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ASSESSING WHOLE BENTHIC COMMUNITIES THROUGH GENOMICS

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Benthic biodiversity studies rarely quantify the whole eukaryotic community. Traditional methods for the quantification of marine benthic biodiversity are labour intensive and time consuming creating a bottleneck in the species recovery from a community. However, in recent years the development of next generation sequencing platforms has created opportunities for developing new genetic methods for rapid species identification called DNA metabarcoding. In our study, we further developed metabarcoding methods to enable accurate extraction and quantification of eukaryotic DNA from bulk sediment samples. We conducted experiments on mock marine benthic communities in order to remove two current limitations of metabarcoding techniques, bias from PCR steps and false positives from extracellular DNA (eDNA) contamination. Our experiments showed that eDNA contamination can be reduced significantly, with two different treatment methods: phosphate buffer washing and enzymatic degradation. Also by removing PCR from the metabarcoding pipeline, and implementing shotgun sequencing and bioinformatic sorting, bias is potentially reduced and accuracy of biodiversity estimates increased. Further developments of metabarcoding techniques along these lines should enable accurate quantification of genetic biodiversity of the whole living marine benthic community. This will be of high relevance for future approaches in environmental monitoring as well as for fundamental community ecology.