
Ecological reliability of eDNA metabarcoding approach for fish biodiversity survey in freshwater ecosystems: comparison to traditional sampling methods

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Abstract

In the past few years, environmental DNA (eDNA) has drawn attention for different reasons, including its potential use for conservation purposes. Currently, more and more publications on macroorganisms in aquatic ecosystems are spotlighting the eDNA metabarcoding approach, *i.e.* group-specific detection at species level able to describe species communities in mesocosms or natural ecosystems. These studies are seeking for a suitable molecular analysis pipeline (*i.e.* analytical protocol from sampling to molecular and bioinformatics analysis). In this study, using Valentini et al. (2016) pipeline, we investigated the ecological reliability of this approach for assessing fish biodiversity in rivers. Three main aspects were tested: (1) the comparison of current traditional field surveys with the eDNA metabarcoding approach; (2) the comparison of more than ten years temporal traditional field surveys with the eDNA metabarcoding approach; (3) the distance detection of the eDNA metabarcoding signal. Our results demonstrated the reliability of the eDNA approach and its higher efficiency compared to the traditional methods to describe species assemblages. Finally, the spatial representativity of this new method and of the detection distance of species is discussed.

Keywords: Environmental DNA, metabarcoding, fish Biodiversity, Freshwater ecosystems, distance detection, ecological reliability

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