Conference Abstract

Developing prokaryotic water quality indicators

Alexander Eiler[‡,§], Domenico Savio[|], Laurent Fontaine[‡], Lorenzo Pin[¶]

‡ University of Oslo, Oslo, Norway
§ eDNA solutions AB, Gothenburg, Sweden
| Karl Landsteiner University, Krems, Austria
¶ NIVA - Norsk Institutt for Vannforskning, Oslo, Norway

Corresponding author: Alexander Eiler (alex@ednasolutions.se)

Abstract

Despite the importance of prokaryotes in aquatic ecosystem and their predictable diversity patterns across space and time, biomonitoring tools relying on prokaryotes are widely lacking. Using metabarcoding, as well as other molecular methods, we were able to identify multiple prokaryotic descriptors and illustrate their reliability and advantages in aquatic environmental assessment. Multivariate statistical and machine learning methods combined with variation coefficient and overall prevalence of taxonomic groups were used to detect possible biological indicators among prokaryotes for various anthropogenic pressures, i.e. acidification, eutrophication and faecal contamination in aquatic environments. In addition, text mining approaches provide powerful alternatives for sequence based status classification and source tracking of contaminants. While these individual sequencing based indicator approaches seem to be powerful, alpha and beta diversity indices provide so far minor precision in ecological status classification. Reasons are the often non-linear association between prokaryotic alpha and beta-diversity with environmental gradients as indicated by first modeling attempts. Still, our results suggest that the limitations in reliably describing reference communities and developing general and robust classification systems for water quality assessment based on prokaryotic sequencing data can be overcome by extensive training data.

Presenting author

Alexander Eiler, Department of Biosciences, Section for Aquatic Biology and Toxicology, University of Oslo, Norway

Presented at

1st DNAQUA International Conference (March 9-11, 2021)

Conflicts of interest

The authors state no conflict of interest