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ENVIRONMENTAL MONITORING THROUGH NEXT-GENERATION SEQUENCING METABARCODING: ASSESSING THE IMPACT OF FISH FARMING ON BENTHIC MACRO-AND MEIOFAUNA COMMUNITIES

Jan Pawlowski*, Philippe Esling,*†, Franck Lejzerowich*, Thomas Cedhagen‡ and Thomas A. Wilding§

*Department of Genetics and Evolution, University of Geneva, Sciences 3, 30, Quai Ernest Ansermet, CH-1211, Geneva 4, Switzerland. †IRCAM, UMR 9912, Université Pierre et Marie Curie, Paris, France. ‡Department of Biological Sciences, Aquatic Biology, Aarhus University, Aarhus, Denmark. §Ecology Department, SAMS, Scottish Marine Institute, Oban, Argyll, UK

ABSTRACT

The measurement of species diversity represents a powerful tool for assessing the impacts of human activities on marine ecosystems. Traditionally, the impact of fish farming on the coastal environment is evaluated by monitoring the dynamics of macrobenthic infaunal populations. However, taxonomic sorting and morphology-based identification of the macrobenthos demand highly trained specialists and are extremely time-consuming and costly, making it unsuitable for large-scale biomonitoring efforts involving numerous samples. We propose to alleviate this laborious task by developing protist and metazoan metabarcoding tools based on next-generation sequencing (NGS) of environmental DNA and RNA extracted from sediment samples. We have analysed the response of benthic foraminiferal communities to the variation of environmental gradients associated with salmon farms in Scotland. We investigated the foraminiferal diversity based on ribosomal minibarcode sequences generated by the Illumina NGS technology. We compared the molecular data with morphospecies counts and with environmental gradients, including distance to cages and redox used as a proxy for sediment oxygenation. Our study revealed high variations between foraminiferal communities collected in the vicinity of fish farms and at distant locations. We found evidence for species richness decrease in impacted sites, especially visible in the RNA data. We also detected some candidate bioindicator foraminiferal species. Based on this proof-of-concept study, we conclude that NGS metabarcoding using foraminifera and other protists has potential to become a new tool for surveying the impact of aquaculture and other industrial activities in the marine environment. The methodology has been developed further and is now possible to use also for metazoans.



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