DNA extraction bias is more pronounced for microbial eukaryotes than for prokaryotes

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Abstract

DNA extraction and preservation bias is a recurring topic in DNA sequencing-based microbial ecology. Different methodologies can lead to distinct outcomes, which has been demonstrated especially in studies investigating prokaryotic community composition. Eukaryotic microbes are ubiquitous, diverse, and increasingly a subject of investigation in addition to bacteria and archaea. However, little is known about how the choice of DNA preservation and extraction methodology impacts perceived eukaryotic community composition. In this study, we compared the effect of two DNA preservation protocols and 6 DNA extraction methods on the community profiles of both eukaryotes and prokaryotes in phototrophic biofilms on seagrass (Zostera marina) leaves from the Baltic Sea. We found that, whereas DNA preservation and extraction method caused significant bias in perceived community composition for both eukaryotes and prokaryotes, extraction bias was more pronounced for eukaryotes than prokaryotes. Especially soft-bodied or hard-shelled eukaryotes like nematodes and diatoms were differentially abundant depending on the extraction method. We conclude that careful consideration of DNA preservation and extraction methodology is crucial to achieving representative community profiles of eukaryotes in marine biofilms, and likely all other habitats containing diverse eukaryotic microbial communities.

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figures/figure1/figure1-eps-converted-to.pdf

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