Many fish communities in Alpine rivers are impacted by anthropogenically altered riverbeds, making effective biomonitoring critical for the long-term sustainability and health of river systems. Traditional surveys require fish to be temporarily captured, an approach that can only be done outside of protected periods and at low water flow. A new method of detecting fish DNA in the environment has the potential to revolutionize monitoring efforts. Our study applied environmental DNA (eDNA) analyses in dynamic Alpine habitats to successfully detect species even at low population densities and to obtain information on the whole fish species community at a regional scale.

Environmental DNA provides high resolution data on Alpine fish populations and facilitates their management

Hydropower plants, transverse structures, and artificially straightened riverbeds are just some examples of how Alpine rivers and the landscapes around them are being altered for the benefit of neighbouring communities. These changes exert negative influences on fish species and make population management challenging. For instance, straightened river segments lack areas with low flow rates, which can be crucial for spawning and refuge seeking during the annual spring and summer high waters. Hence, detailed knowledge on the species present and how they are distributed along rivers is essential for their management, which also needs to incorporate sport fishing and artificial stocking in many places.
Traditionally, fish populations in Alpine rivers are assessed via electrofishing, but this method can only be applied during short periods outside of spawning times and when water levels and turbidity are low enough to effectively see and capture fish. Additionally, the considerable time and people necessary for electrofishing campaigns means only a small number of locations can be assessed, which are then taken as a representation for the whole river.

Environmental DNA (eDNA) – genetic material obtained directly from environmental samples (soil, sediment, water, etc.) without any obvious signs of biological source material\(^1\) – has the potential to revolutionize fish monitoring in rivers as it enables the cost-effective analysis of multiple water samples from different locations within river networks. It allows us to easily pinpoint the upstream distribution limits of species and the changes in their longitudinal distribution. Although Alpine rivers are characterized by a comparably low species diversity, low population densities coupled with high water flow fluctuations represent a significant challenge for the broad-scale application of eDNA-based fish monitoring. Our team, scientists based at the University of Innsbruck and freshwater ecologists from the ARGE Limnologie, is examining what is needed for successful eDNA-based fish detections in Alpine rivers through the Austrian Research Promotion Agency (FFG) project “eDNA-AlpFish”.

First, our team defined detection limits for distinct flow situations in the summer and winter months. We were able to confirm the high sensitivity of our species-specific eDNA amplification approach by detecting signals from fish at low numbers and at considerable downstream distance and water flow. For example, we detected signals stemming from ~50 individuals (200 g) of Eurasian minnow (*Phoxinus phoxinus*) at a downstream distance of 550 m and at a discharge of 0.25 m\(^3\)/s. Under similar circumstances, a detection via electrofishing is uncertain as usually a shorter river stretch is sampled and not all present fish individuals can be caught.

\(^{1}\) Environmental DNA (eDNA) is a term used to describe DNA extracted from environmental samples such as water, sediment, or soil, which can be used to infer the presence and abundance of target species.
In the next step, we evaluated the performance of these molecular approaches in direct comparison to electrofishing by sampling water from an Alpine river and its tributaries in the epirhithral zone. Whilst water samples from the whole river network could be obtained in a day, quantitative electrofishing was only possible at three sites within this timeframe. Additionally, the molecular analysis enabled the detection of bullhead (*Cottus gobio*) upstream of the point where low population levels made catches via electrofishing impossible.

Samples were also taken at epipotamal locations along the river Inn where the fish community is more diverse, and they were analysed with DNA metabarcoding. This approach permits the simultaneous assessment of the whole fish community and led to the detection of all the species known to occur in these waters. Additionally, we also obtained eDNA signals stemming from the surrounding tributaries in these samples.

The results of the eDNA-AlpFish project will inform sampling strategy and data interpretation of future projects and, overall, highlight the massive potential of eDNA for large-scale fish monitoring in Alpine rivers.

References


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