Integrating field data to parameterize a larval transport model of sole and improve knowledge on connectivity in the North Sea

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Among fish, early life stages are critical in determining dispersal. Effective fishery management requires the understanding of how spawning grounds and nurseries are connected and what processes influence larval retention and dispersal.

A Lagrangian larval transport model for sole in the North Sea has shown that hydrodynamics have a strong impact on dispersal (Lacroix *et al.*? 2013). However, it is difficult to obtain observations of life history traits for the proper parameterization of Individual-Based Models. Estimates may strongly influence modelled larval dispersal. Various assumptions about these traits can be tested by comparing simulation results with field data. Here ICES recruitment assessments are used to identify the most plausible model parameterization ('best model').

In addition the genetic population structure of sole was assessed with a panel of 1536 SNPs. The best model and genetic markers were used to compare connectivity patterns.

This initial step is crucial towards the calibration, validation and improvement of the larval dispersal model of sole and its applications, for example in the design of marine protected areas.

References

Lacroix G., G.E. Maes, L.J. Bolle, F.A.M. Volckaert. 2013. Modelling dispersal dynamics of the early life stages of a marine flatfish (*Solea solea* L.). Journal of Sea Research 84:13-25.