Assessing connectivity in young flatfish and its implementation in fisheries management

Delerue-Ricard Sophie [1,2], Ilaria Coscia[1], Léo Barbut[3], Geneviève Lacroix[3], Andreas Vanden Bavière [2], Johan Robbens [2] and Filip A.M. Volckaert[1]

[1] Laboratory of Biodiversity and Evolutionary Genomics, Katholieke Universiteit Leuven,
Ch. Deberiotstraat 32, B-3000 Leuven, Belgium
E-mail: sophie.deleruericard@bio.kuleuven.be

[2] Institute for Agricultural and Fisheries Research (ILVO), Ankerstraat 1, B-8400 Oostende, Belgium

[3] Royal Belgian Institute of Natural Sciences (RBINS), DO 'Nature', Gulledelle 100,
B-1200 Brussels, Belgium

Recently, it has been shown that commercial fisheries target specific size/age classes, causing a loss of genetic diversity as well as altering life cycles (fisheries-induced evolution). This represents a serious threat for the future of commercial stocks. Such features have also been observed in the North Sea stocks of sole (*Solea solea*), which have been overfished in the past 20 years. For example, heavy fishing pressure has led to smaller individuals. Given its commercial importance in the North Sea fishery, a larger effort has to be made to preserve this valuable resource. To improve sole stock management, managers would benefit from an upgraded biological assessment of population structure and connectivity patterns. 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? And once known,
3. Can we predict the impact of changes in physical and biological drivers?
4. Can we define sub-populations based on connectivity patterns?

My research project aims at filling those gaps, by focusing on population connectivity at the larval and postlarval stages. A suite of 200 highly variable SNPs (Single Nucleotide Polymorphisms) and state-of-the-art genotyping (Illumina-Veracode) will be employed to investigate the population structure of sole at a regional scale (<150km) within the North Sea and eastern English Channel. Additional insights will be gained by otolith microchemistry, used to trace the movement of single individuals between spawning and nursery grounds. Temporal variability will be studied through the combination of two years of intensive sampling and historical datasets spanning the last two decades. Finally, results of hydrodynamic modelling of larval dispersal will be compared to collected data in order to investigate the role of selected biotic and abiotic factors in driving connectivity. Overall, this study will help the sustainable management of the 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.