

DIATOM COMMUNITIES FROM ARCTIC DRIFT AND LAND-FAST ICE AS REVEALED BY HIGH-THROUGHPUT PYROSEQUENCING

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Ice-associated diatoms and other large protists have been studied extensively using microscopy. However, little information on the genetic diversity of these eukaryotic cells is available. We applied high-throughput tag sequencing of the V4 region of the 18S rRNA gene to investigate the eukaryotic microbiome of drift and land-fast ice. Ice cores were collected at 6 stations from March to early May 2008 as part of the International Polar Year-Circumpolar Flaw Lead (CFL) system study, in the Canadian Beaufort Sea. The 0-3 cm (bottom) and 3-10 cm (top) horizons were sampled for all cores, as well as the ice-water interface (sub-ice) at one station. All horizon ice communities were very diverse and the diatom sequences in the assemblages included many known sea ice genera. Raphid pennate diatoms (Bacillariophyceae) were by far the most common sequences in all samples, except one where a bloom of the centric diatom *Melosira* was observed. Sequences matching a previously recovered environmental clone, Baltic Sea ice diatom clone 8-90, were the largest contributors to the pennates and were the only taxa shared by all of the samples, regardless of ice type or horizon. Fewer sequences of Mediophyceae (primarily *Thalassiosira*) and Fragilariophyceae were recovered. We also show that the ice-associated communities living within drift and land-fast ice harbored taxonomically distinct communities, with higher occurrences of sequences of *Pseudogomphonema* and *Nitzschia* spp. in the land-fast ice. In addition, *Pleurosigma* and *Entomoneis* spp. were found suspended at the ice-water interface of drift ice. We compare these results with those obtained from traditional microscopy and discuss them in the context of the changing Arctic sea ice cover.