Species (CITES) which provide specific levels of protection for certain chondrichthyan species however there is no published record of these protections being applied. Here we investigated the exploitation of chondrichthyans in ports and markets along the Atlantic and Mediterranean coast of Morocco and reviewed the advantages and disadvantages of genomic assessment to identify IUU fishing in developing countries. We visited a total of 6 towns/cities in the June of 2015 and 2016 for total duration of 8 weeks. Documentary evidence and 231 samples of chondrichthyan individuals were collected. Using the FISH-BOL primers (F1, F2, R1 and R2 combinations) we successfully barcoded 201 samples of chondrichthyan individuals equating to 17 species of shark, 13 species of ray and 2 species of chimaera. Through intelligence with fishermen we recorded a demand and targeted IUU trade of the bigeyed thresher sharks *Alopias superciliosus* in 50% of the towns/cities visited. Through the DNA barcodes we recorded a new landing of the Tortonese's Stingray *Dasyatis tortonesei* in an Atlantic port from an artisanal fishery. Lastly we review the levels of misidentification and the uses of DNA barcoding as a method of recording and preventing IUU fishing of chondrichthyan species in Morocco and other developing countries.

# Potential benefits of population genomics applied to European anchovies

[1]**Rita Castilho,** [1]Regina Cunha and [2]Gonçalo Silva

[1]CCMAR, Universidade do Algarve, Faro, Portugal; [2]MARE-ISPA, Lisboa, Portugal

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Small pelagic fish typically display large effective population size, high fecundity, high levels of dispersal and gene flow which are conducive to weak population genetic structure. We will show-case the population genetics of the European anchovy (*Engraulis encrasicolus*), displaying a complex population structure and evidence for temperature-dependent selection. Next Generation Sequencing (NGS) tools presently enable researchers to cover larger areas of the genomes that traditionally have been probed with comparatively very few markers. Potential results are addressed showing the benefits and drawbacks of the application of these techniques to improve fisheries management by unveiling the evolutionary forces that drive the spatial and temporal heterogeneity of the stocks.

# RAD genotyping to investigate fine scale population structure delineation of the Thornback ray (*Raja clavata*) in the North East

**Sabrina Le Cam**, Florence Cornette, Grégory Charrier, Sylvie Lapègue, Eric Stéphan, Pascal Lorance

Ifremer and LEMAR, France

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At the ecosystem level, sustainable exploitation of fisheries resources depends not only on the status of target species but also on that of bycatch species, some of which are even more sensitive to exploitation. It is especially the case for Elasmobranchs species whose abundance declined during the 20th century. Yet their biology of is still poorly known and traditional fisheries stock assessment methods using fisheries catches and scientific survey data for estimating abundance are expensive or even inapplicable due to the small numbers observed data in such species. This project aims at, first resolving the population genetic structure of the Thornback ray in a large part of its distribution range and second, providing genomic resources to attempt to apply a recent genetic-based methods for absolute population abundance estimation. Over 500 individuals sampled from the North Sea, the Celtic Sea, the Bay of Biscay, down to the Azores islands and the Mediterranean Sea were genotyped at 13,324 filtered RAD loci. Preliminary results showed a strong genetic structure among the samples ($Fst = 0.09$, $p<0.001$) mainly due to differences between Mediterranean, Azorean and Atlantic continental shelf samples. To assess the uses of large population genomic datasets in a context of weak genetic structure, analyses aiming at using a large number of SNPs and outlier loci to investigate fine-scale population structure delineation in the samples of the Atlantic continental shelf ($Fst = 0.007$) will be presented. A set of RAD derived SNPs were also selected to carry out parentage assignments on a large sample from the Bay of Biscay and estimate sibs frequency to derive population abundance.

# Exploring the population structure of European lobster: the utility of SNPs in lobster fisheries management

**Tom L. Jenkins** and Jamie R. Stevens
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In marine species, inference of genetic structure and connectivity is not always trivial because of typically high gene flow and a general lack of barriers to dispersal, leading to weak genetic differentiation. These biological factors are also frequently compounded by the limited resolution associated with many traditional genetic markers. Fortunately, recent advances in sequencing technology have enabled thousands of genome-wide markers to be characterised for non-model organisms, potentially providing greater power and resolution than previously available. In this study, we present a preliminary exploration of genetic structure and connectivity in the European lobster (*Homarus gammarus*), a species of considerable economic and ecological importance which has previously shown little genetic differentiation using microsatellites and other traditional markers. Specifically, we explore the possibility of fine-scale genetic variation within this species and assess the distinctiveness of samples from around Britain and northwest Europe. Subsequently, we explore whether natural patterns of population connectivity are sufficient to enable natural replenishment of threatened stocks. The existence of stable genetic structure can facilitate the tracing of lobsters and aid in understanding the potential impacts of supplementing wild stocks with hatchery-reared juveniles, whilst avoiding long-term deleterious effects on their genetic diversity. To maximise the power for detecting differentiation, we are using restriction-site associated DNA (RAD) sequencing to identify polymorphic single nucleotide polymorphisms (SNPs) across the genome and a SNP panel is under development containing a suite of the most informative SNPs. The results of our study and the SNP panel will likely be of great benefit to stakeholders and fisheries management. Ultimately, we anticipate that our SNP panel will be available to other researchers studying *H. gammarus* and will give managers a tool to monitor the genetic diversity and structure of their stocks over time.

# Development of optimal molecular markers of domestication in Atlantic salmon for assessing introgression in wild populations

[1]**M. Coulson**, [1]L. Marcello, [2]V. Pritchard, [3]K. Glover, [4]K. Hindar, [5]D. Ensing, [6]T. Moen, [7]M. Kent, [7]S. Lien, [8]I. Bradbury, [9]P. McGinnity, [10]J. Gilbey, and [1]E. Verspoor

[1]University of the Highlands and Islands, Inverness College, UK, [2]University of Turku, Finland; [3]Institute of Marine Research, Bergen, Norway, [4]Norwegian Institute of Nature Research, Trondheim, Norway, [5]Agri-Food and Biosciences Institute, Belfast, UK, [6]AquaGen AS, Trondheim, Norway, [7]Centre for Integrative Genetics, As, Norway, [8]Department of Fisheries and Oceans, St. John's, Canada, [9]University College Cork, Ireland, [10]Marine Scotland Science, Pitlochry, UK

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Controversy surrounds the direct genetic impacts of Atlantic salmon farming on wild salmonid stocks. While the majority of farm escapees are expected to die without breeding, some do remain or ascend rivers to spawn. A detailed understanding of the actual levels of interbreeding and introgression in most rivers is lacking which, along with an understanding of the adaptive differentiation of farm and wild salmon, is required to establish the actual impact of this potential interaction on the productivity and viability of wild populations. This project uses a genome-wide association study by screening SNPs between farmed strains and wild stocks of Atlantic salmon across their native range. To this end, representative samples of both farmed strains and wild stocks were collected from each of Scotland, Norway, Ireland and Canada. DNA for each individual was quantified, and normalised and samples for each farmed strain or wild population were pooled into a single tube for allelotyping. A subset of pools were repeated as technical replicates, resulting in a total of 96 pools representing farmed or wild samples. These pools were then genotyped for a panel of 930,000 SNPs at the Centre for Integrative Genomics (CIGENE), Norway. Individual genotype and intensity data from previously genotyped individuals was used to calculate correction factors for allele frequency estimates from pooled intensity data of our samples. From these allele frequency estimates, pairwise differences in allele frequencies, FST, and tests of selection were used to rank the SNPs in their discriminatory power to differentiate among farm and wild samples. We present preliminary results of the identification of the number and genomic distribution of the top SNPs and next steps for undertaking individual genotyping. Furthermore, we discuss the methodological considerations and implications of using a pooling approach for initial filtering of large SNP panels.

# Revealing fine-scale population structure using introgression signals in the European sea bass

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The European seabass (*Dicentrarchus labrax*) is genetically subdivided into two partially reproductively isolated lineages, one living in the Atlantic and the other in the Mediterranean. Previous attempts to delineate stocks for fisheries management within those lineages have struggled with a lack of spatial genetic structure at neutral markers, especially within the Atlantic. Here, we build on the theory of genomic islands of differentiation to provide an empirical assessment of genetic connectivity using introgression signals. Using phased whole-genome sequence data, we show that the length distribution of introgressed genomic fragments of Atlantic origin can be used to reveal genetic connectivity patterns within the Mediterranean Sea. We then test the existence of a cryptic genetic structure within the Atlantic lineage using a 1K SNP chip dataset in 827 individuals. We detect a latitudinal admixture gradient originating at the contact zone with the Mediterranean population, which extends northward and reveals a cryptic barrier to gene flow in Brittany. As predicted by theory, introgression gradients at individual loci are mostly detected in genomic regions located in the periphery of genomic islands of differentiation between Atlantic and Mediterranean lineages. Although introgression gradients may confound the detection of local adaptation loci, they are of prime importance to improve stock delineation when the neutral migration-drift balance is not informative.

## Conservation genomics of the Eurasian shad (*Alosa*)

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We have assembled a de novo genome of the Eurasian shad, *Alosa alosa*, using overlapping-read and mate-pair data, and generated ~ 25-fold coverage Pool-seq data for 15 anadromous and freshwater populations of *A. alosa, A. fallax and A. immaculata*. The resulting Pool-seq data was aligned to the A. alosa genome and used to generate allele frequencies for ~2 million SNP loci for each population. Change in allele frequency (ΔA) and FST in 20Kb genomic windows were then used to identify candidate loci associated with the transition from an anadromous to completely freshwater life history. The assembled genome had a scaffold N50 of 2Mb. The ΔA analysis revealed significant shifts in allele frequencies between anadromous and freshwater population pairs in each species we studied for hundreds of SNP loci, most of which sit in just a handful of the same genomic locations. Similarly, FST for tens of the same 20Kb genomic regions were found to be significantly higher than expected under neutrality in one or all three *Alosa* species. Many of the candidate loci found were in introns, or upstream, from genes involved in ion-transport, stress response and brain and muscle development. Remarkably, several of the candidate genes identified have previously been found to be under selection in anadromous fish species that have adapted to a completely freshwater life history, such as stickleback and salmon. These findings indicate that parallel adaptation to freshwater has occurred within *Alosa*, and that convergent evolution in the traits involved might be common, even among distantly related fish species. Ongoing and future work will include using this genome data to devise plans to maintain the adaptive potential of threatened Alosa species, developing molecular inversion probes to conduct *mixed* stock analysis and establishing methods to accurately identify hybrids in populations in which introgression has been observed.

# Global genetic structure of the swordfish (*Xiphias gladius*, L.) as revealed by microsatellite DNA and ddRAD analyses

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The swordfish is an epipelagic fish found in all oceans around the world. Despite its high migratory potential, various studies have revealed significant genetic structure between Mediterranean, Atlantic and Indo-Pacific, but also within Atlantic. In the current study, we compare the genetic structure revealed using microsatellite DNA and ddRAD analyses. In the first case, 2610 specimens from Mediterranean, Atlantic, Indian and Pacific stocks, were genotyped for fifteen microsatellite markers and analyzed using a Bayesian cluster analysis. The results suggested the presence of three clusters that correspond mainly to Mediterranean, Atlantic and Indo-Pacific regions, with extensive mixing between the two latter. Pairwise FST's and structure analysis further supported the genetic differentiation between north and south Atlantic. For the ddRAD analysis, 140 individuals, corresponding to nine sampling localities from the aforementioned oceans, were sequenced on an Illumina platform. The ddRAD analysis, based on 1600 SNPs, gave similar but more robust results, regarding the genetic structure within the Atlantic Ocean and the participation of each individual in the different genetic groups.

# Towards synthesized knowledge management and transfer for 'omics' data to better advise fisheries management

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Appropriate knowledge management strategies are becoming increasingly important as the amount of data and knowledge being generated by science is skyrocketing. This is true for all stages of a research's lifetime, from data generation all the way through to new discoveries and their publication in scientific journals. Further, the communication and the transfer of scientific knowledge to appropriate end-users like fisheries managers is not trivial. This is a crucial step if research findings are to be integrated into future management strategies. I will talk about methods for knowledge management and knowledge transfer, from collection through analysis to applications in industry and policy. I will use some examples from my own and other’s fisheries and population genomics datasets and research findings to show different strategies, or a lack thereof, and demonstrate what works and what doesn’t in knowledge transfer. So, how can we use this information now, to better inform fisheries policies both at the national and European level? Is there a “recipe” for knowledge transfer of population genomic findings we can develop? I will make a start and invite everyone to engage in a lively discussion towards that goal.

# POSTER PRESENTATIONS

# Genetic identification and connectivity patterns of two threatened smoothhound sharks: insights for conservation

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Sharks are among the most threatened marine fauna due to their life-history traits that reduce populations' ability to recover after intense overharvesting. Effective management of shark fisheries is often compromised by high rates of species misidentification and inaccurate stock assessment. However, the application of genetic tools over the past 25 years has greatly contributed to elasmobranch studies, especially to those aimed at assisting conservation efforts. In this project, the population genetic structure and demography of two endangered smoothhound sharks (*Mustelus mustelus* and *Mustelus punctulatus*) will be investigated across two major sub-basins: the north-central Adriatic Sea and the Strait of Sicily. These bio-economically important species show partially overlapping distribution ranges and are often misidentified due to unclear and sometimes contrasting diagnostic characters. Species-specific assessments are therefore arduous to develop, and thus accurate identification is paramount to properly define and manage populations. In addition, the smoothhounds' migratory behaviour and connectivity, which are key factors to understand the vulnerability of the populations to fishing activities, are poorly known in the Mediterranean Sea. In this context, we will first genetically identify smoothhounds' samples collected in the two sub-basins using two approaches based on species-specific PCR amplification of the mitochondrial cytochrome c oxidase I (COI), and fragment analysis of several diagnostic microsatellite loci. Furthermore, patterns of genetic diversity, gene flow, and populations' connectivity will be inferred from multilocus microsatellite markers. This data will help to correctly assign Management Units (MUs), and it will give

insights about the movements and migratory behavior of both species in the Adriatic Sea.

## Estimates of Ne of sea lamprey in Portugal: a temporal approach using the interannual fluctuations in the genetic composition

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In recent years population genetics have increasingly been used for delineation and management of fish stocks. More specifically, estimates of changes in effective population size (Ne) and population structure stability are crucial to predict their possibilities for adaptation to future changes, including the effect of overexploitation or other adverse environmental changes. The sea lamprey *Petromyzon marinus*, being an anadromous species, is quite vulnerable to a number of disturbances, including a very profitable fishery that places an additional burden on populations. Previous studies revealed no population structure along European coasts and shallow genealogies, with low genetic diversity levels. A total of 158 specimens, comprising individuals collected in 2005, 2012 and 2015 in river Vouga (Portugal), were screened for genetic variation using the mitochondrial non-coding region I. Genetic diversity indices were similar and 3 out of 4 haplotypes were shared between sampling periods. The haplotype network showed a shallow genealogy with few levels of diversification. No temporal structure was found (FST = -0.014, P-value = 0.580). The sea lamprey population yielded lack of genetic drift between the analysed periods (Fs’=-0.028 for the first period and Fs’=-0.099), indicating that genetic stochasticity may play a small role in this population. Revisiting these results with a finer-scale genomic approach may provide a much needed confirmation of this overall scenario of population structure and genetic drift absences.

# Historical gene flow constraints in a northeastern Atlantic fish: phylogeography of the ballan wrasse *Labrus bergylta*

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The distribution and demographic patterns of marine organisms in the north Atlantic were largely shaped by climatic changes during the Pleistocene and influenced by biological and ecological factors intrinsic to each species. The ballan wrasse (*Labrus bergylta*), the largest labrid fish along Europe's continental margins, is a target for fisheries and aquaculture industry. The phylogeographic pattern, population structure, potential glacial refugia and recolonization routes for this species were assessed across its full distribution range. The existence of a marked population structure can reflect both recolonization from three distinct glacial refugia and current and past oceanographic circulation patterns. Although isolated in present times shared haplotypes between continental and Azores populations and historical exchange of migrants in both directions point to a common origin of *L. bergylta*. This situation is likely to be maintained and/or accentuated by current circulation patterns in the north Atlantic, and may lead to incipient speciation in the already distinct Azorean population. Future monitoring of this species with a genomic approach would be crucial to re-assess this pattern at a finer scale and to evaluate how this species is coping with current environmental changes.

# Failure of the classical DNA sequence method to infer the population structure of *Trachurus picturatus* from NE Atlantic

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The blue jack mackerel, *Trachurus picturatus*, is a pelagic fish widely distributed in the NE Atlantic, and in the Mediterranean and Black Seas. It is an economically important resource in the Macaronesian islands of Azores, Madeira and Canaries, but despite its fishery value and ecological importance, fluctuations in the landings are difficult to explain since studies regarding the population dynamics, stocks structure and fish movements are, at present, inexistent. During the year 2016, 120 juvenile individuals were sampled by the artisanal fleets in Azores, Madeira, Canary Islands and Portugal mainland at Matosinhos, Peniche and Portimão. For each individual, genomic DNA was extracted, followed by a Polymerase Chain Reaction amplification of partial mitochondrial (mtDNA) and nuclear DNA genes. Fragments of mtDNA from the control region (D-loop), cytochrome c oxidase subunit I (COI) and cytochrome b (cyt-b) were sequenced following a previous work published for this genus. Nuclear DNA partial genes of both, the first intron S7 and the MN32, were also sequenced for the first time in few individuals. The alignment of the DNA sequence data was performed with the addition of sequences from the Mediterranean and the Atlantic Ocean, available on GenBank. Analyses revealed a very shallow phylogenetic tree. The phylogeographic patterns indicated little or no genetic differentiation for the blue jack mackerel in the NE Atlantic, with COI and cyt-b haplotype network revealing a star-like pattern but with several haplotypes shared among all the populations. All mtDNA genes presented very high haplotype diversity. The absence of genetic differentiation points to the need of a genome-wide population genomics approach. The development of microsatellites and/or SNPs, in order to improve the knowledge of the existent stocks of the blue jack mackerel in the NE Atlantic Ocean, are currently being evaluated.

# Genetics of local adaptation in Atlantic Bluefin tuna from the Mediterranean Sea

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The Atlantic Bluefin tuna (ABFT, *Thunnus thynnus*), one of the largest top-predator fish inhabiting the pelagic ecosystems of the North Atlantic Ocean and Mediterranean Sea, has been extensively overexploited in recent decades. However, in the Mediterranean Sea, the mixing rates between the eastern, central and western basins have not yet been resolved. Both electronic tagging, otolith and genetic markers cannot still depict a clear scenario of tuna movements and structuring, essential requirement for a proper management of ABFT fisheries. Here we used Expressed Sequence Tag-linked (EST-linked) microsatellites to explore the patterns of adaptive evolution of *T. thynnus* population and of its population dynamics in the Mediterranean Sea. For this purpose 16 EST-linked microsatellites were genotyped in 177 tuna individuals from the Mediterranean and several methods were used to explore population genetic structuring and estimate/detect signals of local adaptation. Bayesian clustering results indicated the presence of a single cluster, corroborated also by the Correspondence Analysis and pairwise FSTs. Similarly the two methods, used for the detection of FST outliers, did not reveal any pattern suggesting the presence of selective pressure. Our results advise that the low level of polymorphism detected in EST-SSR loci used in this study could be ascribed to the presence of relatively conserved regions flanking these microsatellites. These genomic regions are probably not involved in physiological responses to local adaptation and we were able to rule out action of divergent or balancing selection on EST-SSR polymorphism.

# Venomous fish transcriptomics - A top-down approach as complement to a bottom-up analysis

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Venomics is a fascinating research area, with different compounds identified in each new venomous species. The potential is wide, including prospecting venom evolutionary conservatism/lability, investigating its biological and physiological properties and drug development. Marine creatures, particularly fish, have been largely overlooked and their venoms are poorly characterized, an unexpected situation since they represent more than 50% of the total known venomous vertebrates. European ichthyofauna includes venomous species from different fish families, namely Dasyatidae, Trachinidae and Scorpaenidae. Although described as nonlethal these venoms are reported to induce cardiovascular and neurotoxic effects and associated to hemodynamic changes. The venom diversity within the genus *Scorpaena* is still unknown, however two venom proteins from a single west Atlantic species (*Scorpaena plumieri*), were recently described. They were isolated from the venom spines and identified as a cytolysin with hemolytic effect and C-type lectin with hemagglutinating effects. Recently our team described the protein profiles of four species from the Portuguese ichthyofauna. The diversity encountered among closely related species is a promising start for future research on fish venom bioprospecting. Traditional SDS-PAGE analysis of protein venomous extract, combined with LC-MS/MS sequencing may be complemented with protein annotation underpinned by venom gland transcriptomes. This approach enables the identification of a large number of venom gland proteins, which may belong to known molecules or new bioactive components yet to be described. Using RNA-Seq, it will be possible to identify species-specific transcripts and overlapping proteins in the venom gland of several species. To our knowledge this study represents the first combined survey of comparative transcriptomics from the venom apparatus of several fish species. A broad scale transcriptomic top-down approach combined with an analysis targeting the major venom components represents a powerful tool for the study of composition/activity correlations and venom evolution in fish, paving the way for future biotechnological and pharmacological applications.

# Application of 18S RNA microarray complemented by microscopy to study dynamics of harmful phytoplankton in an upwelling region with shellfish aquaculture (Sagres, Portugal)

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Harmful algal blooms (HABs) threaten public health through the contamination of seafood with biotoxins and cause economic damage to fisheries and aquaculture. HABs regularly occur in marine and brackish waters worldwide, especially in the regions affected by anthropogenic or natural nutrient enrichment, such as upwelling zones along the western continental margins. The Sagres area is subject to seasonal upwelling, most active during summer (June – September). Shellfish aquaculture is a new economic activity recently developing in the area, and is directly dependent on the phytoplankton primary production but is also threatened by HAB events. The 18S rRNA microarray was applied to detect toxic phytoplankton along with microscopy in surface water samples, taken from July 2014 to June 2016, at the station next to offshore mussel aquaculture farm (approx. 1 km from coast, 25 m depth). Sea surface temperature and Ekman transport were used to identify upwelling conditions. During summer 2014 and 2015, and spring 2016 the study area was generally in upwelling conditions with short periods of relaxation. Phytoplankton community was dominated by diatoms, among which potentially ASP-toxic *Pseudo-nitzschia* genus, represented by both *P. seriata* and *P. delicatissima* species complexes reached high abundances during upwelling periods. DSP-producing dinoflagellates of the *Dinophysis* genus were frequently present at dates following diatom blooms. The 18S rRNA microarray related to observations by microscopy provided more decisive identification of dinoflagellates of the genera *Alexandrium, Azadinium, Karenia, Karlodinium, Gymnodinium* and flagellates *Prymnesium, Heterosigma*. In the case of diatoms from the genus *Pseudo-nitzschia*, more species could be identified by microarray than the two morphological species complexes, *P. seriata* and *P. delicatissima,* identified by microscopy . Thus, we suggest that the applied RNA microarray is a potentially useful tool for harmful phytoplankton monitoring, that provides more precise taxonomic identification compared to microscopy.

# Genopoptaille project: moving stock assessment into the future

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The project GenoPopTaille aims at estimating the census population of the thornback ray in the Bay of Biscay using a close kin approach where the total number of adults in the population is estimated from the number of parent-offspring pairs in a large sample of adults and juveniles. To achieve this goal a number a challenging issues are addressed: the genetic diversity and connectivity of populations of the species throughout the Atlantic and Mediterranean Sea is analysed based upon RAD sequencing, a large sample of adults and juveniles from the Bay of Biscay is collected, the feasibility of genotyping egg capsules, which are stranded on the coast, is investigated, dynamic population modelling is carried out based on available fisheries dependent and independent data. The poster will present an overview of the project.

# Elasmobranchs in numbers: review of the European catches according to official data

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Elasmobranchs are one of the oldest and most diverse group of species inhabiting marine ecosystems. Due to their life-cycle, most of them are sensible to climatic perturbations and anthropogenic activities, like fisheries. Historically, the European Union has carried out the exploitation of elasmobranchs trough commercial fisheries and despite only a few are target species, almost all of them are captured as bycatch. This has led most populations of these species in a poor state of conservation within European waters. In view of this situation, the following study aims to carry out a comprehensive analysis of the catches made by the European fleet in the period 1950-2014 employing the FAO data, in order to understand the state and historical evolution of elasmobranchs stocks. The 15 species selected for the study were grouped according to their distribution in the water column: epipelagic (*Prionace glauca*, *Lamma nasus*, *Isurus oxyrinchus*, *Mustelus mustelus* and *Galeorhinus galeus*), mesopelagic (*Squalus acanthias*, *Dalatias licha* and *Scyliorhinus canicula*), bathypelagic (*Centrophorus squamosus* and *Centroscymnus coelolepis*) and raja sp. (*Dipturus batis*, *Raja clavata, Raja montagui*, *Leucoraja naevus* and *Dipturus oxyrinchus*). The statistical tests employed were ANOVA (Parametric) and Kruskal-Wallis (No-parametric). Mesopelagic species dominated the catches from 1950 to 1998, being replaced by epipelagic ones after that year, mainly *P. glauca*. Significant differences were found between catches per year. Fluctuations in the time series are indicating changes in the strategies of the European fishing fleet, as is the case of *P. glauca* and *I. oxyrinchus*, which value and catches has increased lately due to the increase of commercial demand of meat and the fin trade with the Asiatic market. With fishing pressures mounting, the use of population genomic approaches, will shed light on questions that have practical applications for species conservation and management, such as genomic identification of stock structure, effective population size and genetic diversity. Collaborative and complementary work of different research areas will be pivotal for the successful conservation of these species.

# The blackspot seabream fishery in the Strait of Gibraltar

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One of the most important commercially-exploited fish species in the Strait of Gibraltar is blackspot seabream (*Pagellus bogaraveo*). This demersal fish, usually found between 400 and 700 m deep in this area, is captured by a relatively small number of very specialized artisanal longline vessels that deploy their gear near the coast. Due to the high level of specialization of this fleet, in recent years more than 70% of weight landed in the main harbours corresponded to blackspot seabream. In Spain, this species is in very high demand, which has led to high prices in the local fish markets of the main landing harbours. Therefore, the annual total sales in these fish markets are highly dependent on fluctuations in biomass of blackspot seabream. In this study, we assess the potential for simulation and modelling of the blackspot seabream population in the Strait of Gibraltar, with SimFish 1.0, which allow us implement a discrete biomass-abundance dynamic model to obtain a simulated monthly time series of blackspot seabream biomass. On this simulated time series we fitted Autoregressive Integrated Moving Average (ARIMA) models. The best ARIMA fit provided a significant correlation and high persistence index. The proportion of variance non-explained by the ARIMA models was correlated with a time series of sea surface temperature (SST) and North Atlantic Oscillation (NAO). The analysis of the correlation between the proportion of variance not explained by the ARIMA models and environmental variables showed that significant associations were not detected for the full-time series. By contrast, significant correlations were found in some years, suggesting that overexploitation is a main factor responsible of the commercial depletion of blackspot seabream in the Strait of Gibraltar. This marine resource lends itself to a genomic approach, which would contribute to the evaluation of the present day genetic diversity and could possibly evaluate the connectivity between different coastal locations.

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Faro, Portugal
2017

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