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Conference Abstract

The potential of sediment and fauna microbiomes in water quality assessment

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Abstract

The Water Framework Directive dictates that all European surface waters must have an ecological quality of good or better. The need for regular and comparable ecological quality assessments drives the development of DNA-based approaches for biomonitoring in freshwater systems. Water quality assessments are traditionally based on biological quality elements (BQE) such as fish, plants and other fauna.

Previous studies have shown the potential of metabarcoding as a potential supplement to traditional morphology-based approaches to determine water quality indices. Metabarcoding of the macroinvertebrate community on unsorted bulk samples has the ability to profile freshwater streams into at least 7 water quality categories Kuntke et al. (2020). A follow-up study using the same locations shows that a broad range barcode targeting the ribosomal 16S/18S RNA genes simultaneously demonstrated that ecological quality is reflected in all environmental DNA; the eukaryotic communities, and perhaps even more so, in the microbiome of the sampled streams (unpublished).

The relationship between water quality and microbial communities is well-known, but not well-described. Healthy compositions of microbiota are vital for the functioning of many organisms, and this principle extends to the ecosystem level as well. The microbiome of freshwater streams therefore represents a great untapped potential in the development of DNA-based monitoring methods. The aim of this work was to explore links between water quality, environmental DNA collected from bulk and sediment samples, as well as individual

macroinvertebrates with relevance for freshwater streams. Previous work on invertebrate communities Kuntke et al. (2020), and bulk sample analysis (total 53 streams) (unpublished) was combined with metabarcoding data of microbial communities from an additional 31 Danish stream sediments, as well as 140 macroinvertebrate indicator species.

Metabarcoding of freshwater stream bulk and sediment samples has revealed strong parallels to conventional fauna observations in relation to estimations of water quality. Both the invertebrate and microbial community diversity followed the general trend of increasing to a plateau with higher water quality (data not shown). Macroinvertebrate composition (Fig. 1a) and sediment microbiome composition (Fig. 1b) were observed to be present on a gradient in relation to water quality, with individual taxa being either more, equally or less abundant with changing water quality, and only few solely related to a single category. Microbial populations associated to poor oxygenation (*Methylomonadaceae, Rhodocyclaceae*), as well as faecal contaminations (*Anaerolineaceae*, *Lentimicrobiaceae*) were abundantly observed in sediments of lower ecological quality. This equates to presence of macroinvertebrates able to survive in polluted environments with poor oxygen conditions. Part of the sediment microbiome was also found to be associated to the analysed macroinvertebrate species (Fig. 1c). However, the invertebrates also had their own unique and diverse microbiota, including known endosymbionts (*Wolbachia*, *Rickettsia*) and other insect associated microbiota (*Acinetobacter*, *Chryseobacterium*).
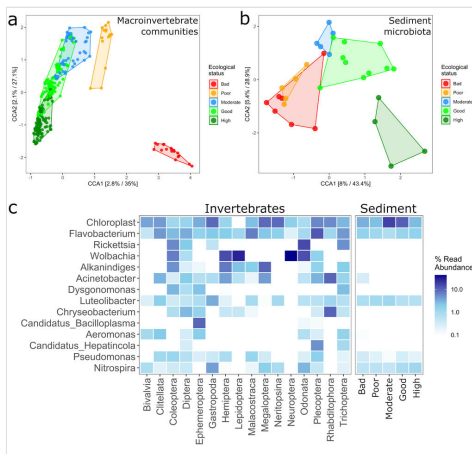

Figure 1. doi

Fig. 1: Relationships between macroinvertebrates (n = 53, 6 replicates per location) (a), sediment microbiomes (n = 31) (b) and water quality, and microbiomes of freshwater invertebrates (n = 140, 16 orders) and sediments of different water qualities (n = 31) (c).

Current sequencing platforms and high quality databases combined with advanced statistical analyses have made it possible to begin the development of modified assessment protocols based on DNA analyses, and could potentially lead to entirely new ecological quality indices for the prediction of water quality. Microbes can be very sensitive

to environmental changes, and harbour potential indicator organisms for e.g. pollution, and by extension, water quality in a given stream. Microbiome data is abundant, and easy to obtain from all types of environmental samples, including those collected for metabarcoding of existing BQE such as macroinvertebrates. Exploring the use of sediment and fauna microbiomes has the potential to yield a wealth of new information relating to how ecosystems reflect water quality, and may provide additional indicators for use in DNA-based water quality assessment methods.

Keywords

Metabarcoding, macroinvertebrates, microbial communities, water quality

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