

THE GENOMICS OF LOCAL ADAPTATION OF A MARINE DEMERSAL FISH

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The classical notion of marine fishes is that they typically have high effective population sizes (low genetic drift) and high levels of dispersal due to an apparent lack of barriers in the marine environment (high gene flow). Therefore the realization of a genetic population structure is a slow process for marine organisms.

Recent theoretical insights indicate that adaptive parts in the genome would show population divergence much faster than neutral parts. The current conservation management that only takes into account neutral variation, is not able to identify locally adapted populations.

The aim of this project is to gain insights in the relationship between the neutral population structure and local adaptation by studying the interaction between selection, gene flow, population history and genetic drift. We've chosen a non-commercial species, the sand goby (*Pomatoschistus minutus*), to distinguish natural selection from anthropologically induced selection.

This project contains two components. First, there will be a statio-temporal analysis with two different types of neutral genetic markers (microsatellites and SNPs). The second component studies genomic characteristics of local adaptation in the marine environment by innovative techniques as a genome scan and a candidate gene approach. These techniques can also provide a better understanding of how fish respond to the environment and by extension how they might respond to environmental change.