

Under-ice bloom: temporal dynamics and biogeography of Arctic sympagic algae and phytoplankton

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The Arctic is one of the most productive regions in the world, owing to the annual phytoplankton spring bloom which develops when light becomes seasonally available. The open water phytoplankton bloom is preceded by an under-ice bloom. To understand the temporal dynamics of these communities, a time series was conducted from April to July 2016 on land-fast ice off the west coast of Baffin Bay. Size-fractionated sea-ice algae and eukaryotic phytoplankton communities were analysed using metabarcoding of the V4 region of the 18S rRNA gene. Sympagic and planktonic photosynthetic communities were dominated by diatoms (Bacillariophyta). Micro- (20-100 µm) and nano-phytoplankton (3-20 µm) communities underwent a pennate-centric-pennate diatom succession through the different stages of bloom. Pico-phytoplankton (0.2-3 µm) was initially dominated by Bolidophyceae followed later by the chlorophyte *Micromonas polaris* and the haptophyte *Phaeocystis pouchetii*.

Biogeographical distribution of key ribotypes (ASVs) retrieved from ice and water were determined from a global analysis of more than 2,500 metabarcoding samples available from the metaPR2 database. Ice algae ribotypes were distributed across ice-covered seas (polar or polar-temperate), reflecting their dependence on sea ice habitat. Some key phytoplankton ribotypes were not restricted to the Arctic, but exhibited polar-temperate or cosmopolitan distributions, suggesting that Arctic spring bloom communities harbour ribotypes from non-Arctic waters, which may take over in the future and alter the phenology of blooms with consequences for the whole ecosystem.