2010

Impact of the Farmington Bay Eutrophication Plume on the Plankton Ecology of Gilbert Bay, Great Salt Lake

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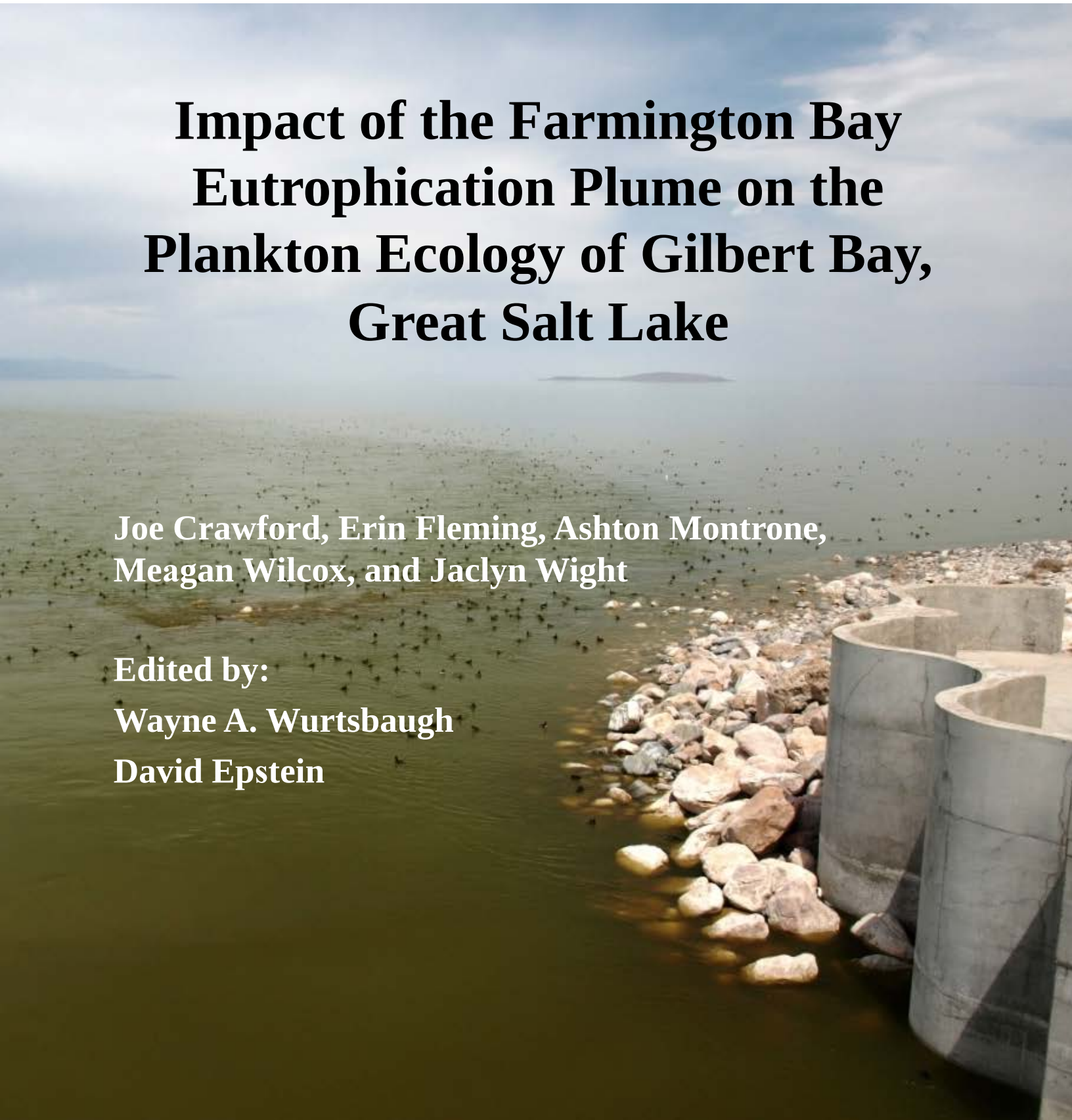

2010 Project Report

Impact of the Farmington Bay Eutrophication Plume on the Plankton Ecology of Gilbert Bay, Great Salt Lake

Aquatic Ecology Practicum (WATS 4510) Class Report
Watershed Sciences Department
College of Natural Resources
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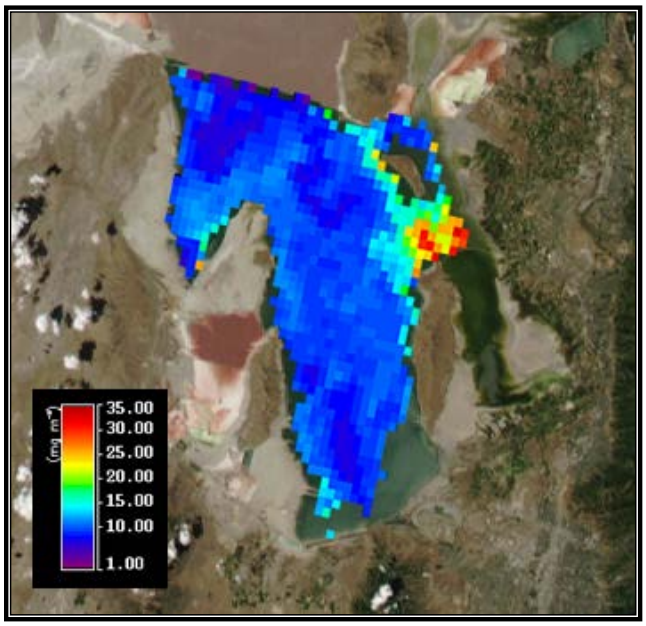

MODIS Satellite Image of Chlorophyll Plume
Extending from Farmington Bay into Gilbert Bay (August 2006)

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Front Cover Photo: Eared grebes concentrated in the plume flowing out of Farmington Bay. Photo by W. Wurtsbaugh, 29 April 2008.

Title Page Photo: MODIS satellite imagery (NASA) of chlorophyll levels in Great Salt Lake, August 2006. Note that MODIS imagery did not reveal a chlorophyll plume 2-3 days prior to the class sampling effort on 30 September 2010.

Back Cover Photo: Sunset over Gilbert Bay. Photo by W. Wurtsbaugh, 1 December 2008.

Acknowledgements

We would like to thank the Utah Division of Water Quality for financial support of the project. Ian Washbourne helped analyze nutrient samples. Michelle Kang assisted in pigment analyses. We especially want to thank Department Head Chris Luecke for his continued support of the class that makes these student projects possible.

Executive Summary

Farmington Bay in the Great Salt Lake is hypereutrophic because of extreme nitrogen and phosphorus loading, largely from greater metropolitan Salt Lake City sewage effluents. Although this causes detrimental impacts within the bay, the influence of the outflow of its algal- and nutrient-rich waters into Gilbert Bay is largely unknown. To address this issue, students in the 2010 Aquatic Ecology Practicum course from Utah State University did a 13-km long transect analysis of trophic parameters from the causeway bridge separating the two bays, out into the pelagic zone of Gilbert Bay (Figure 1; Appendix A). On the September 30th date of the transect, flows out of Farmington Bay were low and consequently the plume did not extend far into the lake and we could not detect a plume using MODIS satellite imagery. Nevertheless, the students were able to measure a distinct gradient in a variety of parameters and used water from Gilbert and Farmington Bay in an experiment to assess how Farmington Bay water influences brine shrimp growth. Conductivity profiles indicated that the less dense Farmington Bay water formed an overflow plume that was only 0.2-0.4 m thick.

Sta	Rep	Station Depth (m)	Latitude	Longitude	Distance From Farmington Bay (km)
0	a	0.80	41° 03' 57.9"	-112° 13' 48.4"	0.00
1	a	1.00	41° 04' 04.6"	-112° 13' 57.9"	0.25
1	b	0.90	41° 04' 08.1"	-112° 13' 54.3"	0.25
2	a	1.40	41° 04' 21.0"	-112° 14' 18.4"	0.92
2	b	1.40	41° 04' 16.8"	-112° 14' 20.2"	0.92
3	a	1.50	41° 04' 28.0	-112° 14' 46.9"	1.65
3	b	1.40	41° 04' 34.1"	-112° 14' 39.7"	1.65
4	a	1.80	41° 04' 38.9"	-112° 16' 20.9"	3.80
4	b	2.20	41° 04' 44.7"	-112° 16' 19.8"	3.80
5	a	1.80	41° 04' 41.3"	-112° 18' 50.1"	7.20
5	b	1.80	41° 04' 48.3"	-112° 18' 50.2"	7.20
6	a	7.25	41° 04' 20.6"	-112° 23' 18.5"	13.30
6	b	7.30	41 04' 26.2"	-112° 23' 19.8"	13.30

Figure 1—Map of Farmington and Gilbert Bay showing the location of the sampling stations used in the plume study.

Joe Crawford's analysis of algal pigments demonstrated that the high chlorophyll level in Farmington Bay (59 µg/L) was quickly diluted as the overflow plume spread and mixed with Gilbert Bay water (figure 2b). By Station 3, 1.3 km from Farmington Bay, chlorophyll levels had decreased to 3.3 µg/L, and by the end of transect at Station 6 (13.3 km) they had decreased to 0.2 µg/L. Phycocyanin levels, an indicator of the prevalent cyanobacteria in Farmington Bay showed a similar trend. Secchi depths were consistent with the chlorophyll concentrations: 1.2 m at Station 1 and increasing to 3.5 m at Station 6. Analysis of respiration and photosynthesis rates of Farmington Bay and Gilbert Bay water reflected the huge gradient in algal biomass in the two zones.

Erin Fleming analyzed the species composition at selected stations along the transect and found large decreases in algal biovolume and changes in taxonomic composition (figure 2a). The high phytoplankton biovolume in Farmington Bay was dominated (71%) by the cyanobacteria *Nodularia*, but with substantial contributions of diatoms and green algae. By Station 3, total biovolume had decreased 91%, and only 1% of this was contributed by *Nodularia*. By

Station 6 biovolumes were extremely low, with only 0.01% of the biovolume that was present in Gilbert Bay, thus reflecting the large decrease seen in chlorophyll levels.

Jacklyn Wight analyzed the *Artemia* populations along the transect gradient (figure 2b). Contrary to the phytoplankton data, *Artemia* biomass increased from low levels at stations close to Farmington Bay to high levels in the pelagic zone of Gilbert Bay. At Stations 1-3 biomass ranged from 30-70 µg/L, but increased to near 190 µg/L at Station 6 in the pelagic zone. Adult and larger juveniles dominated the biomass estimates, but nauplii dominated numerical counts. Estimates of brine shrimp grazing rates were only around 2-5% of the water column per day at Stations 1-3, but increased to around 13%/day at Station 6. The relatively high grazing rate in the open pelagic zone is the likely reason for the strong decline in algal biovolume in the lake.

Megan Wilcox assessed ova abundance and lipid indices in the *Artemia* (figure 2c). The lipid indices, an index of the "fatness" of the brine shrimp, were variable, but highest at Stations closest to Farmington Bay, and decreased substantially in the pelagic zone. The higher lipid ratios close to Farmington Bay were not, however, reflected in the abundance of eggs and cysts carried by females, which were very low at Station 1 and increased substantially along the transect (figure 2d). The low lipid ratios in the pelagic zone likely reflect the very low food abundance there at the time of the sampling, but also the fact that female brine shrimp were shunting lipids from their bodies to produce cysts and eggs.

Aston Montrone used stable isotope mixing models to estimate how important the exported phytoplankton and detrital food from Farmington Bay was for the growth of *Artemia* in Gilbert Bay. Both ^{15}N and ^{13}C isotope data indicated that at Stations 1-2, within 1 km of the Farmington Bay outflow, nearly 60% of the diet of *Artemia* was derived from Farmington Bay organic matter (figure 2e). As distance increased, the importance of this food source decreased markedly, but the carbon model indicated that by Station 5 (7 km) only about 5% of the diet was attributable to Farmington Bay sources, whereas the nitrogen mixing model suggested that nearly 40% of the diet of shrimp at this station was from Farmington Bay.

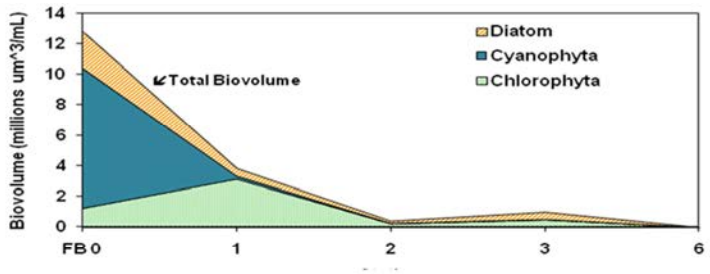
A survey of eared grebes along the transect indicated that they were concentrated close to the Farmington Bay discharge, with densities 10 times higher between stations 1 and 2 than between 5 and 6, even though brine shrimp were more abundant at the more distant stations. Grebe densities increased considerably once the transect was over biostromes, suggesting that the birds might be utilizing brine fly larvae on them.

Jacklyn Wight and Megan Wilcox conducted a 14-day experiment to assess how mixtures of water from Farmington Bay and Gilbert Bay (Station 6) influenced the growth and survival of *Artemia* nauplii. Nauplii grown in 75% Farmington Bay and 25% Gilbert Bay water survived and grew poorly, indicating that the food source or the resulting low salinity (ca. 5%) did not support the growth of the *Artemia*. *Artemia* grown in a 50-50 mixture of the two sources of water survived and grew best, while nauplii in 75% of 100% Gilbert Bay water survived poorly, likely reflecting the very low amount of food available in the pelagic zone at the start of the assay.

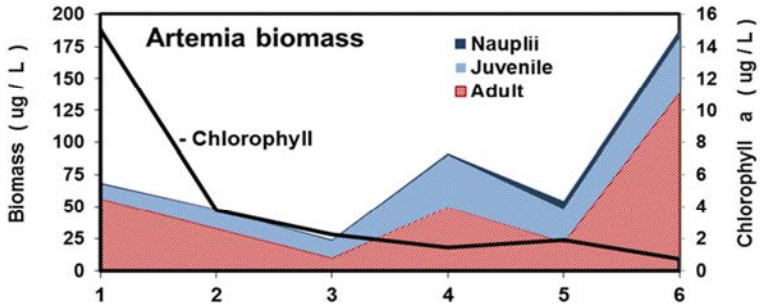
The overall data set suggested that the Farmington Bay plume may help sustain the food web in this region. However, most parameters indicated that the plume was distinguishable out to a distance of 7 km. Consequently; the plume would have been influencing only about 7% of Gilbert Bay. In other seasons when hydraulic discharges are higher from the bay it could have considerably more influence. Consequently, longer-term analyses with good temporal resolution will be necessary to fully assess the impacts of Farmington Bay on the food web in Gilbert Bay.

Figure 2. Summary of changes in limnological parameters along the 13 km overflow plume from Farmington Bay going into Gilbert Bay. Note that some parameters were collected within Farmington Bay (Station 0), whereas others started at Station 1, 250 m from the outfall of Farmington Bay.

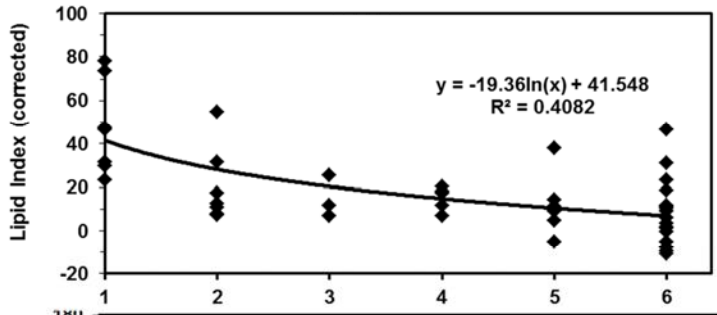
a. Biovolume of different algal taxa along the transect. Note that not all stations were analyzed.



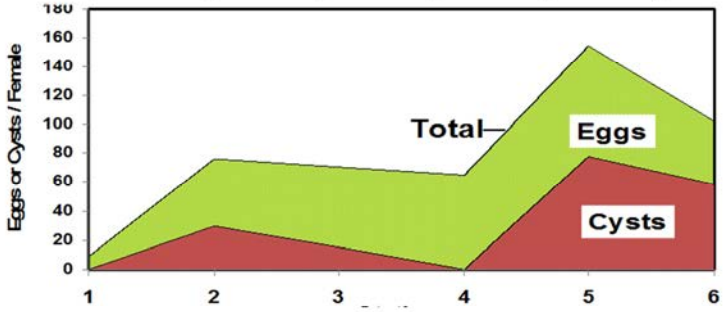
b. Chlorophyll a concentrations and biomasses of different *Artemia franciscana* life stages along the plume. In Farmington Bay chlorophyll concentrations were



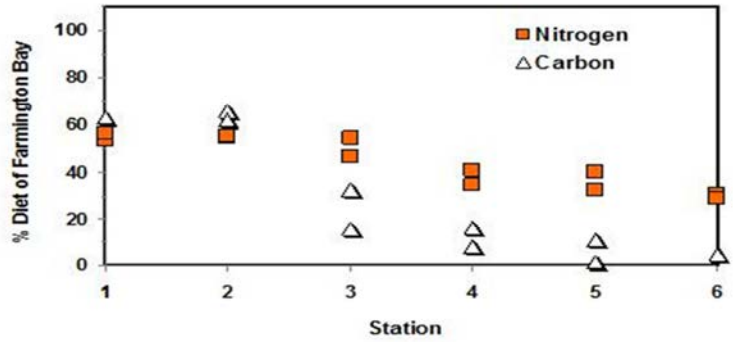
c. Lipid indices (fat droplets) in adult *Artemia* females.



d. Eggs and cysts on *Artemia* females.



e. Isotope mixing model estimates of the importance of Farmington Bay particulate matter for *Artemia* growth.



Chlorophyll, Phycocyanin, and Primary Production Along a Trophic Gradient in the Great Salt Lake

Joe Crawford

SUMMARY

The Great Salt Lake is a saline lake that is divided into several different bays. Large densities of algae in Farmington and Gilbert Bay are the result of effluents being dumped from several wastewater treatment plants. These high levels of algae create a large algal plume that extends several kilometers out into Gilbert Bay that can be seen at different times of the year. This study mainly focused on the different chlorophyll and phycocyanin levels and how they varied between the two bays and throughout the plume. Water samples were taken at seven different sites and then later processed for chlorophyll *a and phycocyanin*. Primary production was measured in the laboratory with water from Farmington Bay and from Gilbert Bay by recording the change in oxygen that occurred during photosynthesis and respiration. Chlorophyll concentrations decreased the farther away the site was from Farmington Bay. Farmington Bay, where the nutrients were discharged into, had higher levels of primary production than Gilbert Bay. It is likely that the chlorophyll plume that occurs in Gilbert Bay is because of the high levels of algae that are being transported from Farmington Bay.

INTRODUCTION

The Great Salt Lake, a shallow saline lake located in the Great Basin of Utah, is divided into several bays (Stephens and Gillespie 1976). This study focused on two of those bays: Farmington Bay and Gilbert Bay. Farmington Bay located in the southern basin of the lake is a recipient of many different tributaries and effluents from several wastewater treatment plants. It is separated from Gilbert Bay by an automobile causeway to Antelope Island. A culvert on the west side of the causeway allows water to flow into Gilbert Bay. The causeway causes the water composition is different between the two bays. For example, since Farmington Bay receives fresh water from tributaries it has low saline levels between 0-3percent while the salinity level in Gilbert Bay has been measured between 11-14% throughout the bay. Furthermore, Wurtsbaugh et al. (2008) found that chlorophyll levels in Farmington bay were much higher than those in Gilbert Bay.

The chlorophyll levels of the Great Salt Lake are influenced by the wastewater treatment plants surrounding the Great Salt Lake. Over the past few decades the population surrounding the lake has greatly increased creating the need for more wastewater treatment plants. These plants release their treated water into the lake causing an increase of nutrients. The high levels of nutrients have led to hypereutrophic conditions, large algae blooms, and toxic levels of cyanobacteria in Farmington Bay (Wurtsbaugh et al. 2008). As the water and algae flows into Gilbert Bay it often creates a large visible plume that often can be seen with satellite imagery to extend far into the bay. These large amounts of algae may lead to high levels of primary production and potentially provide food for invertebrates.

Studies have shown that primary production affects many different organisms in lakes (Wetzel 1964). For example, in the Great Salt Lake the brine shrimp (*Artemia franciscana)* feed on the primary producers (algae and cyanobacteria) (Stephens and Gillespie 1976). There are also many birds that feed off of the brine shrimp and as a result depend on primary production in the Great Salt Lake.

Different methods have been used to measure primary production and its importance. As the amount of primary production increases in a body of water the lake becomes more eutrophic (Goldman 1988). Others studies have used chlorophyll levels, transparency and total phosphorus to determine trophic status (Carlson 1977, from Goldman 1988). In general as the level of chlorophyll and phosphorus increase, the transparency decreases leading to eutrophication. Furthermore, many studies have shown that there is a correlation between the amount of chlorophyll and primary production in lakes (e.g. Hayward and Venrick 1982). Even though the Great Salt Lake is the largest lake in Utah and a popular tourist destination there has only been one study done to determine the amount of primary production in the lake (Stephens and Gillespie 1976). This study focuses on primary production and chlorophyll levels in Gilbert and Farmington Bay.

I predicted that in the Great Salt Lake there would be different levels of chlorophyll along the plume in Gilbert Bay. Assuming that the amount of algae will decrease in the plume the farther out into the lake it goes the levels of chlorophyll should also decline. Therefore, this study tested the hypothesis that the farther away from Farmington Bay you travel the less amount of chlorophyll there will be in the water column. Phycocyanin, a pigment specific to cyanobacteria, was also measured to see how these organisms were transferred into Gilbert Bay. I also analyzed the amount of photosynthesis and occurring in Farmington and Gilbert Bays.

STUDY AREA AND METHODS

Study Site

Currently the Great Salt Lake is approximately 120 kilometers long and about 56 kilometers wide (Utah.com). The main portion of this study was conducted along a transect that began at and the Farmington Bay outflow and extended 13.3 kilometers into Gilbert Bay. The first site was in Farmington Bay at the causeway bridge while the other sites were located in Gilbert Bay at 0.25, 0.92, 1.65, 3.8, 7.2, and 13.3 km away from Farmington Bay (see figure 1 in Introduction). Each site in Gilbert Bay also consisted of a replicate sample site that was 100-250 m away from the original site. At each site water for pigment analyses was collected with a VanDorn bottle at ca. 0.2 m and at 0.3 m above the lake bottom.

Chlorophyll and Phycocyanin Measurements

A common way to measure the amount of algae in these blooms is by measuring the amount of chlorophyll. On September 30, 2010 water samples were collected at the surface of the lake and near the bottom at each site in Gilbert Bay using a Van Dorn sampling bottle (photo 1) and then transferred to 25-mL Nalgene bottles. A surface water sample was also taken at the outflow of Farmington Bay and placed in a 25-mL scintillation vial. The water samples were then placed in a cooler and transported back to the lab and placed in a cooler. The water samples were analyzed within 18 hours for chlorophyll by filtering 25-mL of water through a 25-mm Millipore glass fiber filter with a vacuum pump. Then the filter was placed in 10 mL of 95% methyl-ethanol and left in the dark overnight. The samples were then analyzed with a 10 AU fluorometer non-acidification technique (Welshmeyer 1994). Whole water samples were also analyzed for the phycocyanin pigment of cyanobacteria with *in vivo* fluorescence utilizing the Turner 10 AU fluorometer (Tuner Designs 2008). A Regression analysis was done determine if the levels of phycocyanin and chlorophyll were significantly related. A t-test was also performed to evaluate the relationship between surface and deep level phycocyanin. All statistical analyses were done in Microsoft Excel.

Photo 1—Water sample collection with a Van Dorn sampling bottle.

Photosynthesis and Respiration Measurements

To determine the amount of primary production and respiration taking place along the transect oxygen changes were measured at three depths in the water column. Water samples were taken at the surface, middle and at the bottom of the lake at four stations. The samples were then transferred from the Van Dorn sampling bottle and placed in BOD bottles. To measure respiration BOD bottles were covered completely with electrical tape (dark bottles) to ensure that no light would be able to penetrate inside the bottle. The other bottles were left clear to measure photosynthesis. Two clear and two dark bottles were attached on a rope and incubated in the lake at the surface, middle and bottom depths. Initial oxygen levels were immediately fixed by placing 10-mL of formalin into water samples. After being deployed for ca. 3-6 hours the samples were collected and immediately received 10-mL of formalin. The samples were then transported back to the lab and refrigerated. Within 24 h the samples were analyzed by measuring the amount of oxygen (mg/L) in each sample

with a YSI instrument. To obtain accurate oxygen readings a magnetic stir bar was placed in each sample, placed on a stir plate, and stirred at a constant speed. Measurements were taken after the YSI reading stabilized.

The amount of primary production between Gilbert Bay and Farmington Bay was also measured in a laboratory experiment. Water samples were taken from each bay and placed in a Cubitainer®. I filled two clear and two dark BOD bottles with water from each site and incubated the samples for six hours at a light intensity of 150 uE/m2/sec and a temperature of 20°C. At the initiation of the experiment, and after the incubation the amount of oxygen in each bottle was measured with the YSI instrument. A single factor ANOVA was performed to determine if there was a significant relationship between the amount of photosynthesis and respiration in each bay.

Specific Conductivity

The amount of Farmington Bay water that was in each site of Gilbert Bay was also estimated. This was determined by measuring the specific conductivity (SC) of the water of each bay with a YSI instrument and then using a mixing model to calculate the relative contributions from the two bays with the following equation:

$$SC_{site} = x\ (SC_{FB}) + (1 - x)\ SC_{Gilbert}$$

Where: x = proportional contribution from Farmington Bay (FB)

RESULTS

Specific Conductivity

The specific conductivity mixing model allowed us to estimate the proportion of water at each site that was derived from the less saline Farmington Bay water. At the first site in Gilbert Bay, which was 0.10 m away from the causeway bridge, a mean of 28.5 % of the water was from Farmington Bay. By Station 4, at a distance of 3.8 km, only 2-3% of the water was from Farmington Bay, and at Stations 5 and 6 essentially all of the water was from Gilbert Bay (figure 1)

Chlorophyll and Phycocyanin

The declining relationship between distance from Farmington Bay and chlorophyll levels was significant (figure 2a; Regression analysis, p-value = 0.03, n = 11). The amount of chlorophyll *a* in Farmington Bay was 59 µg/L and the level of chlorophyll *a* decreased the farther out the site was into Gilbert Bay. At the first site in Gilbert Bay, the surface chlorophyll level had decreased to 30.7 µg/L at Station 6 it was only 0.10 µg/L. There was no statistical difference between chlorophyll levels measured at the surface and near the bottom (Paired two sample t-test for means; p-value = 0.43, n = 12).

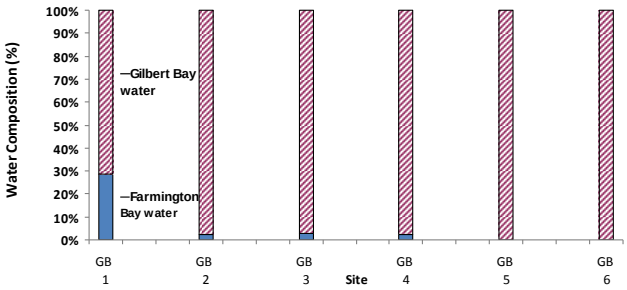


Figure 1—Composition of water in Gilbert Bay Water determined by a conductivity mixing model. The first site, GB 1, is the closest to Farmington Bay and as a result is composed of almost 28.5 % of Farmington Bay water.

Measurement of phycocyanin concentrations provides an index of the biomass of cyanobacteria (Otsuki et al 1994). It was evident that he farther away the site was from Farmington Bay phycocyanin concentrations declined (figure 2b). Furthermore, the levels of phycocyanin at the surface of the lake and those at the bottom were significantly different (p-value = 0.04, n = 12). At the surface, the phycocyanin was twice the amount than those samples collected from the bottom of the sample site (figure 2b). The difference between deep and shallow phycocyanin concentrations was most pronounced at sites near Farmington Bay. However, both pigments followed a similar longitudinal trend, resulting in a significant correlation between the amount of chlorophyll and phycocyanin (figure 3; p-value 0.000, n = 25).

Primary Production

The amount of primary production, as measured by the difference in oxygen levels, resulted in inconclusive data between each site in Gilbert Bay. However, the data that was collected from the laboratory experiment showed photosynthesis and respiration were considerably greater in Farmington Bay than they were in Gilbert Bay (figure 4). The respiration in Farmington Bay was 1.27 mg O_2/L/hr while in Gilbert Bay the analysis indicated it was -0.38 mg O_2/L/hr (i.e. zero), approximately a 3-fold difference. This difference was highly significant (ANOVA d.f.$_{1,2,}$ p-value = 0.01).

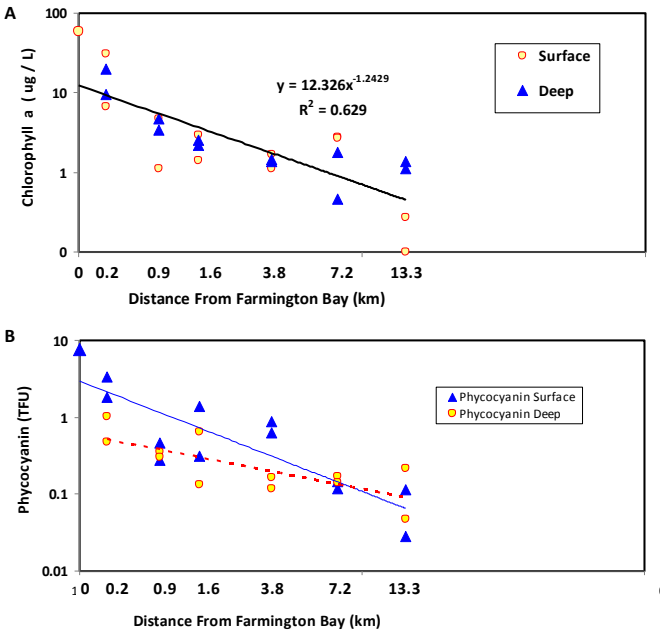


Figure 2—A (above). Chlorophyll a concentrations (log axis) along the sampling transect from Farmington into Gilbert Bay in the Great Salt Lake. B (below). Relative phycocyanin concentrations (log axis) in Farmington and Gilbert Bay in the Great Salt Lake. R2 value for the surface concentrations = 0.728. R2 for the deep concentrations is = 0.568. The first site (0 km) was within Farmington Bay (at bridge), and only a surface sample was taken there. Samples were taken from the surface and near the bottom at each site in Gilbert Bay. See Figure 1 in the Summary for a list of depths at each station. TFU = Turner fluorometer unit (relative values).

There was also a significant difference in the amount of photosynthesis that occurred between each bay (ANOVA d.f.$_{1,2}$ p-value = 0.004). In Farmington Bay estimated photosynthesis was 0.89 mg O_2/L/hr while a negative value of -0.35 mg/L/hr was recorded in Gilbert Bay. Although the negative estimate of photosynthesis has to be anomalous, the relative differences in respiration and photosynthesis in the two bays is consistent with the different levels of chlorophyll and phycocyanin in each system.

DISCUSSION

Farmington Bay is negatively impacted via the effluents from wastewater treatment plants (Wurtsbaugh et al. 2008). Studies have shown that large algal blooms are created by the stimulation of primary production (Fee 1976). As water from Farmington Bay enters Gilbert a large algal bloom can often been seen many kilometers out into Gilbert Bay. This plume is likely due primarily to the exported phytoplankton from Farmington Bay, as evidenced by the high levels of phycocyanin found in Gilbert Bay and moderate levels of the cyanobacteria *Nodularia* that only grows at salinities far less than those in Gilbert Bay (see Fleming chapter, this report). Additionally, nutrients exported from Farmington Bay may stimulate new primary production in Gilbert Bay and contribute to the plume development. However, the levels of chlorophyll, phycocyanin, and probably primary production decrease as the water travels farther into Gilbert Bay. During our study, the specific conductivity data suggested that the plume only extended a few kilometers into Gilbert Bay, and this was largely supported by the pigment data.

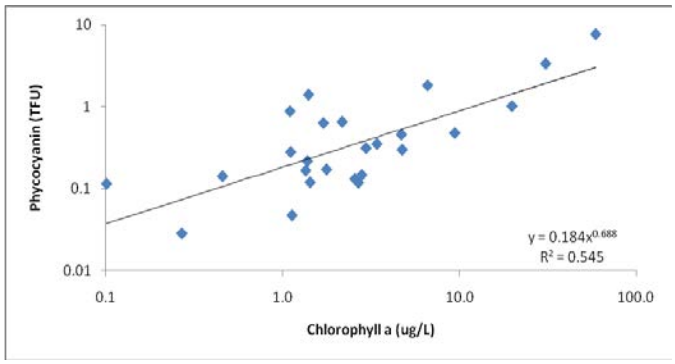


Figure 3—A comparison of the chlorophyll *a* and phycocyanin concentrations from seven sites in Farmington and Gilbert Bays of the Great Salt Lake in relation to each other. TFU = Turner fluorometer unit (relative values).

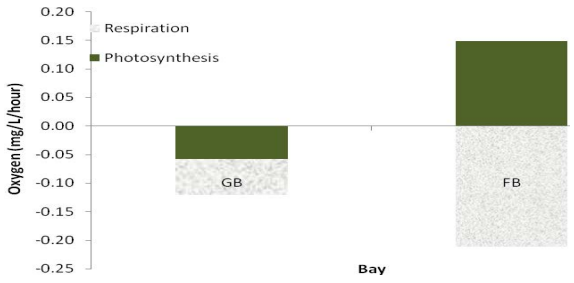


Figure 4—Respiration and photosynthesis rates measured in water samples taken from Gilbert Bay and Farmington Bay. Both respiration and photosynthesis differed significantly between the two sites (see text).

Hayward and Venrick (1982) suggest that when using chlorophyll levels to determine the biological health of a body of water to it is important to measure the surface levels as well as at different depths in the water column. However, there was no difference noted in the chlorophyll levels at each site in our study. All of the sites that were measured, except the last one, at 13.3 km, were < 2.2 m deep and the Secchi depth was greater than the water depth. It is likely that because of the shallow nature and the clarity of the water, photosynthesis and algal growth was possible throughout the water column. Unfortunately, there were also a lot of unexplained variances in the surface and bottom water chlorophyll samples. For example, Station 2 was less than 2.2 m deep and had a chlorophyll difference of 0.63 µg/L between the bottom and the surface. While on the other hand in the replicate Station 2 there was less than 0.2 µg/L difference. A common error with the Welshmeyer method of analyzing chlorophyll is failing to homogenize the sample before measuring it with the fluorometer. It is possible that this error was made while processing samples that caused large variances in the results. At Station 6 there were also large differences between the surface and deep samples. However, in this case the very low chlorophyll concentrations measured in the surface water are consistent with the extremely low algal biomass that was found in the surface water samples (see Fleming, this report). Although these large variances made it difficult to assess the concentrations at a single site, the overall declining trend along the transect was clear.

Conversely, the study concluded that there is a significant difference in the amount of algae (measured in the form of chlorophyll *a*) between Farmington Bay and Gilbert Bay. It was also shown that there was more primary production in Farmington Bay than in Gilbert Bay. These findings are consistent with Wurtsbaugh et al. (2008) who also found large differences between the amounts of chlorophyll in each bay. In Farmington Bay they measured chlorophyll levels that ranged from 38 to 186 µg/L while in Gilbert Bay the average was only 15 µg/L. Moreover, according to the Boundary Trophic Classification System for Lakes (OECE, 1982, from Dodds 2002) Farmington Bay is hypereutrophic, with a chlorophyll level of 59 µg/L. The average chlorophyll level in Gilbert Bay was 4.4 µg/L, yielding a classification of mesotrophic. However, at the open pelagic Station 6, chlorophyll levels were very low (<1 µg/L) suggesting it was oligotrophic. However, the low chlorophyll levels were likely due to high grazing rates of *Artemia* (see Wight, this report). The chlorophyll data also is also consistent with the amount of ^{15}N that was found in the *Artemia* and seston at each site (see Montrone report and figure 5).

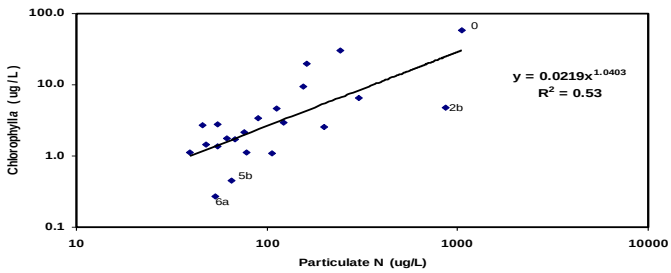


Figure 5—Relationship between particulate N in seston (see A. Montrone chapter) and chlorophyll a concentrations at the seven stations sampled along the plume entering Gilbert Bay of the Great Salt Lake. Two depths were sampled at most stations. Station numbers and replicates are shown for some stations. Note log-log scale.

Otsuki et al. (1994) measured chlorophyll and phycocyanin levels and found that they were significantly related and could both be used to assess the biological health of water bodies. This proved to be the case in this study. The levels of chlorophyll and phycocyanin were indeed significantly related to each other. Furthermore, while there was not enough evidence to determine a difference in the two depth strata measured in the chlorophyll levels there was a significant difference in the phycocyanin densities, indicating that the cyanobacteria from Farmington Bay were in an overflow plume due to the different densities of water in the two bays. It is possible that the densities and life spans of the two pigments are different causing there to be a significant difference in depth for phycocyanin but not of chlorophyll.

Other studies have also shown that there is a positive correlation between primary production and the trophic status of lakes (Goldman 1988). Unfortunately, there was no conclusive evidence from the in situ study between each site after using the oxygen method to measure primary production. This might have been caused by the manner in which they oxygen was fixed and measured. Formalin was placed in each sample after the incubation period to stop photosynthesis, but it is possible that this was not completely successful. Furthermore, instead of immediately processing the samples they were not processed until the next day.

Bubbles were found in all of the samples and these undoubtedly contributed to the poor data. These could have been caused by a failure to put a water seal around the top of all of the stoppers and/or by the change in altitude when transporting the samples from the Great Salt Lake to Logan.

Fortunately, the laboratory primary production study yielded better results, with significantly higher rates in Farmington Bay than in Gilbert Bay. These laboratory results also support the chlorophyll data that showed there was more chlorophyll in Farmington Bay than Gilbert Bay. Stephens and Gillespie (1976) studied the production of phytoplankton in the Great Salt and also showed that the southern basin of the Great Salt Lake primary production rates were also very high**.** Primary production has never been measured previously in Farmington Bay, and our result showing three-fold higher rates there than in Gilbert Bay is further proof of the hypereutrophic nature of Farmington Bay.

This study was done with only one sample date. As a result, it only gave us a snapshot of what is happening at that period of time and does not give us an idea of what is happening in these bays temporally. However, the data that was gained gives a good insight into how far the algal bloom extends into Gilbert Bay. Furthermore, it allows us to find out what primary production and algal production are doing to the water column and how they are affecting the organisms that are living there.

This study shows that chlorophyll can be a useful tool in determining the biological health of a water body (Hayward and Venrick 1982). Moreover, it confirms that there is a direct relationship between the chlorophyll levels and the amount of primary production that occur in the Great Salt Lake. Even though the chlorophyll plume in Gilbert Bay consists of less than 1% of the lake's total area, the chlorophyll plume extended at least 4 km (2.5 miles) into Gilbert Bay. This is similar to the study of Wurtsbaugh et al. (2008). Using a MODIS satellite imagery they found that on some dates the surface chlorophyll plume extended as far as 20 km into Gilbert Bay.

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Phytoplankton in the Plume: Is Nutrient Export from Farmington Bay in the form of Phytoplankton an Important Food Source for Gilbert Bay Brine Shrimp?

Erin Fleming

SUMMARY

A road causeway separates Farmington Bay from Gilbert Bay of the Great Salt Lake, but an opening in the causeway allows fresher, more nutrient rich water to pass into Gilbert Bay. This export is high in phytoplankton, especially the cyanobacterial species *Nodularia*. However, cyanotoxins in the *Nodularia* may decrease the usefulness of nutrients exported in this form. An analysis along a transect of the plume in September 2010 showed a decrease in algal biovolume from 12 million um^3/mL at the Farmington Bay discharge to 1.1 million um^3/mL only 1.6 km into Gilbert Bay. Divisions Chlorophyta, Bacillariophyta, and Cyanophyta were the dominant taxa. *Nodularia* represented 96% of the biovolume in Farmington Bay, but the abundance of this taxa was close to zero at stations farther than a kilometer from the causeway. In a companion study, an isotopic mixing model suggested that Farmington Bay-derived nutrients are major contributors to brine shrimp production. High grazing rates and a variable plume extent may significantly alter the availability of phytoplankton for brine shrimp grazing, but the nutrient content is still a possible source for food webs in Gilbert Bay close to the Farmington Bay discharge.

INTRODUCTION

The Great Salt Lake has a unique hydrology because causeways spanning across the lake create essentially separated bays that have become chemically different from each other. The Jordan River enters Farmington Bay at the southeast end of the lake and subsequent point and non-point sources lead to hypereutrophic conditions and massive algal (specifically cyanobacteria) blooms (Wurtsbaugh and Marcarelli 2006). Water from Farmington Bay is able to flow north by an opening in the causeway into the less productive Gilbert Bay, where salinities are nearly five times higher and the less dense water moving north does not evenly mix into the saltier water and so remains in a chemostratified plume.

The effect Farmington Bay water has on biota within the plume reaching into Gilbert Bay is not well understood, and conflicting reports exist (Naftz et al. 2008; Wurtsbaugh et al. 2008). The range of effects could stretch from being harmful—cyanobacteria blooms produce high cyanotoxin levels with varying toxicity—to having no effect, and being beneficial by providing crucial nutrients to organisms. In particular, this plume may influence the *Artemia franciscana* (brine shrimp) community of the lake, which is of special interest as it supports a large industry of brine shrimp cyst harvesting, and is an import food source for large populations of birds.

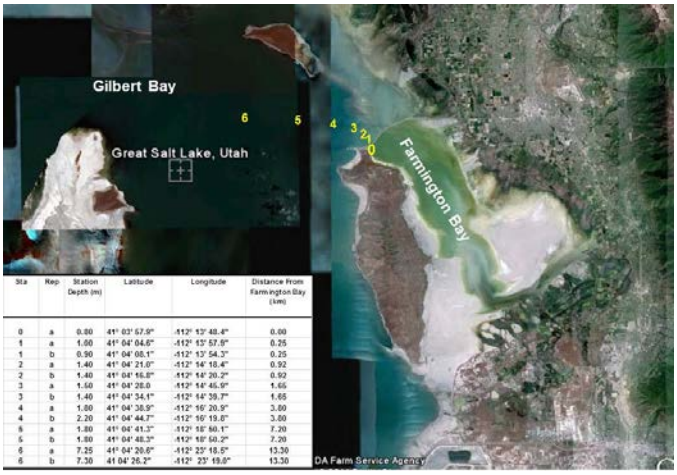
Previously collected phytoplankton samples from a station within the path of the plume show an abundance of *Nodularia*, a cyanobacteria genus specific to lower salinities and therefore cells that must have been exported from Farmington Bay (unpublished data, Wurtsbaugh and PhycoTech Inc. 2010). However, cyanobacteria is generally thought to be poor food quality for invertebrates (Nogueira 2006), so it is possible this organic nutrient export from Farmington Bay may not be available to the brine shrimp. Contrasting reports exist as to whether *Nodularia*—especially slightly decomposed filaments—is detrimental to filter feeders, or whether there is no correlation (Gorokhova 2009).

The exported phytoplankton in the Farmington Bay plume differ in species composition from the underlying Gilbert Bay water because the initial growth conditions vary, limiting which species are able to grow in each area (Stephens and Gillespie 1976). By combining phytoplankton types and densities with additional data from isotopic analysis on field brine shrimp and water column seston, we can better understand how phytoplankton export from Farmington Bay to Gilbert Bay is an important food source for brine shrimp. My hypothesis was that I would find more palatable species further from Farmington Bay, but that production of *Artemia* close to the causeway would still be higher because of the high nutrient input.

STUDY AREA AND METHODS

Study Area

On Thursday September 30th, we sampled seven stations along the plume (Figure 1). The stations were picked from the extent of the plume seen in MODIS satellite imagery in other years. At each station, a second site about 100-250 m away from the first was sampled for replication. The sixth station was sampled first, in the open pelagic area of the lake, where mean lake depth was 7 meters. From this far point, 5 more stations were selected on a path back towards the causeway. An additional site (Station 0) on the south side of the causeway in Farmington Bay was selected and sampled as a reference.



Sta	Rep	Station Depth (m)	Latitude	Longitude	Distance From Farmington Bay (km)
0	a	0.80	41° 03' 57.9"	-112° 13' 48.4"	0.00
1	a	1.00	41° 04' 04.6"	-112° 13' 57.9"	0.25
1	b	0.90	41° 04' 08.1"	-112° 13' 54.3"	0.25
2	a	1.40	41° 04' 21.0"	-112° 14' 10.4"	0.92
2	b	1.40	41° 04' 16.6"	-112° 14' 20.2"	0.92
3	a	1.50	41° 04' 28.0	-112° 14' 45.9"	1.65
3	b	1.40	41° 04' 34.1"	-112° 14' 39.7"	1.65
4	a	1.80	41° 04' 38.9"	-112° 15' 20.9"	3.00
4	b	2.20	41° 04' 44.7"	-112° 15' 19.8"	3.00
5	a	1.80	41° 04' 41.3"	-112° 15' 58.1"	7.20
5	b	1.80	41° 04' 48.3"	-112° 15' 50.2"	7.20
6	a	7.25	41° 04' 28.6"	-112° 25' 18.5"	13.30
6	b	7.30	41 04' 26.2"	-112° 25' 19.0"	13.30

Figure 1—Map of Farmington and Gilbert Bay showing the location of the sampling stations used in the plume study.

Phytoplankton and Isotopic Analyses

At each site, Secchi depth and station depth were recorded using a Secchi disk and measuring tape. At two depths per site, a phytoplankton sample was taken either by dipping 125-mL bottles into surface water or using a Van Dorn bottle to collect water 0.3 above the lake bottom at each site. These samples were preserved using 3% formalin (variation of Lind 1985).

Phytoplankton identifications and counts were done using oil immersion lens on an inverted compound at 1000X without epifluorescence capability, so picoplankton were not analyzed. I counted random fields of subsamples settled using an Utermöhl settling chamber base until total enumerated cells were greater than 100, or until 100 fields had been counted. I recorded the lengths and widths data of ten random cells of each taxon using eyepiece units, which were subsequently converted to micrometers. Lengths and widths were transformed into biovolumes using equations in Hillebrand et al. (1999), as modified by Sun (2003). I made note of any abnormalities in cell shape, to estimate visually the degradation of cells from Farmington Bay in the higher salinity of Gilbert Bay. For Station 1, densities and biovolumes were calculated using replicate A for cyanobacteria and replicate B for all other cells at the shallow depth. This was because I settled a larger volume for replicate B, so it was more accurate. However, in this large sample *Nodularia* floated to the top of the settling chamber, which was out of scanning view.

For the isotopic analyses we used a Van Dorn bottle to collect water and a 250 µm net to collect zooplankton samples. To concentrate seston (particulate organic matter) we filtered water samples on AE Gelman filters. The samples were sent to the UC Davis Stable Isotope Facility for analysis of total C/N and dN15/dC13. See chapter by A. Montrone for further details of the isotopic analysis.

Algal Pigments and Salinity

At both the deep and shallow depth for both sites at each station, a water sample was taken in acid-washed, DI rinsed 125 mL bottles. Bottles were stored in dark coolers on ice and analyzed within 24 h. We measured phycocyanin fluorescence in a Turner 10AU fluorometer (Tuner Designs 2008) using pseudo-triplicate readings of a single cuvette taken from each sample. Chlorophyll samples were filtered, frozen, extracted, and read on the 10-AU Turner fluorometer using a variation of the Welschmeyer method (Welschmeyer 1995. EPA Method 445.0). Salinity was read in the laboratory from water samples, using a refractometer.

RESULTS

Station depths along the transect moved from shallower (about 1 m for Stations 0 and 1) to deeper (7.3 m at Station 6). The salinity data measured at each station along the transect showed a distinct gradient. Between Station 0 and 1 the surface salinity (measured at 0.2 m) jumped from 2.0% to 13.2%. After Station 1, the salinity leveled off to reach 15% at Station 6. Chlorophyll and phycocyanin data showed a similar trend along the transect, with high levels in Farmington Bay, and decreasing exponentially along the plume (Crawford, this report).

The biovolume of cells dropped from a total of more than 12 million um^3/mL at Station 0 in Farmington Bay, to 4.05 million um^3/mL at Station 1 in Gilbert Bay (figure 2). The volume lost was in mainly in cyanophytes; the biovolume of chlorophytes slightly increased. The remainder of the stations had much lower biovolumes, with a high of 1.1 million um^3/mL at Station 3 before dropping to .001 million um^3/mL at Station 6. A list of the different taxa identified can be found in Table 1.

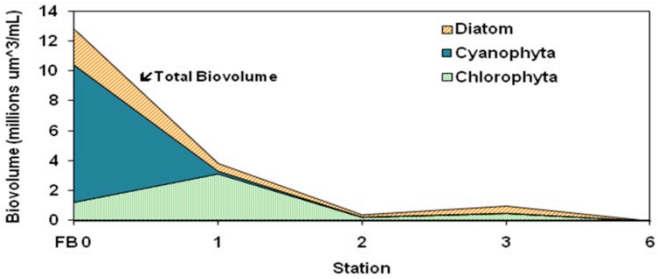


Figure 2—Biovolume of phytoplankton cells at shallow depths for stations across a transect of the Great Salt Lake plume. Top line represents the total biovolume for a given site. The biovolumes of Division pyrrophyta and unknown cells were less than 0.2% and 10% of total at Stations 1 and 3, respectively, and so were excluded this figure.

Taxa Identified

Division	**Genus sp.**
Chlorophyta	*Carteria*
	Dunalielia viridis
	Oocystis
	Pediastrum
	Unknown
Cyanophyta	*Microcoleus*
	Nodularia (vegetative cells)
	Nodularia (Heterocysts)
	Spirulina
Bacillariophyta	*Amphora c.*
	Chaetocerous
	N. epithemoides
	Navicula
	Nitzschia
	Nitschia accicularis
	Unknown
Pyrrophyta	Unknown

Table 1—Phytoplankton taxa identified in Farmington Bay and Gilbert Bay, Great Salt Lake samples, 30 Sep. 2010.

Total algal biovolume was significantly correlated with chlorophyll *a* concentrations (figure 3; r2 = 0.88, p = 0.0005), indicating that the more numerous chlorophyll measurements do provide a good measure of the amount of algae available for brine shrimp grazers. The cyanobacterial pigment, phycocyanin, was significantly correlated with the biovolume of cyanobacteria (figure 4 3; r2 = 0.83, p = 0.0017) indicating that this pigment can be used to estimate the abundance of this taxa.

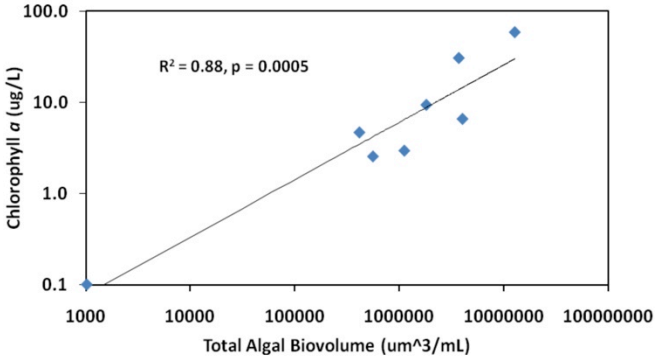


Figure 3—Relationship between algal biovolume and chlorophyll a levels at 8 sites along a trophic gradient from Farmington Bay into Gilbert Bay of the Great Salt Lake. Note the log-log plot.

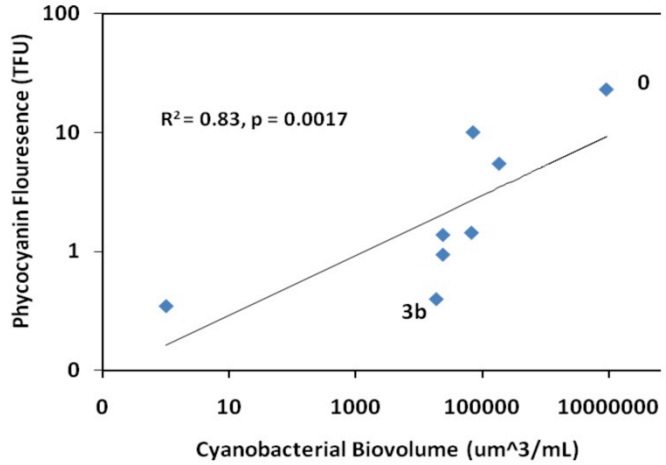


Figure 4—Relationship between cyanobacterial biovolume and phycocyanin levels at 8 sites along a trophic gradient from Farmington Bay into Gilbert Bay of the Great Salt Lake. Note the log-log plot.

Cell densities were 225,000/ml in Farmington Bay, but dropped rapidly with increasing distance from the discharge point into Gilbert Bay (figure 5). The density and biovolume of *Nodularia* relative to other species and relative to salinities along the transect is shown in Figure 6. The salinity increased to greater than 7% before Station 1 and *Nodularia* densities dropped, but did not disappear altogether. The presence of empty and degraded *Nodularia* increased from none present at Station 0 in Farmington Bay to only detrital pieces at Station 6.

The results of an isotopic analysis mixing model for *Artemia* to estimate the percent of Farmington Bay derived carbon and nitrogen can be found in the chapter by Ashton Montrone. Greater than 50% of these nutrients in *Artemia* at Station 1 were derived from Farmington Bay sources, and around 30% at Station 6. Station 1 b was determined to be an outlier and was removed for statistical analysis, which returned $p<0.001$ and $R^2>60$ for regressions of both C and N.

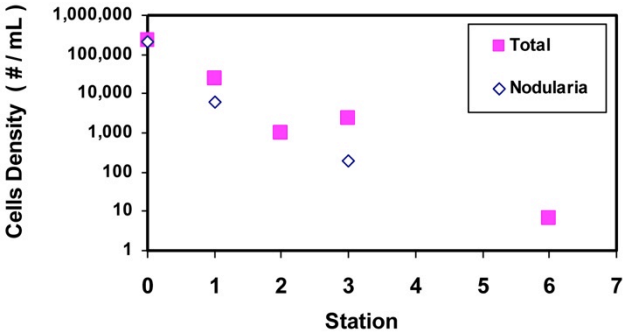


Figure 5—Densities of all algal taxa and those of Nodularia along the Farmington Bay eutrophication plume extending into Gilbert Bay.

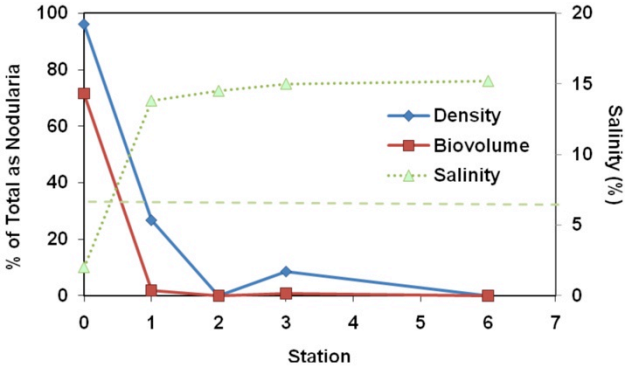


Figure 6—Percent of total cell density and biovolume present as Nodularia, and salinity at shallow sites across a transect of the Great Salt Lake Farmington Bay plume. Dashed horizontal line represents salinity at which Nodularia no longer fix N2 or grow (Marcarelli 2006).

DISCUSSION

The biovolume calculated for the Farmington Bay site and the subsequent decrease is similar to results for the Suwannee River in Florida where it empties into the Gulf of Mexico (Bledsoe 2000). For sites close to the causeway opening (within 1 km) Farmington Bay export is clearly impacting the local algal flora. However, when discharges are higher (e.g. spring), remote sensing data suggest that Farmington Bay may influence sites more distant from the discharge (Wurtsbaugh et al. 2008).

Food quality appears to vary along the plume. At Station 1 in Gilbert Bay, the abundance of chlorophytes represent a good food source for *Artemia*, based on other studies. Sick (1976) found that *Dunaliella viridis* were a nutritious food source for *Artemia salina*. It is likely that another abundant chlorophyte, *Oocystis*, is also a good food source. Vanni (1992) found that Daphnia would feed on *Oocystis* once they were large enough, which would be a less limiting factor for the larger *Artemia*.

A study done on food preference for *Artemia franciscana* indicated that *Artemia* at all life stages selected for food particles that were 3-8 µm (Makridis 1999). This is the size of the common chlorophytes and diatoms in the Great Salt Lake, but smaller than the filamentous phytoplankton, such as *Nodularia*, *Microcoleus*, and *Spirugina*. As part of my notes for anomalies within samples, I noted high numbers of cells in the shed carapace filtering limbs of *Artemia*, but only at Station 2 and beyond. The algal cells in the filtering limbs were not representative of the whole sample, but rather were in only two Divisions (Chlorophyta and Bacillariophyta), and within those, four species (mainly *D. viridis).* It is possible that these highly palatable cells grow in the discarded carapace in order to escape grazing pressure (Gliwicz et al. 2010).

There was a significant amount of *Nodularia* at Station 1, but these cyanobacteria may not be growing there. Marcarelli et al. (2006) provide evidence that N_2 fixation and growth of cyanobacteria from Farmington Bay ceases at salinities greater than 7%. I noted the presence of degraded *Nodularia* filaments at Stations 1-6: at Stations 3 and 6, 100% of the *Nodularia* was a degraded form.

At the distant sites phytoplankton densities were extremely low, particularly those of *Nodularia*, but this does not rule out the importance of cells exported from Farmington Bay. It is still possible that the nutrients from the cells are incorporated into the food web as the cells degrade due to the increased salinity and release labile nutrients that can be used by other plankton. Also, our samples represents a single point in time when grazing rates were high (up to 25%/day) due to high densities of brine shrimp, so any cells exported were rapidly consumed (J. Wight, this report). Two weeks

prior to our sampling excursion, mean Secchi depths in Gilbert Bay were only about 0.7 m and chlorophyll levels were near 20 µg/L (personal communication, P. Brown, DWR), but the distant stations in during our sampling had Secchi depths >3.5 m and chlorophyll levels < 2 µg/L, indicating the high grazing by shrimp had cleared the water column. Consequently, a plume of phytoplankton from Farmington Bay might have extended further into Gilbert prior to our visit. Unfortunately, efforts to detect the plume with MODIS satellite imagery were unsuccessful.

Evidence of Farmington Bay phytoplankton being used by the zooplankton in Gilbert Bay can be seen through isotopes. Coincident isotopic analysis of *Artemia* and seston samples from the transect suggested that in the food of brine shrimp originating from Farmington Bay was still 30% at Station 6, based on a nitrogen mixing model, but 0% based on a carbon mixing model (See Montrone, this report). The density of algal cells and the chlorophyll levels we found at the further stations on the date we sampled were very low, indicating that the growth rates of the shrimp then would have been limited by the low food levels. With low overall food in the pelagic zone, any phytoplankton exported from Farmington Bay would have had extra significance. It is also likely that most of the shrimp growth and biomass accumulation occurred prior to our sampling, and we do not know the nature of the plume then.

Although the relationship between the cell biovolumes and their associated pigments is not one-to-one, it is a strong relationship with R^2 >0.80 for both pigments. The strong relationship between the sites that were analyzed and their measured pigment data show that even with a small data set of counts, the total algal biovolume and cyanobacterial biovolume correlates to the respective trends in chlorophyll and phycocyanin data. Because chlorophyll and phycocyanin data exist for each station, their cell abundances can be inferred.

Phytoplankton densities found in 2009 by Wurtsbaugh (unpublished data) in areas close to Station 6 were 16,000-200,000 cells/mL, which are much higher than the density I estimated. For the Secchi depth at Station 6 (3.5 meters), the densities I found were extremely low. Nevertheless, the algal counts from the surface water at Station 6 were consistent with the extremely low chlorophyll levels found at that depth (figure 2). Chlorophyll concentrations were greater and consistent with Secchi depths in mid-water and deep samples at Station 6 (see Crawford, this report). Apparently, the upper 0.2 m of water at the distant station was depopulated with respect to phytoplankton, perhaps because of heavy grazing there. Gas vacuoles, particularly those in *Nodularia*, could have impacted the accuracy of my field sampling, as I collected beneath the surface film. However, wave action from wind turbulence likely prevented all *Nodularia* from rising to the surface and no surface scums were visible. Gas vacuoles were not burst before settling in the Utermohl chambers prior to counting. At Station 1 replicate B, I noticed a large number of strands entrained in the neuston layer. These cells were easily counted when a small volume (1 mL) was used, but were out of scanning view for the taller settling chambers used to settle larger volumes. Field densities of *Nodularia* at further stations would have been low, and I also tapped on subsequent samples to check for the presence of *Nodularia*, so errors were likely small.

My results demonstrate the importance of phytoplankton and nutrients being exported from Farmington Bay for *Artemia* feeding in Gilbert Bay. However, during our September sampling trip, elevated phytoplankton biovolume was only noted at the Gilbert Bay station within 0.25 km of the Farmington Bay discharge. By Station 2, only 0.9 km distant from Farmington Bay, cell biovolume had decreased to quite low levels, suggesting that at the time of our sampling trip, Farmington Bay was having a limited impact. However, isotopic evidence presented latter in our class report suggests that the plume may have extended further into Gilbert Bay and provided food for brine shrimp. Clearly, additional samples over time are needed for a more conclusive understanding and quantitative estimate of how Farmington Bay nutrients exported through the causeway impact production in Gilbert Bay.

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Farmington Bay Plume Influence on Brine Shrimp Distribution, Survival and Growth in the Great Salt Lake

Jaclyn Wight

SUMMARY

To study the influence of hypereutrophic water from Farmington Bay on brine shrimp, six stations were sampled along the discharge plume extending 13 km into Gilbert Bay of the Great Salt Lake, Utah. All sampling for this study was conducted on 30 September 2010, including 18 samples of brine shrimp and the collection of water used in an *Artemia* growth experiment. Although chlorophyll levels declined markedly from sites close to Farmington Bay out into the pelagic zone, brine shrimp biomass more than doubled along the plume, from 69 mg/L to 139 mg/L, while *Artemia* density more than tripled, from 1.2 individuals/L to 4.0 individuals/L. Estimated community grazing rates by *Artemia* at stations close to Farmington Bay were 5%/day, but increased to ca. 13%/day at the most distant station sampled. The gradient in brine shrimp distribution was inversely correlated with the gradient of chlorophyll α.

A 14-day bioassay testing survival and biomass production in different ratios of Gilbert and Farmington Bay water supported the link between brine shrimp biomass and chlorophyll α. Survival and biomass production of nauplii were greatest in a mixture of 50% Gilbert Bay and 50% Farmington Bay water in the experiment. Organic matter exported from Farmington Bay may have a positive influence on brine shrimp within the plume in Gilbert Bay, but on the date we sampled, the extent of the positive impact was limited.

INTRODUCTION

Farmington Bay hosts massive algal blooms due to high levels of nutrient input from waste water treatment plants surrounding the lake (Wurtsbaugh and Marcarelli 2006). Farmington Bay water mixes with Gilbert Bay water as it travels through a causeway near Antelope Island (Gliwicz et al. 1995). The influence of the algal plume stemming from Farmington Bay may be understood through the plume's interactions with *Artemia franciscana*, an abundant species of zooplankton in Gilbert Bay. *Artemia*, or brine shrimp, have access to algal food resources because of the mixing occurring between Farmington Bay and Gilbert Bay.

Brine shrimp are an important economic resource of the Great Salt Lake. The harvest of brine shrimp cysts alone often reaches millions of kilograms annually (Wurtsbaugh and Gliwicz 2001) and is worth around $100 million annually (Goel and Myers 2009). Therefore it is important to understand how *Artemia* are interacting with the Farmington Bay plume. Brine shrimp can control the amount of algal biomass through grazing, or conversely may be controlled by the amount of algae available (Wurtsbaugh and Gliwicz 2001; Wurtsbaugh et al. 2008). Whether or not the shrimp utilize the plume as a food resource has had little attention (unpubl. UDWQ Request 2010). However, one isotopic analysis suggested that brine shrimp do consume algae in varying amounts from Farmington Bay during different seasons (Naftz et al. 2008), but a second isotopic analysis was inconclusive (Wurtsbaugh et al. 2008).

One factor that may affect the distribution of *Artemia* along the plume is the amount and type of algae offered at different distances from Farmington Bay. There are several species of algae available to feed on: Two species of algae from the *Dunaliella* genus, one species from the genus *Oscillatoria*, and one from the genus *Coccochloris* (Post 1977). In addition to these, Farmington Bay also hosts a species of cyanobacteria, *Nodularia*. *Nodularia* is the most abundant form of algae in Farmington Bay; however this species does not do well in salinities greater than about 5%, so it will not grow in Gilbert Bay (Marcarelli et al. 2006). Also, *Nodularia* is thought to be a poor food resource for brine shrimp (Wurtsbaugh and Marcarelli 2006). Therefore a gradient of food quality will form as algae moves from fresher water in Farmington Bay to highly saline water in Gilbert Bay.

This study tested several hypotheses. The foremost hypothesis is that the abundance of brine shrimp will increase along the plume. Because the water from Farmington Bay disperses and spreads out as it leaves the causeway into Gilbert Bay, there will be gradients in the chemistry and food quantity and quality along the

plume. I hypothesized that the distribution of brine shrimp will reflect these gradients: The abundance, health, and biomass of the shrimp will increase as the plume spreads from the source into Gilbert Bay. Abundance and distribution of brine shrimp is likely linked to the food source.

Another hypothesis this study tested was that the nutritional quality of the plume is low. Because *Nodularia* does poorly in highly saline environments, and because it is thought of as a poor food resource, the nutritional quality of the plume should increase when moving away from the Farmington Bay source, as cyanobacteria becomes less abundant. This lends credibility to the prediction that the brine shrimp will feed, and appear in higher densities, at areas further from Farmington Bay rather than close to the causeway. I hypothesized that abundance of *Nodularia* will decrease as distance from Farmington Bay increases, and so food quality will increase. In this study, the main nutritional factor considered was chlorophyll α in respect to abundance and biomass of *Artemia*, while a companion study by Wilcox (this report) focused more on the health of *Artemia* in relationship to the plume.

Alternatively, there could be no relationship, or there are other limiting factors affecting shrimp distribution along the plume. Salinity could be one of these limiting factors. Though *Artemia* are able to tolerate a wide range of salinities, they are often not found in high densities in environments with lower salinities than that of Gilbert Bay (Wurtsbaugh and Gliwicz 2001). This is due mainly to their poor competitive abilities and higher predation in lower salinity waters. Predation is also a possible factor affecting brine shrimp distribution. The invertebrate *Trichocorixa* may keep the brine shrimp from consuming the plume. *Trichocorixa* is the dominant brine shrimp predator in the Great Salt Lake, and thrives in the fresher waters of Farmington Bay (Wurtsbaugh 1992). Even if food quality throughout the plume is high, other variables may impact brine shrimp distribution.

This importance of the plume for brine shrimp was further tested in a bioassay experiment. I hypothesized that brine shrimp would have a higher percent survival and greater biomass production in treatments of water mixtures containing a greater proportion of Gilbert Bay water. If the food quality of the phytoplankton from Farmington Bay is low, then this outcome is possible. If the food quality of the plume is high, survival and biomass may alternatively reflect the value of the Farmington Bay resource in the bioassay.

If the food quality of the plume is high, contrary to my prediction, then it is possible for grazing by brine shrimp to act as a top-down control on the size of the algal plume. If this is true, there will be high densities of shrimp in the plume feeding, and less of a distributional gradient along the gradient of the plume, assuming nutrient quality is equal along the plume.

Photo 1—Sampling brine shrimp.

METHODS

Study Area and Field Study

The Great Salt Lake is broken up into four main bays. Each bay has a unique composition of salinity, nutrients, and biota (Wurtsbaugh et al. 2008). The bays included in this study were Farmington Bay and Gilbert Bay. The low salinity in Farmington Bay, as well as high nutrient input, allow for massive algal blooms that flow out into Gilbert Bay (Wurtsbaugh and Marcarelli 2006). Farmington Bay water and algae are exchanged with Gilbert Bay water through a causeway near Antelope Island. Satellite imagery confirms the presence these algal plumes into Gilbert bay on many occasions (Wurtsbaugh et al. 2008).

Samples for analysis were collected at six different stations in the Gilbert Bay arm of the Great Salt Lake on 30 September 2010 (photo 1). The sample stations stretched across 13 km, from the causeway leading from

Farmington Bay into Gilbert Bay. Replicate samples were collected at each station after moving the boat 100-300 m. A total of 18 samples were collected (photo 2). A zooplankton tow net 30 cm in diameter and a mesh size of 250 µm was used for 12 of the samples, two at each of the six stations. Each sample was collected from 0.1 m from the lake bottom and towed vertically to the surface. Six additional samples were collected with an 8 L Van Dorn bottle at Station 3, at depths near the bottom of the lake (0.1 m from the bottom), halfway through the water column (near 0.7 m), and just below the lake surface (0.2 m deep). Between samples the zooplankton net and the Van Dorn bottle were rinsed twice with a wash bottle of lake water. The zooplankton were preserved in clean 250 mL screw cap plastic bottles with 3-4% formalin.

Photo 2—Bioassay containers.

Preparation for a laboratory experiment included collection of Gilbert Bay and Farmington Bay water. First 10 L of water was collected in Farmington Bay near the bridge over the causeway, filtered to remove zooplankton, and stored in a clean Cubitainer for the bioassay. Next 10 L of Gilbert Bay water collected and filtered at Station 6 (replicate A) and stored in a clean Cubitainer for the bioassay. They were placed in a cooler for the remainder of the sampling time to inhibit further phytoplankton production.

Laboratory Processing and Bioassay

All zooplankton were measured at 15x magnification on a Meiji dissecting microscope. The samples were subsampled to give minimum counts of 30 individuals. The lengths of brine shrimp were recorded for the first ten males, females, juveniles, and nauplii found. The entire subsample was counted and broken up into the same four groups; male, female, juvenile and nauplii. After every sample was measured, the lengths (L) were used to estimate dry weight using the formulas $W=3.14L^{0.56}$ for *Artemia* nauplii and $W=0.90L^{3.02}$ for *Artemia* post-nauplii (Wurtsbaugh 1992). The count and length data was also used to estimate filtering rates (FR; ml individual/day) of the brine shrimp according to the formula: $FR=5.45L^{1.82}$ (Wurtsbaugh 1992). The analyses were performed in Excel.

To test brine shrimp nauplii survival and biomass production in Gilbert Bay water, four treatment waters were mixed using the 10 L of Farmington Bay and 10 L of Gilbert Bay water collected during the field sampling. The experiment was conducted in white translucent plastic containers (1.3 L). The four treatments that each consisted of a total of 1 L of water were: 100% Gilbert Bay water, 75% Gilbert Bay and 25% Farmington Bay, 50% of each water, and 25% Gilbert Bay and 75% Farmington Bay. There were two replicates of each treatment. The water in the Cubitainers was homogenized before pouring out into the treatment containers. Great Salt Lake brine shrimp nauplii were hatched from cysts in the lab, and 20 nauplii were placed in each 1 L container. The experiment was run in a controlled temperature room for 14 days, at a mean temperature of 24.6˚ C (range 22.7˚ C to 25.3˚ C). Lighting in the room was at 150 uE/m2/sec on a 16:8 light-dark cycle. After 14 days the brine shrimp were collected and preserved in 3-4% formalin. All of the bioassay shrimp were measured and counted the same way as the field samples. Additionally, chlorophyll data was collected halfway through the experiment (day 7) and on the final day (day 14). The initial chlorophyll values (day 1) were estimated based on chlorophyll data collected during field sampling in Farmington Bay and Gilbert Bay Station 6, where the cubitainers were filled. The survival and biomass accumulation data from the bioassay,were tested with ANOVA in Excel. The ANOVA tested, in general, whether Gilbert Bay or Farmington Bay water was a preferred food source for brine shrimp.

RESULTS

Artemia Distribution

The highest overall *Artemia* biomass and density occurred at Station 6. When looking at the life stages of brine shrimp separately, Station 6 had the greatest density for all life stages (figure 1). This was also true for biomass, separated into life stages (figure 2). Station 3 had the lowest overall biomass and density. A

regression analysis showed an obvious trend indicating an increase in both biomass and density as distance from Farmington Bay increased (appendix 1). Specifically, density increased nearly three-fold from Station 1 to Station 6 from 2.4 individuals/L to 4.0 individuals/L. Biomass also increased from 69 mg/L to 188 µg/L, more than a two-fold increase from Station 1 to Station 6. Statistically the relationship between *Artemia* biomass and distance from Farmington Bay was strong (R^2=0.61, p=0.003).

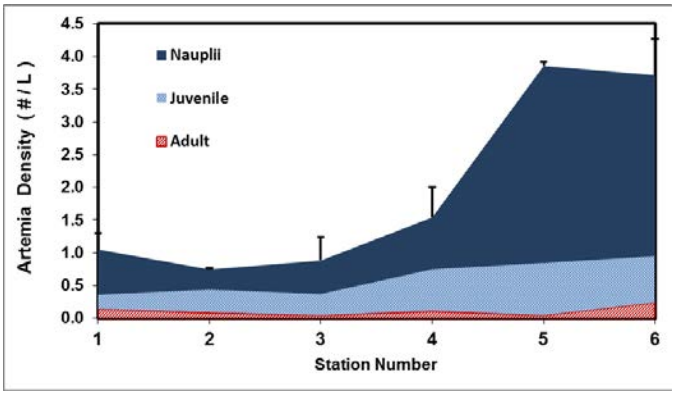

Figure 1—*Artemia* density by life stage, given in individuals/L, at each station along the Farmington Bay (Station 1) to pelagic (6) transect in Gilbert Bay. Error bars show s.d. for the sum of all life stages

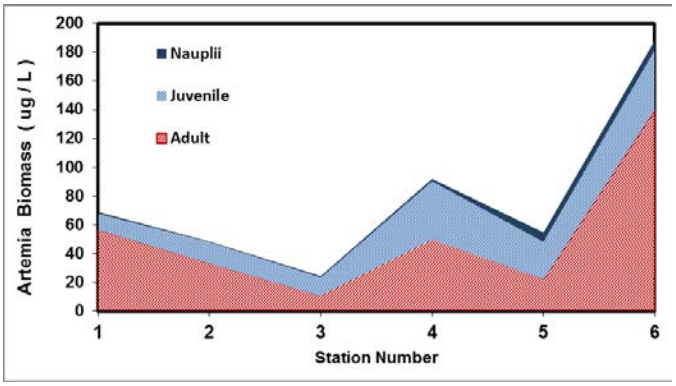

Figure 2—*Artemia* biomass by life stage, given in µg/L, at each station along the Farmington Bay (Station 1) to pelagic (6) transect in Gilbert Bay.

The increased *Artemia* biomass led to p = 0.02) increased community grazing rate in the pelagic zone (figure 3). The grazing rates more than doubled, from 5% of the water column per day at Station 1, to 13% of the water column per day at Station 6 (figure 3). As brine shrimp biomass increased, chlorophyll decreased by a factor of four (figure 3). However, there was not a significant relationship between grazing rates and chlorophyll α (figure 4; p=0.11)

In addition to distance and chlorophyll, this study also examined the vertical distribution of brine shrimp in relation to the Farmington Bay plume. The depth samples collected with the Van Dorn bottle at Station 3 were used for a regression analysis testing the relationship between depth and *Artemia* biomass. Overall, brine shrimp biomass decreased by 50% with increasing depth and this relationship was marginally significant (p=0.06).

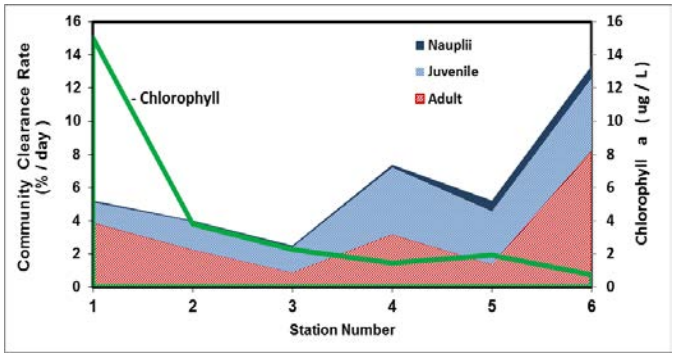

Figure 3—Estimated community filtration rates by *Artemia* (area plot, left axis) and chlorophyll concentrations at each station along the 13 km plume gradient in Gilbert Bay.

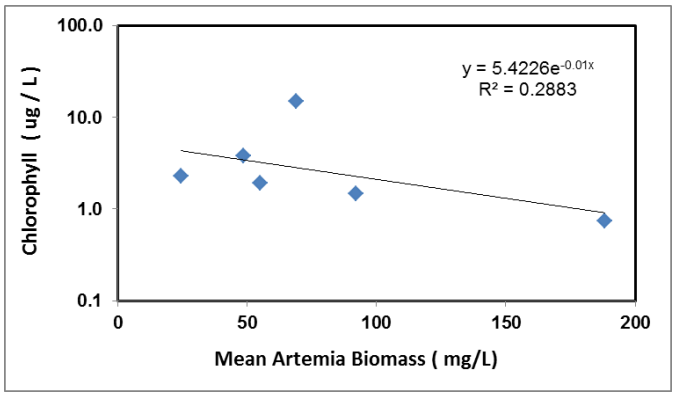

Figure 4—Relationship between mean *Artemia* dry biomass in each sample along the plume transect and mean chlorophyll concentrations (µg/L).

Bioassay

The result of the bioassay showed *Artemia* survived and grew best when Farmington Bay water was mixed with that from Gilbert Bay (figure 5). The treatment with the highest average survival of 80%, with an average of 16 remaining individuals, was a mixture of 50% Gilbert Bay water and 50 % Farmington Bay water. The treatment with the lowest survival of only 7% was in 100% Gilbert Bay water. Survival was significantly different between treatments (ANOVA; p=0.0001). The *Artemia* also grew best in the 50/50 mix of Farmington

and Gilbert Bay water. At the end of the 14 day experiment individual dry weights in these treatments were over 300 µg/L, compared to <200 µg in all other treatments. The total biomass was also highest in the 50/50 mix, with over 5000 µg/L. Biomass production was particularly low in the 100% Gilbert Bay treatment, with only moderate growth and a mean survival of only 7%. Biomass production was significantly different between the treatments (ANOVA; p=0.03).

The bioassay demonstrated the importance of grazing for controlling algal levels. In treatments with high survival of nauplii chlorophyll levels declined markedly by day 7 and remained low (figure 6). Conversely, treatments with low nauplii survival showed an increase in chlorophyll over time, with concentrations reaching over 50 µg/L.

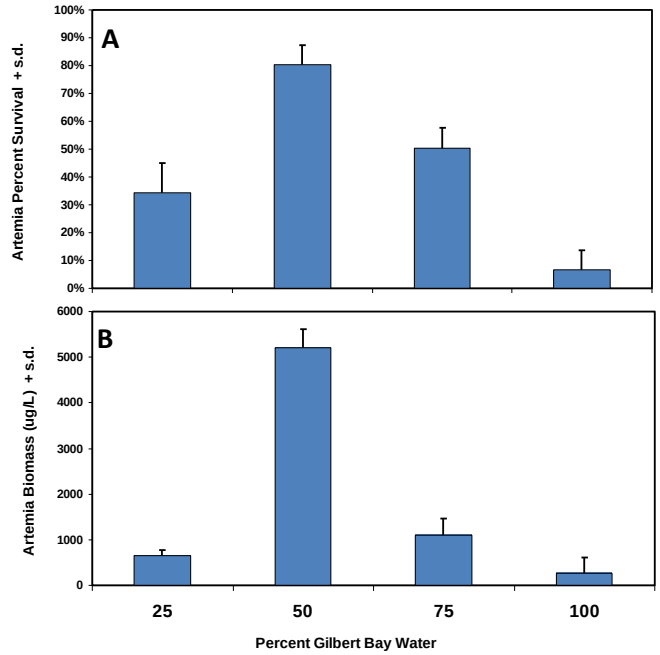

Figure 5—(A) Percent survival of *Artemia* nauplii in each treatment of the bioassay with mixed percentages of Farmington Bay and Gilbert Bay water, (B) The final biomass of *Artemia* in each treatment. Error bars show standard deviations of the two replicates.

DISCUSSION

There was a strong gradient of *Artemia* distribution in Gilbert Bay along the algal plume. As distance from Farmington Bay increased, *Artemia* biomass increased. The cause of this gradient, however, is not as clear. Depth was shown to be a factor in brine shrimp distribution vertically, however not a very important one. This is likely because the depth samples were collected only at Station 3. So the lake-wide application of this relationship is not advised. Further sampling would be needed to better test this relationship.

Because no corixids were found in any of the samples collected, one may say that predator density is not controlling the gradient in *Artemia* for the sampling period. However, corixids were a major predator on brine shrimp in the Great Salt Lake when salinity is less than 5% (Wurtsbaugh 1992). Even though their presence, or lack thereof, does not explain brine shrimp distribution in Gilbert Bay in this study, it very well could when conditions are more favorable for the corixids.

Chlorophyll appeared to be an important factor in brine shrimp distribution. Which variable is the independent one in this situation is difficult to delineate though. There have been recorded periods of grazing in the Great Salt Lake where the brine shrimp control the amount of phytoplankton in Gilbert Bay, as the population grows and feeds (Wurtsbaugh and Gliwicz 2001; Wurtsbaugh et al. 2008). However, during my survey grazing rates increased as distance from Farmington Bay increased, even though chlorophyll α was less abundant. There was some factor keeping the brine shrimp from consuming the abundant food in the plume close to the causeway.

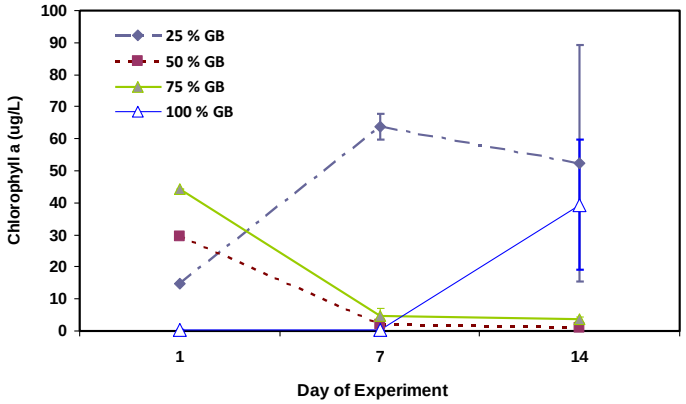

Figure 6—Chlorophyll a concentrations in the bioassay experiment with varying proportions of Gilbert Bay (GB) and Farmington Bay water. Error bars show +-s.d. except for the first date (day 1) when these amounts were estimated from Great Salt Lake measurements.

The bioassay provided insight to the chlorophyll relationship. *Artemia* survived the best and grew the most in the treatment of 50% Gilbert Bay and 50% Farmington Bay water. The observation that brine

shrimp did quite poorly in 100% Gilbert Bay water (survival was 0 individuals and 2 individuals for each replicate of this treatment) indicates that food levels were extremely limited for nauplii because the water was collected from a low chlorophyll level in the lake where adult grazing rates were high. Under these low-food conditions, Farmington Bay plume is like providing a valuable food resource in the low-chlorophyll areas of Gilbert Bay. However, because the brine shrimp did not do best in the 75% Farmington Bay–25% Gilbert Bay treatment there must be a restrictive factor in the Farmington Bay water, or else we would expect the brine shrimp to have done even better in this treatment than the 50% treatment.

It is interesting to note that the decrease in chlorophyll was linked to the survival of *Artemia* in the bioassay. This pattern mimics, to some degree, what was observed for Gilbert Bay. On September 13th, the Utah Division of Water Quality obtained samples of chlorophyll, and noted that they were higher (20 µg/L at pelagic stations, i.e.Station 6) than our chlorophyll samples were on September 30th (less than 1 µg at Station 6). A new stock of brine shrimp may have grazed down the plume the weeks prior to our sampling date, as they did in the bioassay.

Where does *Nodularia* come in? Schmidt and Jonasdottir (1997) found that this cyanobacteria was not a healthy food resource for copepods when in bloom. However, this study also found that as *Nodularia* blooms decompose, and colonization by smaller organisms increases, this food resource is utilized more frequently by copepods. The bioassay experiment reflects these findings to some degree. It could be that the increased amounts of *Nodularia* in the 25% Gilbert Bay water treatment remained healthy, without significant breakdown in the two-week period, to provide a substantial food resource to the nauplii. The combined 75%/25% Farmington/Gilbert water would have had a salinity of ca. 5%, which would have allowed survival and perhaps growth of the *Nodularia* (Marcarelli et al. 2006). In contrast, the salinities in treatments with higher proportions of Gilbert Bay water would have been too high for *Nodularia* to survive (Marcarelli et al. 2006) and they may have decomposed. What aspects of *Nodularia* that limits this algae's value as a food resource is unclear, though studies suggest it could be that it lacks the molecules that support zooplankton growth (Schmidt et al. 2002). Additionally, it could be the filamentous character of the algae, or it could be the toxin it produces (Twist and Codd 1997).

Other studies provided alternative explanations for zooplankton distribution in areas with gradients, like the Farmington Bay plume. In the Mississippi River and Columbia River plumes, zooplankton distribution depends on the interaction between fresh and salt waters (Grimes and Finucane 2001; Morgan et al. 2005). As fresher Farmington Bay water spills into Gilbert Bay through the causeway, the water runs over the top of the denser salt water, which was witnessed on the day of our sampling at Stations 1A and 1B. This water may push brine shrimp and other large zooplankton that get caught in the overflow current out and away from Farmington Bay. This would also explain high densities and biomass occurring at Stations 6A and 6B, and is what was found to occur in the Mississippi River and Columbia River plumes.

With any study, the statistical power of the results increases with number of samples. Because of time limitations on the sampling day and during the sample analysis, the number of samples was limited compared to what was initially desired. Therefore the conclusions of the results of this study are narrow in scope and applicability. However, they are still useful in describing the distribution of brine shrimp along the Farmington Bay plume in Gilbert Bay.

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Appendix 1—Summary Output Log Distance from Farmington Bay in km (X) vs. *Artemia* biomass in µg/L (Y)

Regression Statistics	
Multiple R	0.78
R Square	0.61
Adjusted R Square	0.57
Standard Error	146.28
Observations	12

ANOVA

	df	*SS*	*MS*	*F*	*Significance F*
Regression	1	338839.30	338839.30	15.83	0.00
Residual	10	213982.46	21398.25		
Total	11	552821.75			

	Coefficients	*Standard Error*	*T Stat*	*P-value*	*Lower 95%*	*Upper 95%*
Intercept	-81.46	80.55	-1.01	0.34	-260.94	98.01
log Distance from FB (km)	460.83	115.81	3.98	0.003	202.80	718.87

Physiological Health of Brine Shrimp along the Farmington Bay Eutrophication Plume in Gilbert Bay of the Great Salt Lake

Meagan Wilcox

SUMMARY

I determined the physiological health of adult brine shrimp in a 13-km long plume that extends out of Farmington Bay and out into Gilbert Bay of the Great Salt Lake. Vertical hauls with a zooplankton net were used to collect brine shrimp from six stations along the plume. Female brine shrimp from these stations were analyzed for lipid content and cyst and egg abundance. I found that as lipid droplets increased the brine shrimp had cysts instead of eggs. This conclusion corresponds with the idea that brine shrimp shunt their lipid droplets in order to produce live eggs. The highest amounts of lipid droplets were found in brine shrimp living closest to Farmington Bay where chlorophyll levels were high and the greatest amount of eggs were found in Station 5 and 6, 7 and 13 km from the Farmington Bay discharge into Gilbert Bay. A bioassay utilizing varying mixtures of Farmington Bay and Gilbert Bay water demonstrated that brine shrimp nauplii survived and grew poorly in either pure Gilbert Bay water or 75% Farmington Bay water, and did best in a 50-50 mixture of the two water sources (photo 1).

Photo 1—Image of four of the experiments from the experimental bioassay. Note the green color of the two containers on the left that had 75% and 50% Farmington Bay water, respectively.

INTRODUCTION

Brine shrimp, *Artemia franciscana*, are found throughout the world in different sizes and varieties of saline lakes (MacDonald and Brown 1990). The Great Salt Lake contains these brine shrimp in several bays, with an automobile causeway as a dividing line between two major bays I studied. These two areas of interest are Gilbert Bay and Farmington Bay. Farmington Bay receives waste loading from different surrounding sources in Salt Lake and Davis Counties, including sewer treatment plants (Wurtsbaugh and Marcarelli 2006). Farmington Bay is said to be one of the most polluted bodies of water in Utah (Marcarelli and Wurtsbaugh 2004). There are large fluxes of nutrients, cyanobacteria, and other phytoplankton from Farmington Bay and flowing as a plume into Gilbert Bay. It has not been determined whether this plume is harmful or beneficial to brine shrimp and other organisms there. The plume may be an important food source for these organisms, or extremely harmful.

Brine shrimp densities in Farmington Bay are usually lower than the densities found in Gilbert Bay. However, in the surface waters of Gilbert Bay, Marcarelli and Wurtsbaugh (2004) found low densities of brine shrimp, perhaps due to low food levels in the open water (Marcarelli 2004). Reasons for a smaller number of brine shrimp in Farmington Bay could be a result of 1) a large populations of predators, *Corixids Trichocorixa*, 2) a high hydrogen sulfide concentration and anoxia, or 3) high nutrient loading resulting in extreme eutrophication and poor water quality (Marcarelli and Wurtsbaugh 2004). Brine shrimp dominate food webs in hypersaline environments and have been introduced to areas of high salinity to control algal blooms because of their grazing capabilities, which results in clearer water (Sorgeloos et al., 1986). Macdonald and Browne (1990) showed experimental data recording a significant increase of water clarity and a decrease of an algal bloom in a pond, due to brine shrimp grazing, further clarifying the influence brine shrimp may have on bodies of water.

Brine shrimp are an important food source for waterfowl that live in and around the Great Salt Lake (Marcarelli and Wurtsbaugh 2004) and brine shrimp cysts are a valuable commercial resource and are collected yearly by the millions. The life cycles, reproductive output and inputs, and other fitness traits of brine shrimp have been studied. However, physiological and fitness status of the shrimp in the Great Salt Lake have not been studied in detail. The health and survival of brine shrimp are imperative for the health of the Great Salt Lake and are indicators of the physiological standing of other species. The physiological health and the number of cysts compared to eggs of the brine shrimp also relate to the condition of the lake; when food resources are high, live eggs will be produced by the females, and when resources are low or conditions are unfavorable, the females will produce dormant cysts (Gliwicz and Wurtsbaugh 2001). Wurtsbaugh and Gliwicz (2001) found that the number of lipid droplets in brine shrimp females decreased from spring through the late fall, and that this decrease paralleled a decrease in the C:N ratio.

The focus of my research was to use the number of lipid droplets, eggs, and cysts of adult brine shrimp to determine their physiological health in the plume that extends out of Farmington Bay and into Gilbert Bay. A bioassay was also performed to determine the whether or not brine shrimp nauplii found the Farmington Bay water suitable for growth. Field data was collected from the Great Salt Lake at six stations along the Farmington Bay plume extending into Gilbert Bay. An experiment was also done to determine whether or not the plume is beneficial or harmful to brine shrimp. If the plume is beneficial, we would have expected to find high brine shrimp densities in the area along the plume with a significantly high number of lipid-droplets and ovoviviparous eggs. The hypothesis of this research was that the brine shrimp will not be found in high densities near the plume from Farmington Bay due to toxicity and/or poor algal food quality from the water discharging into Gilbert Bay. Brine shrimp will be found in higher densities further away from the plume. The number of lipid-droplets will show how healthy the brine shrimp are and their location will determine which bay is a more suitable environment. The prediction is that the physiological health (lipid droplets and egg numbers) of brine shrimp will be better in Gilbert Bay because there will be better food resources there.

METHODS AND STUDY AREA

Study Area and Field Collections

To determine the physiological status of the brine shrimp, samples were taken on September 30, 2010 from six different stations along the plume extending from Farmington Bay into Gilbert Bay. Stations 1 – 6 started 0.25 km north side of the causeway and continued out at specific intervals until we were well into Gilbert Bay at about 13.3 km. There was also a second replicate site for each station collected within 100-250 m of the first replicate. Water for chlorophyll analysis was also collected at Station 0 was on the south side of the causeway in Farmington Bay. Although I only collected samples on September 13th, the Division of Wildlife Resources had collected chlorophyll samples on September 13, 2010 and recorded the levels at 20 µg/L.

J. Wight and I collected samples from the entire water column with a vertical zooplankton sampling net. The brine shrimp were filtered out and stored in labeled jars with the lake water from the specific station and formalin was added as a preservative. See Wight (this report) for additional details on the field collections.

Chlorophyll *a* at both the deep and shallow depths for all stations and replicates were measured by J. Crawford (this report). The chlorophyll samples were filtered, frozen and read on the 10-AU Turner fluorometer using a variation of the Welschmeyer method. The deep and shallow depths were averaged together from each station and used for the results in my data set.

Laboratory Analyses

Three to seventeen gravid adult female brine shrimp were randomly selected from each of the jars from the stations. These brine shrimp were observed under a microscope to count lipid-droplets on the fifth leg on the right side of the shrimp along the spine by this leg until the sixth leg was reached. This method was adopted from Gliwicz and Wurtsbaugh (2001). The number of cysts or eggs being carried was also recorded by pulling the egg sac apart and counting the individual ova. Cysts were differentiated from eggs by their much darker orange color and a “flat” side. Analyses were also done on the total ova (eggs + cysts). Adult female brine shrimp were the only organisms used to simplify the data and reduced variance that would be present if males, juveniles, or nauplii had been included.

Bioassay Analysis

Undiluted water from Farmington Bay and Gilbert Bay was gathered in the field, stored in Cubitainers, transported to the lab and mixed at different ratios into 1.3 liter translucent white plastic buckets for the bioassay. Only 1 liter of water was put into the containers and deionized water was added to make up for evaporation throughout the experiment. White containers were used to allow light penetration to the sides and also would reflect the overhead light back into the container to support photosynthesis. The treatments were set up as followed:

Treatment	%Gilbert Bay	%Farmington Bay water
1	100	0
2	75	25
3	50	50
4	25	75

100% Farmington Bay water was not used in the bioassay due to a previous experiment completed with this information (Marcarelli and Wurtsbaugh 2006).

Each treatment was duplicated in order to assess variability. Nauplii were hatched from cysts in the lab and 20 were placed in each of the eight 2-L buckets that contained the different ratios of Gilbert Bay water to Farmington Bay water. The experiment was run in a controlled temperature room at 20°C and checked and recorded daily. Lighting in the room was at 150 uE/m2/sec which allowed algae to grow and support the brine shrimp. To measure food availability for the shrimp chlorophyll *a* levels were determined on October 1st, October 8th, and October 14th which were the first, middle, and last day of the bioassay. The initial chlorophyll *a* level was taken from J. Crawford's data of the field sampling. The bioassay ran for 14 days in order to provide a sufficient time for a full growth cycle of the brine shrimp without producing a second generation. After 14 days, the brine shrimp were removed from the containers and preserved in formalin until they were counted and measured.

RESULTS

The smallest brine shrimp, on average, were found at Station 3 with a length of 6.9 mm and the longest at Stations 1 and 2 with a length of 8.8 mm. The size of the brine shrimp had a significant effect on the number of lipid droplets and eggs and cysts of the females:

Lipid droplets	= 8.261 L – 50.821	$r^2 = 0.184$
Eggs/female	= 6.561 L – 12.27	$r^2 = 0.035$
Cysts/female	= 19.99 L – 106.49	$r^2 = 0.242$
Ova/female	= 11.68 L – 51.028	$r^2 = 0.100$

Because female size varied between stations (particularly at Sta. 3 where very few females were present), I corrected the data from each station to the mean length of all females measured in the study (8.31 mm). For example, corrected lipid droplets were calculated as:

Corrected Lipid Droplets =
Lipid Droplets counted + (8.261 * (8.31 – L))

Lipid content of the female shrimp decreased significantly at stations further from the Farmington Bay discharge into Gilbert Bay (figure 1). At Station 1, closest to Farmington Bay, mean corrected lipid droplet numbers were 47/female, but this decreased to 8/female at Station 6. Variability, however, was high at all of the stations.

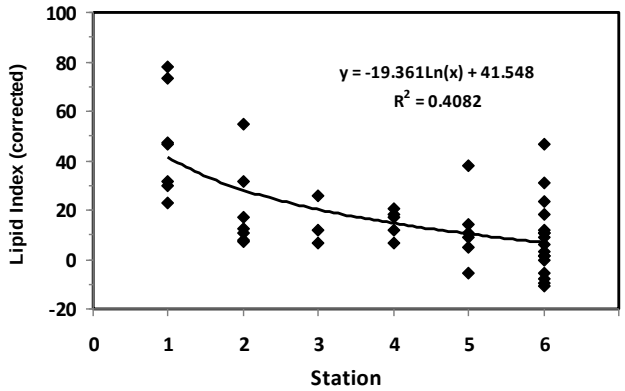

Figure 1—Lipid droplet index per female *Artemia* at six stations along the Farmington Bay algal plume extending into Gilbert Bay. The lipid numbers were corrected to the mean size of the *Artemia*, and this resulted in negative numbers for some of the shrimp. $P < 0.000$.

Ova/female showed the opposite trend along the transect with the highest numbers at Station 6, 13 km from the Farmington Bay discharge (figure 2). Females there had an average of 51 ova, with a relatively even split between eggs and cysts. In contrast, females at Stations 1 and 2 had few ova, and they were nearly all eggs, with negligible numbers of cysts.

Surprisingly, the corrected ova per female (combined number of eggs plus cysts) decreased significantly ($p = 0.01$) with increasing concentrations of chlorophyll *a* (figure 3). When chlorophyll levels were near 10 µg/L (Sta. 1), there were only 6 ova/female, whereas at chlorophyll concentrations of 0.7 µg/L (Sta. 6), there were 51 ova/female.

Ova per female and lipid indices were negatively correlated (figure 4). Female brine shrimp with ca.70 ova/female had corrected lipid indices near zero, whereas shrimp with very few ova had lipid indices over 50 droplets/female.

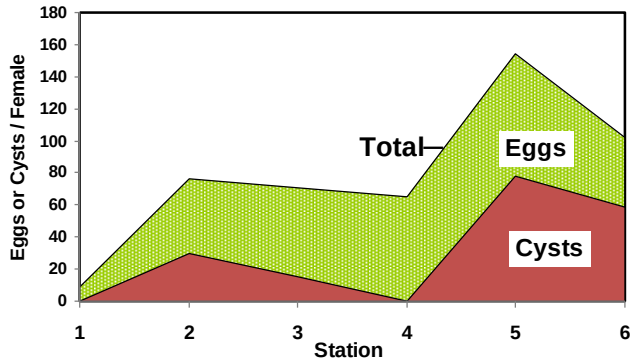

Figure 2—Changes in the corrected number of eggs and cysts in female brine shrimp along the plume transect. Data from Station 3 was omitted because of the low number of brine shrimp there available for processing. The top line shows the total number of ova/female.

Figure 5 shows the percent survival rate of the brine shrimp for each treatment of the bioassay. The highest percent survival rate was found in the 50-50 mix of Farmington Bay and Gilbert Bay water with an average survival rate 80%. In contrast, in 100% Gilbert Bay water or in the 25%/75% mix of Gilbert and Farmington water, survival rates were much lower. Analysis of variance tests done on percent survival, and on biomass accumulation in the bioassay indicated that there were significant differences between the treatments (survival, $p < 0.000$; biomass, $p = 0.037$).

DISCUSSION

The highest percentage survival rate from the bioassay was found in the treatment with the 50-to-50 ratio of Gilbert Bay to Farmington Bay water with an initial chlorophyll level at 29 µg/L. The correlation of the chlorophyll levels and the survival percentage of 80% can be explained by a greater amount of food available compared to the treatment with more Gilbert Bay water (figure 2).

Contrary to our hypothesis, the bioassay demonstrated that brine shrimp may benefit from phytoplankton exported from Farmington Bay, provided that the concentrations from the bay are not too great. The survival rates were lowest in the 100% Gilbert Bay water, which had an initial chlorophyll level of only 0.2 µg/L, further confirming the implication that the brine shrimp preferred water with higher chlorophyll levels because of the amount of food available. Research from Wurtsbaugh and Marcarelli (2006) resulted in a similar manner; brine shrimp nauplii in their bioassay with Gilbert Bay water also had a low survival rate. The explanation drawn from their result of a low survival rate was the lack of food available; the phytoplankton biomass was low in the Gilbert Bay water (Wurtsbaugh and Marcarelli 2006).

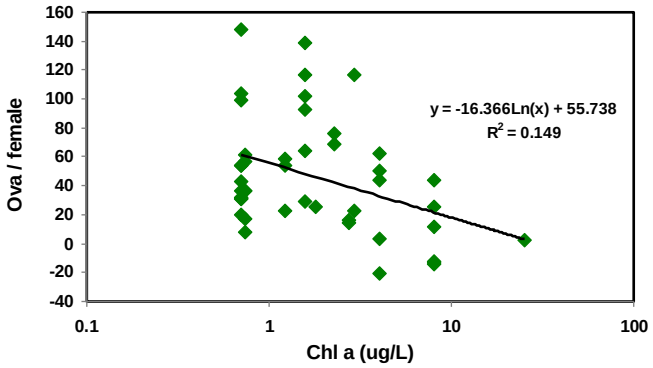

Figure 3—Relationship between chlorophyll a at the different stations and the corrected number of ova in brine shrimp sampled along the eutrophication plume entering Gilbert Bay. The regression was significant ($p = 0.01$).

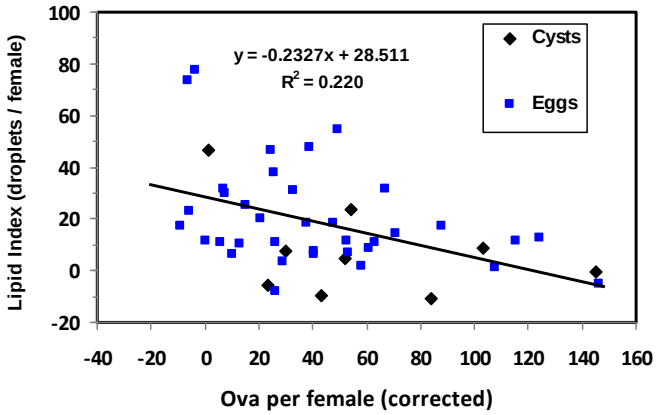

Figure 4—Relationship between the lipid index in female brine shrimp and the ova per female. The regression line is for total ova. The lipid index and the ova/female are corrected for the mean size of brine shrimp in the analysis (8.3 mm), and this correction resulted in some negative numbers for both parameters.

However, in support of our hypothesis, the brine shrimp survival rates improved in the treatment with a ratio of 25% to 75% Gilbert Bay water. This result shows that only a small portion of Farmington Bay when mixed with Gilbert Bay water can be beneficial to the physiological health of brine shrimp. Overall, brine shrimp preferred mixtures of the two bay waters because Farmington Bay initially produced enough chlorophyll to provide a food source, but when there was a greater amount of Farmington Bay water it was harmful to the brine shrimp.

In association to the bioassay results of brine shrimp preferring high chlorophyll levels, I found an inverse relationship between lipid indices and the number of ova on a female (figure 4). This supports the assumption that brine shrimp shunt their lipid droplets in order to produce eggs. Ovoviparious eggs are thought to be produced only when food levels are high and conditions are high-quality for nauplii growth and survival. The greatest amount of brine shrimp with high numbers of eggs were found in Stations 5 and 6 with 74 as an average. The highest amounts of lipid droplets were found closest to Farmington Bay at averages of 52 and 24 per appendage, indicating there was likely lower production of nauplii in this area.

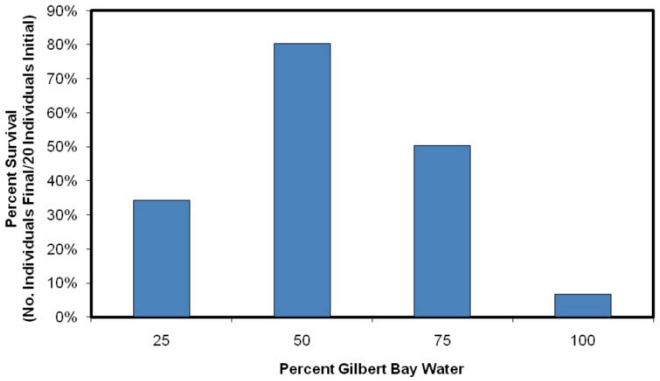

Figure 5—Relative survival of brine shrimp nauplii in a bioassay utilizing different proportions of Gilbert Bay and Farmington Bay water.

Chlorophyll levels also had a positive influence on the number of lipid droplets (Chl a; p= 0.000). In the most distant stations where grazing rates were high and chlorophyll levels extremely low, lipid levels were also quite low (figure 1). However, the regression analysis relating chlorophyll levels and the amount of eggs was not significant (p= 0.41). Though a little unexpected, we did find a significant influence of chlorophyll levels on the abundance of cysts (p= 0.01). A possible explanation for this relationship could be explained by when there are low amounts of chlorophyll there is an increase in the number of cysts due to a lack food for the brine shrimp. Also, there was a significant relationship between the total number of ova and chlorophyll levels (Chl a; p= 0.01) which correlates to the relationship between cysts and chlorophyll. An observation I found in the field data was the number of ova decreases with increasing amounts of chlorophyll *a*. This result was not expected but could be explained by the high chlorophyll levels recorded by the DWR a few days previously. The brine shrimp could have thrived in the high amounts of chlorophyll and it supported them through the flux of chlorophyll we recorded.

With all these variations in the data and sources, more research is necessary to truly understand if the plume from Farmington Bay is beneficial to the brine shrimp or not. However, with the present data it shows brine shrimp are able to survive close to Farmington Bay. The plume coming from this bay may not necessarily be unhealthy for brine shrimp, although it may not suitable for live eggs. Wurtsbaugh and Marcarelli's (2006) research indicates that Farmington Bay is not suitable for brine shrimp survival which contradicts the recent findings from the bioassay completed in this research. However, Wurtsbaugh and Marcarelli could not determine the reason for the high mortality rates in their bioassay of Farmington Bay water (Wurtsbaugh and Marcarelli 2006). With all this controversies found in previous data and the data in my research, it is obvious more research is necessary to understand the plume from Farmington Bay.

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A Study of *Artemia franciscana* Diet along a Salinity Gradient in the Great Salt Lake Using Isotopes

Ashton Montrone

SUMMARY

The dietary sources of *Artemia franciscana* in Gilbert Bay of the Great Salt Lake, a large terminal saline lake, were studied using isotopic analysis. Carbon and nitrogen isotopic ratios were measured for both seston and *Artemia* over a 13-km long trophic gradient that extended from hypereutrophic Farmington Bay into Gilbert Bay. Particulate organic nitrogen and particulate organic carbon was 8-10 times higher at the station near the discharge of Farmington Bay compared to the open waters of Gilbert Bay. Isotopic mixing models indicated that 5-60% of *Artemia's* diet along the transect was seston originating from Farmington Bay. The proportion of diet of *Artemia* originating from Farmington Bay decreased further from the causeway that joins the bays.

INTRODUCTION

Artemia are an important component of the Great Salt Lake (GSL) food web. There is a large demand for harvesting their cysts as they are ideal for providing live aquaculture food for hatcheries (Sorgeloos et al. 1978) and they support a multimillion dollar per year business (Hummell. 2006). The causeway that separates Farmington Bay and Gilbert Bay has disrupted the north-south flow of brine and has created different ecological habitats with Farmington Bay having lower salinity (Rushforth and Felix, 1982). The GSL is highly varied in temperature and salinity spatially and temporally. The temperature varies from -5 °C to 35 °C and 45 °C in the shallow regions (Post 1977). The Southern Arm is around 130 g/mL (Post 1977) but even these numbers change as inflows and evaporation change. The colder temperatures limit bioprocesses and the higher salinity gradient created by the causeway has led to lower biodiversity in Gilbert Bay (Rushforth and Felix 1982) than in Farmington Bay. *Artemia* are frequently the exclusive macrozooplankton herbivore in the pelagic region of Gilbert Bay (Wurtsbaugh et al. 1991). High nutrient loading and lower salinities lead to eutrophic conditions in Farmington Bay (Wurtsbaugh et al. 1991). These highly eutrophic waters flow from Farmington Bay into Gilbert Bay often resulting in a green plume that can extend 20 km (Wurtsbaugh et al. 2008). The primary goal of my study was to understand the proportional dietary sources of the *Artemia* population in the plume.

Carbon and nitrogen have stable isotopes that naturally occur in various ratios in all material. As these isotopes go through various biochemical reactions, the ratios of stable isotopes to non-isotopes change by a process known as fractionation (Fry, 2006). The biochemical processes slightly favor that heavier molecules stay in the organism and the lighter molecules are expelled (Fry, 2006). Fractionation is subtle but predictable. Percent change in the heavier isotope is too large of a unit to explain the process, thus either "per mil", or δ from the Greek word delta is used. δ X, where X is the chemical being considered, is how much a value differs from an established benchmark. δ X is defined as:

$$\{(\text{Ratio of Sample isotopic level} / \text{Ratio of Standard} - 1)\} * 1000.$$

The unique characteristics of each bay in the Great Salt Lake result in unique signatures for both carbon and nitrogen isotopes and should be tractable in a mixing model. The lower salinities of Farmington Bay (~ 3%) are sufficiently low for nitrogen fixing cyanobacteria to thrive, along with other phytoplankton. This, coupled with high nutrient loading leads to highly eutrophic conditions. The flow of water primarily is primarily from Farmington Bay into Gilbert Bay. As Farmington Bay is much more eutrophic than Gilbert Bay, the result is a green plume that extends into Gilbert Bay (Wurtsbaugh et al. 2008). As nitrogen fixing cyanobacteria have theoretically significantly lower $\delta^{15}N$ levels and they compose a significant portion of the plume (see Fleming 2010, this report), their nitrogen δ value is distinct and allows for water columns containing them to have unique signatures for tracking *Artemia* diets. Farmington Bay and Gilbert Bay have different tributaries which lead to different nutrient loading. Systems like Farmington Bay, which have a relatively large sewage effluent, have unique $\delta^{13}C$ values (DeBruyn and Rasmussen, 2002). In my study the carbon isotope values were used to assess the general contribution of seston (particulate organic matter) from Farmington Bay, whereas ^{15}N was used more as a reference to determine the contribution of cyanobacteria from Farmington.

STUDY AREA AND METHODS

Study Area

Our study area was comprised of seven stations that extended from the causeway bridge near Antelope Island to 13.3 kilometers west-northwest of the bridge. We sampled on September 30, 2010 from 7:00 until 19:00. Station 0 was located on the Farmington Bay side of the bridge and was considered to be "pure" Farmington Bay water while Station 6 was 13.3 kilometers away and considered to be "pure" Gilbert Bay water. Distance between stations increased as our distance from Farmington Bay increased (see table in the Executive Summary). Water at Farmington Bay had a salinity of 2% and a depth of 0.8 m at the sample site near shore. A second replicate at each station were constructed by traveling obliquely across the lake to maintain a similar radial distance from Farmington Bay. Water became slightly deeper along the transect with little variation from Stations 1 to 5 (depths between 0.9 and 2.2 meters). At Station 6 the water became much deeper–7.3 m. Salinity increased rapidly between Station 0 and Station 1. At Station 1 replicate B (250 m from the causeway) the surface water salinity was 12.5% and reached a maximum at Station 6 with a mean of 15.2% between replicates. The average temperature for the entire transect was 21.9 ˚C with a minimum at Station 0 of 20 ˚C and a maximum at Station 1 replicate A of 27.7 ˚C. Phycocyanin, a pigment from nitrogen fixing cyanobacteria, was highest at Station 0 (23 TFU, Turner fluorescence units), and lowest at Station 6, with a mean value of 0.43 TFU.

Artemia Methods

Artemia were collected by vertical hauls using a 250 µm Wisconsin net of 0.5 meter diameter. The net was lowered to within 0.2 m from the bottom of the lake and raised to the surface. The *Artemia* were placed in acid-washed and deionized rinsed scintillation vials. Samples were then placed in a cooler with ice for transport to the laboratory. At Stations 0, 1, 2, and 3 for both replicates, more than one haul was needed to collect a sufficient amount of *Artemia*; > 1 milligram dry weight for the isotopic analysis.

The night of collection, the *Artemia* were placed on a 250 µm filter and rinsed with deionized water to remove all salt and particulate matter. Samples were then put back into the scintillation vials with the lids off and dried at 70˚C for 24 h. The samples were then acid fumed in a desiccator with an open beaker containing concentrated HCl to remove carbonates. The samples were then homogenized by grinding and then weighed and placed in 5mm x 8mm tin capsules for isotopic analysis. Isotopic analyses were then performed at UC Davis Stable Isotope Facility.

Seston Methods

With the exception of Station 0, seston was collected at two depths, 0.2 m from the surface and 0.4 m above the bottom with an 8-L horizontal Van Dorn water bottle. Lake depth measurements were taken prior to taking a deep sample. It should be noted that at Station 6 replicate A the van Dorn bottle bumped the bottom when collecting the deep sample and may have stirred up sediment. The $\delta^{15}N$ value at this Station was abnormally low, possibly due to sediment being included in the sample. Acid washed 1-L bottles were then rinsed with lake water and completely filled from the Van Dorn bottle. Samples were then placed in a cooler with ice to prevent decomposition.

Later that night, the seston samples were filtered on 25-mm glass fiber Gelman A/E filters (1 µm pore size) with a vacuum manifold. Sample water was then added until the filter clogged. The amount of water required to clog the filter was then recorded. Station 6 replicates were combined as 1 liter was insufficient to clog the filter. Thus, the two replicates at Station 6 were combined. The filters were folded using tweezers and were inserted into open scintillation vials. The scintillation vials were then dried at 70˚C for 24 h. and then acid fumed to remove carbonates. Filters were placed in 5mm x 8mm tins for isotopic analysis at the UC Davis Stable Isotope Facility.

Phycocyanin was measure using in-vivo fluorometry and a Turner 10AU fluorometer. For more detail on methods on pigment analyses, see Crawford (this report).

Post Processing Methods

UC Davis provided carbon and nitrogen weights for each sample. From these weights, particulate carbon and nitrogen were then back calculated by using the amount of water filtered. Also provided were $\delta^{13}C$ and $\delta^{15}N$ values for all samples except Station 3 replicate A shallow. It contained an insufficient seston for processing and was therefore eliminated from the analysis.

It was assumed that the diet for *Artemia* was some combination of the isotopic signatures of Farmington Bay and Gilbert Bay. A mixing model to determine the

source of diet was created for both seston and *Artemia*. The mixing model was created to approximate the weighted averages of the δ values for each isotope from surface water collected at Stations 0 and 6. As the most extreme values of each isotope were at Stations 0 and 6, every intermediate value could be described as a weighted average of the two values. By linear regression it was determined that the trophic enrichment from seston to *Artemia (* the change in δ value due to fractionation) for nitrogen and carbon were 5.95 and 0.3 δ values, respectively. The isotopic values for Farmington Bay were -18.20 for $\delta^{13}C$ and 2.70 for $\delta^{15}N$. The values used for Station 6 in Gilbert Bay were -20.50 for $\delta^{13}C$ and 9.39 for $\delta^{15}N$. Thus the equation for % diet from Farmington Bay based nitrogen was:

% diet from Farmington = (δ N *Artemia*-5.95-9.39) /(2.7-9.39)

The equation for % diet from Farmington Bay based on carbon was:

% diet from Farmington = (δ C *Artemia*-0.3-21.8) /(-18.20-(-20.5))

RESULTS

Particulate Nitrogen and Carbon

Both nitrogen and carbon showed a logarithmic decline in particulate nitrogen and carbon from Station 0 to 6 (figure 1). At Station 0, there was 1058 µg of organic nitrogen per liter. At the other extreme, at Station 6 (deep sample), there was only 39.3 µg of organic nitrogen per liter. Regression analysis of particulate nitrogen/liter against log (1 + distance) indicated there was a significant decrease (p-value of 0.013, r^2=0.16). At Station 0, there were 4586 µg C/L. At Station 6 deep, there were 172.6 µg C/L. When particulate carbon/liter is regressed against log (1+distance), there is a significant (p = 0.014 and r^2 =0.17) decrease in particulate carbon from Station 0 to Station 6. Because of such strong statistical significance, one might expect a higher r^2 value. This isn't the case because of three factors. Both carbon and nitrogen concentrations decline logarithmically. There is also an implicit assumption that the water is moving away from Farmington Bay linearly. In reality, wind currents create eddies and transport water in all directions. Finally, there is temporal and spatial variability of *Artemia* grazing. The amount of *Artemia* grazing at each station may have contributed to the amount of particulate carbon and nitrogen in the seston. Despite the reasons for a low r^2, there was 8-10 times more particulate carbon and nitrogen closer to Farmington Bay than Gilbert Bay. This indicates that more particulate organic matter, and thus food, was available for *Artemia* closer to Farmington Bay than in the open waters at Station 6.

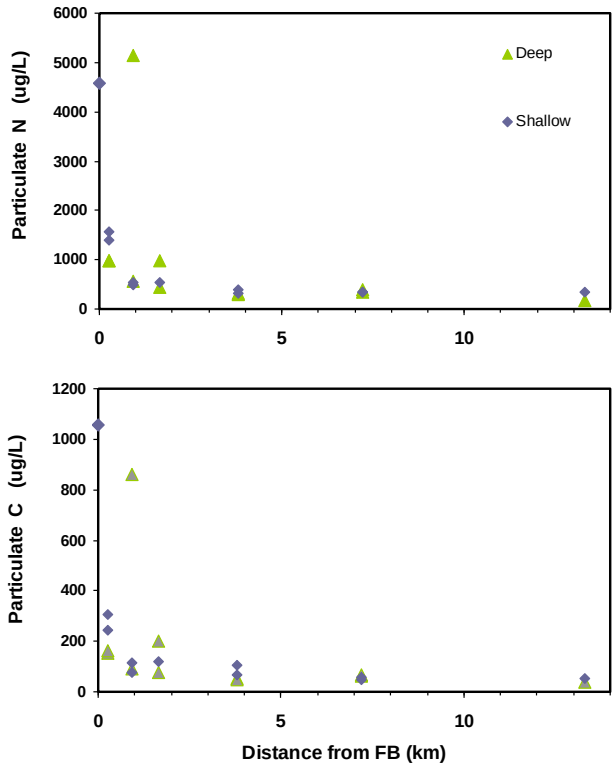

Figure 1—Above─Particulate nitrogen seston along the Farmington Bay-Gilbert Bay transect from Station 0 (0 km) to Station 6 (13 km). Below─Particulate carbon concentrations along the transect. Diamonds show values for shallow seston samples and triangles show values for deep seston samples.

$\Delta^{13}C$ of Seston and Artemia

The values for $\delta^{13}C$ became increasingly negative for both *Artemia* and seston as we moved from Station 0 to Station 6 (figure 2). The lowest δ13C value for shallow seston, -18.2, was at Station 0 and the highest value, -21.1, was at Station 6. When δ13C shallow seston is regressed against log (1 + distance), a p-value of 0.004 is generated. For the deep seston, δ13C values decreased markedly from Station 1 to Station 4, and then leveled off or increased somewhat at Stations 5 and 6. When δ13C for deep seston is regressed against log (1+ distance), it also significantly decreased (p-value of 0.012) from Station 0 to 6, but a linear regression actually did not fit the data well. The highest $\delta^{13}C$ value for *Artemia*, -16.7, was at Station 1 replicated B. $\delta^{13}C$ values decreased considerably until Station 4 and then leveled off with values near -20. If $\delta^{13}C$ for *Artemia* is

regressed against log (1 + distance), it also significantly decreased (p-value of 0.0019) from Station 1 to 6.

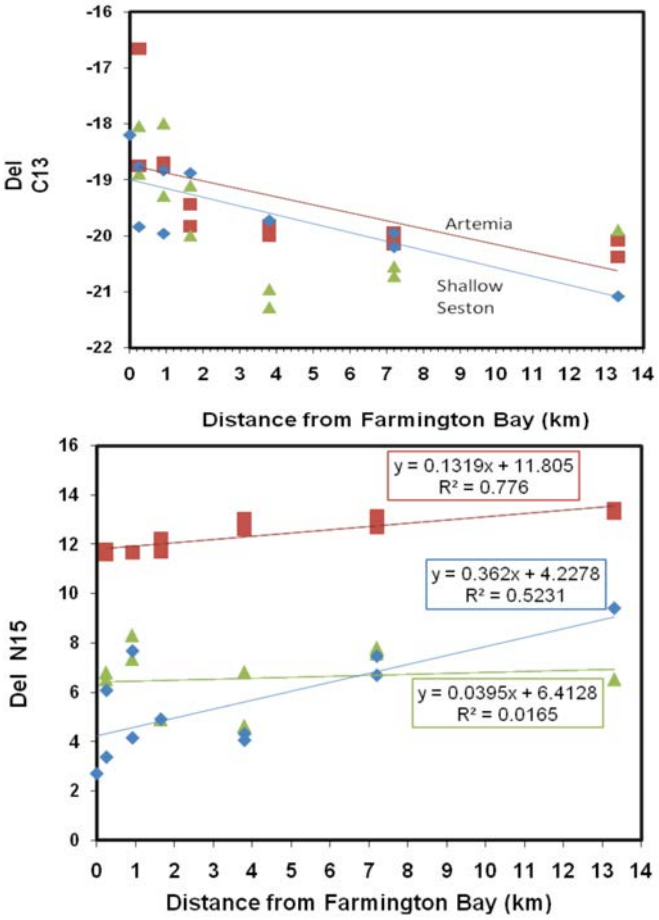

Figure 2—Above–δ13C values for both *Artemia* and seston along a transect from Farmington Bay into Gilbert Bay of the Great Salt Lake. Station 0 (0 km) was in Farmington Bay and the most distant station (Station 6; 13.4 km) was in the pelagic zone of Gilbert Bay. Below– δ14N isotopic composition of seston and *Artemia* along the transect. Key: *Artemia*–red squares; Seston Deep–green triangles; Seston Shallow–blue diamonds. Only surface water seston samples were available in Farmington Bay.

The *Artemia's* isotopic composition reflected a diet composed of seston of Farmington Bay origin near Farmington Bay. The linear regressions of *Artemia* and seston for both shallow and deep are all nearly parallel. While there was a fair amount of noise, the lines nearly perfectly reflect the theory that13C fractionates one half of a δ value for every trophic level higher carbon moves up (Fry, 2006).

δ ^{15}N *in Seston and Artemia*

δ^{15}N values increased for shallow seston and *Artemia* from Station 0 to Station 6 (figure 2). The values for δ^{15}N for shallow seston were lowest at Station 0 (2.7), and highest at Station 6 (9.4). When δ^{15} N values for shallow seston are regressed against log (1 + distance), δ^{15} N values significantly (p-value of 0.030) increased. Deep seston δ^{15}N values varied considerably. The highest value was at Station 2 replicate A (8.3), while the lowest was at Station 6 (3.8). Deep seston did not show a statistically significant gradient from Farmington Bay to Gilbert Bay (p-value of 0.17). *Artemia* δ^{15}N values were lowest at Station 1 replicate B (11.6), and highest at Station 6 (13.4). When *Artemia* δ^{15} N values are regressed against log (1 + distance), they significantly increased from Station 1 to 6 (p-value of 6.78E-06).

Closer to Farmington Bay, the salinity gradient between the shallow and deeper water was greater (see Introduction, figure 1). At Station 1, a 0.1-0.2 m thick layer of less saline and therefore less dense Farmington Bay water was visibly running over top of the more saline and therefore denser Gilbert Bay water. The surface water carried the nitrogen fixing biota from Farmington Bay. Note that the differences between shallow and deep δ^{15} N values were greater in the stations closer to Farmington Bay (figure 2). Theoretically, the shallow and deep values would converge as the water column became mixed from top to bottom as the salinity gradient decreased and lowered the density differences. I therefore believe the difference between shallow and deep ^{15}N values at Station 6 were erroneous.

There was not a significant difference between δ^{15} N values of deep seston from Station 0 to 6 (figure 3). This would suggest there was limited mixing occurring from the top of the water column to the bottom at stations very near Farmington Bay. When there were differences, it seems to be spatially and temporally isolated. The deep station 6 value is particularly troubling, as it is much closer to a value you would expect for a near Farmington Bay reading for shallow seston. On the station 6 deep seston sample, the van Dorn bottle bumped the bottom and may have stirred up some sediment. One explanation may be nitrogen fixing seston that may have settled out of the column from earlier plumes.

Mixing Models of Artemia Diet

The ^{15}N mixing models indicated that POM from Farmington Bay was important in the diet of *Artemia* in Gilbert Bay (figure 3). That importance declined markedly as the distance from Farmington Bay increased. The δ^{15}N mixing model suggested that the

diet of *Artemia* at Station 1 reflected a mean of 55% Farmington Bay food. The diet of *Artemia* reflected 29% Farmington Bay seston at Station 6. The mixing model was quite robust for nitrogen. The linear regression of percent diet of Farmington Bay using nitrogen against station had a p-value of 1.05 E-6. The nitrogen mixing model shows that the Farmington Bay seston were an important food source near Station 1 with decreasing dependency as Station 6 was approached.

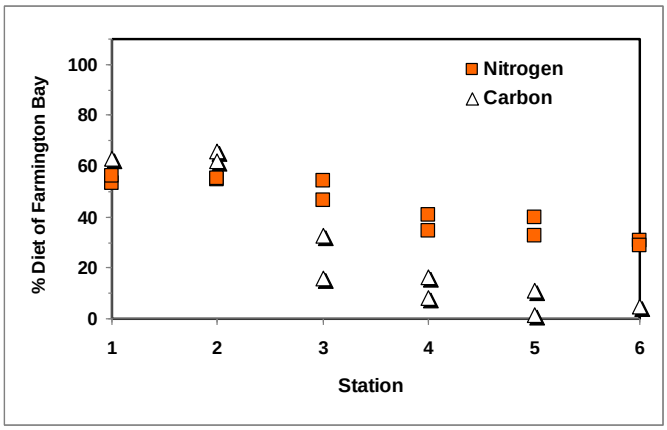

Figure 3—Mixing model estimates of the contribution of Farmington Bay seston to the diet of *Artemia* along a transect from the Farmington Bay discharge (Station 1) into Gilbert Bay of the Great Salt Lake. Mixing models were constructed using both carbon and nitrogen isotopic mixing models.

The carbon mixing model reflected the results of the nitrogen model, but the data were noisier. The estimated contribution of Farmington Bay seston to the *Artemia* diet decreased significantly from Station 1 to 6 (linear regression; p = 0.0009). However, the model suggested that Farmington Bay particulate matter was really important only as far as Station 2. Furthermore, the estimated value for percent diet of Farmington Bay at Station 1 replicate B was 134%. This was generated by an unusually high δ^{13} C value for the *Artemia* at this station (-16.7) and could be considered an outlier. Overall, both models agree that the *Artemia* rely on Farmington Bay water that flows into Gilbert Bay for food, and the dependence decreases as they are further from Farmington Bay.

DISCUSSION

The isotopic mixing model analyses suggest that seston exported from Farmington Bay may be important for brine shrimp feeding in parts of Gilbert Bay, but the importance of this seston is, however, not entirely clear. The mixing model estimates based on ^{13}C and ^{15}N differed considerably in how much of the diet at Station 6 was derived from Farmington Bay seston (0-30%, respectively). Furthermore, the end members presented in the analyses above were dependent on a single sample at Stations 6. Alternatively, if mean values for seston at Stations 5 and 6 are used for the Gilbert Bay end member, the ^{15}N model only indicates that Farmington Bay seston contributed to *Artemia* nutrition only as far out as Station 3 (1.65 km). It is unfortunate that more seston samples could not be analyzed for isotopic content at Station 6 for the end-member contribution to the mixing model. Nevertheless, the mixing models analyses do indicate that seston from Farmington Bay contributes to the brine shrimp diets, but because of the limited data, the extent of that contribution remains unknown. Our results contradict Wurtsbaugh et al. (2008), as their isotopic data suggested that the *Artemia* in Gilbert Bay did not use the plume from Farmington Bay as a food source.

Another complication in the data analysis was that there were some isotopic differences between shallow and deep seston, but we do not know what layer(s) the *Artemia* were feeding in. Overall, there was not a significant difference between δ^{15}N values of deep seston from Station 0 to 6 (figure 1). This would suggest there was considerable mixing and/or sedimentation occurring from the top of the water column to the bottom at stations very near Farmington Bay. When there were differences, they seemed to be spatially and temporally isolated. The deep Station 6 value (+3.8) is particularly troubling, as it is much closer to a value you would expect for a near Farmington Bay reading for shallow seston. On the Station 6 deep seston sample, the Van Dorn bottle bumped the bottom and may have stirred up some sediment. It is possible that nitrogen-fixing seston with low isotopic enrichment may have settled out of the column from earlier plumes that extended that far into the lake.

Naftz et al. (2008) also studied δ^{15} N values of *Artemia* and particulate organic matter (seston) at many sites within the Great Salt Lake. With the exception of one station (3510), which is located in the south-central portion of Gilbert Bay, they found *Artemia* δ^{15}N values between +13 and +8. These are relatively similar to values I found. Additionally, with the exclusion of two points for all stations but 3510, or 90% of the points, the values ranged between 13 and 10. However, at Station

3510 Naftz et al. recorded seven readings between May and September of 2004 below a δ^{15} N value of 10. The lowest δ^{15} N value for *Artemia* he found was near 5.8 in July. I did not find a single reading below 11 even at the Farmington Bay discharge into Gilbert Bay. His particulate organic matter δ^{15} N value for Station 3510 in July was 2.5–similar to the +2.7 value I found for Farmington Bay seston. I found nitrogen fractionation to be +5.95 δ values for the transfer between seston and *Artemia*. *If* we apply this fractionization value to Naftz et al's early July recording of +5.8 for *Artemia* it suggests that the shrimp then were feeding on a diet with an isotopic δ^{15} N value of -0.15. This is near δ^{15}N of 0 that could occur in cyanobacteria that had satisfied all of their nitrogen needs by fixation alone. Because nitrogen fixation doesn't occur in the hypersaline waters of Gilbert Bay (Wurtsbaugh 1988; Marcarelli et al. 2005, 2006), phytoplankton with δ^{15}N values near 0 would most likely have to come from lower salinity sites like Farmington Bay. While large shallow lakes are likely to have great spatial variability in algal distribution due to relatively reduced water transport and geomorphic constraints (Doi et al. 2006), the consistency at which Naftz et al found δ^{15} N values below 10 for Station 3510 is inconsistent with my results, particularly given that Station 3510 is approximately 22 km from the discharge of Farmington Bay into Gilbert Bay. In my study *Artemia* collected only 0.25 km from Farmington Bay had mean δ^{15}N values of +11.7, well above those found by Naftz et al. (2008) at Station 3510. I should caution that a fractionization value of +5.95 is quite unusual, and a median value near +3 is more normal (Fry 2006). If that value were applied to the seston–Artemia link, the isotopic value of Artemia at Station 3510 would be less problematic. Clearly, more work is needed on the feeding ecology of brine shrimp in the Great Salt Lake to understand the contribution of Farmington Bay seston export for their nutrition.

Crawford's (this report) measurements for phycocyanin, a proxy measurement for cyanobacteria indicated that these organisms decreased markedly from Station 0 to Station 6. Beyond Station 4, phycocyanin readings were <2% of those in Farmington Bay, suggesting substantial dilution and/or grazing on the exported cyanobacteria. Although analyses of chlorophyll utilizing MODIS satellite imagery did not detect a plume extending into Gilbert Bay, a report from DWR (Phil Brown, personal communication) suggested that there was a plume extending into our study site several weeks leading up to our sampling. This is reflected in our δ^{15}N values for *Artemia* and our nitrogen mixing model.

Our study documented distinctive isotopic signatures of both nitrogen in carbon in Farmington Bay that could be used to trace the plume into Gilbert Bay. Nitrogen fixing *Nodularia* cease growing and fixing nitrogen at salinity levels above 6-7% (Robinson 2004; Marcarelli et al. 2008). Gilbert Bay's south arm typically has salinity levels > 12%. During our sampling, salinity was 2% at Farmington Bay and rose immediately above 12% at Station 1. Thus, *Nodularia* found in Gilbert Bay were entirely of Farmington Bay origin and accumulated all of its biomass there. As *Artemia* at as far out as Station 6 had isotopic signatures different than Gilbert Bay (depending on the mixing model), it indicates that they are dependent on plumes originating from Farmington Bay. The gradient for δ^{13}C was likely due to the large amount of sewage effluent discharged into Farmington Bay that subsequently flows into Gilbert Bay. DeBruyn and Rasmussen (2002) were able to use the high δ^{13}C signature of sewage effluent to trace the food web in a river below the discharge point. A potential complication for the use of this approach is that Doi et al. (2006) found that δ^{13} C values increased with increasing pH, and there are substantial gradients in pH from Farmington Bay into Gilbert Bay (W. Wurtsbaugh, unpublished data). Unfortunately, we did not take pH measurements as this would have been an opportunity to compare results.

Ideally, the extent of the study would have been larger in both temporal and spatial scale as the variability in seston and *Artemia* densities and isotopic composition is considerable. Both time and budget constraints were prohibitive in extending the study. Due to the necessity of combining the seston replicates because of unexpectedly low levels seston at Station 6, more weight had to be given to the reading that justifiably should have. One more sample in mid-summer might have given some reference as *Nodularia* levels increase significantly during this time (Wurtsbaugh et al. 2008). This would lead to higher concentrations of *Nodularia* entering Gilbert Bay. Likely finding higher concentrations would contribute to the discussion of Naftz finding such a high proportion of Farmington Bay

water in *Artemia* diet so far from the causeway and might give some insight to the large range of values found at Station 3510.

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Eared Grebe Abundance along the Farmington Bay Plume in Gilbert Bay

Wayne Wurtsbaugh

SUMMARY

On the return trip from the pelagic zone to the Antelope Island causeway bridge, eared grebes were counted by two students on both sides of the boat to a distance of approximately 50 meters. In the pelagic zone where the water was >6 m deep, relative grebe abundance was low. Closer to Farmington Bay and in shallower water, relative densities increased considerably, and between Stations 2 and 1 reached about 10-fold greater than in the open pelagic zone. Because brine shrimp were least abundant near stations 1 and 2, it likely that the grebes were foraging on invertebrates swept out of Farmington Bay, or on brine fly larvae on the abundant stromatolites in that area.

INTRODUCTION

Birds utilize the high productivity of the Great Salt Lake to help fuel their migrations and in some species, to feed their young. Large-scale analyses of bird distribution in the lake have been done by shoreline and aerial surveys. These surveys show that bird abundance is often high in the region of the lake near Ogden Bay and near the automobile causeway leading to Antelope Island. Large concentrations of eared grebes (*Podiceps nigricollis*) often concentrate within a few hundred yards of the Farmington Bay outfall. To provide a more detailed analysis of how the outfall and resulting plume might influence bird densities, we did a transect count along the route between Station 6 and Station 1 in the lake on our return from the pelagic zone.

METHODS

Two students enumerated birds on both sides of the boat as we cruised at about 30 km/hr. The students were directed to estimate bird densities in a swath within 50 m of the boat. The transect was done between 16:30 and 17:00 hours on 30 September 2010. Station locations and water depths are shown in Figure 1. Relative densities are given as birds observed per minute of observation between stations. Because sighting distances were not measured, the resulting density estimates are only approximate, but should give a reasonable estimate of relative abundances at different stations. Eared grebes were the only bird that was abundant, and consequently only their densities were calculated.

RESULTS

Grebes were far more abundant near the Antelope Island causeway bridge and declined markedly along the transect. Between Stations 5 and 6 grebes were 10 times less abundant than in the area close to the Farmington Bay outflow (figure 1).

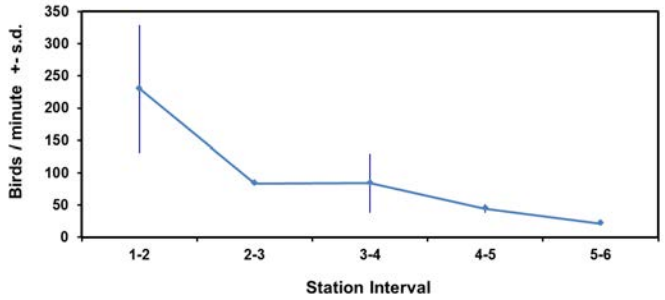

Figure 1—Relative abundance of eared grebes (*Podiceps nigricollis*) observed between the different sampling stations along the Farmington Bay algal plume extending into Gilbert Bay. Error bars (when larger than the points) show the standard deviations of duplicate observations on the two sides of the boat. Stations 1 and 2 were within 1 km of the outflow of Farmington Bay, whereas the interval between Stations 5 and 6 was located 7-13 km from the outflow.

DISCUSSION

Grebe abundance is frequently very high near the outflow of Farmington Bay. The birds there may be feeding on abundant invertebrates such as corixids coming out of the hypereutrophic bay, and/or they may be taking advantage of invertebrates stunned when they are mixed into the hypersaline waters of Gilbert Bay.

Although grebes feed on brine shrimp, the birds were most concentrated where brine shrimp were least abundant on the date of the transect (see chapter by Wight). The area where the birds were concentrated is quite shallow (Summary-Figure1) and covered by stromatolites with abundant brine fly larvae (Wurtsbaugh 2009). It is possible that the grebes utilize the area because of this additional food resource. I have frequently observed that grebes in the lake are most abundant in area between Fremont Island and the northern tip of Antelope Island where stromatolites are abundant. However, grebes are not abundant over the stromatolite fields on the east side of Stansbury Island. Consequently, some other characteristic associated with the nutrient- and algal-rich area near the Farmington Bay outflow may provide more abundant prey for the birds.

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Appendix A. Selected parameters measured in the Farmington Bay Plume Study. Most parameters except those for Artemia abundance and physiological state show results from the surface (0.2 m) depth. See individual student reports for data collected in deeper strata. Secchi depths were only greater than the station depth in the pelagic zone (Sta. 6). At Stations 1 and 2, Secchi depths were estimated based on the near-disappearance of the disk close to the bottom.

Bay	Sta	Rep	Station Depth (m)	Secchi (m)	Latitude	Longitude	Distance From Farmington Bay (km)	Salinity (‰)	TP (ug/L)	TN (ug/L)	Chl *a* (ug/L)	Phycocy_anin Fluorescence (TFU)	Phytoplankton Total Biovolume (um^3/mL)	Nodularia Biovolume (Millions um^3/mL)
Farmington	0	a	0.80		41° 03' 57.9"	-112° 13' 48.4"	0.00	2.0	265	5815	58.9	23.0	12.837	9.180
Gilbert	1	a	1.00	~1.2	41° 04' 04.6"	-112° 13' 57.9"	0.25	13.8	447	5714	6.6	5.5	4.051	0.180
Gilbert	1	b	0.90		41° 04' 08.1"	-112° 13' 54.3"	0.25	12.5	417	5679	30.7	10.0	3.735	0.000
Gilbert	2	a	1.40	~1.8	41° 04' 21.0"	-112° 14' 18.4"	0.92	14.5	419	6254	4.7	1.4	0.417	
Gilbert	2	b	1.40		41° 04' 16.8"	-112° 14' 20.2"	0.92	14.9	434	5253	1.1	0.8	0.001	
Gilbert	3	a	1.50		41° 04' 28.0	-112° 14' 45.9"	1.65	14.2	417	5511	1.4	4.2		
Gilbert	3	b	1.40		41° 04' 34.1"	-112° 14' 39.7"	1.65	15.0	422	4937	3.0	0.9	1.123	0.010
Gilbert	4	a	1.80		41° 04' 38.9"	-112° 16' 20.9"	3.80	14.8	438	5963	1.1	2.6		
Gilbert	4	b	2.20		41° 04' 44.7"	-112° 16' 19.8"	3.80	14.9	428	5234	1.7	1.9		
Gilbert	5	a	1.80		41° 04' 41.3"	-112° 18' 50.1"	7.20	15.0	444	5907	2.8	0.4		
Gilbert	5	b	1.80		41° 04' 48.3"	-112° 18' 50.2"	7.20	15.1	432	5775	2.7	0.4		
Gilbert	6	a	7.25	3.60	41° 04' 20.6"	-112° 23' 18.5"	13.30	15.2	416	5655	0.3	0.1		
Gilbert	6	b	7.30	3.50	41 04' 26.2"	-112° 23' 19.0"	13.30	15.2	452	5286	0.1	0.3	0.001	0.000

Bay	Sta	Rep	Artemia (#/L)	Zooplankton Grazing rate (%/day)	Artemia cysts (#/individual)	Artemia eggs (#/individual)	Artemia Lipid droplets (#/limb)	Seston C (ug/L) Surface	Seston N (ug/L) Surface	Seston del 13C (surface)
Farmington	0	a								
Gilbert	1	a	1.36	7.0	0.0	9.3	49.8	1743	402.2	-18.2
Gilbert	1	b	1.02	3.3	0.0	30.6	24.4	822	179.8	-18.8
Gilbert	2	a	0.84	4.1	0.0	15.2	25.6	406	84.5	-20.0
Gilbert	2	b	0.81	4.0	0.0	40.5	15.1			
Gilbert	3	a	0.65	2.0	0.0	66.8	12.6	429	114.1	-19.7
Gilbert	3	b	1.16	2.6	33.5	39.8	0.7	336	55.2	-19.9
Gilbert	4	a	1.32	4.5	0.0	6.8	31.4	420	63.9	-21.1
Gilbert	4	b	1.98	9.9	30.1	65.1	10.1	475	73.5	-19.8
Gilbert	5	a	3.94	5.2	0.0	5.1	9.1	543	86.4	-18.8
Gilbert	5	b	3.86	5.1	0.0	101.5	14.5	602	133.7	-18.9
Gilbert	6	a	3.56	15.1	77.6	40.7	11.5	353	73.7	-19.7
Gilbert	6	b	4.34	11.8	17.6	27.9	22.0	355	45.7	-20.2

Sunset over Gilbert Bay