

Master 2 project

Genetic diversity and structure of thornback ray (*Raja clavata*)

Introduction

Several marine fish species have strongly declined during the 20th century as a consequence of overfishing, including certain rays and sharks (Quéro and Cendrero, 1996; Dulvy et al., 2008; Dulvy et al., 2014). Therefore, the conservation of these species has become a major objective for ensuring sustainable exploitation of marine resources. An important consideration for long term conservation is genetic diversity and structure which depend on population size and connectivity between populations. Population genetic structure is one of the indicators proposed for gauging population health in the framework of the European Marine Strategy Framework Directive (MFSFD) (Bourlat et al. 2013). However, to date no studies have actually tested population genetic structure indicators using empirical data.

Objectives and methodology

The aim of the project is to study the genetic population structure of thornback ray in the Mediterranean Sea and the Northeast Atlantic and to test the pertinence and practical feasibility of a suite of genetic indicators.

First, the null hypothesis of panmixia within the Mediterranean Sea will be tested using the Bayesian analysis implemented in the program STRUCTURE (Pritchard 2010), similar to Doyle et al. (2016).

Second, for each putative population several genetic indicators will be computed. The first indicator is effective population size N_e . This parameter is related to the number of individuals which actually participate to produce the next generation and thus informs on population viability (Soulé 1987). N_e will be estimated using the Linkage Disequilibrium (LD) method which is based on linkage disequilibrium due to the non-random association of alleles at different gene loci. The package NeEstimator V2.1 (Do et al. 2014) will be used for this. The second indicator is the inbreeding index F_{IS} . It informs on the extent of genetic inbreeding within populations. The third indicator is the fixation index F_{ST} which measures the reduction in heterozygosity due to subpopulation divergence in allele frequency. These three indicators will be calculated for the Mediterranean Sea and used to contrast these populations with two from the Northeast Atlantic (Bay of Biscay and West Portugal).

Third genetic indicators will be related to abundance indices derived from bottom trawl survey data (Medits program) to determine whether differences might be linked with population size.

In summary, the following steps will be carried out

- 1) Literature review
- 2) Preliminary data analysis and cleaning
- 3) Test of panmixia and identification of putative populations
- 4) Calculation and interpretation of genetic indicators for putative populations relative to abundance indices
- 5) Report writing

Data

The ANR funded GenoPopTaille project (2014-2018, coordinator P. Lorance) developed SNP (Single-Nucleotide Polymorphism) markers (Marandel et al. submitted). Around 7000 SNPs were then genotyped for individuals sampled from six ecosystems in the Mediterranean Sea and two in the Northeast Atlantic (Bay of Biscay and West Portugal). Bottom trawl data from the Medits survey program will be used for deriving relative abundance indices. Within the Mediterranean Sea a standard trawl is used (Bertrand et al. 2002), hence abundance indices are comparable.

Candidate profile

- Familiarity with statistical programming language (R,...)
- Good working level of English (oral and written)

Contact

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