

Genetic adaptation in common sole (*Solea solea*) under natural and artificial selection

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The management of commercial marine fish species requires a thorough understanding of natural and anthropogenic selective influences that impact natural populations. The study of the level of adaptive genetic variation in natural sole populations across Europe to assess the geographical distribution and the influence of overfishing on functional genetic diversity at relevant genes, might provide indications for genetic (local) adaptations. My study has four main objectives: (i) the bioinformatic analysis of sole transcriptome sequences (based on next generation sequencing) to develop markers linked to candidate genes potentially involved in life-history traits such as growth, maturation, and temperature adaptation; (ii) the high-throughput screening of contemporary and historical sole populations using both neutral and gene-linked SNPs/microsatellites to assess jointly the connectivity and potential local adaptation in sole; and (iii) the experimental validation of genetic adaptations in a controlled breeding population of sole to assess genotype by environment interactions. Preliminary results have already revealed the existence of various interesting polymorphisms in candidate genes, now analysed on a spatio-temporal scale. This project is highly relevant to sole management by mapping genetic management units and by pinpointing potential irreversible anthropogenic effects on adaptive genetic variation. The project is integrated into the EU projects FishPopTrace and FinE, studying the traceability/connectivity and evolutionary impact of fisheries on marine populations.

Keywords: aole, connectivity, functional diversity, high-throughput screening, management, overfishing, SNPs, traceability.

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