

Connectivity and genetic structure of flatfish for fisheries management and traceability in Belgium

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Early life stages are critical in determining connectivity. Effective fishery management requires understanding of how spawning grounds and nurseries are connected and what processes influence larval retention and dispersal. These mechanisms maintain a high genetic diversity which is essential to guarantee population resilience to environmental changes. Marine populations are often believed to be panmictic because there are few obvious barriers to gene flow in the ocean. However, recent work based on Next Generation Sequencing has shown that even highly mobile species have a population structure at reduced spatial scale. Once determined, population structure is the best level to monitor fish stocks. Each population has its own genetic signature therefore traceability system in the industry would highly benefit from a precise mapping and monitoring of stocks, especially for sole in the North Sea.

Given its commercial importance in the North Sea fishery, a larger effort has to be made to preserve the flatfish valuable resource. In this project we will address the following questions:

1. Does larval dispersal vary in time and space?
2. What biotic and abiotic factors are driving larval connectivity?
3. Can we define sub-populations based on connectivity patterns?

A suite of 1536 SNPs (Single Nucleotide Polymorphisms) and state-of-the-art genotyping (Illumina Golden Gate genotyping) have been employed to investigate the genetic population structure of sole larvae and post-larvae at the European scale. We have obtained four groups: (1) a mixed group with populations within the North Sea and eastern English Channel; and the three most geographically extreme populations were clearly separated: (2) the German Bight on one side and (3) the Celtic Sea and (4) the Irish Sea on the other side.

Finally, results of hydrodynamic individual based model of larval dispersal developed by Lacroix and collaborators will be compared to collected data in order to investigate the role of selected biotic and abiotic factors in driving connectivity. Temporal variability will be studied combining three years of intensive sampling and historical data spanning the last two decades.

Overall, this study will help the sustainable management of fishery by defining significant ecological units, while the molecular markers will allow tracing any fish present on the market to its origin, hence fighting illegal fishing and enabling efficient traceability.