



Conference Abstract

Assessment of the macroinvertebrate community of the Vjosa river through non-destructive DNA metabarcoding of preservative ethanol

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Abstract

Streams and rivers represent hotspots of biodiversity in their natural state. This biodiversity is declining worldwide due to pollution, exploitation and hydromorphological degradation of these systems. One of the last big, natural rivers in Europe is the Vjosa in the Balkan region. The catchment is characterized by natural flow dynamics, resulting in high habitat diversity and turnover, and hosts several sensitive and endemic species (e.g. *Isoperla vjosae*). DNA metabarcoding represents a promising approach to characterize this biodiversity but methodological drawbacks such as primer bias or incomplete reference databases limit the application, particularly in taxonomically underexplored regions.

Here, we assessed stream biodiversity with a focus on macrozoobenthic (MZB) taxa via a non-destructive, voucher-preserving DNA metabarcoding protocol. In this approach, ethanol used for preservation of multi-habitat samples in the field was used as DNA

template, allowing to retain the integrity of the original sample and further comparison of molecular and morphological taxa lists. Samples were taken in spring and autumn 2018 at 48 sites allocated over the Vjosa catchment. The preservative ethanol was filtered through 0.43 µm nitrocellulose membranes from which DNA was extracted. Subsequently, a 421 bp fragment of the COI gene was amplified with the primer pair BF2/BR2 and Illumina sequenced. After filtering for sequences with similarity to reference entries >85%, 4,123 OTUs were obtained, of which 921 were identified as MZB taxa. Dipterans and ephemeropterans were most abundant, followed by plecopterans. Some taxa (e.g. molluscs) were not identified due to a known primer bias and >7,000 OTUs could not be assigned above 85 % similarity. Using the here presented voucher-preserving approach allowed us to identify the pitfalls of DNA metabarcoding as tool for biodiversity assessment in taxonomically unexplored regions such as the Vjosa catchment. However, the comparison of specimen abundance data and molecular data showed the power of non-destructive fixative metabarcoding for detecting MZB communities with highly increased taxonomic resolution.

Keywords

free DNA, fixative, voucher-preserving, biodiversity assessment

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