

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



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Introduction

Inter-annual recruitment variability of sole (*Solea solea*) is high in the North Sea. It has been shown, with a Lagrangian larval transport model, that hydrodynamics explains part of this variability in sole [1]. IBMs require a good knowledge of the biological processes governing larval dispersal. However, it is difficult to obtain observations of life history traits; their estimates may strongly influence larval connectivity / retention and successful migration as predicted by the model. Various assumptions about these traits can be tested by comparing simulation results with field data.

Objective

Assess the model performance: Comparing simulated test cases with data to establish the most likely parameterization set.

Sole Larval transport model (LTM)

The sole LTM results from the coupling between the 3D hydrodynamic model COHERENS and an Individual-Based Model (IBM) for sole larvae [1].

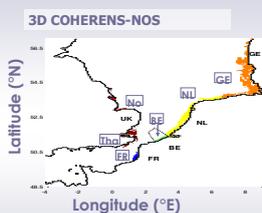


Fig. 1. Geographic implementation of the model, and main nurseries in the North Sea, France (FR), Belgium (BE), Netherlands (NL), Germany (GE), Norfolk (No), Thames (Tha).

Larval parameterization.

Larval stage duration and mortality depend on the environmental conditions met by the larvae.

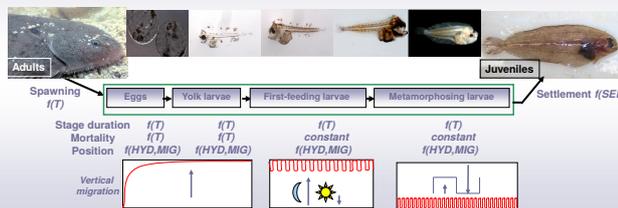


Fig. 2. Schematic representation of the sole larvae IBM. T: Temperature, HYD: hydrodynamics, MIG: vertical migration, SED: sediment type.

Methodology

Test cases, 12 parameterization sets are tested

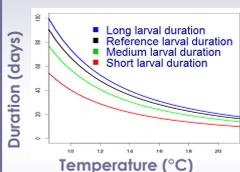


Fig. 3. Total duration of larval pelagic stage in function of temperature. These curves cover the range found in the literature (compiled in [2]).

4 larval durations: $\alpha_i T^{-\beta_i}$
 Reference: summary in [1]
 Medium: $\alpha_i \rightarrow 0.85 * \alpha_i$
 Long: $\alpha_i \rightarrow 1.1 * \alpha_i$
 Short: $\alpha_i \rightarrow 0.6 * \alpha_i$

3 mortality levels: $c_i T^{b_i}$
 Medium: summary in [1]
 High: $c_i \rightarrow 1.1 * c_i$
 Low: $c_i \rightarrow 0.9 * c_i$

with T the instantaneous temperature and $\alpha_i, \beta_i, c_i, b_i$ specific stage coefficient.

Criteria:

1. *d*, the local anomaly indicator shows the local recruitment anomaly in each nursery (NL, UK, GE, BE, see fig 1).

Data [3] and [4] and results are standardized, and a discrepancy indicator is built for each nursery:

$e_i = \frac{Ind - \widehat{ind}}{Ind}$ where *Ind* and \widehat{ind} are observed and simulated standardized recruitment in nurseries *i*.

An overall discrepancy criterion summarizes the local anomaly

$d = \sqrt{\sum_{i=1}^n e_i^2}$ where *n* is the number of nurseries

2. *g*, global recruitment indicator, representing global recruitment discrepancy in IVb and IVc ICES division.

$g = \frac{|N_i - \widehat{N}_i|}{N_i}$ where *N_i* and \widehat{N}_i are the total recruitment observed and predicted by the model

Results

The local anomaly shows that variability between test cases is bigger than inter-annual variability (Fig.4). In particular for the short larval duration test case.



Fig. 4. yearly *d* indicator for each test case where all model results are pooled before standardization of the recruitment in each nurseries.

The performance of each test case, (from 1995 to 2011 in Reference runs and for the years 1995, 1997, 2003 and 2004 for Long, Short and Medium larval duration and 3 mortality level) is estimate to take into account the ability of the model to reproduce observed global recruitment and local anomaly (Fig.5).

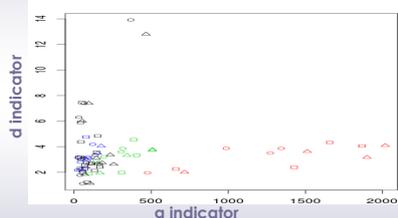


Fig. 5. Performance of 75 test cases (4 larval durations Long, Reference, Medium, Short and 3 mortality rates: High, Low, Medium) as synthesized by the two indicators *d* and *g*. The lowest values of these indicators indicate the best parameterizations.

Long and reference larval durations for the sole seem the best performing test case. A short larval duration over estimates the global recruitment in IV ICES division.

For mortality, no clear pattern seems to emerge, although high mortality (circle) is slightly better, the high value of *g* indicator show that all model overstate the recruitment.

Conclusions & Perspectives

- Increasing of larval duration improves recruitment predicted by the model.
- Many biotic and abiotic parameters might influence dispersal patterns. Before building more complex models, it is necessary to better represent the biological processes influencing the dynamics of marine species.
- This study represents a first step towards the calibration and improvement of a larval dispersal model of sole in the North Sea and the development of a tool for fisheries management.

PERSPECTIVES:

- Investigate the influence of spawning (zone, period and egg number) on the recruitment.

- Validate the model with other approaches (otoliths, genetic, demography).

REQUEST: We are looking for life-history data of sole to validate the model

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Reference:

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