Prokaryotic community structures along salinity gradients of melt ponds on sea-ice floes in the Chukchi Sea

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Sea-ice floes in the Arctic Ocean are extreme environments with variable nutrients, light availability and salinity. Melt ponds are formed on sea-ice in summer by thawing of surface ice and melting snow. Recently, melt pond areas have increased in Arctic summer. In the present study, we had questions (1) who "seed prokaryotes" (*Bacteria* and *Archaea*) are in fresh melt ponds in an early stage of development, (2) how they change in community compositions with development of melt ponds, and (3) which environmental factors drive the change of prokaryotic communities. To answer the questions, prokaryotic community structures were investigated using pyrosequencing of 16S rRNA gene for 27 melt ponds (salinity of 0.2-26.8) on 2 sea-ice floes along with ambient seawater in the Chukcki Sea in August, 2014. Eleven and two phyla belonging to *Bacteria* and *Archaea*, respectively, were identified in melt ponds. The "seed prokaryotes" in melt ponds (salinity of 0.2-5) were predominantly comprised of *Bacteroidetes* (44-90%). A drastic change of prokaryotic community structures was observed along the salinity gradient of melt ponds. In the presentation, results will be shown in detail and discussed.