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Published in:
Aquaculture Europe 2019

Publication date:
2019

Document Version
Publisher's PDF, also known as Version of record

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MODELLING MUSSEL LARVAL DISTRIBUTION FOR OPTIMAL SITE SELECTIONS OF MUSSEL FARMING

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Introduction

Eutrophication is one of the largest threats to the Baltic Sea manifested by algal blooms, turbid waters, loss of submerged vegetation and hypoxic and anoxic conditions at the sea bottom in large areas (Holmer et al., 2015). The potential of using bivalves such as blue mussels to mitigate effects of eutrophication in the coastal zone has been proved environmental effective in Danish waters (Timmermann et al., 2019). Mussels remove nutrients from the water through filtration of particles, which are incorporated into mussel biomass and removed from the system by harvesting. However, it is still a challenge to optimize mussel farms and mussel production. The farm design and locations need to be adapted to different environmental conditions in order to handle e.g. high predation pressure, low salinity, exposure to high wind, waves or ice coverage, but also in terms of efficient mussel larvae settling on the long-lines. Spawning takes place in the natural mussel beds in spring and the resultant larvae are spread by the water currents to other areas before settling on the bottom or on the long-lines in the mussel farms. In the following study, we use 3D ecosystem modelling to estimate the mussel larval distribution on fine spatial and temporal scales in a local set-up of the Limfjorden

Materials and methods

We couple a 3D physical Limfjord model with an agent based model (ABM) using the Flexsem system (Larsen et al., 2017). The hydrodynamic model has been validated against observations. Mussel larvae are defined by two main biological parameters: the pelagic larval duration (PLD) and a main spawning event in spring. To simulate the dispersion of mussel larvae we use numerical particles released from the mussel bed sampling stations acting like a source area (figure 1). The mussel densities in the stations are considered for the amount of larvae released. The individual trajectories of the particles are stored for the temporal extent of the pelagic phase. No random vertical or horizontal movements of the particles are included. At the end of the pelagic larval duration, settling occurs once for particles ending anywhere within the model domain. The model provides maps of mussel larvae distribution and connectivity between sub-areas, which can be used for site-selection processes of mussel farming in the Limfjorden.

Results and Discussion

Preliminary results on larval connectivity in the area show that there is a high probability of larvae to be recruited in the same location where they were originally released (self-recruitment). This is the case in all areas except for 1, 2, 4, 6 16 and 17 where no mussel were released. Self- recruitment is higher for short PLDs, and as we increase the number of days that the larvae remain in the water column, larvae will move to other areas within the Limfjorden (results not shown). Main donor and receiver areas can also be identified by the model for different scenarios. For 2010, area 5 corresponding to Kås Bredning is the main donor area and areas 10 and 11(Løgstør Bredning) and 13 (Risgårde Bredning) the main receiver areas. These connectivity results can be explained by the circulation current patterns in the area. Current mean speed and standard deviation in the studied month was calculated and it was observed to be higher in area 5. This area is a strait and therefore we expect higher current speeds that disperse the larvae to the inner parts of the Limfjorden (not shown).

Conclusion and Outlook

Larval dispersal is a complex process mediated by several factors acting at different scales. In this study, we are able to identify the main donor and receiver areas, as well as the areas with high self-recruitment and isolated areas for the specific year and season modelled. Note that the model does not account for post-settlement survival. Other factors such as bottom trawling, oxygen depletion and marine protected areas are also important to consider when modeling the spawning areas and potential settlement sites. Thus, this variability in density of larvae newly settled is caused by complex interactions between hydrodynamics, habitat structure, predation and species-specific traits. Further work will include (1) annual variability in mussel larvae distribution, (2) changes in climate affecting the physical conditions and biological traits of the species and (3) model validation against mussel beds densities, genetics and larval sampling. The tool developed in this study can provide useful information for decision makers to be used for management applications and aquaculture purposes in the inner Danish waters.
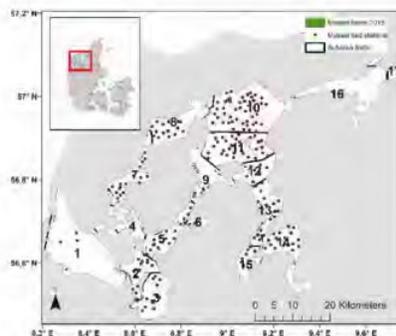
Fig. 1. Map of the sampling stations (red dots) in the mussel beds existing in the Limfjorden. The Limfjorden is divided into 17 areas for the connectivity study (subarea limits shown in black).

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