Microbial community structure of Arctic multiyear sea ice and surface seawater by 454 sequencing of the 16S RNA gene. - DTU Orbit (17/10/2019)

Microbial community structure of Arctic multiyear sea ice and surface seawater by 454 sequencing of the 16S RNA gene. Dramatic decreases in the extent of Arctic multiyear ice (MYI) suggest this environment may disappear as early as 2100, replaced by ecologically different first-year ice. To better understand the implications of this loss on microbial biodiversity, we undertook a detailed census of the microbial community in MYI at two sites near the geographic North Pole using parallel tag sequencing of the 16S rRNA gene. Although the composition of the MYI microbial community has been characterized by previous studies, microbial community structure has not been. Although richness was lower in MYI than in underlying surface water, we found diversity to be comparable using the Simpson and Shannon's indices (for Simpson $t=0.65$, $P=0.56$; for Shannon $t=0.25$, $P=0.84$ for a Student's t-test of mean values). Cyanobacteria, comprising 6.8% of reads obtained from MYI, were observed for the first time in Arctic sea ice. In addition, several low-abundance clades not previously reported in sea ice were present, including the phylum TM7 and the classes Spartobacteria and Opitutae. Members of Coraliomargarita, a recently described genus of the class Opitutae, were present in sufficient numbers to suggest niche occupation within MYI.

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