



Biostrome communities and mercury and selenium bioaccumulation in the Great Salt Lake (Utah, USA)

Wayne A. Wurtsbaugh^{a,*}, Jodi Gardberg^b, Caleb Izdepski^{a,1}

^a Dept. of Watershed Science and the Ecology Center, Utah State University, Logan, UT 84322-5210, USA

^b Utah Department of Environmental Quality, Salt Lake City, Utah, P.O. Box 144870, Salt Lake City, UT 84114-4870, USA

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ABSTRACT

The Great Salt Lake has a salinity near 150 g/L and is habitat for over 200 species of migratory birds. The diet of many of these birds is dependent on the food web of carbonaceous biostromes (stromatolites) that cover 260 km² of the lake's littoral zone. We investigated the biostrome community to understand their production processes and to assess whether they are a potential vector for bioconcentration of high mercury and selenium levels in the lake. The periphyton community of the biostromes was >99% colonial cyanobacteria. Periphyton chlorophyll levels averaged 900 mg m⁻² or nine times that of the lake's phytoplankton. Lake-wide estimates of chlorophyll suggest that their production is about 30% of that of the phytoplankton. Brine fly (*Ephydra gracilis*) larval densities on the biostromes increased from 7000 m⁻² in June to 20000 m⁻² in December. Pupation and adult emergence halted in October and larvae of various instars overwintered at temperatures <5 °C. Mean total dissolved and dissolved methyl mercury concentrations in water were 5.0 and 1.2 ng L⁻¹. Total mercury concentrations in the periphyton, fly larvae, pupae, and adults were, respectively, 152, 189, 379 and 659 ng g⁻¹ dry weight, suggesting that bioconcentration is only moderate in the short food web and through fly developmental stages. However, common goldeneye ducks (*Bucephala clangula*) that feed primarily on brine fly larvae at the Great Salt Lake had concentrations near 8000 ng Hg g⁻¹ dry weight in muscle tissue. Data from a previous study indicated that selenium concentrations in periphyton, brine fly larvae and goldeneye liver tissue were high (1700, 1200 and 24,000 ng g⁻¹, respectively) and Hg:Se molar ratios were <1.0 in all tissues, suggesting that the high mercury concentration in the ducks may be partially detoxified by combining with selenium. The study demonstrated that the high mercury levels in the Great Salt Lake are routed through the biostrome community resulting in invertebrate prey that may provide health risks for birds and humans that consume them.

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1. Introduction

The Great Salt Lake, the largest saline lake in North America, is extremely important for migrant birds that forage in its productive waters and along its margins (Aldrich and Paul, 2002). Salinities above 120 g/L in most parts of the lake exclude predacious fish, so that the invertebrates produced in the system can be channeled to the birds. The lake's pelagic zone produces abundant brine shrimp (*Artemia franciscana*; hereafter *Artemia*) but the only other abundant macro-invertebrate in the lake tolerant of high salinity is the brine fly (*E. gracilis*; formerly *E. cinerea*). The brine fly larvae feed primarily on periphyton growing on, and forming the abundant biostromes covering much of the shallow littoral area of the lake (Collins, 1980; Eardley, 1938). Although considerable work has been done on the lake's pelagic food web composed of phytoplankton and *Artemia* (e.g.

Stephens and Birdsey, 2002; Wurtsbaugh, 1992; Wurtsbaugh and Gliwicz, 2001), very little is known about the benthic food web in the lake. In saline Mono Lake and Aber Lake the ecology of brine flies are better understood (Herbst, 1988; Herbst, 1990; Herbst and Bradley, 1993), and the brine flies (*E. hians*) in those locations are important prey for several bird species. Collins (1980) studied the population ecology of brine flies associated with biostromes in the Great Salt Lake during the summer, but provided little information on the biostromes themselves, nor about the seasonality of the brine flies. Wurtsbaugh (2009) recently provided some preliminary information on the biostrome food web. However, the ecology of these structures is poorly understood, not only in the Great Salt Lake, but elsewhere. The biostromes food web in the Great Salt Lake is particularly important because it provides abundant brine flies that help fuel the enormous migratory bird populations utilizing the lake (Wurtsbaugh, 2009).

The biostrome food web is important not only as a food resource, but because it may also contribute to high mercury levels observed in some bird species that utilize the lake. The Great Salt Lake was recently found to have some of the highest mercury levels in water documented in the United States (Naftz et al., 2008), and in 2005 the State of Utah placed

* Corresponding author. Tel.: +1 435 797 2584; fax: +1 435 797 1871.

E-mail addresses: wayne.wurtsbaugh@usu.edu (W.A. Wurtsbaugh), jgardberg@utah.gov (J. Gardberg), caleb.izdepski@gmail.com (C. Izdepski).

¹ Current address: CH2M Hill, New Orleans, LA, 70002-7272, USA.

three waterfowl species on a consumption advisory list because of their high mercury levels (Scholl and Ball, 2005). The species with the highest mercury concentration, the common goldeneye duck (*Bucephala clangula*), has a diet consisting of 70% brine fly larvae when it is at the lake (Vest et al., 2009; J. Vest, personal communication). Formation of toxic methyl mercury usually occurs in benthic environments (King et al., 2000) and thus could potentially be associated with the biostromes. Additionally, methylation is strongly associated with sulfate-reducing bacteria in anoxic zones and sulfate levels are extremely high in the Great Salt Lake, thus facilitating methylation (Brandt et al., 2001). However, the expected high primary production by periphyton on biostromes would provide an oxic environment, at least during the day, so strong methylation in this environment would not be expected. Because of the high mercury levels in common goldeneye, and the unique ecology of biostromes, we were consequently interested in understanding the bioconcentration of mercury in the biostrome food web.

The Great Salt Lake and its biota also have high concentrations of selenium (Conover and Vest, 2009a; Conover and Vest, 2009b; Oliver et al., 2009; Vest et al., 2009; Wurtsbaugh, 2009). Because selenium can counteract the toxic effects of mercury (Khan and Wang, 2009) a final objective of our study was to relate the mercury in the biostrome communities to previously reported concentrations of selenium to determine if there might be some antagonistic interactions between the two contaminants.

2. Methods

2.1. Study sites

The Great Salt Lake (Fig. 1) is a 5200 km² closed-basin system in Utah, USA (41.04 N, 112.28 W) bordered on its eastern and southeastern shores by the Salt Lake City metropolitan area. The lake has been

impacted by industrial and municipal discharges, as well as by transportation causeways that divide the system into four large bays. Gunnison Bay (2520 km²), located in the northwest of the lake, has salt concentrations over 270 g/L. The biostromes in Gunnison Bay are nearly unstudied. Preliminary observations indicate that they do not have any periphyton associated with them, but there are pink and bright-green microorganisms in different layers, probably representing Archaea and sulfur-reducing microbes. Shallow Farmington Bay (260 km²; mean depth <1 m) in the SE has biostromes along the east side of Antelope Island (Wurtsbaugh, unpublished data), but these are not likely growing as severe eutrophication in the bay limits light penetration. We studied Gilbert Bay (2400 km²), in the central portion of the lake. This bay is separated from Gunnison Bay by a railway causeway. Gilbert Bay typically has surface salinities ranging between 110 g/L and 180 g/L, but salinities have ranged from 60 to 270 g/L over the past 160 years (USGS, 2010. <http://ut.water.usgs.gov/greatsaltlake/> Accessed Nov. 2010). Gilbert Bay supports a large population of *Artemia* (Stephens and Gillespie, 1976; Wurtsbaugh, 1988). The mean lake elevation during the study was 1278.6 m (USGS, 2010. <http://ut.water.usgs.gov/greatsaltlake/> Accessed Nov. 2010). At this elevation, the respective mean and maximum depths of Gilbert Bay are 4.9 and 9.4 m (Baskin, 2005). The bay is meromictic due to flow of saturated brines from Gunnison Bay through culverts in the railway causeway into the deeper strata of Gilbert Bay (Loving et al., 2002) creating a deep-brine layer (monimolimnion) below approximately 6.7 m. The upper 6.7 m of Gilbert Bay is well-mixed and oxic. The deep-brine layer is anoxic with substantial hydrogen sulfide, and consequently has no macroinvertebrates. Gilbert Bay has high nutrient levels and is mesotrophic (Stephens and Gillespie, 1976; Wurtsbaugh, 1988). With the exception of meromixis due to the railway causeway, Gilbert Bay is the most natural remaining part of the Great Salt Lake with populations of brine shrimp, brine flies and actively growing biostromes.

Biostromes occur along the perimeter of much of the Great Salt Lake (Fig. 1), and at the water surface elevation at the time of the study, occurred at depths from 0 to approximately 3.9 m where there was sufficient light for photosynthesis. Eardley (1938) provided a detailed map of the benthic structure of the Great Salt Lake, although no methods were provided on how this information was collected. The deep brine layer now underlies approximately 44% of Gilbert Bay. In the remaining sediments covered by the oxygenated mixed layer, biostromes, oolitic sand and mud represent 23%, 62%, and 15% of the substrate, respectively (Table 1). Recent work suggests that biostromes may be more extensive than what Eardley suggested (R. Baskin, personal communication). Some of these are laminated and thus can be considered stromatolites, but the composition of few of them has been documented, so we use the more general term “biostrome” here. In Gilbert Bay we have encountered nearly pure cultures of *Aphanothece* sp. in the biostromes. (Halley, 1976) also described the biostromes as being composed of coccoid cyanobacteria characteristic of *Aphanothece* sp. when the salinity was ca. 160 g/L, and (Carozzi, 1962) described them as being formed by *A. packardii* when the salinity was near 270 g/L. Collins

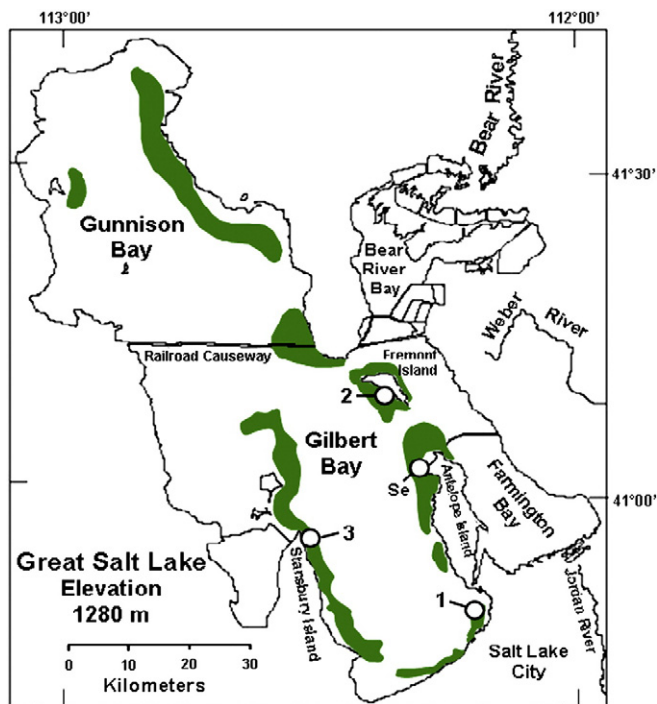


Fig. 1. Sampling stations in Gilbert Bay, Great Salt Lake, and the approximate distribution of biostromes (dark shaded areas; after Collins, 1980; Eardley, 1938). The stations used for mercury sampling were: Sta. 1 – SE Gilbert Bay; Sta. 2 – Fremont Island; Sta. 3 – Stansbury Island. Biostromes at Station 1 were also sampled in 2007 for selenium (Se), as was a station at the northern tip of Antelope Island (Se). Dark shading indicates areas of biostromes.

Table 1

Morphometric characteristics of Gilbert Bay of Great Salt Lake at a lake elevation of 1280.2 m (4200 ft), which is near the mean historical elevation. The data exclude areas of the southern salt ponds and Farmington Bay. Gilbert Bay's area was derived from Baskin (2005). The areas of biostromes, oolitic sand and mud were derived from the proportional areas shown in the map of Collins (1980), with an adjustment to a lake level of 1280.2 m. At that lake elevation the lake's mean depth is 5.55 m.

| Region | Area of sediments (km ²) | Volume (m ³ × 10 ⁹) |
|---------------------|--------------------------------------|--|
| Gilbert Bay (total) | 2057 | 11.42 |
| Deep-brine layer | 912 | 1.73 |
| Mixed layer | 1145 | 9.69 |
| Biostromes | 261 (23%) | |
| Oolitic sand | 712 (62%) | |
| Mud | 172 (15%) | |

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