

# Using high-throughput sequencing and quantitative molecular techniques to investigate ~3800 years of diatom diversity and sea-ice variability in the North Water polynya (Baffin Bay), Canada

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Changes in global temperatures have a direct impact on oceanic and atmospheric processes, and at present, the Arctic is experiencing a rise in near-surface air temperatures. As a consequence, multi-year sea-ice extent has significantly declined in the last two decades. These changes have a direct impact on the pelagic and ice-associated (sympagic) photosynthetic communities that form the foundation of marine food webs. The North Water (NOW) polynya is one of the most productive areas in the arctic and therefore represents a critical site for studying the impacts of climate-induced environmental changes. Although recent monitoring of the area revealed important changes in productivity and microbial species composition, proxy datasets that span large temporal periods are required to place these environmental changes into a long-term context.

To reconstruct past changes in sea-surface conditions, biogenic proxies derived from diatoms and preserved in seafloor sediment are commonly used. These include microfossil assemblages, biogenic silica, and IP<sub>25</sub>. However, limitations to the use of these proxies include low species-level resolution and the biased preservation of heavily silicified specimens. Sedimentary ancient DNA (*sedaDNA*) is an emerging proxy which, in the light of recent advances in molecular biology, has the potential to become a very useful tool for paleoenvironmental reconstructions.

In this study, we will quantify and characterize diatom *sedaDNA* extracted from twelve samples collected along a 5.43 m long sediment core retrieved from the NOW polynya in order to: (1) characterize past diatom diversity using genetic barcodes and high-throughput sequencing (metabarcoding) techniques. Diatom-specific primers will be designed to target short (~75 bp), variable regions of two gene markers (*rbcL*, 18S rRNA V4 region) that will be used for genetic species identification. These results will be combined with diatom abundances and assemblage determinations to reconstruct past environmental conditions; (2) investigate changes in sea-ice conditions during the last 3800 years. The absolute quantification of both diatom *sedaDNA* and copies of a specific *rbcL* gene from two species representing pelagic and sympagic assemblages will be obtained using droplet digital PCR. The absolute quantification data will be compared to BSi and IP<sub>25</sub> abundances for evaluating proxy reconstructions of productivity and sea-ice history in the NOW.