

## **B06-O02**

### **USE OF NEXT-GENERATION SEQUENCING IN STUDYING BIOGEOGRAPHY OF SEA-ICE PROTISTS**

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Protistan communities are known to harbor a large number of species that are easily overlooked or missed in sampling and counting due to very low cell abundance. These rare taxa may be inert or may turn into active components of the communities when the environmental conditions change. Therefore, ignoring them may result in an insufficient overview of protistan diversity of a given environment. With next-generation sequencing (NGS) approach, where 90–500 bp long segments of the DNA are massively sequenced, tens of thousands of sequences can be collected from one sample. Thus, also the rare taxa are detected and the protistan richness can be estimated more reliably. The prize of NGS has dropped substantially, in parallel with the development of more easy-to-use and standardized bioinformatics analysis pipelines. In the Arctic, there is a clear lack of knowledge on sea-ice protistan diversity. Here, we propose a pan-Arctic sampling plan for studying biogeography of sea-ice protists using an NGS approach, with detailed cost and time-table estimates.