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Conference Abstract

Biogeographic structuring of benthic microbial communities influence the establishment of global bioindicators for coastal aquaculture impact monitoring

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Abstract

With an increasing demand for finfish from aquaculture, the importance of monitoring the impact of aquaculture installations on coastal ecosystems becomes more and more important. The traditional approach employs macroinvertebrates as bioindicators to assess the ecological quality (EQ) of near-field benthic ecosystem, which is costly and time consuming. Modern approaches using environmental DNA metabarcodes of microbial organisms (eukaryotes and prokaryotes) have shown to be a powerful alternative. It is crucial that the ecological quality determined by molecular bioindicator signatures mirrors the results of standard macroinvertebrate inventories. Previous studies looking for bioindicators of organic enrichment have so far only analyzed samples within a specific geographic location (e.g. one farm, farms from one country). To answer the question if there are global bioindicators (or core communities) across different biogeographic regions, we analyzed 328 samples from three salmon producing countries (Norway, New Zealand,

Scotland) to find commonalities in bacterial and ciliate DNA metabarcodes communities within the same ecological quality groups. We used supervised machine learning (SML) to predict both country origin and ecological status for both bacterial and ciliate eDNA markers. We then investigated if prediction accuracy for ecological quality increases if the dataset is reduced to single-country or two-country subsets to eliminate country/region specific effects. Further, core communities including only cosmopolitan ASVs were tested to detect possible global bioindicators for each individual EQ class. Based on the obtained results, we discuss the potential of a globally applicable database and a global training of an SML algorithm to predict ecological quality in aquafarm sediments using eDNA metabarcodes from benthic bacterial and ciliate communities.

Keywords

biogeography, supervised machine learning, monitoring, aquaculture, eDNA metabarcoding, bioindicators

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