



Conference Abstract

(e)DNA-based assessments within one of the World's largest river survey programs: summarized insights from the 4th Joint Danube Survey

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Abstract

With the 4th Joint Danube Survey in 2019 (JDS4), for the first time, DNA- and environmental DNA-based approaches were integrated into the program of the JDS, focussing on the three biological quality elements of fish, macrozoobenthos and phyto-benthos, and additionally on the sediment community (Liska et al. 2021, Weigand and Astrin 2021). The rationals for including (e)DNA-based tools into the survey's program were that i) many hard-to-identify organism groups can be assessed down to their species level, ii) taxonomic information can be unlocked even in cases where morphotaxonomic knowledge and expertise are limited, iii) all developmental stages, cryptic species and indeterminable sexes can be potentially identified, iv) taxalists relying on sequence-based information are reproducible and comparable in space and time (aspects, which are particularly important for a longitudinal survey involving many countries), and, v) this additional line of taxonomic evidence will help to draw a more precise and comprehensive picture of the Danubian biota.

The target groups were assessed using group-specific (e)DNA-based metabarcoding approaches (for fish: Pont et al. 2021; macrozoobenthos: Beermann et al. 2021;

phytobenthos: Zimmermann et al. 2021; sediment community: Cordier et al. 2021). The coverage of barcode libraries for Danubian biota were checked prior to conducting the metabarcoding approaches. Coverage values based on JDS3 outcomes were >90% for fish (12S, but depending on reference database), 84% for macrozoobenthos (COI) and 69% and 88% for all, respectively, only abundant phytobenthos species (18S + rbcL), so that (e)DNA-based approaches were expected to be implemented effectively from this perspective (Weigand and Astrin 2021).

Although still a certain degree of methodological variation exists, the outcomes clearly demonstrate the huge potential of (e)DNA-based approaches for complementary biodiversity and ecological status class assessments: eDNA water analysis of fish revealed most of the taxa also detected by the traditional fish survey, but was particularly effective in detecting hard-to-capture benthic taxa (including endangered sturgeon species) and fish traces originating from waste water treatment plants (Pont et al. 2021). Many of the traditionally assigned macrozoobenthos species were detected by DNA metabarcoding as well, but sequence data allowed to add a plethora of new chironomid and oligochaete species to the taxalist. Molecular ecological status class assessments based on presence-absence values of macrozoobenthos species were largely congruent to traditional abundance or presence-absence-based outcomes (Beermann et al. 2021, Weigand 2021). Although traditional light microscopy, which is based on identifying phytobenthos species by their frostules, revealed a higher number of diatom species, the molecular assessment detected much more taxa (i.e. MOTUs), which await species-level taxonomic annotation in the future (Zimmermann et al. 2021). Metabarcoding of the sediment community was particularly effective to assess meiofaunal species and allowed the molecular inference of fine sediment quality based on local community structures of vulnerable nematode species (Cordier et al. 2021). Finally, all (e)DNA-based taxalists were compiled to inform invasive alien species detection in the Danube River Basin.

However, despite their promising performance and large coherence with traditional outcomes during JDS4, the full potential of (e)DNA-based approaches in the context of larger environmental surveys might be further released by

1. developing and curating catchment-specific DNA barcode reference libraries,
2. focussing on a small(er) set of standardized (e)DNA-based approaches,
3. integrating genetic diversity (and spatiotemporal changes thereof) in ecological status class assessments,
4. installing a dense, large-scale environmental DNA-based screening, based on which traditional surveys can be performed at conspicuous sites, and,
5. educating and training national authorities in state-of-the-art molecular tools.

Already today, (e)DNA-based methods can be seen as an effective and complementary tool to provide consolidated results for biodiversity and ecological status class assessments in a highly integrative and international setup, as pursued during JDS4.

Keywords

JDS4, Water Framework Directive, Biological Quality Elements, Bioassessment, Environmental DNA (eDNA), NemaSPEAR[%] index

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