

## Developing genomic resources of marine fish for sustainable stock exploitation GENOFISHRESOURCES

Population genetics have been used in the last decades to investigate the population structure of marine fish resources in order to discriminate separate stock to be harvested separately in order to better manage these resources (Carvalho & Hauser, 1995). Subsequently, novel techniques that made possible to discriminate even weak population structure, led to the discovery of extensive genetic population structure in many marine species, overturning the past dogmas of large and homogenous marine populations with limited local adaptation and speciation (Hauser & Carvalho, 2008). In the last decade, the advent of the increasingly cheaper Next Generation Sequencing (NGS), Reduced-Representation Sequencing (RRS), and the application of Single Nucleotide Polymorphisms (SNPs) have played a game-changing role in the study of population genomics of non-model species such as several fish species (Helyar, et al. 2011).

This project aims to apply the ultimate bioinformatics approach for studying the population structure and the potential genomic signature of local adaptation of different fish species, including both large pelagic and small benthic fish species such as sharks (see <https://fishreg.jrc.ec.europa.eu/web/medbluesgen>), tunas (FARB Unibo Prot. RFBO125984), red mullet (Progetto RITMARE), etc., in order to characterize their stock boundaries and enhancing better stock management.

The blue shark, *Prionace glauca*, is one of the most abundant epipelagic sharks that is found in all oceans, but its population structure along the Atlantic-Mediterranean gradient is still poorly characterized despite past attempts using conventional genetic markers such as microsatellites and mtDNA (Verissimo, et al. 2017; Bailleul, et al. 2018). Bailleul, et al. (2018) highlighted through simulations, the extensive time-lag between a demographic change and its detectable imprint in the population genetic structure, suggesting that genome scans may outperform conventional markers to detect patterns of population structure out of this 'grey zone'.

The use of genome-representative markers will enable to discriminate this "grey-zone" effect, allowing to clarify if the Mediterranean populations of blue shark have different genetic and demographic structure, helping to better conserve the species in this area, where it has been subject to a drastic population decline in the last decades (Ferretti, et al. 2008).

On the other hand, even benthic species shows no clear genetic structure in the Mediterranean Sea, such as the red mullet, *Mullus barbatus*. In fact, the use of conventional microsatellite markers didn't solve the population genetics structure of the species along the Italian coasts (Matić-Skoko, et al., 2018). However, these results are in contrast with previous works which suggest a strong population structure, even if using a small sample size and poorly structured sampling design (Galarza, et al., 2009).

New genomics resources and analytical tools, such as reference genome (Fietz, et al., 2020) and scan for selection would be of help in better understand how this benthic species are structured along different Geographical Sub Areas (GSA) in the Mediterranean Sea.

In this project, ready-to-use Restriction site associated DNA (RAD) markers, such as ddRAD and 2bRAD, from different species will be analysed to clarify the population structure of ecologically different species, and will inform stakeholders, organizations and commissions involved in the managing of these fishing resources, as well as disseminate the results through publications on peer-reviewed journals.

The successful candidate will be aqua-intended with the main bioinformatic tools used for population genomics analysis and related programming languages (bash, python, R), and would have experience in the analysis of RADseq data, such as ddRAD and 2bRAD.

Activity Plan:

### 1° quarter

During the first quarter, the candidate will undergo to a deep bibliographic revision of the state of the art for the population connectivity, ecology and fishery of the target species, and will do a summary of the main bioinformatic tools available to date for RADseq analysis for population genetics and scan for selection that may suite the study cases. Specifically, the candidate will investigate the actual stock delineation and fishing pressure of the target species before applying a bioinformatic pipeline to challenge the assumptions from bibliography and to test alternative hypothesis of population structure.

### 2° quarter

During the second quarter, the candidate will analyse ready-to-use RAD data of the target species taking into the account the knowledge acquired from the bibliographic revision done in the first quarter of the project.

The preliminary results from these analyses will be presented constantly in form of report in weekly internal meeting to the lab group, feeding the discussion, generating new ideas and questions which will be taken into consideration for further steps in the analyses. The preliminary results may be disseminated through conferences and meetings.

The RAD reads will, initially, mapped against available reference genomes (if any), and the resulting contigs, and possibly scaffolds, will be scanned for potential selection (if any), updating the preliminary result reports.

In this step of the project, the candidate may supervise lab's student during their Ph.D./M.Sc. thesis.

### 3° quarter

During the final quarter of the project, the candidate will revise the final results from the analyses which may have undergone to an internal review process. Then, the candidate will invest the final part of the project writing the manuscripts for disseminating the results for all the parallel works through peer-reviewed journals.

### References:

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MedBluesGen: <https://fishreg.jrc.ec.europa.eu/web/medbluesgen>

Veríssimo A, Sampaio Í, McDowell JR, Alexandrino P, Mucientes G, Queiroz N, da Silva C, Jones CS, Noble LR. 2017. World without borders—genetic population structure of a highly migratory marine predator, the blue shark (*Prionace glauca*). *Ecology and Evolution*, 7(13): 4768–4781. doi: 10.1002/ece3.2987