

## Unique membrane lipids typify adaptations of halophilic archaea and bacteria across a salinity gradient at the Great Salt Lake

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Microbial membrane lipids play an important role in the physiological adaptation of organisms to changes in temperature, pH, nutrients or salinity. Halophilic archaea contain very characteristic membrane lipids in comparison to other archaea, including bacterial cardiolipin analogs with C<sub>20</sub> and C<sub>25</sub> isoprenyl groups and abundant archaeol and extended archaeol (containing a C<sub>20</sub> and a C<sub>25</sub> isoprenyl group) with unique headgroups such as sulfated sugars (SG) and phosphoglycerolmethylphosphate (PGP-Me) [1,2]. These predominantly anionic lipids have been associated to function to shield the membrane from high Na<sup>+</sup> ion concentrations by providing a high negative charge surface density [1].

In this study we investigated eight sites ranging from freshwater to brackish to hypersaline conditions using 454 pyrosequencing, quantitative PCR, and intact polar lipid analysis to describe changes in the microbial community composition and their lipid content. Archaeal lipid contributions increase with increasing salinity, but bacteria remain dominant. Bacterial lipids include phospholipids, glycolipids, sulfolipids and aminolipids, some of which have been described for halophiles [3]. With increasing salinity we see an increase of the above described isoprenoidal cardiolipins, archaeols and extended archaeols, with a wide range of headgroup diversity, including PGP-Me, SG, glyco- and glycoposphate. Notably, typical archaeal tetraethers (GDGTs) were absent at higher salinities, but instead newly identified unsaturated GDGTs of unknown biological origin [4], become abundant. Their co-occurrence with isoprenoidal cardiolipins having multiple unsaturations suggests a similar physiological role for yet unassigned halophilic archaea.

[1] Kates (1993) *Experientia* **49**, 1027-1036. [2] Angelini *et al* (2011) *Biochim. Biophys. Acta* **1818**, 1365-1373. [3] Lopalco *et al* (2013) *Environ. Microbiol.* **15**, 1078-1087. [4] Zhu *et al* (2014) *RCM under review*