



Conference Abstract

Analyzing multiple stressor effects on EPT taxa in a mesocosm experiment with DNA metabarcoding

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Abstract

Multiple stressors diversely and often adversely affect stream ecosystems around the globe. Therefore, understanding multiple stressor effects on different organisms is essential for a better ecosystem understanding, an accurate water quality assessment and improved ecosystem management. However, while multiple stressor effects should be assessed at species level this taxonomic resolution is often not achieved e.g. for stream macroinvertebrates. Due to their high abundance and diversity, species-level identification is often not feasible with morphology-based approaches. DNA metabarcoding represents an alternative approach for studying multiple stressor interactions at species level.

In an outdoor experiment over 10,000 specimens from the insect orders Ephemeroptera, Plecoptera and Trichoptera (EPT), which are routinely used as bioindicators, and their responses to stressors were studied. In the experiment salinity, fine sediment deposition and flow velocity were manipulated in a full-factorial design in 64 mesocosms with two microhabitats each (streambed and leaf litter), resulting in eight replicates per treatment. DNA metabarcoding revealed 122 EPT Operational Taxonomic Units (OTUs), from which the most abundant 27 alone showed 14 different response patterns to the applied stressors. The high taxonomic resolution achieved by DNA metabarcoding revealed species specific stressor responses that were hidden at a lower taxonomic resolution. As a prominent example, *Rhithrogena semicolorata* responded negatively to fine sediment

deposition and flow velocity reduction, while *Ecdyonurus torrentis* (both Heptageniidae, Ephemeroptera) was insensitive to experimental manipulation, highlighting different stressor responses among species within the same family (Fig. 1, Beermann et al. 2020).

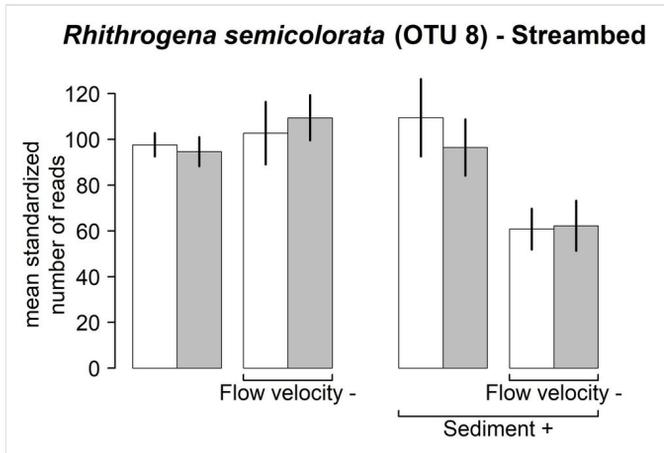


Figure 1. [doi](#)

Mean standardized number of reads for OTU 8 (*Rhithrogena semicolorata*, Heptageniidae, Ephemeroptera) in the microhabitat streambed for all experimental treatment combinations. White bars indicate ambient salinity, while grey bars indicate increased salinity. Error is shown as standard error.

Even for well-studied organisms such as EPT taxa, this study shows that DNA metabarcoding has the potential to depict response patterns at species or OTU level despite high specimen abundance. Consequently, DNA metabarcoding promises to be a rewarding method when investigating and assessing multiple stressor effects on stream water quality.

Keywords

freshwater, stream ecosystems, stressor effects, taxonomic resolution, macroinvertebrates

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