

## Intercepting invaders: metabarcoding for monitoring non-indigenous species in a North Sea harbour

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My thesis is embedded in the EU Interreg project GEANS (Global Ecosystem Health Assessment for the North Sea), which aims to facilitate the implementation of genetic-molecular tools for routine ecosystem assessment in the North Sea region. To this end, the project consists of various pilot studies that aim to compare DNA-based and traditional survey methods of the marine environment. One of the research areas of GEANS is monitoring of non-indigenous species (NIS) in harbours. NIS are a growing concern in coastal areas and have the potential to become invasive and displace native organisms and harm economic activities. Marine NIS are primarily spread via ballast water. Vessels are required by the International Maritime Organisation to treat their ballast water before entering a port. Exemptions to this requirement can, however, be granted if it can be shown that the voyage undertaken by the ship does not carry a significant risk of introducing new or dangerous alien species from one port to another. To evaluate the risk, a survey of the biota of all the harbours encountered during the voyage must be conducted. Biological surveys for NIS have traditionally relied on morphological identification of biota, but this approach is time- and labour-intensive and prone to errors or biases induced by a lack of taxonomic expertise. DNA-based survey methods, such as metabarcoding, have the potential to ameliorate these issues but are still not commonly implemented by stakeholders for the North Sea region.

In my thesis, I evaluated the performance of metabarcoding for detection of NIS in the harbour of Oostende (Belgium). I first compared the total numbers of native and non-native species detected from settlement plates via visual identification with the numbers reported from these plates via metabarcoding of the 18S rRNA gene. Next, I compared the performance of two different marker genes (COI and 18S rRNA) in detecting species composition from plankton samples via metabarcoding. Metabarcoding was able to detect many more species from the settlement plates than morphological examination alone, and it also enabled the rapid identification of planktonic species, which would otherwise be extremely difficult to identify morphologically. Non-native species were found from both planktonic and plate samples via metabarcoding. Some of these taxa were never recorded for the North Sea while others were well-known invasive species. However, the lack of consensus seen among the different species detection methods, coupled with many dubious identifications, indicate shortcomings of DNA-based methods. In this study, I demonstrated that metabarcoding may be feasible to detect NIS in North Sea harbours, but that current technical limitations of the method warrant caution and further explorative research.