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Conference Abstract

Sediment eDNA Metabarcoding for monitoring impacts from offshore oil extraction

Anders Lanzén[‡,§], Jon Thomassen Hestetun[|], Andrea Bagi[|], Thomas D Dahlgren[|]

‡ AZTI, Pasaia, Spain
§ IKERBASQUE, Basque Foundation for Research, Bilbao, Spain
| NORCE, Norwegian Research Centre, Bergen, Norway

Corresponding author: Anders Lanzén (alanzen@azti.es)

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Abstract

Routine biological monitoring of the areas affected by offshore oil drilling and extraction is critical for ensuring proper environmental management. In addition to sufficient knowledge of the ecosystem affected, formalised e.g. as biotic indices of indicator species, adequate temporal and spatial resolution is also required, to provide accurate information. As already demonstrated in several types of environments, environmental DNA (eDNA) metabarcoding offers an attractive alternative to current morphology-based assessments, including for impacts of oil extraction or spills.

We have recently studied the influence of different experimental strategies on the accuracy of marine sediment metabarcoding, suggesting minimum criteria for technical and spatial replication (Hestetun et al. 2020). Here, we aim to evaluate the predictive power of this strategy, through agreement with assessments based on physicochemical measurements and current bioindicators. To this end, we targeted the metazoan, and total eukaryotic benthic communities, using COI and 18S V1-V2 markers, respectively. Sampled sites ranged from high to low impacts. The studied areas were located near active production installations and reference sites on the Norwegian continental shelf, in the North Sea and Barents Sea.

As a proxy for accumulated impact, we developed a simple physicochemical pressure index (PI) based on total hydrocarbons, PAH16, barium and copper, all of which agreed well with impact reported from recent routine monitoring. Alpha diversity of both molecular datasets, as well as of morphology data, correlated strongly with this PI. However, the correlation was stronger yet with the macroinvertebrate-based Norwegian Sensitivity Index (NSI) derived from COI metabarcoding data, which also agreed well with NSI values derived from morphology-based monitoring. We also identified a set of bioindicator taxa from each of the two metabarcoding datasets, used to develop two novel metabarcoding-based biotic indeces. Using cross-validation, we demonstrated that predictions based on these indeces agreed well with PI. Predictive performance was better, and similar to NSI, for the COI-based index, but also high for the 18S-based version.

In conclusion, this study demonstrates how *de novo* biotic indices can be developed, that perform comparably to existing biotic indices. We are confident that, using a larger set of samples, performance can be improved beyond that of current monitoring practices. Thanks to the reduced costs of eDNA analysis in comparison to morphological identifiation, this would also pave the way for improved spatial and temporal resolution employed in routine environmental monitoring. In doing so, it can also provide valuable raw data for improving our understanding of benthic ecology, biodiversity and its sensitivity to anthropogenic pressures.

Keywords

monitoring, microbenthos, sediment, eDNA, de novo biotic index, oil extraction, hydrocarbons, metabarcoding, 18S

Presenting author

Anders Lanzén

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References

- Hestetun J, Lanzén A, Skaar K, Dahlgren T (2020) The impact of DNA extract homogenization and replication on marine sediment metabarcoding diversity and heterogeneity. Authorea https://doi.org/10.22541/au.160486389.98416006/v1