

CONNECTIVITY AND DEMOGRAPHIC STABILITY OF NORTH SEA SOLE POPULATIONS

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Several commercial marine fish stocks show signs of collapse due to the synergy between climate change and adverse human impacts, such as habitat degradation and overfishing. Besides the reduction in abundance of the exploited species, intense fishing activities have an array of additional ecological impacts. Fisheries may cause irreversible evolutionary changes in life history traits and the genetic structure of populations. One of the species for which such phenotypic-genetic changes are likely to occur is common sole (*Solea solea*). This project aims at studying the connectivity and demographic stability of sole populations in the North Sea and adjacent waters before and after heavy (beam trawl) fishing.

First, we will characterize the spatial and temporal connectivity of the different life stages of *Solea solea*. Are the spawning populations of *Solea solea* separated in time and space or are they well mixed? Do adult fish spawn near the nursery ground where they grew up? Do they return to the same spawning ground year after year? Through the combined analysis of otolith microchemistry and neutral genetic markers, we will answer these questions and investigate the extent to which spawning grounds, nursery areas and feeding grounds are linked. The level of gene flow between different populations will be estimated and adult fish from the feeding grounds will be assigned to their nursery origin. As such, we will evaluate the relative importance of different North Sea nurseries to adult populations.

Secondly, we will analyze the long-term demographic stability of the sole population in the North Sea. Using DNA extracted from historical otolith collections (1960's-1990's), we will investigate possible fluctuations in genetic variability through time, in relation to fishery pressure and methods. The evolution of the effective number of breeding fish will be followed through time, providing a good indicator for the 'genetic health status' of the North Sea stock(s).

Results will improve our understanding of the population genetic structure and the connectivity of spawning grounds, nurseries and feeding grounds of common sole. This knowledge is relevant for fisheries management, in order to identify appropriate management units and to evaluate the benefits of marine protected areas.