



Conference Abstract

A large-scale ecological assessment of Swiss rivers using environmental DNA for the monitoring of macroinvertebrates

Jeanine Brantschen^{‡,§}, Rosetta Charlotte Blackman^{‡,§}, Jean-Claude Walser^{l,¶}, Florian Altermatt^{‡,§}

[‡] Eawag, Dübendorf, Switzerland

[§] University of Zurich, Zurich, Switzerland

^l GDC, Zurich, Switzerland

[¶] Swiss Federal Institute of Technology, Zurich, Switzerland

Corresponding author: Jeanine Brantschen (jeanine.brantschen@eawag.ch), Florian Altermatt (florian.altermatt@eawag.ch)

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Abstract

Anthropogenic activities are changing the state of ecosystems worldwide, affecting community composition and often resulting in loss of biodiversity. Riverine ecosystems are among the most impacted ecosystems. Recording their current state with regular biomonitoring is important to assess the future trajectory of biodiversity. However, traditional monitoring methods for ecological assessments are costly and time-intensive. Here, we compare environmental DNA (eDNA) to traditional kick-net sampling in a standardized framework of surface water quality assessment. We use surveys of macroinvertebrate communities to assess biodiversity and the biological state of riverine systems. Both methods were employed to monitor aquatic macroinvertebrate indicator groups at 92 sites across major Swiss river catchments. The eDNA data were taxonomically assigned using a customised reference database. All zero-radius Operational Taxonomic Units (zOTUs) mapping to one of the 142 traditionally used indicator taxon levels were used for subsequent diversity analyses (n = 205). At the site level, eDNA detected less indicator taxa than the kick-net method and alpha diversity correlated only weakly between the methods. However, the methods showed a

strong congruence in the overall community composition (gamma diversity), as the same indicator groups were commonly detected. In order to set the community composition in relation to the biotic index, the ecological states of the sampling sites were predicted by a random forest approach. Using all zOTUs mapping to macroinvertebrate indicator groups (n = 693) as predictive features, the random forest models successfully predicted the ecological status of the sampled sites. The majority of the predictions (71%) resulted in the same classification like the kick-net based scores. Thus, the sampling of eDNA enabled the detection of indicator communities and provided valuable classifications of the ecological state, when combined with machine learning. Overall, eDNA based sampling has the potential to complement traditional surveys of macroinvertebrate communities in routine large-scale assessments in a non-invasive and scalable approach.

Keywords

environmental DNA, metabarcoding, biotic indices, macroinvertebrate, biomonitoring, random forest

Presenting author

Jeanine Brantschen

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