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Effect of salinity on mercury methylating benthic microbes and their activities in Great Salt Lake, Utah

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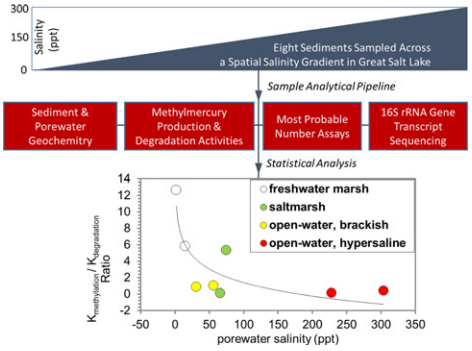
HIGHLIGHTS

- Great Salt Lake waters and biota are elevated in methylmercury (MeHg).
- Rates of MeHg production in GSL sediments inversely correlate with salinity.
- Numbers of sediment sulfate reducing bacteria (SRB) correlate with MeHg production.
- Salinity constrains SRB activity and the availability of mercury for methylation.

GRAPHICAL ABSTRACT



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ABSTRACT

Surface water and biota from Great Salt Lake (GSL) contain some of the highest documented concentrations of total mercury (THg) and methylmercury (MeHg) in the United States. In order to identify potential biological sources of MeHg and controls on its production in this ecosystem, THg and MeHg concentrations, rates of Hg(II)-methylation and MeHg degradation, and abundances and compositions of archaeal and bacterial 16 rRNA gene transcripts were determined in sediment along a salinity gradient in GSL. Rates of Hg(II)-methylation were inversely correlated with salinity and were at or below the limits of detection in sediment sampled from areas with hypersaline surface water. The highest rates of Hg(II)-methylation were measured in sediment with low porewater salinity, suggesting that benthic microbial communities inhabiting less saline environments are supplying the majority of MeHg in the GSL ecosystem. The abundance of 16S rRNA gene transcripts affiliated with the sulfate reducer *Desulfobacterium* sp. was positively correlated with MeHg concentrations and Hg(II)-methylation rates in sediment, indicating a potential role for this taxon in Hg(II)-methylation in low salinity areas of GSL. Reactive inorganic Hg(II) (a proxy used for Hg(II) available for methylation) and MeHg concentrations were inversely correlated with salinity. Thus, constraints imposed by salinity on Hg(II)-methylating populations and the availability of Hg(II) for methylation are inferred to result in higher MeHg production potentials in lower salinity environments. Benthic microbial MeHg degradation was also most active in lower salinity

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environments. Collectively, these results suggest an important role for sediment anoxia and microbial sulfate reducers in the production of MeHg in low salinity GSL sub-habitats and may indicate a role for salinity in constraining Hg(II)-methylation and MeHg degradation activities by influencing the availability of Hg(II) for methylation.

1. Introduction

Great Salt Lake (GSL) is the largest lake in the western United States and the fourth largest terminal lake in the world (52,000 km^2) (Fig. 1) (Keck and Hassibe, 1979). With over 200 avian species known to inhabit GSL over the course of a year, it has been suggested to be the most important inland shorebird site in North America with millions of birds visiting annually (Aldrich and Paul, 2002; Paul and Manning, 2008). A recent study of the most abundant avian species that utilize GSL revealed diets that consist predominantly of brine shrimp (*Artemia franciscana*) and brine flies and their larvae (*Ephydra* spp.) (Roberts, 2013), which themselves feed on phytoplankton and periphyton (Barnes and Wurtsbaugh, 2015; Collins, 1980; Wurtsbaugh and Gliwicz, 2001). Thus, carbon and energy from primary producers (phytoplankton and periphyton) are channeled to bird populations through invertebrate grazers.

Some of the highest concentrations of total mercury (THg) and methylmercury (MeHg) documented in the United States are found in the waters of GSL (Naftz et al., 2008). This is due, at least in part, to GSL being a terminal lake (Tayler et al., 1980) but also because of elevated rates of atmospheric Hg deposition in the region (Naftz et al., 2009; Peterson and Gustin, 2008). As a consequence, biomass of periphyton, *Artemia*, and *Ephydra* in GSL was shown to contain elevated concentrations of THg (Peterson and Gustin, 2008; Wurtsbaugh et al., 2011). Moreover, muscle tissues from common goldeneye duck, along with several other bird species, were shown to contain THg at concentrations up to 42-fold greater than *Ephydra*, a common food source for these birds (Scholl and Ball, 2005; Vest et al., 2009; Wurtsbaugh et al., 2011). Further, birds and brine flies with elevated THg concentrations were located proximal to waters with the highest measured MeHg concentrations in GSL (Johnson et al., 2015). Together, these observations suggest bioaccumulation of Hg in the form of MeHg (Naftz et al., 2008) which typically enters the base of aquatic food webs as a result of uptake by primary producers (Boyd et al., 2009; Mason et al., 1996; Pickhardt and Fisher, 2007). Bioaccumulation occurs in higher trophic levels (periphyton, birds) when consumers absorb MeHg from this food source and then respire carbon faster than they excrete the metal (Watras et al., 1998).

The formation of MeHg from inorganic Hg in aquatic environments occurs under anoxic conditions and is catalyzed by a diverse group of anaerobes, including those involved in sulfate reduction, iron reduction, methanogenesis, and fermentation (Compeau and Bartha, 1985; Fleming et al., 2006; Gilmour and Henry, 1991; Gilmour et al., 2013; Parks et al., 2013; Podar et al., 2015). While GSL is primarily a sodium chloride lake (Oren, 2013), concentrations of sulfate are high (Spencer et al., 1985), representing up to 7% of the total soluble salt (Wurtsbaugh et al., 2011). This fact coupled with the abundance (10^7 to 10^8 cells cm^{-3} sediment) of sulfate reducing bacteria (SRB) and

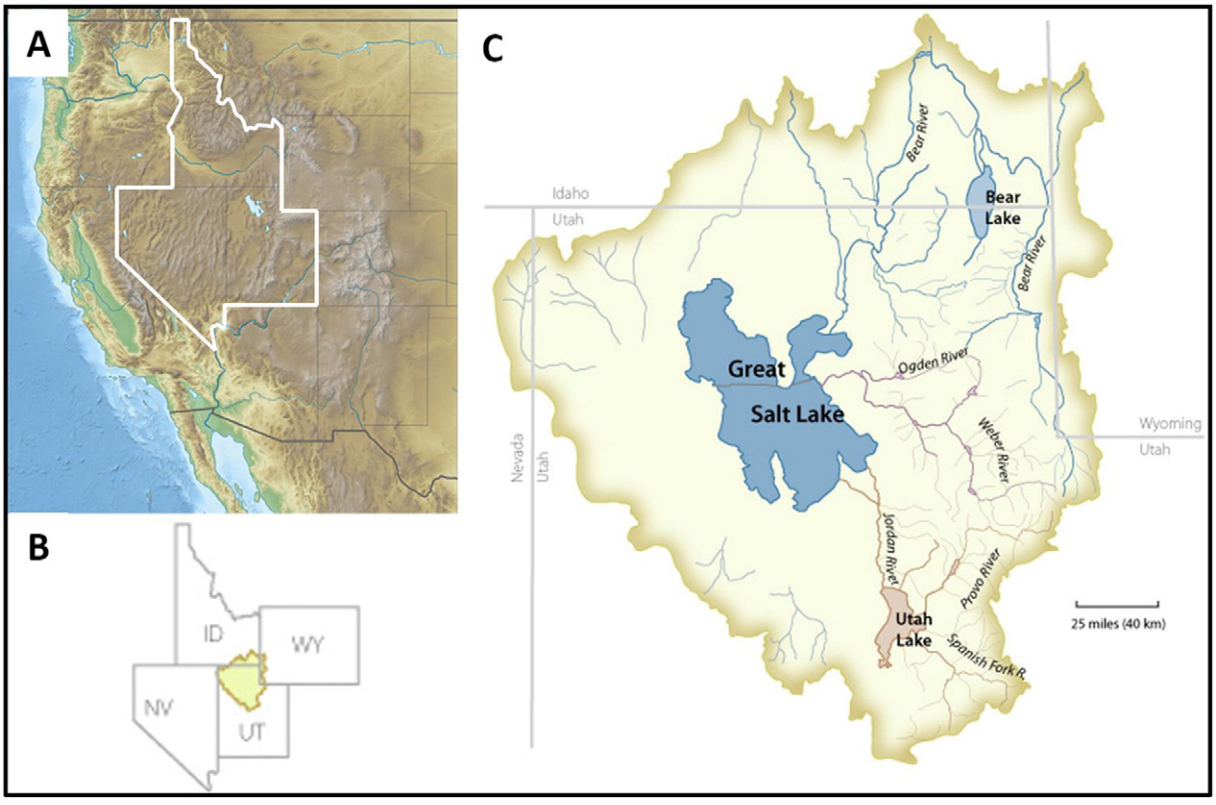

Fig. 1. (panel A) Relieve map of the western United States (Map modified from Wikimedia Commons). (panel B) Close up image of western mountain states with the greater GSL ecosystem indicated. (panel C) Location of Great Salt Lake within the statue of Utah, with primary river inputs depicted (maps in panels B and C were modified from Learn.Genetics.utah.edu).