

# Space-time dynamics in monitoring neotropical fish communities using eDNA metabarcoding

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## Abstract

The biodiverse Neotropical ecoregion remains insufficiently assessed, poorly managed, and threatened by unregulated human activities. Novel, rapid and cost-effective DNA-based approaches are valuable to improve understanding of the biological communities and for biomonitoring in remote areas. Here, we evaluate the potential of environmental DNA (eDNA) metabarcoding for assessing the structure and distribution of fish communities by analysing sediments and water from 11 locations along the Jequitinhonha River catchment (Brazil). Each site was sampled twice, before and after a major rain event in a five-week period and fish diversity was estimated using high-through-put sequencing of 12S rRNA amplicons. In total, 252 Molecular Operational Taxonomic Units (MOTUs) and 34 fish species were recovered, including endemic, introduced, and previously unrecorded species for this basin. Spatio-temporal variation of fish assemblages was detected, richness during the first campaign was nearly twice as high as in the second sampling round; though peaks of diversity were primarily associated with only four locations. No correlation between  $\beta$ -diversity and longitudinal distance or presence of dams was detected, but low species richness observed at sites located near dams indicates that these anthropogenic barriers might have an impact on local fish diversity. Unexpectedly high  $\alpha$ -diversity levels recorded at the river mouth suggest that these sections should be further evaluated as putative “eDNA reservoirs” for rapid monitoring. By uncovering spatio-temporal changes, unrecorded biodiversity components, and putative anthropogenic impacts on fish assemblages, we further strengthen the potential of eDNA metabarcoding as a biomonitoring tool, especially in regions often neglected or difficult to access.

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