

Assessing genomic consequences of intense exploitation and climate change in Atlantic bluefin tuna

Project description:

Overexploitation has directly, negatively affected marine fish populations in the past half-century, modifying not only their abundance but their behaviour and life history traits. The recovery and resilience of such populations is dependent upon their exploitation history, which often extends back millennia. Hence, information on when exploitation intensified and how populations were composed in historical periods, has the potential to provide context on the baselines currently used in fisheries management and conservation.

Like many commercial marine fish populations, the eastern Atlantic and Mediterranean population of Atlantic bluefin tuna (*Thunnus thynnus*) has experienced dramatic changes in abundance and complexity during the past 50 years due to overexploitation. Since 2014, this population has shown signs of recovery, yet we have a poor understanding of how it was composed prior to 1970, and thus how those more recent changes reflect long-term population dynamics when exploitation rates were lower and climate conditions were different.

Genomic data provides an opportunity to investigate how this species has responded to climate and the Anthropocene in terms of its demography and adaptive traits. This information is much needed to reduce the likelihood of future population declines and predict ecosystem function during dramatic climate events to come. Therefore, in this project we will conduct the first analyses on nuclear whole-genome data of this species, which includes sample groups of archaeological and archived ABFT dated to between the 10th century and early 20th century. Furthermore, we will use ancient genomes to investigate the potential loss of a putative Black Sea population of ABFT, which disappeared rapidly during the 1970's and has been the subject of much debate on the stock-structure of ABFT. In this project, the candidate will study both demographic and adaptive responses to environmental and ecological change by applying a battery of methods to identify adaptive loci and study allele frequency changes between spatiotemporal sample groups using both hard-called genotypes and genotype likelihoods.

These novel data will have implications for the management of ABFT since they elucidate the current population structure and allow for the forecasting of responses to climate and anthropogenic exploitation following what has been observed with this robust dataset during several climatic and cultural events during the last millennia.

Plan of activities:

Month 1-2: Bioinformatic training.

The candidate will familiarise themselves with UNIX and Python scripting, using a variety of online and taught courses at the University of Bologna, Biocomputing Department.

Month 2-8: Demographic and adaptive analysis.

The candidate will use a range of UNIX and python programs, to analyse nuclear whole genome data using both hard-called and genotype-likelihood approaches. Specifically, Bayesian model-based demographic programs and assumption-free approaches will be used to assess population structure, meanwhile genomic diversity estimates will be produced as evidence for population bottlenecks using a variety of linkage, direct estimation, ROH and inbreeding approaches. The candidate will also use distance and haplotype-based approaches to assess the adaptability of bluefin tuna at the genomic level, performing genome-wide scans and association tests to link loci with traits, environmental and ecological conditions. The candidate will also be expected to explore the annotation of the bluefin tuna genome to link signatures of selection with gene function.

Month 8-10: Publication preparation.

The candidate will prepare a minimum of two high-impact publications for open-source, widely consumed academic journals.

Month 10-12: Outreach.

The candidate will attend a range of international and national conferences or symposiums, to share research outputs and will also develop skills in science communication to engage with the wider public.