BIOMARKER SIGNALS FROM MICROBIAL MATS IN MELT WATER PONDS FROM BRATINA ISLAND ON THE MCMURDO ICE SHELF, ANTARCTICA

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The McMurdo Ice Shelf is an ablation zone that covers more than 1500 km² (Howard-Williams et al., 1990), making it one of the largest polar deserts on Earth. During summer, however, networks of melt water ponds develop within this extreme environment, typified by the “dirty ice” at Bratina Island (Hawes et al., 2018). These ponds, which are characterized by highly different physiochemical conditions (e.g. salt concentrations, pH and temperature), are of particular interest for organic geochemists and microbiologists due to their high biomass and microbial diversity (Jungblut and Neilan, 2010). The microbial mats in these “biological oases” can be up to several centimeters thick and are typically stratified. So far, only one study has analyzed lipid biomarkers in three Antarctic melt water ponds (Jungblut et al., 2009). Here, we investigated the microbial community in twelve melt water ponds from the McMurdo Ice Shelf by intact polar lipids (IPLs) and bacteriohopanepolyols (BHPs) for the first time. The analysis of IPLs and BHPs provides important chemotaxonomic information on how microbes can cope with the low temperatures and energy limitation in this extreme environment. Only ester bound IPLs were detected in the melt water ponds, indicating that bacteria and eukarya strongly predominate over archaea in this cryosphere. Most of the samples revealed a prevalence of phosphate free IPLs over phosphatic lipids (Figure 1). The only sample that showed a strong predominance of diphosphatidylglycerols (DPG) over glycosidic IPLs was a fossil mat collected from the margin of one of the ponds. The phosphate-free lipids were mainly composed of mono- and diglycosidic lipids (MGDG and DGDG), whereas phosphatidic lipids were dominated by phosphoglycerol (PG-DAG) and phosphocholine (PC-DAG) in most of the samples (Figure 1). The predominance of MGDG and DGDG is in accordance with previous results, suggesting that the melt water ponds are mainly inhibited by cyanobacteria (Jungblut and Neilan, 2010), which predominantly build their lipid membrane with glycosidic lipids (e.g. Bauersachs et al., 2009). Extraordinary high abundances of MGDG and DGDG were detected in samples that are rich in cyanobacteria of the family of Nostocaceae (Figure 1). This agrees with previous lipid analysis of pure Nostoc strains (Bauersachs et al., 2009).

In total, 12 different BHPs were identified in the ponds from the McMurdo Ice Shelf. The BHP analysis revealed a very heterogeneous distribution of these compounds in the different ponds. However, in most samples, aminotriol, bacteriohopanetetrol and bacteriohopanetetrol cyclitol tetraether were predominant, as previously reported for samples from arctic soils (Höfle et al., 2015).

The analysis of IPLs and BHPs constrained the lipid adaptation mechanisms of microbial communities in the melt water ponds to low temperatures and severe energy limitation. This enables us to better understand how microbes can thrive under extreme conditions in modern settings and their paleoenvironmental analogs.
Figure 1: the relative abundance of IPLs in melt water ponds from the McMurdo Ice Shelf. (MGDG/DGDG = Mono-/diglycosidic diacylglycerol; SQDG = Sulfoquinososyl diacylglycerol; BL = Betaine lipid; OL = Ornithine lipid; PC-DAG = phosphocholine diacylglycerol; PG-DAG = phosphoglycerol diacylglycerol; DPG = diacylglycerol; PE-DAG = phosphoethanolamine diacylglycerol; PI-DAG = phosphoinositol diacylglycerol)

References


