



Conference Abstract

# Metabarcoding with MinION: Speeding up the detection of invasive aquatic species using environmental DNA and nanopore sequencing

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## Abstract

Traditional detection of aquatic invasive species, via morphological identification is often time-consuming and can require a high level of taxonomic expertise, leading to delayed mitigation responses. Environmental DNA (eDNA) detection approaches of multiple species using Illumina-based sequencing technology have been used to overcome these hindrances, but sample processing is often lengthy. More recently, portable nanopore sequencing technology has become available, which has the potential to make molecular detection of invasive species more widely accessible and to substantially decrease sample turnaround times. However, nanopore-sequenced reads have a much higher error rate than those produced by Illumina platforms, which has so far hindered the adoption of this technology. We provide a detailed laboratory protocol and bioinformatic tools to increase the reliability of nanopore sequencing to detect invasive species, and we test its application using invasive bivalves. We sampled water from sites with pre-existing bivalve occurrence and abundance data, and contrasting bivalve communities, in Italy and Portugal. We extracted, amplified and sequenced eDNA with a turnaround of 3.5 days. The majority of

processed reads were  $\geq 99$  % identical to reference sequences. There were no taxa detected other than those known to occur. The lack of detections of some species at some sites could be explained by their known low abundances. The approach is now being tested on other target taxa such as fish and other vertebrates.

## **Keywords**

eDNA, minion, nanopore, mussels, invasive

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