Sustainable monitoring of commercial fish in the Belgian part of the North Sea through eDNA ddPCR analyses

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Traditional monitoring of fish stocks in the North Sea mainly occurs via trawling, yet this method is invasive and destructive to the environment as it disturbs the seafloor and causes bycatch of non-target species. Furthermore, due to regulations it is not allowed to monitor via trawling in certain regions, such as windfarms. Recent advancements in environmental DNA (eDNA) applications offer opportunities as more sustainable alternatives for fish monitoring. eDNA comprises all intra- as well as extracellular genetic material present in an environmental sample. In the case of fish, this DNA can come from the shedding of scales and mucus or the release of gametes for example. A great advantage of using eDNA is that only a small amount of water is required to analyse it. Therefore, samples can be taken from smaller vessels or even automated samplers, without having to catch any fish or disturbing the environment. By analysing the eDNA, species presence/absence and community composition can be inferred. This method is very sensitive and often detects rare and elusive species that traditional methods tend to miss. In this study, we wanted to take this one step further and investigate whether species-specific eDNA concentrations in marine water samples may be used to estimate local fish abundances, by determining eDNA concentrations through droplet digital PCR (ddPCR), a very sensitive technique that can detect and quantify even a few molecules of DNA in a sample. We tested whether eDNA concentrations of three economically important species, common sole (*Solea solea*), plaice (*Pleuronectes platessa*) and whiting (*Merlangius merlangus*), correlate with their abundances based on traditional beam trawling data. To this end, water samples were collected in tandem with beam trawl 1 km transects in March 2020 at 12 sites in the Belgian part of the North Sea (BPNS). These sites were selected based on previous monitoring data, indicating absence, low and high abundances of the three fish species. Species-specific ddPCR primer/probe assays were developed for sole and whiting, and an existing assay was implemented for plaice. Results indicate promising correlations for all three species, although with some “false” positives. Yet, these may actually be true positive detections, which were as such not recorded within the beam trawl samples. This warrants further investigation to see at what distance a fish eDNA signal can still be detected. Therefore, 50 water samples were collected in Autumn 2020, involving more locations with and without the three fishes, again based on traditional beam trawl data. This time samples were taken at the beginning, middle and end of the 1 km transects to assure that the eDNA better represents the trawling transect and to investigate local variation in eDNA concentrations. These results will allow to fine tune the eDNA abundance correlations for the BPNS. In a next step, species-specific DNA shedding rates and local eDNA patterns will be investigated, which are likely to be more complex in the marine environment compared to freshwater systems. The combined results of these experiments will show whether the correlations allow for accurate abundance estimations, in order to evaluate if eDNA can serve as a potentially efficient and sustainable alternative or addition to traditional abundance estimates.

Keywords: Environmental DNA; Fish abundance estimation; Genomics; Sustainable monitoring