



Conference Abstract

eDNA metabarcoding survey of fish communities in the Danube and its tributaries

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Abstract

In complement to the JDS4 traditional fish survey (TFS, mainly by electrofishing), a fish eDNA metabarcoding-based survey has been implemented within the framework of the monitoring program organized by DNAqua-Net and in collaboration with the INTERREG "MEASURES" program. Water samples were collected at 29 sites from the source to the mouth of the Danube River, and at 18 tributaries. Two water samples (mean volume 29 L per sample) were collected at each site and the water filtered in situ. Twelve PCR replicates were performed per sample using teleo primers.

In total, 80 taxa were detected, of which 19 corresponded mainly to farmed fish or food fish due to eDNA release in waste waters, most often downstream of large cities. Of the remaining 61 taxa, 50 taxa were identified at the species level, six taxa at the genus level,

and five taxa at a higher taxonomic level. Concerning the Danube river itself, 69 and 57 species/markers were detected along the Danube River by TFS and eDNA surveys, respectively. 50 of these taxa were detected by both methods. Nine species were captured by TFS alone, mainly due to gaps in reference libraries and too closely related barcodes. Eight species were only detected by eDNA. Except for the *Salvelinus* group, these were all benthic species, which are difficult to catch by electrofishing in large rivers (*Acipenser ruthenus*, *Acipenser stellatus*, *Benthophilus sp.*, *Romanogobio uranoscopus*, *Sabanejewia balcanica*, *Umbra krameri*).

The species richness tended to increase from upstream to downstream and the relative number of DNA sequences per taxa showed a clear succession of species along the river. *Barbatula barbatula*, *Cottus gobio*, *Hucho hucho*, *Lamprolepis planeri*, *Phoxinus phoxinus* and *Thymallus thymallus* were restricted to the Upper Danube whereas *A. ruthenus*, *Neogobius fluviatilis*, *S. balcanica* and *Scardinius erythrophthalmus* were detected from Vienna to the Danube river mouth. *Abramis brama*, *Alburnus alburnus*, *Cyprinus carpio*, *Silurus glanis*, *Sander spp.*, *Zingel streber* were detected all along the river course; *Alosa spp.* and *Syngnathus abaster* downstream from the Iron Gate; *A. stellatus* and *U. krameri* only on the most downstream site (Danube delta).

The calculation of a fish index, based on the common metrics used to intercalibrate national fish assessment methods on a European scale, classified most of the sites as being in moderate ecological status. Comparison of the indicative ecological status calculated using the same assessment method based on TFS and eDNA data at the common Danube sites showed a similar classification for six of the 13 sites and a difference of one class for the remaining seven sites.

Keywords

eDNA, metabarcoding, fish community, ecological assessment, Danube river

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