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

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Introduction

Sole (*Solea solea*) is a highly exploited fish with a high economic value that may benefit from integrative management measures (e.g. MPA) based on a better understanding of the relationship between spawning grounds and nurseries. Based on a Lagrangian larval transport model, inter-annual recruitment variability has been shown to be high in the North Sea, partly explained by hydrodynamics [1]. As soles spawn offshore and recruitment is strongly constrained by access to coastal nurseries, the correct parameterization of larval duration, tidal migration and mortality levels is crucial to fine-tune more biologically relevant/complex larval transport models (LTM) for efficient management implementation.

Objective

Evaluate the LTM model performance by:
1) Comparing simulated larval dispersal scenarios with observed data
2) Establishing the most likely and realistic parameterization set
3) Contrast sole connectivity based on our model and other methods (e.g. genetics).

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].

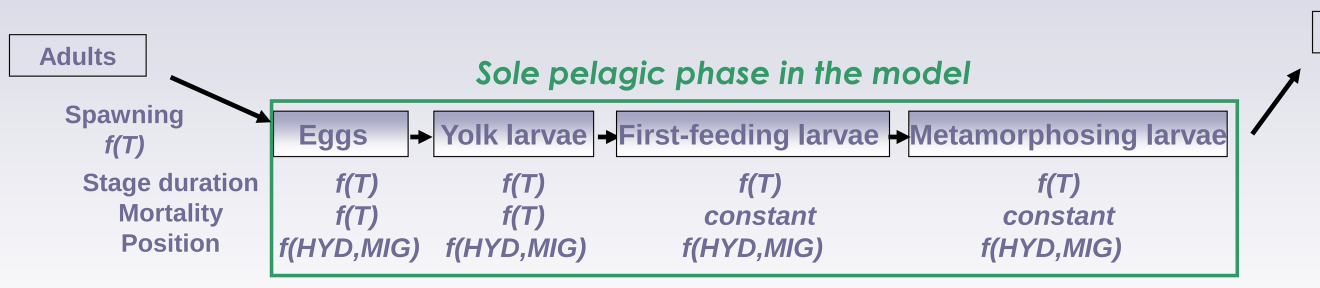

Fig. 1. Schematic representation of the sole larvae IBM. T: Temperature, HYD: hydrodynamics, MIG: vertical migration, SED: sediment type.

Larval parameterization: IBMs require a detailed knowledge of the biological processes governing larval dispersal. However, obtaining such direct observations of life history traits is challenging, requiring the mining of the literature exploring a wide range of these parameters.

LTM scenarios:
72 parameterization sets are tested

- 3 Mortality levels:
  high, medium and low
- 3 Larval durations:
  long short and medium
- 8 Migration behaviors (stage dependent):

Mig0:	passive drift	+ passive drift	+ passive drift	+ passive drift
Mig1:	move up	+ move up	+ passive drift	+ move down
Mig2:	move up	+ move up	+ nycthemeral mig.	+ passive drift
Mig3:	move up	+ move up	+ nycthemeral mig.	+ tidal mig. 1
Mig4:	move up	+ move up	+ passive drift	+ passive drift
Mig5:	move up	+ move up	+ passive drift	+ tidal mig. 1
Mig6:	move up	+ move up	+ passive drift	+ tidal mig. 2
Mig7:	move up	+ move up	+ nycthemeral mig.	+ tidal mig. 2

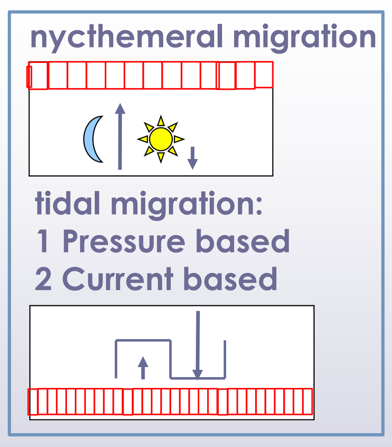

Fig. 2. Type of vertical migration observed on flatfish

Inter-annual variability vs larval dispersal variability

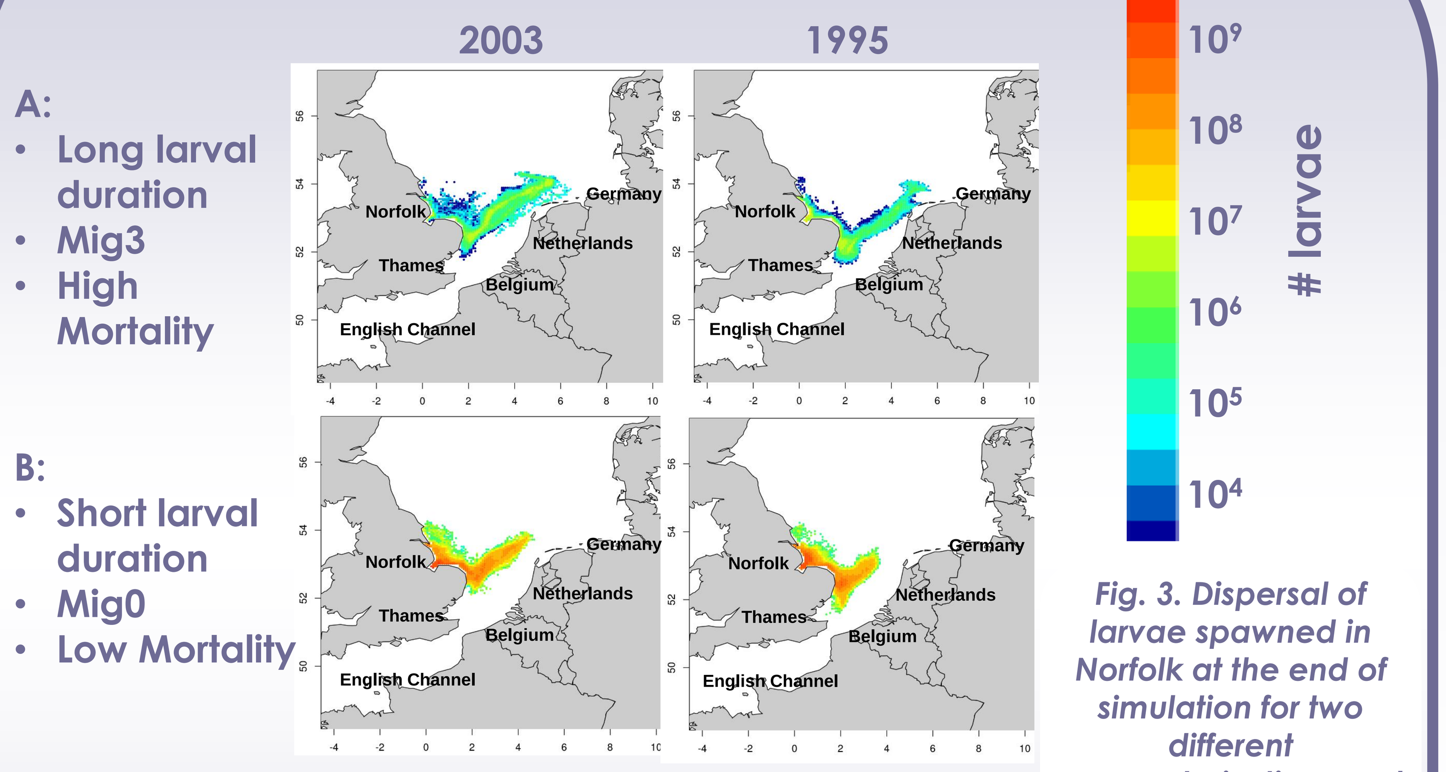

Fig. 3. Dispersal of larvae spawned in Norfolk at the end of simulation for two different parameterizations and two years

The inter-annual variability explains a part of recruitment variability [1]. Model parameterization may strongly influence larval connectivity / retention and successful migration as predicted by the model (Fig. 3).

Model selection

The "best model" should be able to reproduce local and global year-to-year anomalies observed in data [2]. Each test case was assessed with 2 criteria.

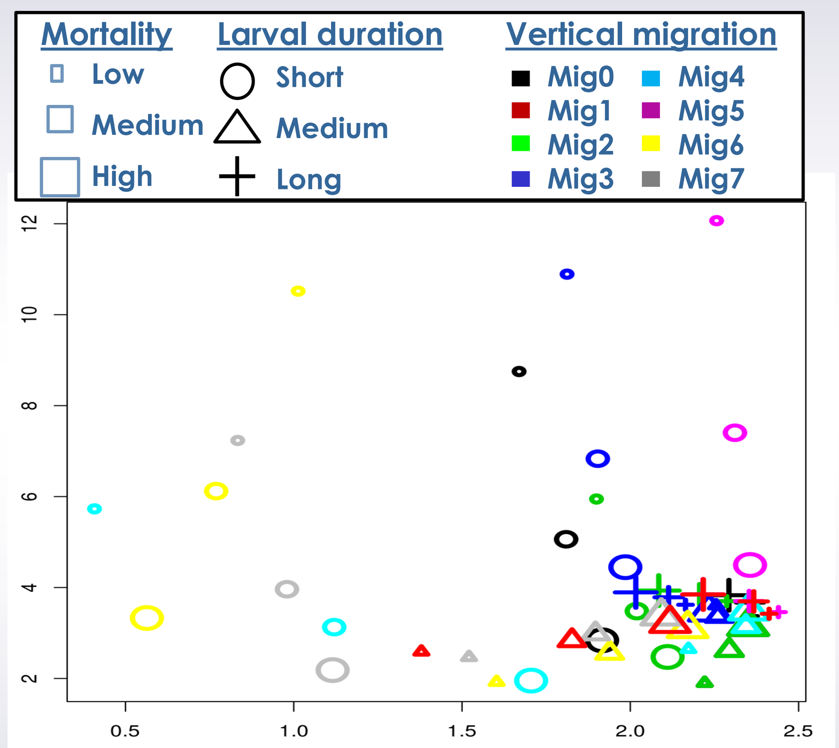

Fig. 4. Performance of 72 test cases as synthetized by the two indicators. Model results are averaged over the years 1994, 1995, 2003 and 2004. The lowest values of these indicators indicate the best parameterizations.

Assessment criteria:

Data [2] and results are normalized, and a discrepancy indicator is built:

1. *Local tendency*, this criterion shows the local year-to-year anomaly recruitment in each nursery.

$e_i = \frac{loc - \widehat{loc}}{loc}$ where loc and $\widehat{loc}$ are observed and simulated normalized recruitment in nursery i.

Overall discrepancy criterion summarizes local anomaly

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

2. *Global tendency*, this criterion shows the global recruitment anomaly in IVb and IVc ICES division.

$g = \frac{|glob - \widehat{glob}|}{Ni}$ where $\boldsymbol{glob}$ and $\widehat{glob}$ are the total normalized recruitments observed and predicted by the model

The "best model" seems to associate a short larval duration and a high mortality with a passive vertical migration behavior for early larvae and synchronous with tide at the end of pelagic phase.

Connectivity

Genetics

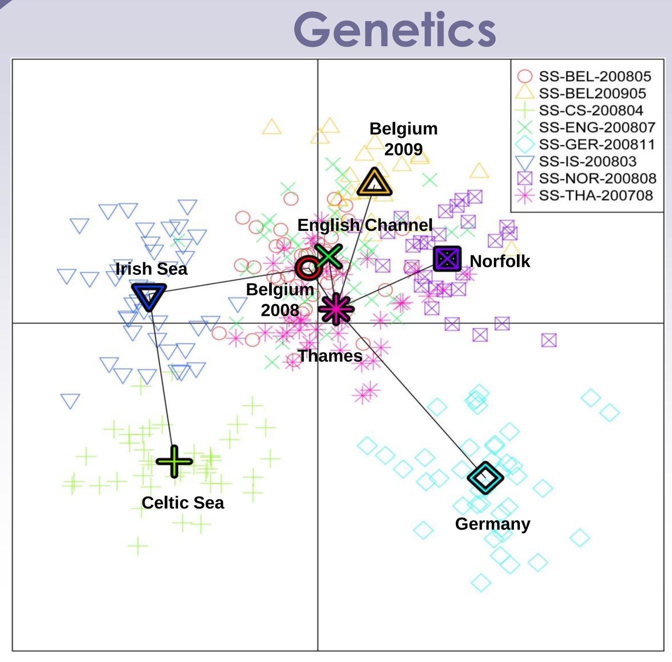

Fig. 5. Discriminant Analysis of the Principal Components (DAPC) on the genetic data based on the 200 best SNPs biomarkers. Statistical assignment power between populations is of 70%. [3]

Predicted by the model

Larvae origin in each nursery (%)

Spawning ground \ Nurseries	ENG	BEL	NL	GER	NOR	THA
THA	0,01	0,42	0,00	0,00	0,00	86,39
NOR	0,00	0,00	0,00	0,00	100,00	0,05
GER	0,00	0,00	0,01	82,24	0,00	0,00
NL	0,00	0,07	63,59	17,75	0,00	0,00
BEL	0,01	60,19	36,35	0,00	0,00	1,48
ENG	99,98	39,32	0,04	0,00	0,00	12,09

Connectivity:
- High (>65%)
- Medium (25-65%)
- Small (0%-25%)
- No connection

Fig. 6. Mean connectivity matrix predicted by the "best model" for the years 1995, 1997, 2003 and 2004. (Area on Fig. 3.)

Connectivity pattern from genetic data shows that all populations in the North Sea are well mixed with the Irish-Celtic Sea and German bight more divergent (following an IBD pattern) (Fig. 5.). Conversely, our model predicts that Norfolk seems most isolated, requiring more in depth investigations. A high level of connectivity between ENG, BEL, NL and THA is predicted by the model (Fig. 6.).

Conclusions & Perspectives

- A short larval duration, tidal migration and high mortality seems the most probable parameterization for sole larvae in the North Sea.
- 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 Marine Protected Area design and 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).
- Investigate adult movements, historical events, selection, exploitation levels, … that may explain population genetic structure and resilience.

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Reference:
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[2] ICES. 2013. Report of the Working Group on Beam Trawl Surveys (WGBEAM), 23-26 April 2013, Ancona, Italy. ICES CM 2013/SSGESST:12. 260 pp.
[3] Diopere et al. (in prep)

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