Royal Belgian Institute of Natural Sciences (RBINS)
Operational Directorate Natural Environments (DO Nature)

B-FishConnect

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

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Introduction

Connectivity 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.

Objective

To investigate the impact of larval stage duration parameterization on sole larval dispersal and recruitment at nurseries with a Larval Transport Model

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].

The larval stage duration depends on the environmental conditions met by the larvae. In this study, we compare two parameterizations (temperature dependent) issued from [1][2] and derived from the same data set (mainly [3]) (Figs. 1 & 2).

	Egg	Embryonic	Larval pelagic				Settling	Settled
	0	1	2	3	4a	4b	5a	5b
Lacroix et al. 2013 [1]	Egg	Yolk sac larvae	First-feeding larvae		Metamorphosing Larvae			
Rochette et al. 2012 [2]	Egg	Yolk sac larvae	First-feeding larvae					

Settlement if suitable substrate

*Fig. 1. Modelling of larval stages between spawning and recruitment at nurseries according to [1] and [2].
The classification of Lagardère et al. (1999) [4] is used as reference.*

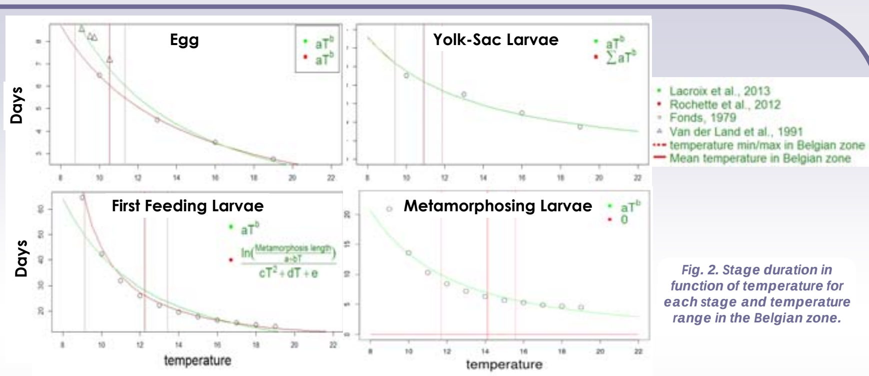
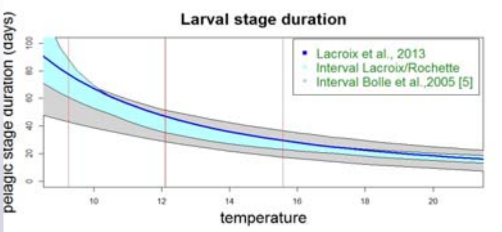


Fig. 2. Stage duration in function of temperature for each stage and temperature range in the Belgian zone.



The total pelagic stage duration shows a large variation (Fig. 3) particularly important when comparing different models based on different studies [1][2] and [5].

Fig. 3. Random combination of the pelagic phase duration for different models

Results

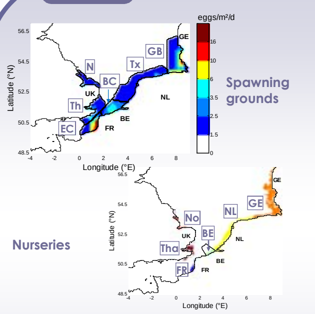


Fig. 4. Up: main spawning grounds in the North Sea and mean number of eggs spawned. Eastern Channel (EC), Belgian Coast (BC), Texel (Tx), German Bight (GB), Norfolk (N) and Thames (Th). Down: nurseries. France (FR), Belgium (BE), The Netherlands (NL), Germany (GE), Norfolk (No), Thames (Tha).

Four simulations, considering the minimum and maximum pelagic stage duration within the range of Fig. 3 (on the basis of [1][2]) for two mean temperatures (10°C and 15°C) have been performed for the year 1998. Fig. 5 shows the larval distribution and the connectivity matrix (spawning grounds and nurseries in Fig. 4).

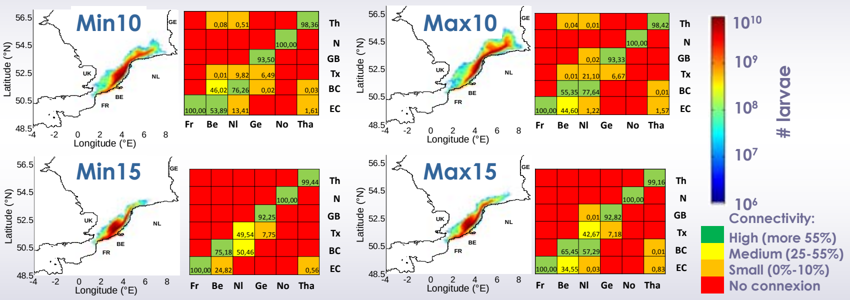


Fig. 5. Left: Final larval distribution for each simulation for eggs spawned in the BC spawning grounds. Right: connectivity matrix between spawning grounds and nurseries (see in Fig. 4). Min10: minimum larval stage duration at 10°C, Max10: maximum larval stage duration at 10°C, Min15: minimum larval stage duration at 15°C and Max15: maximum larval stage duration at 15°C (Fig. 3, based on [1][2]).

Small differences in the pelagic stage duration parameterization may induce significant differences in the dispersal pattern (Fig. 5, left), larval recruitment at nursery and connectivity (Fig. 5, right).

Connections appear or disappear when the highest values [max] of the range are considered instead of the lowest values [min]: +1/-1 at 10°C and +3 at 15°C.

Such differences might be of great importance in fisheries management.

Conclusions & Perspectives

- 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 highlights the importance to parameterize biological processes with accuracy and the need to collect sufficient data and conduct experimental studies to derive biological processes parameterizations in order to improve model's reliability.

RECOMMENDATIONS:

- Cross models of larval duration to maximize the likelihood
  - Take into account result uncertainties

PERSPECTIVES:
Model validation with other approaches (otoliths, genetic, demography).

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

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