At present time, overfishing is known for increasing the risk of stocks' local decline across the Mediterranean area and for rapidly leading to the loss of long-term benefits of fishery products that have been historically shared by coastal communities (Tsikliras et al., 2013; Berkowitz et al., 2018). Although some measures have been already recommended by the Common Fisheries Policy (EU COM(2016)263), it appears necessary to define a blueprint aiming to implement an effective change in the management of the marine resources and ecosystems for the future generations through the integration of eco-social solutions and a proper knowledge and management of fishery stock units (Begg et al., 1999). Indeed, the survival of local stocks containing adaptive diversity is linked with the sustainability and resilience of marine fisheries towards climatic and anthropogenic impacts. This is also true for the Adriatic Sea, where precious demersal and small pelagic resources (i.e. sardine, European anchovy, striped venus and European hake) have already suffered of trans-border competitiveness and historical exploitation (Ungaro et al., 1998; Jukic-Peladic et al., 2001; FAO, 2018).

Twelve years of advances in genetic and genomic technologies went along with more rigorous species identification and stocks’ delimitation (Carvalho et al., 1995; Ward, 2000; Hauser et al., 2008; Waples et al., 2018), as well as seafood traceability along the chain from producer to consumer (Miller & Mariani 2010; Leal et al., 2015). At present time, Next Generation Sequencing (NGS) techniques are able to produce genome-wide molecular data enhancing the resolution of population structure studies (Milano et al., 2014; Hemmer-Hansen et al., 2014; Willette et al., 2014) and the detection of seafood mislabelling or species substitution (Martinsohn et al., 2009; Miller et al., 2012; Marin et al., 2018; Milan et al., 2019).

Given the high potential of genetic and genomic molecular markers, the PRIZE YOUR FISH project will mainly rely on these approaches that will be integrated with other sources of information (e.g. otolith chemistry) in a joined effort aiming to buffer the severe exploitation of small-pelagic fish stocks in the Adriatic Sea. In order to reach this goal, the research fellow will be tackling four main objectives:

1. The implementation of a quality control and traceability system for seafood using key-enabling technologies (e.g. genetic labels);
2. The development of certification schemes including eco-labelling standards to enhance the competitiveness of the Adriatic fishery industry to become more sustainable;
3. The preliminary identification of signals of species and/or stock delimitation using genetic and/or genomic data;
4. The alignment between fishery production and marketing of ecolabelled products.

The expected outcomes will be used to set the groundwork for new fisheries sustainable management approach based on eco-labelled, quality-checked and trackable seafood and to fulfil requirements of environmental, economic and social sustainability of the emerging blue economy and boosting the potential of the Adriatic resources, whose management will change into a more efficient workflow, fostering shared responsibility for environmental and social sustainability in the Adriatic coastal territories, adding new tiles to the bigger picture of a sustainable future.
The one-year Project will be carried out within an interdisciplinary and trans-border collaborative framework, joining Italian and Croatian partners, within the activities of the INTERREG ITALY-CROATIA Project PRIZEFISH “Piloting of eco-innovative fishery supply-chains to market added-value Adriatic fish products”. The workplan foreseen for the research fellow will be organised into three main activities:

- **Literature and methods review (M1-2)**

A comprehensive literature review will be carried out in order to a) identify *a priori* biogeographical boundaries or any signals of population structure of the target species within the in the Adriatic Sea, b) analyse the state, management and seasonality of fisheries c) design a sampling scheme on the information gathered, d) compare with a “state of the art” approach the molecular methods available, the data analysis and bioinformatic pipelines used for population genetics and genomics.

- **Sampling (M3-4)**

The project will include a sampling phase to collect specimens from specific geographical areas, together with biological and collection data (i.e. total length, date of catch, sex, maturity staging and geographical coordinates). A proper sampling protocol will be specifically defined in order to ensure the best quality of DNA, essential for downstream genomic analyses. The sampling phase will be carried out during commercial fishery.

- **Genetic and data analyses (M5-12)**

The number of sampled individuals per site will be defined according to previous case studies (i.e. FishPopTace [http://fishpoptrace.jrc.ec.europa.eu]; AquaGen [https://aquagen.jrc.ec.europa.eu]; MedBlueSGen, [https://fishreg.jrc.ec.europa.eu/web/medbluesgen]). An extra subset of samples will be used for testing different DNA extraction protocols and ensure the best quality of extracted genomic DNA. DNA quality and quantity will be systematically measured with dedicated instruments (e.g. fluorimeter, spectrophotometer or similar tools).

Genotyping analyses will mainly rely on high-throughput sequencing (HTS), successfully employed in many non-model marine fish (Hemmer-Hansen et al., 2014). All specimens will be genotyped following the double-digest Random Amplified DNA (ddRAD) sequencing or other similar cost-effective approach. To this end, the preparation of genomic libraries will be performed according to the chosen sequencing platform. A suitable bioinformatic workflow will be set in order to carry out the quality control of the reads obtained from HTS, identify the genomic loci sequenced, obtain the genotype of each individual, measure the SNP data variation and then use the information gathered for both traceability and population genetics analyses. Among them, standard population genetics parameters as allelic richness, heterozygosity indices and inbreeding coefficients will be estimated with open access software. At the same time, these steps will be fundamental to investigate, at the regional scale, the stocks boundary delimitation within the Adriatic basin.

**PROGRAMMA FORMATIVO (O PIANO DI ATTIVITÀ) DELL’ASSEGNISTA**

Along with the duration of the project, the research fellow will be handling the sampling, lab work, bioinformatic workflow, and other analyses requested to conclude each task. The research fellow will enhance and curate the collaborations with external Universities, Institutions and International Organizations (e.g. FAO). In particular, the research fellow will be contributing to cross border exchange of best practices and experience, allowing other partners to benefit from the increased technical and institutional cooperation. On a broader perspective, the research fellow will improve technical knowledge on sustainable seafood traceability as well as to enlarge institutional and technical intervention fields and networks. The research fellow will participate at data analysis workshops in order to improve skills, to learn and test new platforms, packages and software. The research fellow will present carried work and results obtained at international meetings as oral communications or posters. The research fellow will be
collaborating with the team where it will be inserted as a teaching tutor and co-supervisor for Masters’ students.

REFERENCES


