

Assessing the efficiency of eDNA metabarcoding for documenting patterns of metazoan communities in the Arctic.

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Arctic biodiversity has been for a long time underestimated, situated in a region considered as an austere environment combined to the lack of knowledge. The analysis of environmental DNA (eDNA), a new method tracing DNA from macro-organisms, is changing the way we monitor aquatic biodiversity and has the potential to answer large-scale fundamental biodiversity questions in remote regions such as the Arctic. This study aims to evaluate the eDNA dispersal by contrasting the difference between eDNA metabarcoding and classical sampling methods of the alpha, beta and gamma biodiversity index across the Canadian Arctic latitudinal gradient. Water samples of 250mL were collected in 13 sites within three Arctic ports: Churchill, Iqaluit and Deception Bay. Our results showed a species richness of 422 marine invertebrates, while the number of species detected decreased with latitude with more than 100 less species in the northern port. Contrasting the alpha biodiversity index between eDNA metabarcoding and species spatial distribution may be used to evaluate the eDNA spatial dispersion, thus answering important questions related to the ecology of eDNA and improving the integration of this new molecular tool within applied sciences.