
TOWARDS A QUANTITATIVE INTERPRETATION OF METABARCODING DATA, A FRESHWATER ZOOPLANKTON CASE STUDY

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Résumé

Combining DNA barcoding with high-throughput sequencing, i.e. metabarcoding, is a powerful tool to obtain qualitative estimates of species communities. Furthermore, some studies have indicated that metabarcoding results can be interpreted in a quantitative manner even though the variation in the obtained data is typically high. Methods to reduce the variation and improve the quantitative interpretation of metabarcoding data have been assessed for some aquatic groups (e.g. fish and diatoms) but have not been evaluated for zooplankton communities. Zooplankton taxa, however, respond quickly to environmental changes thus making them good indicator species and are an essential link in the aquatic foodweb. Through an annual sampling campaign of 3 large peri-alpine lakes and the collection of samples from 3 experimental systems we obtained zooplankton community data through traditional microscopy counts and, DNA and eDNA metabarcoding. We further evaluated whether coupling metabarcoding results with a correction for amplification biases

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and/or a quantitative assessment of DNA concentrations for the taxonomic groups will improve the quantitative nature of the metabarcoding data. Combining both metabarcoding results with group specific quantification data improved correlations between molecular and traditional abundance measures but corrections for amplification biases has mixed effects. Overall, we show that quantitative monitoring of zooplankton communities is possible with (e)DNA metabarcoding thus opening up opportunities for metabarcoding analyses to be implemented in routine biomonitoring surveys.

Mots-Clés: Metabarcoding, Zooplankton, Freshwater, environmental DNA, Quantitative biomonitoring