Project *brief*

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Do our marine protected areas function as a network? – An interdisciplinary assessment

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- **European legislation requires that marine protected areas (MPAs) be established in a network in such a way that their effects reinforce each other**
- **We have developed an interdisciplinary method for evaluating such functional connectivity and tested it using the example of the European flat oyster *Ostrea edulis* in the North Sea**
- **Combining genetic evidence of presence with biophysical modelling revealed that oyster larvae from the MPA Borkum Reef Ground only reach the MPA Sylt Outer Reef under extremely favourable wind conditions**

Background and objectives

Marine protected areas (MPAs) are expected to play a crucial role in conserving biodiversity, not only by protecting critical habitats, but also by supporting the functional connectivity of populations. However, until now, there has been no recording or assessment of such a network function for individual species in MPAs in German waters. In our project CREATE, we developed an interdisciplinary approach and applied it to the example of the native European flat oyster *Ostrea edulis* in order to record and quantify the functional connectivity between MPAs in the North Sea. The European flat oyster is a local species that was considered virtually extinct and was only artificially reintroduced in 2020 in the Borkum Reef Ground (BRG) MPA. The project focused on the question of whether this oyster species can spread from there via its planktonic larvae to the Sylt Outer Reef (SOR) MPA and potentially establish a new reef there.

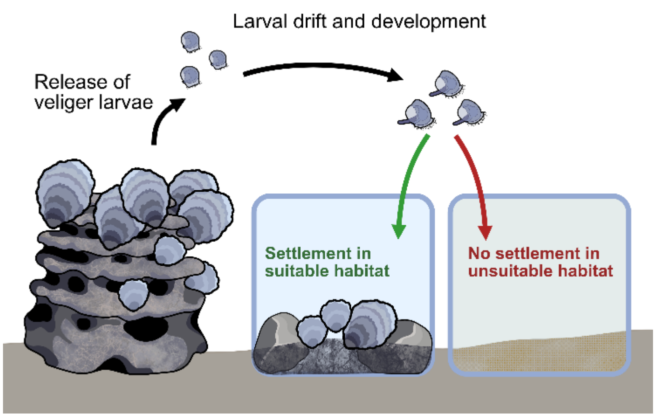

Figure 1: Planktonic larval stages spread from an existing oyster reef (in this case, a reintroduction with artificial substrate). Only in a suitable habitat can they form a new reef (graphics: Pauline Wagner/Thünen Institute).

Approach

To assess the functional connectivity which potentially emerged from the restored European flat oyster reefs, we proceeded as follows:

1. During several research cruises, we sampled environmental DNA (eDNA) in the sea water and/or plankton at strategically selected stations to genetically detect local occurrences of the oyster and their larvae.
2. In laboratory analyses at the HIFMB, we could identify genetic traces of the oysters and their larvae at some of the stations using a technique known as metabarcoding.
3. A newly developed species-specific biophysical model simulated the dispersal pathways of the larvae. It took into account environmental conditions and the swimming behaviour of the larvae. We then compared the model predictions with the molecular evidence.
4. As little is known about the swimming activity of the larvae, we simulated possible dispersal pathways based on alternative swimming behaviours. This enabled us to quantify and map the connectivity between BRG and SOR for individual years, taking the prevailing wind and current conditions into account.
5. The combined analysis revealed the possible dispersal routes of the oyster larvae and the conditions for connectivity. This allowed us to evaluate the current restoration measures in the BRG with regard to the achieved functional connectivity between MPAs.

Results

Evidence of the presence of the European flat oyster, *Ostrea edulis,* was found around the reintroduction area in the BRG as well as at various distant locations.

The two types of samples taken during several research cruises yielded different results: the water samples taken for eDNA analysis confirmed the presence of oysters at four stations in 2022. This method provides an indication of the presence of the species in the immediate vicinity of the sampling site. However, the genetic signal detected in the water does not allow us to determine whether it stemmed from adult oysters on the seabed or from their larvae, which live as plankton in the water column. Larvae play a key role in population connectivity, as they are the only life stage capable of spreading populations via drift (Fig. 1). Using DNA from the plankton samples, however, we were able to specifically detect larvae of *O. edulis* at 18 stations.

We have developed a biophysical model for oyster larvae, combining hydrodynamic and particle drift models provided by our project partner at the Alfred Wegener Institute with key biological characteristics of *O. edulis* larvae. These included temperature-dependent growth rates and duration of the larval stages as well as possible regulation of the depth in the water column. The model was used to simulate near-surface and depth-averaged larval drift, taking into account wind, atmospheric pressure, tidal forces and [baroclinic pressure gradients](#).

Two model scenarios demonstrated the effects of alternative vertical distributions of the larvae: larval drift at the water surface was compared with an even distribution across all depth layers. Comparison with genetic evidence obtained during the field campaign in the summer of 2022 suggests that at least some of the larvae drift at the surface. If the larvae moved at deeper layers or near the seabed, only the oyster occurrences in the immediate vicinity of the reef restoration site could be explained.

The integration of genetic evidence from oyster larvae with biophysical modelling of their potential drift paths shows that the conditions for connectivity between MPAs in the North Sea vary greatly. In years such as 2022, the drift of larvae is severely restricted by relatively weak wind speeds and north-westerly winds during the relevant phase (Fig. 2, top right). In years such as 2023, on the other hand, stronger westerly and south-westerly winds cause widespread dispersal towards the SOR (Fig. 2, bottom right). Such conditions offer a much greater probability of achieving functional connectivity between the two MPAs than those in 2022. The percentages of modelled larvae reaching the second protected area (MPA 2), calculated as connectivity indices, increased from 3% to 22% (Fig. 2).

Conclusions

This case study demonstrates how connectivity indices and connectivity maps derived from them can be used to quantify and evaluate network functions between marine protected areas. In the follow-up project [CREATE II](#), we are transforming these approaches into user-friendly tools. We are testing these tools in practice with various stakeholders in order to adapt them as best as possible to the needs of users.

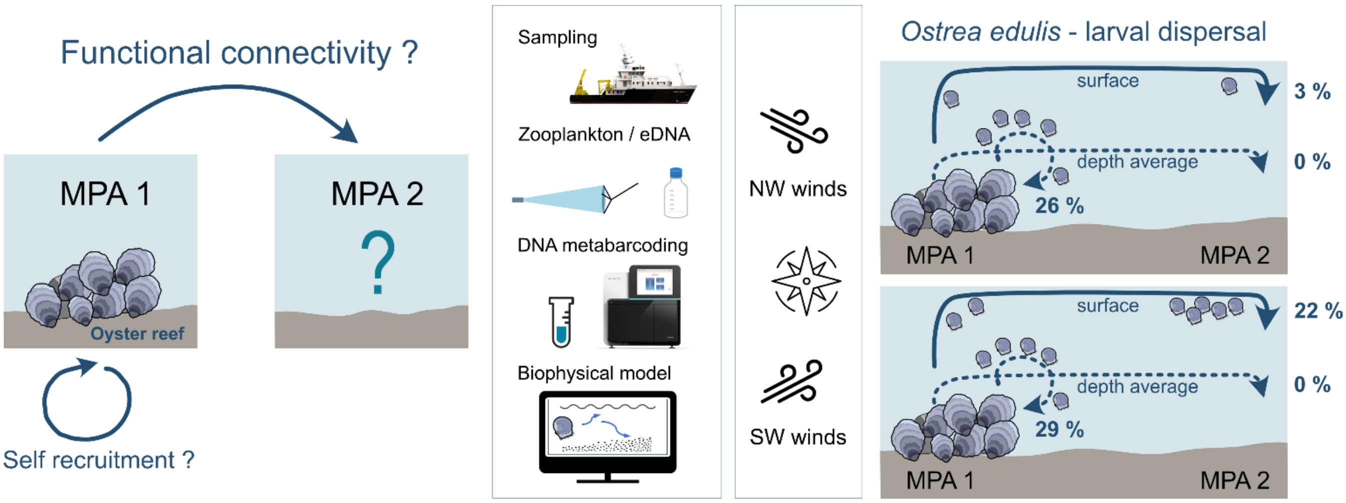

Figure 2: Schematic summary of the key findings of the CREATE connectivity assessment (graphics: Anne Sell/Thünen Institute).

Further Information

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Publications

Beng et al. (2025). Integrating molecular methods and biophysical modelling to assess functional connectivity between marine protected areas. Ecological Applications. https://doi.org/10.1002/eap.70150

Sidorenko et al. (2025). Connectivity and larval drift across marine protected areas in the German Bight, North Sea: Necessity of stepping stones. Journal of Sea Research. https://doi.org/10.1016/j.seares.2025.102563

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