

Where goes the flow? – Tracing sole of the North Sea with genomics and otolith shape

Delerue-Ricard Sophie^{1,2}, Stynen Hanna¹, Barbut Leo^{3,4}, Vanden Bavière Andres^{1,2}, Goscia Ilaria¹, Robbens Johan², Lacroix Geneviève³ and Volckaert Filip A.M.¹

¹ Laboratory of Biodiversity and Evolutionary Genomics, University of Leuven, Deberiotstraat 32, 3000 Leuven, Belgium
E-mail: sophie.deleruericard@kuleuven.be

² Research Institute for Agriculture, Fisheries and Food Research (ILVO), Ankerstraat 1, 8400 Oostende, Belgium

³ Royal Belgian Institute of Natural Sciences, OD Natural Environment, Rue Vautier 29, 1000 Bruxelles, Belgium

⁴ KU Leuven, Deberiotstraat 32, 3000 Leuven, Belgium

Fisheries managers should monitor fish stocks at an ecologically meaningful scale. Better understanding of population structure and movements of individuals between populations would be helpful. However it is difficult to measure connectivity between populations, especially because early-life stages cannot be tagged physically. Therefore we resort to information embedded in the genome and the otoliths. Population structure of adult sole *Solea solea* seems to be low but meaningful at the European scale. However this is less clear at the regional level of the North Sea. Our research focuses on Young of the Year sole caught off the Belgian coast and in the Wadden Sea in 2013 and 2014. Using Single Nucleotides (SNPs) molecular markers we trace the spawning origins of juveniles reaching the Belgian nursery. What is the contribution of the different spawning grounds to the Belgian nursery? Is there a reproductive strategy favouring different cohort origins throughout the season? We also compare the assignment of juveniles caught in the Belgian nursery with the ones caught in the Wadden Sea nursery. In order to assess connectivity, 200 juveniles have been genotyped using ddRAD sequencing and Fourier descriptors have been used to describe the otolith shape of the same individuals. First, we computed population genetic measures and observed variation in population structure between years. Then, the genomic data were compared with otolith shape. Our research reveals origins of fish contributing to the Belgian nursery stock, hence improving management perspectives.

Keywords: connectivity; traceability; early-life stages; genomic; otolith shape; flatfish; North Sea; Wadden Sea