EFFECT OF DNA EXTRACTION METHODS ON METABARCODING SUCCESS OF HOMOGENIZED FRESHWATER MACROINVERTEBRATE COMMUNITY SAMPLES

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Introduction

Metabarcoding based on homogenized bulk samples holds great potential for larger-than-ever scale monitoring of freshwater. Several studies show that DNA extraction methods developed and optimized for specific samples give the best results. Rather than being an exhaustive comparison, this study exemplifies that the choice of DNA extraction method may have a profound effect on the biodiversity analysis.

Conclusions

Based on our results, choosing the DNA extraction method for lotic environments is not as critical as it is for lentic environments - especially if the deep lentic samples contain only few target specimens in excess non-target material. The lotic monitoring sample is based on kick-samples, and those samples contain mainly the target specimens while the lentic sampling is performed using grabs and the deep lake bottom samples contain mainly sediments. In our case, the PowerPlant kit with beads and inhibitor removal steps performed most consistently. However, none of the compared DNA extraction methods were able to recover the same community composition in the lake 15m subsamples (approximately 20 target specimens), indicating serious issues for repeatability of such samples.

Methods

Methods of DNA extraction methods may have a profound effect on the biodiversity analysis. For instance, while the PowerPlant kit with beads and inhibitor removal steps performed most consistently, none of the compared DNA extraction methods were able to recover the same community composition in the lake 15m subsamples (approximately 20 target specimens), indicating serious issues for repeatability of such samples.