



Conference Abstract

Preliminary results of sediments eDNA metabarcoding along arctic fjord

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Abstract

Ecosystems of arctic fjords are exposed to various natural and human-induced stressors that shape the taxonomic structure and functioning. Glacial activity and meltwater inflows together with advection of sea water masses from shelves form variety of environmental gradients that have been shown to influence marine biota. Some of these stressors like sedimentation of inorganic matter, instabilities of bottom sediments or food supply have been recognized as drivers of benthic species richness and diversity with use of traditional (morphology based) methods (Węśławski et al. 2011, Włodarska-Kowalczyk et al. 2005, Włodarska-Kowalczyk et al. 2012). In this study we aimed to use eDNA metabarcoding based methods to discriminate ecological diversity of benthic Eukaryota along environmental gradient (fjord mouth – glacier) at 6 stations in Hornsund fjord (Svalbard). At each station we collected 9 surface sediment samples. To cover a wide diversity of eukaryotic taxa we sequenced mitochondrial COI and nuclear 18S VIV2 genes to. Computational pipeline (SLIM, Dufresne et al. 2019) was used to de-multiplexed sequences, cluster them into ASVs and then taxonomically assigned. For the COI marker we distinguished 4486 unique ASVs, which in majority (95%) remained unassigned but constituted 51% of all sequences. Among sequences with assigned taxonomy 98% of them belonged to Opisthokonta clade, which consisted of 12 phyla in majority Annelida (80% of sequences) followed by Nemertea (13%) and Echinodermata (6%). In case of 18S marker we obtained 1309 unique ASVs, almost 70% of them were taxonomically assigned, constituting almost 97% of all sequences. Seven clades were assessed with dominance of

Opisthokonta (44%) followed by Stramenopiles (29%) and Rhizaria (18%) of all sequences. Among Opisthokonta we noted 17 phyla, which were dominated by Annelida (54% of sequences) with significant share of Arthropoda (20%), Nematoda (10%) and Nemertea (8%). Analysis of alpha diversity expressed as number of unique ASV and Shannon-Wiener index showed different results for COI and 18S markers. For the first marker we did not notice any trend along fjord except much lower indices at the station nearest to the glacier, while for the second marker we observed a decline of both indices from fjord mouth towards glacier, however when data were limited only to benthic metazoans (e.g. excluding Calanoida or Chaetognatha) the trend was not that evident. Our results show that eDNA metabarcoding based methods may be successfully used for diversity assessments of arctic benthic fauna. Among the two markers we used 18S V1V2 allowed to assign higher number of taxa, however high proportion of sequences belonged to non-benthic and unicellular organism. Nevertheless, using 18S V1V2 data we observed similar biodiversity pattern along fjord (decreasing biodiversity with decreasing distance to glacier) that is known from traditional, morphological studies.

Keywords

eDNA, Arctic, benthos, 18S, COI

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