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Abstract

Application of eDNA Metagenomics to Describe Freshwater Fish Communities †

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Abstract: Freshwater fish communities are highly threatened by human activities, making it necessary to establish methodologies able to efficiently monitor possible change. Recently, environmental DNA (eDNA) has shown to be one of the most promising sources of biodiversity information, especially when combined with high throughput sequencing approaches, such as DNA metabarcoding, allowing a simplified and efficient description of fish communities. However, metabarcoding relies on PCR amplification of eDNA, which has some limitations, such as priming biases, exclusion of shorter target eDNA fragments, limited taxonomic range, and limited taxonomic information in a single barcode. Alternatively, metagenomics sequences all eDNA fragments present in a sample without enriching for a specific taxonomic group, locus, or fragment length, overcoming these limitations. So far, eDNA metagenomics has mostly been implemented to describe microorganism communities and its applicability to large metazoans, such as fishes, is still understudied. In the current study, we test the power of this method to describe freshwater fish communities using water samples from the Ave and the Tagus rivers. Metagenomics is able to describe the whole freshwater biome by detecting taxa across the tree of life. When compared with eDNA metabarcoding, eDNA metagenomics provides more information in two aspects: First, a higher detection ability for fish species represented by low abundant and highly degraded DNA. Second, it differentiates between local and transported eDNA, which is not possible with eDNA metabarcoding. Our results also show a higher detectability for taxa represented by a whole genome sequence in the reference database. Therefore, some of the diversity is still being missed, since not all organisms have a genome available. Efforts are being made to produce genomic resources for all eukaryotes, meaning that in the future metagenomic data produced now will still be useful for the description of new diversity and characterization of community change.

Keywords: eDNA shotgun sequencing; eDNA metabarcoding; sequence length; multi-loci

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