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Conference Abstract

Commercial fish abundance estimation in the Belgian part of the North Sea through eDNA ddPCR analyses

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Abstract

Monitoring of fish assemblages in the Belgian part of the North Sea (BPNS) mainly happens through trawling. While effective, this method is invasive and destructive as it disturbs bottom communities, catches non-target species and removes organisms from the environment. A more sustainable alternative for monitoring marine diversity is the use of environmental DNA (eDNA) which comprises intra- and extracellular genetic material that comes from the shedding of organic material, like scales and mucus in the case of fish. When applying metabarcoding on eDNA, community composition can be inferred simply by analysing a small volume of water. Therefore the technique does not disturb the environment, and the high sensitivity of eDNA allows the detection of rare and transient species that are frequently missed by traditional sampling methods. Next to determining community composition, the amount of eDNA copies in the water could potentially be used to quantify target fish species in the marine environment. Here, we investigate whether eDNA concentrations from marine water samples correlate with local fish abundance estimates obtained via traditional beam trawling. Species specific Droplet Digital Polymerase Chain Reaction (ddPCR) assays were designed and tested for three

economically important species: common sole (*Solea solea*), plaice (*Pleuronectes platessa*) and whiting (*Merlangius merlangus*). In march 2020, 12 sites in the BPNS were selected based on absence, low and high abundances of the three target species as observed in epibenthos monitoring data from previous years. In each site, 2L of seawater was collected with a niskin bottle from ca 1m above the sea floor. Subsequently, beam trawl transects of 1 km were conducted and all epibenthos species caught in the trawling net were morphologically identified, counted and weighted. Our results indicate promising correlations between eDNA concentrations obtained with the ddPCR assays and the number of specimens in the net for all three species. Some “false” positive results were obtained with the ddPCR, but these may actually be “true” positive detections because the fish might be present in the area but were not caught in the trawling transects. This warrants further investigation to see how far eDNA signals can be detected in the North Sea system. Next, 50 water samples were collected in Autumn 2020, involving more locations with or without the three fishes. This time samples were taken at the beginning, middle and end of the 1 km transects to investigate small scale horizontal variation in eDNA concentrations. The autumn samples are currently being processed. In March 2021, samples will be taken at different depths (surface, middle of the water column and ca 1m above the seafloor) to investigate whether there are any vertical patterns in eDNA distribution in a very well mixed system such as the BPNS. A DNA shedding experiment will be performed as well to estimate the rate at which the three fishes shed DNA. This will provide important information on how quickly fishes can be detected when they swim by. The information obtained with the field sampling and experimental setting will help to strengthen the correlation to a point that reliable abundance estimations of our target species become possible and will allow us to evaluate the potential of eDNA as a sustainable alternative/addition to traditional monitoring methods.

Keywords

environmental DNA; abundance estimation; genomics; sustainable monitoring

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