

2. To implement standardised genetic tools and SOPs in routine biological assessments
3. To develop a framework to apply and implement DNA-based tools in policy and transnational management of the NSR.

To this end, field pilots have been set-up to clearly demonstrate the benefits and/or added value of DNA-based methods and to validate the SOPs. The final output integrating all outputs will be a decision support framework for application of genetic tools in routine biological monitoring, and implementation of the outputs in ecosystem health assessment in support of policy and transnational management. ICES has endorsed this project at the start as they see a clear advancement into the current benthic monitoring for seafloor ecosystems. Furthermore, the ICES network can be used to further spread the developed methods by for instance publishing the SOPs in the ICES TIMES series in which state-of-the-art description of methods and procedures relating to chemical and biological measurements in the marine environment are presented.

Work related to ICES via:

- WGEXT (Working Group on the Effects of Extraction of Marine Sediments on the Marine Ecosystem);
- BEWG (Benthos Ecology Working Group);
- WGIMT (Working Group on Integrated Morphological and Molecular Taxonomy).

(17) Seascape-mediated patterns and processes of population differentiation in European seabass

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Identifying biologically relevant levels of population structure and demographically independent populations is imperative for sustainable fisheries management but challenging because of high levels of gene flow and large population sizes leading to weak genetic structure. However, increasingly good access to genome-wide variation and architecture have facilitated accurate determination of fine scale genetic population structure. Here, we studied the population structure of European seabass (*Dicentrarchus labrax* L.), a commercially exploited and farmed fish with high dispersal capacity. In addition, we examined the influence of geographic distance and abiotic environmental variables on the observed genetic structure with a seascape genomics approach. Seabass showed a largely panmictic pattern within the Atlantic Ocean, whereas several genetic clusters were distinguished within the Mediterranean Sea based on 2,549 SNP markers genotyped using ddRAD (Restriction site Associated DNA markers) sequencing. Introgression of Atlantic alleles was detected throughout the western Mediterranean Sea, but introgression of Mediterranean alleles was only found in a restricted area in the Atlantic Ocean off the Strait of Gibraltar. Seascape analysis suggested that genetic population structure is mediated by both dispersal limitation and environmental gradients, indicating local adaptation. As such the study provides key information for fisheries and conservation management of European seabass.

Work related to ICES via WKBASS (the benchmark Workshop on Seabass).

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