

# How sensitive is sole larval dispersal in the North Sea to the parametrization of larval duration? A modelling study

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Connectivity throughout the life cycle of flatfish remains an open question, especially at the early life stages. The case of sole (*Solea solea*) is of particular interest because it is one of the most valuable commercial species in the North Sea. It is crucial to understand how the spawning grounds and nurseries are connected and what are the processes influencing larval retention and dispersal in order to propose appropriate management measures. Especially, dispersal during the larval stage is still poorly known. The transport of sole larvae from the spawning grounds to the nurseries is driven by hydrodynamic processes but the final dispersal pattern and larval abundance at nurseries might be affected by biological processes and environmental factors. Larval Transport Models (LTMs) coupled to Individual-Based Models (IBMs) are more and more commonly used to assess the relative contribution of these processes on the larval dispersal. IBMs allow to take into account growth to estimate the duration of dispersal based on environmental conditions met by the larvae. These models may be sensitive to process parametrization and may give different results for parametrizations derived from the same data set. The LARVAE&CO model (Lacroix *et al.*, 2013) used in the frame of B-FISHCONNECT project couples the 3D hydrodynamic model COHERENS with an IBM of sole larvae. It is used here to investigate the impact of parametrization of the stage duration on the dispersal of sole larvae in the North Sea. In this study, we compare two parametrizations (Rochette *et al.*, 2012 and Lacroix *et al.*, 2013) of the stage duration (temperature dependent) derived from the same data set (mainly Fonds, 1979). We show that only small differences of the stage duration parametrization may induce significant differences of the dispersal pattern, connectivity and larval recruitment at nursery. This highlights the importance to parametrize biological processes with accuracy and the need to collect sufficient data (samples, genotypes and otoliths) and conduct experimental studies to derive biological processes parametrizations in order to improve model's reliability.

## References

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