Sea ice protists in arctic marine sedaDNA records: origins, diversity, and vertical export of DNA from the sea surface to the seafloor

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Arctic sea ice is declining at an unprecedented pace as the Arctic Ocean heads towards ice-free summers within the next few decades. Because of the role of sea ice in the Earth System such as ocean circulation and ecosystem functioning, reconstructing its past variability is of great importance providing insight into past climate patterns and future climate scenarios. Today, much of our knowledge of past sea-ice variability derives from a relatively few microfossil and biogeochemical tracers, which have limitations, such as preservation biases and low taxonomic resolution. Marine sedimentary ancient DNA (marine sedaDNA) has the potential to capture more of the arctic marine biodiversity compared to other approaches. However, little is known about how well past communities are represented in marine sedaDNA. The transport and fate of DNA derived from sea-ice associated organisms, from surface waters to the seafloor and its eventual incorporation into marine sediment records is poorly understood. Here, we present results from a study applying a combination of methods to examine modern and ancient DNA to material collected along the Northeast Greenland Shelf. We characterized the vertical export of genetic material by amplicon sequencing the hyper-variable V4 region of the 18S rDNA at three water depths, in surface sediments, and in a dated sediment core. The amplicon sequencing approach, as currently applied, includes some limitations for quantitative reconstructions of past changes such as primer competition, PCR errors, and variation of gene copy numbers across different taxa. For these reasons we quantified amplicons from a single species, the circum-polar sea ice dinoflagellate Polarella glacialis in the marine sedaDNA, using digital droplet PCR. The results will increase our understanding on the taphonomy of DNA in sea ice environments, how sedimentation differs among taxonomic groups, and provide indications to potentially useful marine sedaDNA-based proxies for climate and environmental reconstructions.