



Nordic Council
of Ministers

Spatial population structure and connectivity among marine populations in the Skagerrak: implications for marine biodiversity conservation



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Summary

Most species in the Skagerrak have populations that are genetically distinct from populations in the surrounding North Sea, Kattegat, and Baltic Sea. A considerable number of these species also have multiple distinct populations within the Skagerrak, particularly along the coast and inside fjords. Highly mobile fish species, such as cod, herring and bluefin tuna, have multiple distinct populations that temporarily coexist in the Skagerrak during specific parts of the year, or during certain parts of their life cycle. Overall, the Skagerrak is well connected with adjacent seas through passive dispersal of eggs and larvae and active migration of adults. The persistence of distinct local populations despite the large potential for connectivity calls for population-specific conservation and management of marine biodiversity in the Skagerrak. Management, while maintaining an overall ecosystem approach, needs to be species- and population-specific to avoid neglecting or overexploiting vulnerable local populations.

Background

Biodiversity loss is a global crisis that negatively impacts ecosystem functioning at both local and global scales. The UN CBD Kunming Montreal Biodiversity Framework specifically states maintenance of **genetic biodiversity** as equally important to species and ecosystem diversity. Failure to correctly identify genetic population structure and connectivity in the marine environment can result in the isolation and disappearance of vulnerable and threatened local populations, as well as the overharvesting of depleted fish stocks. Summarising current scientific knowledge on genetic population structure and connectivity in marine species inhabiting the Skagerrak Sea, we here provide information that can improve species- and ecosystem conservation, harvesting and marine spatial planning in the area.

Definitions and Methods

DEFINITIONS

Population structure is the tendency of species to separate into more or less distinct spawning groups or populations. Such populations will independently evolve and maintain genetic differences and adaptations, unless there is genetic connectivity between them.

Connectivity is the passive or active dispersal of individuals – eggs, larvae, spores, seeds, swimming adults, etc. – from one location or population to another. If some individuals reproduce in the new location, this leads to **genetic connectivity** (gene flow), important for evolution and local adaptation. If the dispersal affects numbers and biomass in the receiving population there is **demographic connectivity**, important for ecological interactions and fisheries management.

METHODS

This policy brief is based on a systematic review of 172 scientific studies published between 1990 and 2023, assessing population structure and connectivity in 48 marine species, both within the Skagerrak and in relation to the adjacent North Sea, Kattegat and Baltic Sea. Population structure was assessed primarily using molecular genetic tools, but also with morphometry and chemical isotope analyses. Connectivity was assessed either by studies of tagged individuals or by oceanographic modelling of propagule dispersal. The scientific literature was strongly dominated by fish species, particularly cod and herring.

Key findings

The Skagerrak harbours distinct populations for the majority of species. For these species, there are clear genetic and/or morphological differences between Skagerrak populations and populations in a least one of the adjacent seas (Figure 1). In some of those species, including herring, lumpfish, cod, plaice, sea trout, harbour porpoise, bladderwrack and toothed wrack, the Skagerrak populations are divergent from populations in both the North Sea and the Kattegat. Several species share a genetic barrier on the south-western tip of Norway, between the Skagerrak and the North Sea, and also in the south, between the Skagerrak and Kattegat. For a few species no population structure was detected in the North Sea-Skagerrak-Kattegat area: three-spined stickleback, European plaice, brown crab, Norway lobster, and green sea urchin.

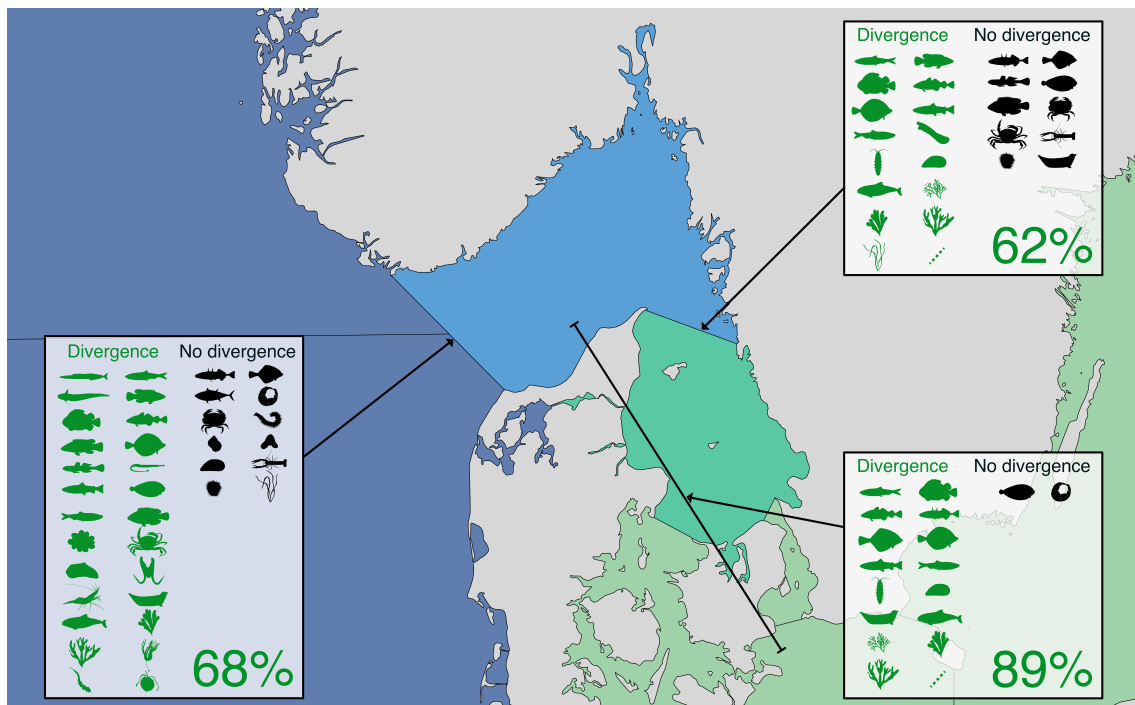


Figure 1. Population structure between the Skagerrak and the adjacent North Sea, Kattegat, and Baltic Sea. The boxes show the species for which population structure between two areas has been assessed, and the percentage of these species for which population structure was found (in green).

More than half of the assessed species also have multiple distinct populations **within** the Skagerrak (Figure 2A). Population structure is most common among coastal sites (Figure 2B), and between coastal and offshore populations (Figure 2C). Population structure is rare in offshore areas, and has only been described for lumpfish, Atlantic bluefin tuna, the cold-water coral *Lophelia pertusa* and the phytoplankton *Skeletonema marinoi* (Figure 2D).

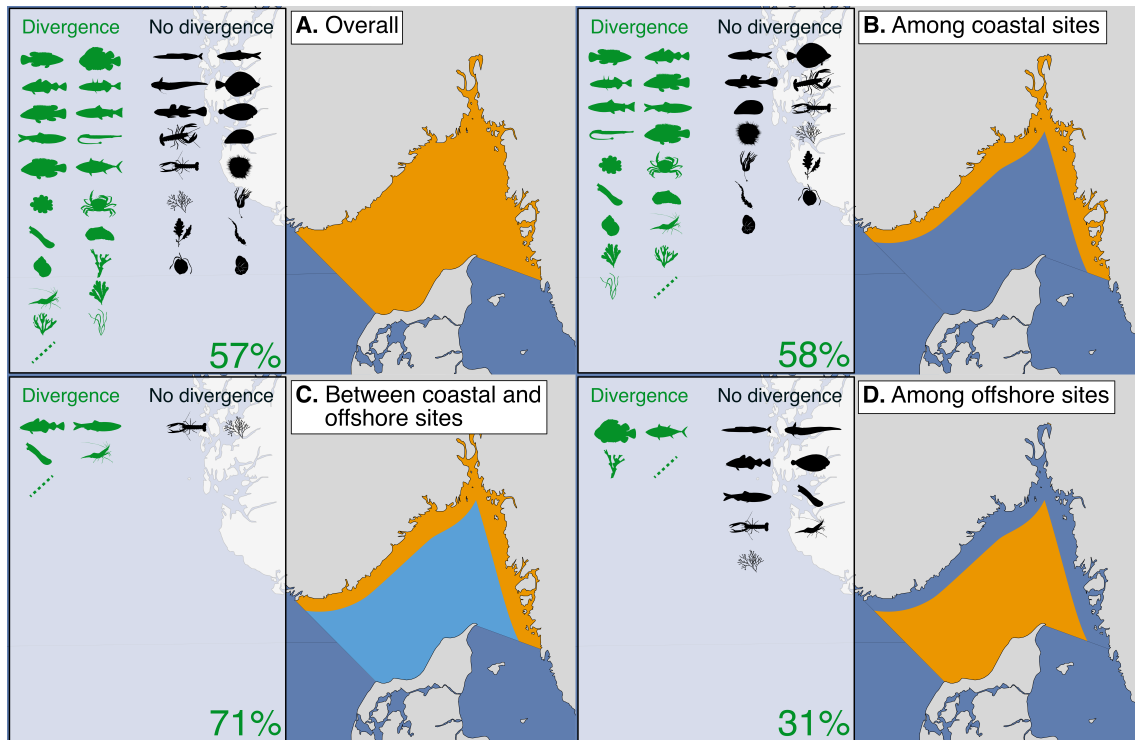


Figure 2. Population structure within the Skagerrak for species assessed in the scientific literature. Subplots show whether any population structure has been found A) broadly within the Skagerrak, B) among coastal sites, C) between coastal and offshore sites or, D) among offshore sites. The boxes show which species have been assessed, and the percentage of these species for which population structure has been found (in green).

Skagerrak populations generally have the potential to disperse to the adjacent North Sea, Kattegat, and Baltic Sea. Dispersal of organisms, i.e. connectivity, **into** the Skagerrak from adjacent seas is high in most assessed species (Figure 3A), whereas connectivity **out** of the Skagerrak is high to the North Sea for all assessed species, but slightly lower southward into the Kattegat and the Baltic Sea (Figure 3B). Dispersal distances **within** the Skagerrak are highly species-specific and may range from a few to hundreds of kilometres, meaning that management needs to be species-specific.

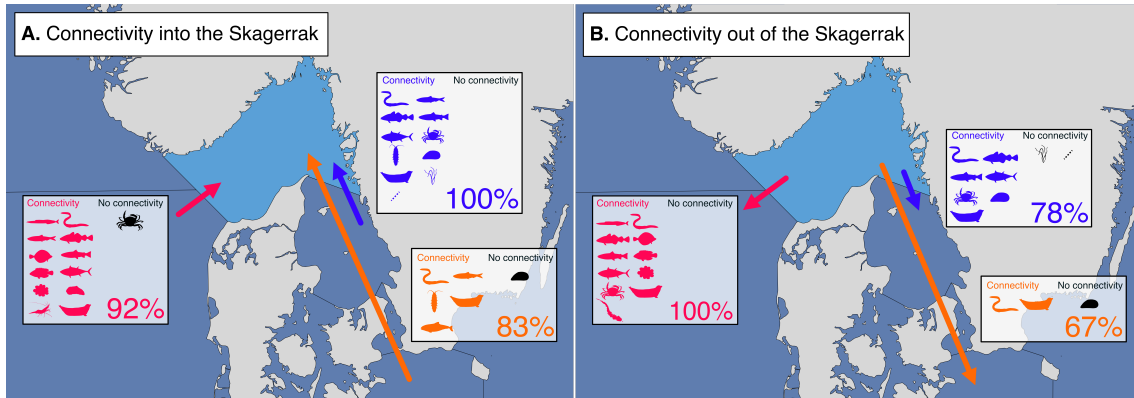


Figure 3. Connectivity of Skagerrak species with the adjacent North Sea (pink), Kattegat (blue), and Baltic Sea (orange). The figure summarises connectivity A) into, and B) out of the Skagerrak, assessed either by tagging or oceanographic modelling. The boxes show which species have been assessed, and the proportion of these species for which high connectivity has been found (in colour).

Recommendations for management

- Management of marine biodiversity in the Skagerrak needs to be based on knowledge about species population structure and connectivity.
- Management should be fine-scaled enough to capture population structure within the Skagerrak, often on the scale of 10s of km, especially along the coast and within fjords.
- Fisheries management, MPA design and marine spatial planning need to consider both coastal and offshore marine areas.
- Management needs to consider that different populations may coexist at certain times in a given area. This is especially relevant in fisheries management, when different stocks coexist, and where genetic mixed-stock analysis should be implemented to disentangle and estimate the proportions of the different stocks.
- More information on population structure and connectivity is needed, both for sessile and mobile species.
- Adaptive strategies that incorporate both spatial and temporal management are more likely to succeed in creating a robust and future-proof biodiversity management in the Skagerrak.

This Policy brief is produced by University of Gothenburg (GU), the Swedish University of Agricultural Sciences (SLU), the Technical University of Denmark (DTU) and the Institute of Marine Research (IMR) under the project "*SAMSKAG – Samarbeid om forbedring av miljøsituasjonen i nordiske hav- og kystområder, med fokus på Skagerrak*", funded by the Nordic Council of Ministers.

Further reading

Henriksson et al. 2024 Connectivity and population structure in a marginal sea – a review. BioRxiv Preprint

Contact

Carl André (carl.andre@gu.se)

Simon Henriksson (simon.henriksson@gu.se)

Marlene Jahnke (marlene.jahnke@gu.se)

About this publication

Spatial population structure and connectivity among marine populations in the Skagerrak: implications for marine biodiversity conservation

Authors: Carl André (GU), Simon Henriksson (GU), Marlene Jahnke (GU), Pierre De Wit (GU), Halvor Knutsen (IMR), Per Erik Jorde (IMR), Guldborg Søvik (IMR), Even Moland (IMR), Charlotte Berkström (SLU), Mikael van Deurs (DTU)

Nord 2024:033

ISBN 978-92-893-8077-5 PDF

ISBN 978-92-893-8078-2 ONLINE

<http://dx.doi.org/10.6027/nord2024-033>

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Cover photo: Adobe Stockphoto

Published: 13 November 2024

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Nordens Hus

Ved Stranden 18

DK-1061 Copenhagen

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