

## Testing genetic tools for marine ecosystem health assessment: a pilot on non-indigenous species.

Delacauw Sander, Deneudt Klaas, GEANS Consortium and Hablützel Pascal

Flanders Marine Institute (VLIZ), InnovOcean site, Wandelaarkaai 7, 8400 Oostende, Belgium  
E-mail: [sander.delacauw@vliz.be](mailto:sander.delacauw@vliz.be)

GEANS (Genetic tools for Ecosystem health Assessment in the North Sea region), an Interreg North Sea region project aims to introduce DNA-based methods in biological monitoring. Within this project, seven North Sea countries collaborate to develop standard operating procedures (SOPs), test them by means of pilot studies and translate the results into a decision support framework to support stakeholders in biological monitoring. Among the pilot studies, one specifically aims for on the detection non-indigenous species (NIS), since accurate monitoring is a key prerequisite to limit the spread of NIS among harbours. While traditional survey methods require species identification upon visual inspection of each sampled individual organism, they heavily depend on taxonomic expert knowledge. Alternatively, species can be distinguished based on their unique DNA sequence. Such species-specific DNA barcodes can be read from DNA extracted from bulk samples consisting of many species without prior sorting (so-called meta-barcoding). During late spring, VLIZ initiated a NIS pilot study in the harbor of Ostend. Three sample sites were selected at which plankton samples and eDNA samples were collected. Also, settlement plates were installed at each location. Later, in high summer, these plates were recovered along with plankton, eDNA and scrape samples. These samples are now being processed using both traditional morphological analysis and DNA-based techniques. Through GEANS, traditional NIS monitoring in harbours could be improved and rendered more cost- and time-efficient as well as more accurate. HELCOM and OSPAR developed a port survey protocol to monitor non-indigenous species. This protocol is customized for morphological species identification of the sampled organisms. Using the HELCOM/OSPAR protocol as a baseline, we investigate to which extent morphological examination can be complemented or replaced by meta-barcoding. Since organisms will not be examined individually, but simultaneously from a bulk sample, identification should be more time- and as such more cost-efficient. In addition, we expect a significant improvement in detection power for non-indigenous species that are difficult to distinguish from similar native or other non-indigenous species. This particularly applies to planktonic larval stages, which are often impossible to identify at species level using morphological examination. While focusing on the North Sea region, the methods we apply are highly generic and can readily be transferred to other use cases worldwide. As such, our efforts to improve NIS monitoring will also improve standardization at the international level.

Keywords: GEANS; Non-indigenous species; Pilot; Monitoring; DNA-barcoding