

## Unravelling the stock identity and biomass of common sole (*Solea solea*) using DNA and eDNA

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Stock assessments are frequently hampered by limited data of the target fish stock. The lack of data on the common sole (*Solea solea*), a commercially important demersal flatfish species in Europe, has led to adopting the precautionary approach to fisheries management in several data-poor ICES areas. The SoleDNA project aims at a more efficient and sustainable management of sole in the southern Celtic Sea and southwest of Ireland (i.e., ICES areas 27.7hjk) by focussing on two major knowledge gaps: stock identity and biomass. In the first part of the project, our aim is to identify genetic differences among sole from several geographical regions which can be used to estimate patterns of gene flow and the stock structure of the species. Between January and June 2022, a total of 600 sole specimens were collected in the Celtic Seas, North Sea and Bay of Biscay. Based on single nucleotide polymorphisms (SNPs) obtained from HiSeq X sequencing, we can determine if sole from ICES areas 27.7hjk belong to other neighbouring stocks or form one or more unique stocks. In the second part, we investigated the use of environmental DNA (eDNA) concentrations as indirect measure of biomass. First, we successfully developed and validated a species-specific, probe-based assay targeting the mitochondrial cytochrome c oxidase subunit I gene of sole using ddPCR. Next, a significant and positive relationship between biomass and eDNA concentration at three eDNA emission time periods (5 min, 1 hour and 24 hours) was revealed in a mesocosm experiment. Finally, eDNA concentrations were obtained from seawater collected in the Belgian part of the North Sea (BPNS) in March 2020 and an extended area in the southern North Sea between 51 and 54°N in autumn 2020 and 2021. The presence of sole eDNA in nearly all sampling stations implies a considerable population size in the sampled areas. A significant and positive relationship between observed biomass (kg/km<sup>2</sup>) and eDNA (copies.L<sup>-1</sup>) collected in water samples from concurrently trawled stations was found in the BPNS ( $r = 0.63$ ,  $p = 0.04$ ). This significant relationship between observed biomass and eDNA concentration from concurrently collected seawater samples was not found in the extended area in the southern North Sea in 2020 nor in 2021. Hydrographic and environmental conditions strongly affect the local variability in eDNA concentrations in the water column, particularly in a dynamic environment such as the North Sea. Therefore, a hydrodynamic dispersion model simulating the distribution of eDNA concentrations under certain assumptions can be valuable in estimating fish biomass in the future. This detailed knowledge on eDNA detection and quantification in both controlled and natural environments highlights the potential and challenges of eDNA as a reliable and non-invasive method to improve and complement current stock assessments of sole. The latter in combination with improved knowledge on the stock identity is essential to enable more sustainable and efficient fisheries management.

### Keywords

Environmental DNA; Population Genetics; Fisheries Management; Biomass; Flatfish