eDNA as a non-invasive method to study distribution, migration and reproduction of coastal North Sea fish

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Coastal environments serve as essential nursing, feeding, and spawning grounds for commercially and ecologically important fish species, some of which use nearshore habitats as transitional steps in their ontogenetic migration. Under climate change and intensive fishing pressure, environmental conditions and fish communities' seasonal migration and dynamics are shifting. Such changes highlight the importance of understanding fish spatial and temporal distribution in coastal habitats for sustainable ecosystems and fisheries management. Despite the importance of long-term monitoring to obtain information on fish movements and distribution, fine-scale temporal datasets on fish communities remain scarce, and the spatial range is often limited due to the intense field work required.

Fish spatial distribution has been thoroughly studied with both long-term beam trawl and eDNA-based surveys in the Belgian part of the North Sea (BPNS). However, seasonal changes in fish assemblages remain understudied despite the seasonality of structuring environmental factors. In the present study, we explored the use of eDNA 12S metabarcoding of seawater samples to monitor fine-scale temporal and spatial patterns in fish communities. In total, 168 samples were collected across 20 sampling campaigns conducted monthly between August 2021 and August 2023. Within the 12 nautical miles of the BPNS, nine fixed stations were evenly spread across a west-to-east and near-to offshore gradient. Our results revealed no temporal patterns at the community level due to the lack of species turnover and the ubiquitous presence of dominant Southern North Sea fish species using coastal Belgian waters as spawning and nursing grounds. However, species-specific temporal changes in eDNA effectively reflected their known biology, reproductive activity, and seasonal migrations in the study area. Similarly, eDNA revealed no distinct spatial patterns in coastal fish communities but unveiled species-specific spatial distribution consistent with beam trawl and eDNA-based surveys previously conducted within the BPNS. The species distribution highlighted the importance of the freshwater input from the Scheldt estuary and the resulting environmental gradient (sediment type, nutrient loading, salinity, and SPM) in shaping fish communities.

Our findings underscore that eDNA metabarcoding is a valuable biomonitoring tool for fish. Moreover, our results further support the link between eDNA and fish biology, as the observed species-specific eDNA trends aligned with a priori expectations based on the literature on lifecycle, migration patterns, and habitat use.

Keywords
EDNA Metabarcoding; Spawning, Nursery; Fish Communities; Monitoring; Fish Lifecycle