



Conference Abstract

New insights into Danube's macroinvertebrate communities from DNA metabarcoding as part of the Joint Danube Survey 4 (JDS4)

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Abstract

The Joint Danube Survey (JDS) is a multinational effort in monitoring Danube's water quality, including its major tributaries. The Danube river stretches over a distance of 2,800 km and flows through or borders 10 different countries to which it is of utter importance as a source of potable water and hydrodynamic power. The JDS is conducted every 6 years and provides a unique opportunity to collect comprehensive data on both abiotic parameters and organisms and to raise awareness of the importance of water as a natural resource. As part of JDS and as a biological quality element in many monitoring programs worldwide, macroinvertebrates are monitored as indicators for various environmental conditions. However, due to their diverse taxonomic composition, associated difficulties with their morphology-based identification as well as their sheer abundance, macroinvertebrates are often analysed with a low taxonomic resolution (i.e., above species level). As an alternative, DNA metabarcoding offers a promising approach to capture this species diversity more accurately.

Here, we used DNA metabarcoding to investigate the macrozoobenthic diversity of 46 sites from the latest JDS sampling campaign in 2019. To analyse macroinvertebrate diversity,

bulk samples were taken by kick-net sampling and analysed using two different approaches, analysing the bulk sample fixative and analysing homogenised organisms from complete bulk samples. DNA metabarcoding of the sample fixative revealed 1,146 Operational Taxonomic Units (OTUs) and 231 species compared to 833 OTUs and 333 species from homogenised sample analysis. While more dipterans, in particular Chironomidae, were detected in fixative (136 species) than homogenised bulk (90 species) analyses, the latter picked up more Trichoptera (19 vs. 2), Amphipoda (10 vs. 4) and Bivalvia species (13 vs. 5). Even though these results of a DNA-based assessment deliver new insights into species richness and composition of Danube's macroinvertebrate communities from the Danube source to its delta already, it is evident that the majority of OTUs was not assigned to species. While filling this lack of reference sequences poses a major challenge, the JDS consortium also offers a unique opportunity to complement reference databases in a multinational effort towards a more comprehensive Danube assessment and monitoring.

Keywords

bulk sample, fixative, preservative, reference database, macrozoobenthos, Chironomidae

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