

Time and cost efficient DNA-based monitoring of marine non-indigenous species in the harbour of Ostend (Belgium) using nanopore sequencing

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Non-indigenous species (NIS) continue to be a major threat for the ecological health of our environment and often are a nuisance for society. Regular monitoring is a key factor for prevention and mitigation of negative impacts caused by NIS. In many countries, including Belgium, monitoring programs for NIS in marine environments are limited in spatio-temporal scope as well as taxonomic coverage. DNA-based monitoring is a promising approach to solve this problem as it is potentially time and cost efficient as well as scalable for high spatio-temporal coverage. In the framework of the GEANS and LifeWatch projects, we conducted a quick survey of the fauna in the harbour of Ostend (Belgium) using traditional microscopic examination of the collected specimens. In parallel, we metabarcoded environmental samples (settlement plates and plankton net samples) at two genetic markers (the mitochondrial COI and nuclear 18S rRNA). The two approaches detected different subsets of the NIS pool present in the harbour. But the DNA-based approach significantly outperformed its morphology-based counterpart as it detected more NIS and was also more time efficient. We show that recent advances in sequencing technology and the availability of fast bioinformatic tools for data analysis allow a rapid turnover time of potentially less than two working days between sample collection and final results. Decreasing sequencing costs and increasing training of practitioners in molecular genetic techniques enable large scale NIS monitoring, leaving the lack of embedding in national and regional monitoring plans and corresponding funding schemes as the primary bottlenecks for implementation.

Keywords: Non-indigenous species; Biodiversity monitoring; Metabarcoding; Nanopore sequencing