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Abstract Book





eDNA metabarcoding biodiversity of freshwater fish in the Alpine area

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Environmental DNA (eDNA) based methods are proving to be a promising tool for freshwater fish biodiversity assessment in Europe within the Water Framework Directive (WFD, 2000/60/EC) especially for large rivers and lakes where current fish monitoring techniques have known shortcomings. Many freshwater fish are experiencing critical population declines with risk of local or global extinction because of intense anthropogenic pressure and this can have serious consequences on freshwater ecosystem functioning and diversity. Within the EU project Eco-AlpsWater, advanced high throughput sequencing (HTS) techniques are used to improve the traditional WFD monitoring approaches by using environmental DNA (eDNA) collected in Alpine waterbodies. An eDNA metabarcoding approach specifically designed to measure freshwater fish biodiversity in Alpine lakes and rivers has been extensively evaluated by using mock samples within an intercalibration test. This eDNA method was validated and used to study fish biodiversity of eight lakes and six rivers of the Alpine region including four EC countries (Austria, France, Italy, Slovenia) and Switzerland. More in detail, this metabarcoding approach, based on HTS sequencing of a section of the 12S rRNA gene, was used to assess freshwater fish biodiversity and their distribution in the different habitats. These data represent the first attempt to provide a comprehensive description of freshwater fish diversity in different ecosystems of the Alpine area confirming the applicability of eDNA metabarcoding analyses for the biomonitoring of fish inhabiting Alpine and perialpine lakes and rivers.