Multi-year Investigations of Complex Interactions Between Cyanobacteria Blooms and the Food Web in Farmington Bay, Great Salt Lake, Utah

A Progress Report of Scientific Findings

2013 to 2015 Field Sampling Seasons

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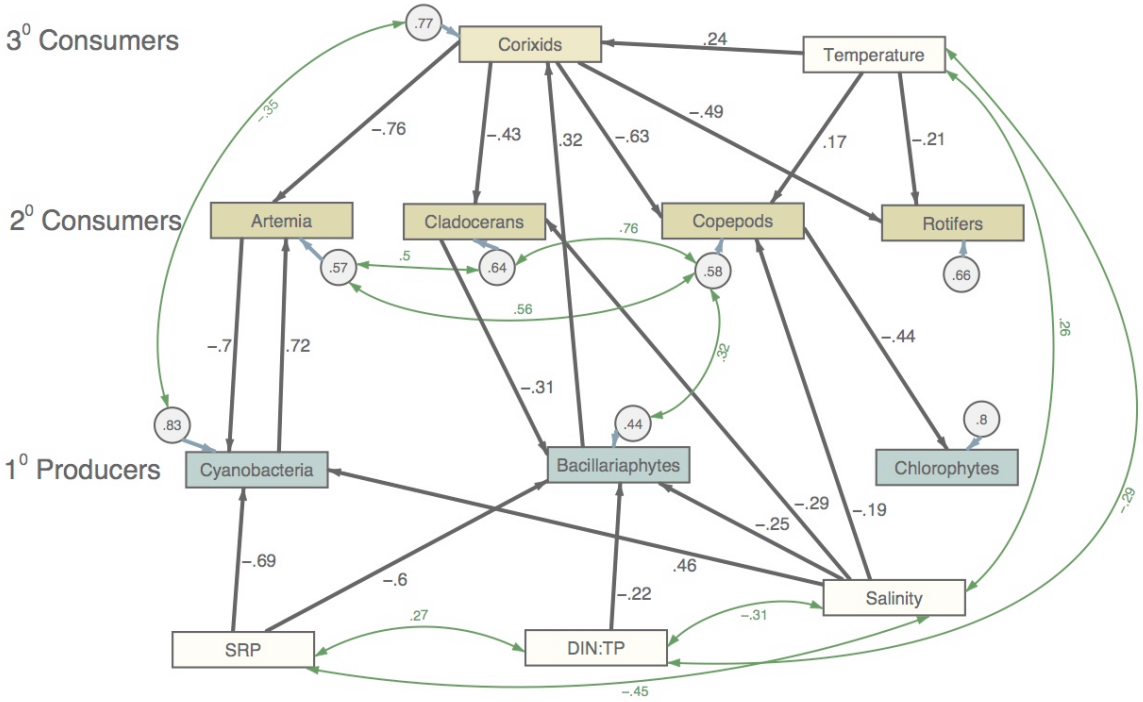

Report Submitted To:

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CONTENT OF REPORT

The following is summary of our multi-year study of the aquatic food web of Farmington Bay (FBay) with special focus on the factors influencing cyanobacteria blooms. Our first few years of research were intended to provide a strong foundation for subsequent investigations that would provide more detail and confirmation on the causes and consequences of cyanobacteria blooms in FBay. Systematic sampling of FBay was undertaken in 2013 and 2014. The sampling frequency was reduced in 2015 to four sampling events, which somewhat restricted our inference ability to confirm trophic relationships. Data from all sampling programs were analyzed and the results are contained in this report including several major findings and insights into top- down and bottom- up, direct and indirect effects of salinity, TN:SRP, SRP, phytoplankton, zooplankton groups, and corixids on cyanobacteria blooms. The influential effects of factors such as salinity, predation, grazing pressure, TN:TP, NO_3&NO_2, were observed for other algal taxa. The cumulative results have provided a wealth of insights into the ecology of FBay and of the role that cyanobacteria serves in the broader GSL ecosystem.

Recommendations are included that are being used to redefine the experimental approach for the expanded 2017 field season. Our 2017 research will continue to focus on nutrient dynamics and their association with the onset of cyanobacteria blooms. The study program will involve greater temporal and spatial detail and will include the overlooked but crucial link between benthic invertebrates and HABs. We will document the remarkable ecological characteristics of FBay with special attention devoted to the nutrient-algal-zooplankton linkages, as well as the role of N_2 fixation for the overall nitrogen balance of GSL.

EXECUTIVE SUMMARY

The potential impacts of cultural eutrophication on water quality and biota of FBay are a high priority because of FBay's extraordinary biological productivity, unique ecology and importance to the Great Salt Lake (GSL) ecosystem. Although FBay represents only about 5.7% of the total area of the GSL, it is critically important to the processing and cycling of nutrients and may contribute as much as 45% of tributary nutrients entering Gilbert Bay. Farmington Bay has a remarkably high capacity for primary and secondary productivity supporting large and diverse populations of zooplankton assemblages not found in other bays of the Great Salt Lake. These zooplankton populations provide abundant foraging opportunities for nesting and migratory waterbirds and shorebirds. Farmington Bay also provides a vital linkage and buffer between urban development and the main bodies of the GSL--Gilbert and Gunnison Bays. Despite cyanobacteria blooms in mid-summer, FBay continues to provide ecological functions that are essential for the maintenance of GSL's ecosystem integrity throughout the year.

Our investigation focused on nutrient concentrations (nitrogen--N and phosphorous--P), phytoplankton and zooplankton population composition, size and dynamics, abiotic factors, and the linkages between trophic levels (i.e., food web associations). Farmington Bay biota were substantively spatially and temporally heterogeneous and statistically differed between sites, months, and years. Pronounced growth of diverse algal groups supported similarly large populations of zooplankton taxa, which cycled throughout the study. The diversity and abundance of zooplankton across FBay provides for the well-characterized beneficial use of supporting waterbirds and shorebirds. Cyanobacteria blooms occurred from late May to September primarily in the central and northern regions of FBay. *Trichocorixa verticalis* (the predaceous corixid bug) became the dominant macroinvertebrate in June, July and August and appeared to facilitate a pronounced shift in the zooplankton assemblage via predation, which indirectly benefited cyanobacteria, chlorophytes, and diatoms. Soluble/bioavailable inorganic forms of nitrogen and phosphorus were low throughout the Bay except for one or two sites located in the southern region of the Bay near sewage outfall canals and tributaries. Near site #7 (close to the Salt Lake County sewage outfall canal) nutrient levels differed significantly from other locations in the Bay--always more than all other regions of FBay. In this region of the Bay cyanobacteria blooms did not occur.

The paucity of cyanobacteria blooms in the southern region of the Bay, coupled with measurable inputs of nitrogen, and essentially fresh water inflow, in this region suggests that the combination of elevated nitrogen levels and low salinity were sufficient to diminish the competitive advantages of cyanobacteria blooms, whereas in the mid-Bay nitrogen became a limiting factor and salinity increased slightly thereby conferring a pronounced competitive advantage for N_2 fixing algae such as *Nodularia* and *Pseudanabaena*. Salinity was the most important bottom-up predictor of cyanobacteria biomass which supports our conclusion that cyanobacteria are slightly halophilic. Although there were times when the cyanobacteria blooms extended north to the causeway, there were other sampling time periods that suggested that other factors, such as further increases in salinity, might be limiting the growth and competitive edge for cyanobacteria.

The fact that hypereutrophic conditions and cyanobacteria blooms develop in FBay during the summer is irrefutable; such blooms have been clearly documented in our study and in previous research programs on FBay. Increases in cyanotoxins in the water column often accompany the large accumulations of cyanobacteria, but not in a fully predictable manner. Insofar as cyanotoxins were

recorded at elevated levels, direct harm to zooplankton populations via acute toxicity from the cyanotoxins was not evident and necessitates further investigation in controlled toxicity studies with representative zooplankton species. Our controlled studies of nodularin effects on *Artemia* survival showed no impacts at environmentally realistic concentrations—including levels well above the highest values observed in FBay. The proposition that cyanobacteria blooms translate into unacceptable levels of harm to other biota and consequently cause a discernable demise in desired beneficial uses of the Bay is understandable given impacts observed in fresh water lakes. However, the fundamental question of whether cyanotoxins are causing direct harm to beneficial uses of GSL is currently not supported by our field results nor in our controlled toxicity study of nodularin impacts on Artemia and thus remains to be fully answered in terms of harm to other taxa.

The cyclical growth and dominance of cyanobacteria blooms in FBay may also be viewed as trophic inefficiency in which the flow of energy and carbon from autochthonous primary producers is temporarily stalled vis-à-vis the production of extensive accumulations of inedible filamentous algae rather than as a definitive measure of harm to the GSL ecosystem. This elevated level of trophic inefficiency is relatively short-lived and gives way to natural processes of deposition and subsequent decomposition by heterotrophic bacteria, which then usher in beneficial changes in the structure and abundance of algal and zooplankton assemblages in the Bay. During the decomposition phase of algal much of the stored N is remineralized, released and exported into the GSL ecosystem for uptake and assimilation, thereby serving as a remedy for N limitation and constraints on biological production in Gilbert Bay.

Farmington Bay boasts greater diversity, species richness, and total biomass per unit volume than is often reported in other regions of the GSL despite, or possibly because of elevated nutrient input and subsequent eutrophic conditions. We suggest that the ability of FBay biota to coexist and thrive when confronted with seasonal and annual cyanobacteria bloom cycles is a function of coevolutionary interactions between cyanobacteria and zooplankton grazers—interactions in which behavioral, genotypic and phenotypic variations that confer tolerance to cyanobacteria and cyanotoxins have been evolutionarily selected for among FBay zooplankton. This presumed co-evolution of biota in FBay provides advantages at the individual and population level and may be the reason why expansive cyanobacteria blooms occur with regular frequency, but have no apparent adverse impacts typically associated with HABs in fresh water systems. In fact, N_2 fixation by cyanobacteria is quite likely a net benefit for the broader GSL ecosystem.

Alternative views of FBay, and its associated cyanobacteria blooms, are suggested as a conceptual platform from which to examine, in much greater scientific detail, the remarkable complexity of FBay trophic interactions, and to serve as a restraint on the oft-cited inclination to immediately classify FBay as a harmed waterbody simply by recording a handful of generalized indicators of hypereutrophic conditions. The essence of these alternative views is that the integrity of the entire GSL ecosystem is a function of water and nutrient input and that severe or long-term reductions in either, or especially both, of these will have demonstrable negative consequences for the ecosystem—consequences that may be very difficult to remedy. Our research on FBay suggests that there are far more important and interesting direct and indirect ecological interactions taking place in the Bay than just a simple negative cause-and-effect relationship between cyanobacteria, resident FBay biota, and beneficial uses of the Bay. Farmington Bay's food web is substantially more complex and much more ecologically valuable than

previous investigations have realized and deserves our most rigorous attention prior to any permanent or semi-permanent modifications in nutrient loads.

DETAILED SUMMARY OF MAIN FINDINGS

1. Results from transect site assessments reveal a remarkable diversity and production of algal, zooplankton, and macroinvertebrate biomass in FBay. It is evident that the biological productivity of FBay supports a wide variety of ecological functions necessary for the broader GSL ecosystem. It is also apparent that the uptake, utilization and cycling of nutrients in FBay serve an important role in the food web of the larger and more saline Gilbert Bay. The remarkable biodiversity of FBay provides foraging opportunities for birds that are not found in Gilbert Bay nor Gunnison Bay and is therefore a critical component of the GSL food web and designated beneficial use.

2. There was pronounced spatial and temporal heterogeneity in all abiotic elements and biotic assemblages assessed. Salinity gradients were identified along the north to south transect and salinity was shown to be a dominant factor determining community structure and function. Nutrient loading was highest in the southern region of the bay. The central region of Fbay showed the highest plankton biomass production. Invertebrate assemblages were predominately defined by season, location, salinity and direct and indirect predator/prey relationships. Algal assemblages were strongly influenced by time of year, location, nutrient molecular form and bioavailability, grazing pressure, and salinity.

3. Soluble inorganic forms of N and P were rapidly depleted/assimilated once they entered the bay. Nutrient limitation varied spatially and temporally. Nitrogen limitation yielded to P limitation in regions where N_2 fixation by cyanobacteria solved nitrogen limitation constraints on growth.

4. Nutrient results suggest that inflow sources near site #7 (southern end of FBay) were the most significant in terms of nutrient loading into the bay. Site #8 (southern end of FBay) also showed substantial loading of P and to a lesser extent N. The TN:TP ratio suggests that various regions of the bay are either N or P limited depending upon location and time of year. Nitrogen limitation dominates in the southern regions of the bay while mid-bay to northern bay sites become P limited when N_2 fixing cyanobacteria resolve N limitation.

5. Algal abundance and diversity demonstrated strong spatial and temporal dynamics; spring and early summer phytoplankton exhibited a distinctly different profile than later in the summer. The initial algal population structure was composed of diatoms, chlorophytes, and to some extent euglenophytes, but was later dominated by cyanobacteria. Cyanobacteria blooms typically began in May and by June cyanobacteria were the dominant algal group in the bay. Cyanobacteria continued to dominate until the October and November, although there was a pronounced return of chlorophytes in July and August. This dynamic differed among years with diminished dominance of cyanobacteria in 2015.

6. The most abundant cyanobacterium was *Nodularia,* followed by *Pseudanabaena*. The *Nodularia* bloom usually began in May then diminished in October. *Pseudanabaena* began its bloom in August and continued into September/October. Although the data are non-conclusive, it appears that cyanobacteria gain a competitive advantage over other algal species once the bioavailable forms of nitrogen are assimilated and nitrogen becomes a limiting factor for algal growth. Phosphorous levels appear sufficient to support the robust growth of cyanobacteria during summer months. It is, however, unclear how much of the bioavailable P is a function of contemporary loading versus internal cycling and mobilization of "legacy" P loads already present in the bay. Although it seems prudent to limit P loading in the bay to reduce the magnitude of cyanobacteria blooms it is not entirely evident that this alone would have an immediate beneficial outcome. The results also suggest that under current conditions of legacy P and allochthonous input of P into the bay nitrogen reductions may in fact enhance the competitive dominance of N_2 fixing cyanobacteria and therefore promote the bloom of *Nodularia* and *Pseudanabaena*.

7. Algal biomass as indicated by chlorophyll-a concentration varied substantially throughout the study period. The peak measurement of chlorophyll-a occurred during 2013 at the end of May with a maximum single site value of 506 ug/L. Average yearly chlorophyll-a levels across the bay were: 114.6 ug/L, 63.9 ug/L and 40.7 ug/L respectively for 2013, 2014 and 2015. The minimum value recorded was 2.7 ug/L.

8. Of the two cyanotoxins examined, nodularin and anatoxin, only nodularin was found to be present in elevated levels. Nodularin concentrations were first observed in significant concentrations in May 2013 and reached peak concentration in July 2013 (88 ug/L). The average concentration across the bay for the entire study was 13.4 ug/L with a median value of 3.4 ug/L. Nodularin production followed a threshold model ("hockey stick") of presence in the water column and appeared to be a density-dependent relationship with *Nodularia* cell numbers $\geq$100,000 cells per ml. No definitive relationship between nodularin concentration and adverse impacts on zooplankton were identified.

9. Dissolved oxygen (DO) was measured during the routine sampling programs only; hence diel changes were not recorded. The minimum DO measurement of surface water was 0.160 mg/L in June 2015. The average yearly DO across the bay was 7.08 mg/L, 8.76 mg/L and 5.78 mg/L for 2013, 2014 and 2015 respectively. The highest value recorded was 19.54 mg/L being recorded in March 2014 when grazing pressure on phytoplankton was minimal. Dissolved oxygen tended to decline in May-June after the initial HABs blooms and may have reflected an increase in oxygen demands imposed on the system. Oxygen consuming biochemical decomposition processes by heterotrophic bacteria, zooplankton respiration requirements, reductions in oxygen generation via shading of subsurface phyto- and benthic algae, or the combination of these and other oxygen

depleting chemical reactions may have contributed to the decline in oxygen during the summer. Notwithstanding the summer declines daily average DO levels appeared sufficient to support zooplankton population growth.

10. Salinity was consistently low in the southern region of the bay where it had a maximum level of 1.4%. Salinity increased along a south to north transect with a yearly average across the bay of 3.8%, 1.1% and 0.4% for 2013, 2014 and 2015 respectively. The highest value of 8.3% being measured at site #1 in 2013—near the breach in the Antelope Island causeway. The maximum value for salinity roughly followed a north to south gradient: Site 1 (8.3%), Site 2 (4.5%), Site 3 (6.3%), Site 4 (3.4%), Site 5 (3.6%), Site 6 (1.7%), Site 7 (1.4%), and Site 8 (1.0%). During 2013 one sampling location was located on the Gilbert Bay side of the Antelope Island causeway had an average of 11.1% and a maximum value of 14.0%.

11. Zooplankton and macroinvertebrates were found in abundance in FBay and predominantly included Rotifera—*Brachionus plicatilis*; Cladocera—*Moina macrocarpa*; Copepoda (Harpacticoid)—*Cletocamptus sp*.; Branchiopoda—*Artemia franciscana*; Insecta (Hemiptera)—*Trichocorixa verticalis*. From April until July there were tremendous numbers of zooplankton in FBay particularly in the central region of the bay. However, coinciding with the emergence and maturation of the corixid *Trichocorixa verticalis* the diversity and abundance of other zooplankton plummeted and essentially never recovered until corixid abundance declined in September. There was strong evidence of a top-down influence of *T. verticalis* on the zooplankton composition of the bay. There is also strong evidence of bottom up effects of nutrients, chemistry, phyto- and zooplankton on *T. verticalis*. There may, however, be multiple other factors also influencing the decrease of zooplankton biomass including; food limitation, intra and inter-specific competition, predation by invertebrates other than corixids, predation by vertebrate species, dissolved oxygen levels, cyanotoxins, other stressors that can serve to constrain zooplankton growth and development. Normal life span and generation times also exert an influence on the temporal pattern of zooplankton abundance and diversity. Simultaneous Quantile Regression, Regression Tree, Random Forests and structural equation models (SEM) highlighted and confirmed many of these interactions.

12. The results from these first years of study were used to identify bottom up and top down effects on cyanobacteria, chlorophytes, and diatoms and complex direct and indirect effects, and to develop total effects food web models (i.e. SEMs). SEM type food web models are data intensive models and those presented here are in their secondary stages and will be used to help identify data gaps necessary to tailor future research so that we may more thoroughly document causal relationships among the abiotic and biotic elements of the Bay. Suffice it to say, food web interaction effects on cyanobacteria blooms are far more complex than most investigators realize and this complexity introduces substantial challenges for resource managers.

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PRINCIPAL INVESTIGATORS

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PROJECT OBJECTIVE

To provide the Wasatch Front Water Quality Council detailed scientific information on the causes and consequences of cyanobacteria blooms and to document biodiversity and biological production as well as complex ecological interactions in Farmington Bay, Great Salt Lake, Utah.

SCIENTIFIC OBJECTIVES

1. Collect a systematic record of spatial and temporal changes in the biotic community and abiotic characteristics of Farmington Bay.
2. Identify key factors that influence phytoplankton, and in particular cyanobacteria, population size, composition and structure.
3. Evaluate spatial and temporal changes in the zooplankton population composition and abundance with respect to abiotic and biotic factors as well as predator-prey relationships.
4. Document the linkage between cyanobacteria blooms and cyanotoxin production in Farmington Bay and examine the effect(s) that cyanotoxins have on resident zooplankton.

DURATION OF PROJECT

March 1, 2013 to February 28, 2016

BACKGROUND AND JUSTIFICATION

It is well-known that the Great Salt Lake (GSL) ecosystem serves multiple critical ecological and biological functions of hemispheric importance, influences the weather, and contributes substantially to the economy of Northern Utah (Paul and Manning, 2001). Although Farmington Bay has been studied intensively over the past few decades, there remains much uncertainty about the role of anthropogenic inputs and their impact on the ecology of the bay (Moser et. al., 2012; Goel and Meyers, 2009; Goel 2008; Schulle, 2008; Miller and Hoven, 2007). Of particular scientific and regulatory interest is the ecological response of Farmington Bay (FBay) to nutrient inputs from various sources including POTWs. Other researchers have examined nutrient loading into FBay periodically and have shown high levels of nutrients (especially nitrogen and phosphorous) and substantial algal growth in response to elevated nutrient levels (Wurtsbaugh, Naftz and Brandt, 2009; Wurtsbaugh, 2008; Marcarelli et. al., 2005). These authors report extremely high levels of chlorophyll-a and cyanobacteria blooms and the subsequent establishment of hypereutrophic conditions in FBay. These authors have also reported

periodic episodes of high levels of cyanotoxins. The USEPA along with the Utah State Division of Water Quality are under obligation to ensure that wastewater discharges into the Great Salt Lake comply with the Federal Clean Water Act (CWA, 33 U.S.C. §1251 et seq. (1972)). Implementation and enforcement of the CWA is challenging giving the unique characteristics of the GSL and it requires an in-depth and site-specific understanding of the complex ecological responses of the GSL to nutrient inputs. The only site specific standard that exists to date for contaminants or nutrients input into the GSL is for selenium (Ohlendorf et. al., 2009; Brix and DeForest, 2004) and the multi-year process involved establishing the selenium standard for GSL illustrates the importance and challenges of deriving such a site-specific standard. It is therefore of paramount importance to critically and systematically document and interpret the role that nutrients serve in the algal and food web dynamics of FBay, as they relate to the designated beneficial uses of the Bay that include support for waterfowl and shorebirds and the aquatic life in their food chain. Identifying and characterizing these linkages is critical in order to determine whether there is evidence of impairment. Such questions are complex as they should include the levels of productivity necessary to support the millions of waterfowl and shorebird that depend on FBay, the overall nutrient load in the greater GSL ecosystem and the possibility that substantial decreases in nutrient input into Farmington Bay might cause harm to the ecology and beneficial uses of Farmington Bay and GSL ecosystems. It is due to our concern about potential harm to GSL ecosystems from nutrient reduction strategies that we undertook a multi-year process of examining the details of nutrient concentrations and biotic responses in Farmington Bay.

INTRODUCTION

The initial goal of this study was to rigorously document biotic and abiotic characteristics of FBay. Included in this multi-year objective was to record limnological conditions in FBay from the early stages of biological production following the melting of ice in March to the onset of winter in November. The goal was to have a continuous record of both biotic and abiotic conditions in the bay and to use this detailed record to understand the factors that lead to cyanobacteria blooms and eutrophic conditions in FBay. Emphasis was placed on the nutrients nitrogen and phosphorous, their spatial and temporal variations, and the correlation between nutrient concentrations and cyanobacteria blooms. The secondary and long-term goals of the project are to discern the effects that cyanobacteria blooms have on the biotic community and the adverse impacts, if any, that such blooms have on beneficial uses of the bay. The third, and equally important goal, is to document the extraordinary diversity and abundance of biota in Farmington Bay and to discern the role that nutrients have for supporting biological production in the bay.

Objectives

The objectives for this multi-year project are shown in the following list of objectives. Realities of lake elevation resulted in a loss of access to some of the sites and financial constraints in 2015 resulted in a

reduction in the scope and frequency of the sampling program. Therefore, not all sites were sampled on all the surveys and the number of surveys differed among years.

Objective #1. Collect a systematic record of spatial and temporal changes in the biotic community and abiotic characteristics of Farmington Bay from March through November.

Routine systematic assessments of biological and abiotic conditions were completed during surveys of FBay. These assessments provided the foundation for understanding algal and aquatic invertebrate population dynamics and the factors that influence their growth. Nine sites along a north-south transect were sampled and, due to the shallow water column, water was collected from only a single depth (25 cm below the surface). Sampling began in March with the initial stages of ice-melt and continued monthly or on a semimonthly basis until the end of November. Limitations imposed by low lake elevation precluded access to some of the sites, especially those in the southern region of the bay.

Objective #2: Identify key factors that influence phytoplankton and cyanobacteria population size, composition and structure.

Information collected under Objective #1 was used to statistically and ecologically investigate relationships between observed changes in the algal population size and structure and environmental and biological factors. This field data was used to refine experimental methodology in subsequent years and design in-situ or laboratory experiments that address the specific reaction of algal colonies to changes in nutrient concentrations.

Objective #3: Evaluate spatial and temporal changes in the zooplankton population composition and abundance with respect to abiotic and biotic factors as well as predator-prey relationships.

Information collected under Objective #1 was used to statistically investigate the relationships between observed changes in the macroinvertebrate abundance, species composition, and age-class structure with factors that potentially influence such changes. Of interest is the relationship between macroinvertebrate population size and composition and algal population composition and abundance and the concentrations and extent of cyanotoxins. Abiotic factors were also analyzed in terms of their relationship and potential influence on macroinvertebrates in FBay as well as predator/prey relationships. The role of corixids in defining zooplankton assemblage composition and size was a focal point of this line of inquiry.

Objective #4: Document the linkage between cyanobacteria blooms and cyanotoxin production in Farmington Bay and examine the effect(s) that cyanotoxins have on resident zooplankton.

While cyanobacteria blooms have been well documented in FBay, the production of cyanotoxins and their impact(s) on other biota in FBay has not been well understood. The presence of cyanobacteria

blooms, as indicated by dramatic changes in phycopigments, dissolved oxygen, and the presence of algal mats, were used to determine when cyanotoxin analyses were required. Concentrations of cyanotoxins were analyzed in terms of algal population size and structure. The range and type of cyanotoxins observed was used to design a thorough laboratory experiment that examined the impact of nodularin on various age classes of *Artemia*.

METHODS AND STUDY DESIGN

Study Area

Our study focused Farmington Bay, Great Salt Lake, Utah. Farmington Bay is a highly unique body of water that provides many beneficial uses for the GSL ecosystem and for the surrounding areas. Some of these beneficial uses include, but are not limited to: providing essential nutrients into Gilbert Bay and the greater GSL ecosystem, fixing atmospheric nitrogen and releasing this additional source of nitrogen to both Farmington Bay and Gilbert Bay, providing critical habitat that supports an extraordinary number and diversity of aquatic invertebrates and avifauna, nutrient cycling essential for maintaining the biological integrity of the GSL, aesthetic value, supporting waterfowl reserves and hunting clubs, serving as a receiving water for treated sewage discharges, modulating ambient temperature fluctuations through its thermal mass, and reducing dust loads, and as a location for recreational activities. In short, Farmington Bay is an incredibly biological diverse bay of GSL and a waterbody that contributes directly to the maintenance of the ecological integrity of the entire GSL ecosystem. Harm to Farmington Bay resulting from decreased biological production is vectored throughout the entire ecosystem.

Farmington Bay is an isolated bay of the GSL that is defined geographically by both natural and manmade features; it is bordered on the west by Antelope Island, on the north by the manmade Antelope Island causeway, on the east by extensive wetlands and urban areas, and to the south by a network of wetlands, waterfowl hunting clubs and managed water impoundments. Farmington Bay is a shallow basin and under the drought conditions of the last 15 years, it has a maximum depth of 1.3 meters and an average depth of 20-35 cm and has an area of approximately 135 km^2 during our study. Water entering Farmington Bay is primarily regulated and enters the bay via the Jordan River, State Canal, the Surplus Canal, the Northwest Oil Drain, direct POTW discharges and the outflow from urban drainage basins. The Jordan River, State Canal and Surplus Canal water passes through a series of impoundments that are managed to grow pondweed to attract and support waterfowl. Discharges from these ponds, as well as the POTW discharges, the NW Oil Drain and unregulated runoff water and spring water along its eastern and western margins provide 10s of thousands of acres of shallow, sheetflow wetlands that provide nesting, foraging and staging habitat for shorebirds as well as waterfowl. Farmington Bay is connected to the main body of the GSL (Gilbert Bay) by means of a breach in the Antelope Island rock causeway. This breach allows bidirectional flow of water to and from Farmington Bay depending on lake elevation, relative hydrological forces, and weather events. During spring runoff and throughout much of the year the flow is predominantly south to north; meaning from Farmington Bay into Gilbert Bay. However, wind events can dramatically alter the flow of water through the breach resulting in a

north to south flow during certain times of the year. Abiotic and biotic features of Farmington Bay are characterized by high spatial and temporal diversity attributable to its shallow depth and the influence of bidirectional flow from the higher saline water of Gilbert Bay. There is generally a salinity gradient from south to north with the southern extension of the bay demonstrating relatively very low salinity (2-5 g/L) while the northern region near the causeway can achieve salinity concentrations approaching 100 g/L (Marcarelli, Wurtsbaugh, and Griset; 2009). This salinity gradient exerts a substantial influence on the population structure and composition of algae and zooplankton. Pronounced temporal changes in the biotic community of Farmington Bay have been documented by previous investigators and include dramatic shifts in algal species composition and abundance as well as substantial transitions in the population size and species composition of zooplankton. The bay often freezes in the winter and is typically ice free from mid-March to late December. The bay often exhibits eutrophic conditions (i.e., chlorophyll-a in excess of 400 ug/L and dissolved oxygen levels dropping to below 1.5 mg/L) during the summer months with eutrophic conditions corresponding to high abundance of cyanobacteria. Although characteristics of eutrophic conditions do exist, the extent to which these conditions exert an adverse influence on beneficial uses of the bay remains unanswered.

Sample Site Location

Sample site locations were assigned based on a north-south longitudinal transect that was established for previous scientific studies conducted by the Central Davis Sewer District and other investigators. Use of these site locations was chosen to afford an important degree of continuity from previous research investigations and because the existing site locations follow a biologically logical and defensible transect from north to south along the bay. Additionally, due to the shallow nature of the bay there are few other options (east-west) that can be reliably surveyed without undue risk of grounding. Of the nine sample sites used for this study eight were in Farmington Bay and one additional site was located on the Gilbert Bay side (north) of the Antelope Island causeway breach that allows bi-directional flow between the bays. The existing 8 Farmington Bay sites have a diversity of benthic environments and allowed for meaningful interpretations to be made about the overall condition of the bay.

Frequency and Timing of Sampling

The sampling schedule was based on the following three goals: 1) collect samples beginning at the time of ice-melt from the bay; 2) sample more frequently during months when dramatic changes in algal blooms have been previously reported; 3) continue with sampling well into the late fall and the onset of winter. A total of 28 synoptic sampling programs were completed. Additionally, 58 single site samples were collected at Site #1. These were used for cyanobacteria and cyanotoxin assessments. Most research investigations in FBay have been limited to just a few systematic surveys and none have documented conditions throughout the entire spring and therefore were limited in their interpretive capabilities. The intent of this project was to have a full record of algal dynamics during the ice-free growth season and to evaluate the algal dynamics in relation to nutrient concentrations and zooplankton population size and structure and to augment this information with more frequent tracking of the cyanobacteria growth and cyanotoxin production.

Sample collection

Separate water samples were collected for nutrient, chlorophyll-a, and algal analysis. Cyanotoxin concentrations were determined for water samples collected for algal analysis. All water samples were collected in pre-cleaned 500 ml HDPE bottles. Bottles were filled to over-flowing and capped securely to minimize head space. All samples were immediately stored in the dark and on ice and were either preserved or shipped the same day of sampling via express overnight shipping. Samples for nutrient and chlorophyll analysis were shipped to Aquatic Research Laboratory in Seattle Washington. Samples for a combination of algal enumeration and cyanotoxin analysis were shipped same day of collection to GreenWater Laboratory in Palatka Florida. Water samples used only for algal analysis were preserved using 7 ml concentrated Lugol's iodine solution, stored in the dark and on ice and then delivered to Rushforth Phycology in Orem, Utah for phytoplankton identification, enumeration and biovolume determination.

Zooplankton were collected by means of a vertical net haul using a 50 cm diameter plankton net with a 65-micron mesh and affixed with a removable collection cup. Vertical net haul depth was recorded and used to calculate the total volume sampled to report zooplankton on a per volume basis (i.e., per liter). Zooplankton were rinsed from the collection cup into 4 liter containers, transported on ice, then subsequently isolated on 30-micron sieve and discharged into 475ml glass jars. A pH buffered formaline (10% solution) was added to a final formaline concentration of 2.5%. Samples were then immersed in an ice bath and delivered to Dr. Lawrence Gray, Utah Valley University in Orem Utah for zooplankton identification and enumeration.

SAMPLING PROGRAM

Sample Site Locations

- Farmington Bay
    - 9 locations
    - Sample sites follow transect
    - Specific locations coincides with previous scientific investigations
    - GPS coordinates during 2013
        - Site 1 N: 41.03.58 , W: 112.13.46
        - Site 2 N: 41.03.09 , W: 112.11.17
        - Site 3 N: 41.01.40 , W: 112.09.23
        - Site 4 N: 40.59.34 , W: 112.08.36
        - Site 5 N: 40.57.30, W: 112.07.36
        - Site 6 N: 40.55.33, W: 112.06.09
        - Site 7 N: 40.54.43, W: 112.02.39
        - Site 8 N: 40.55.12, W: 112.01.31
        - Site 9 N: 41.04.04, W: 112.14.00

    - GPS coordinates during 2014-2015
        - Site 1 N: 41.03.56 , W: 112.13.42
        - Site 2 N: 41.03.41 , W: 112.12.40
        - Site 3 N: 41.03.13 , W: 112.12.16
        - Site 4 N: 41.03.17 , W: 112.10.10

        - Site 5 N: 40.58.12, W: 112.06.54
        - Site 6 N: 40.58.12, W: 112.06.54
        - Site 7 N: 40.56.33, W: 112.06.01
        - Site 8 N: 40.56.07, W: 112.05.38
        - Site 9 N: 40.55.47, W: 112.05.06

- Ogden Bay
    - 1 location
    - Random location near area of Antelope Island Causeway breech entrance to the open water of Gilbert Bay.
    - GPS Coordinates:
        - Site 9 N: 41.04.02 , W: 112.14.00
        -
- Transect Sample Schedule: 2013
    1. March 14, 2013
    2. April 18, 2013
    3. May 13, 2013
    4. May 30, 2013
    5. June 10, 2013
    6. June 13, 2013
    7. June 25, 2013
    8. July 11, 2013
    9. July 22, 2013
    10. August 6, 2013
    11. August 26, 2013
    12. September 19, 2013
    13. October 17, 2013
    14. November 14, 2013
- Additional Single Site Sample Schedule:
    1. January 8, 2013
    2. January 22, 2013
    3. February 5, 2013
    4. February 19, 2013
    5. March 5, 2013
    6. March 12, 2013
    7. March 19, 2013
    8. March 26, 2013
    9. April 2, 2013
    10. April 9, 2013
    11. April 16, 2013
    12. April 23, 2013
    13. April 30, 2013
    14. May 7, 2013
    15. May 22, 2013
    16. June 4, 2013
    17. June 18, 2013
    18. July 2, 2013
    19. July 9, 2013
    20. July 16, 2013
    21. July 30, 2013
    22. August 14, 2013
    23. August 21, 2013
    24. September 4, 2013

25. September 10, 2013
26. September 24, 2013
27. October 9, 2013
28. November 6, 2013

Sample Schedule 2014

January 28, 2014
March 5, 2014
March 19, 2014
March 31, 2014
April 2, 2014
April 15, 2014
April 24, 2014
May 7, 2014
May 15, 2014
May 21, 2014
June 3, 2014
June 19, 2014
July 9, 2014
August 3, 2014
September 17, 2014
September 30, 2014
October 16, 2014
December 18, 2014

Sample Schedule: 2015
January 13, 2015
February 10, 2015
March 11, 2015
March 31, 2015
April 15, 2015
April 28, 2015
May 12, 2015
May 21, 2015
May 27, 2015
June 9, 2015
June 23, 2015
June 26, 2015
July 7, 2015
July 23, 2015
August 18, 2015
August 19, 2015

September 10, 2015
September 22, 2015
October 1, 2015
October 13, 2015
November 10, 2015

Sample site locations are shown in Figures 1 and 2. Sample locations were modified slightly during 2014-2015 to cluster three sites in each designated region of the bay. The designated regions were: north, central and south. This was done because analysis of the 2013 data indicated that there were broad geographical locations that demonstrated similar biological responses and therefore were amenable to spatial grouping designation.

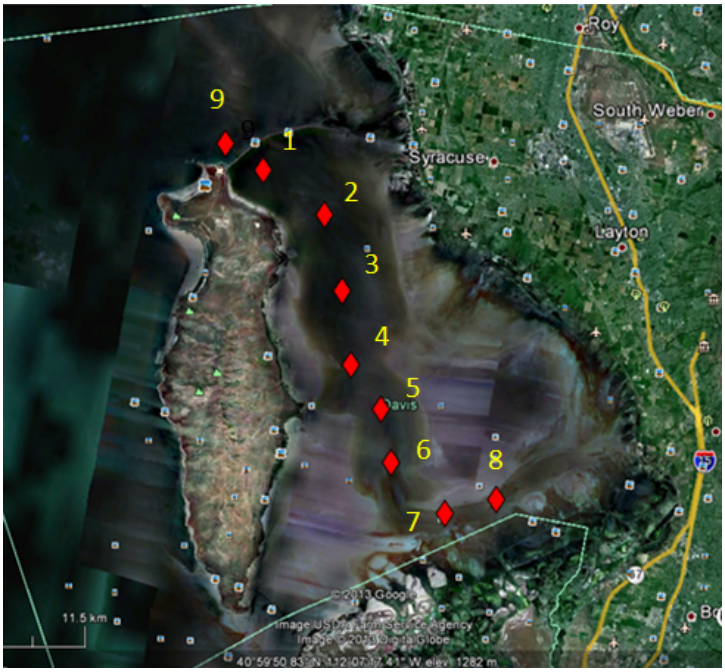

Figure 1. Sample site (total N=9) locations during 2013 in Farmington Bay (n=8) and in Gilbert Bay (n=1). Sample sites are designated along a predetermined transect through the bay and follow the midline for the 4196-elevation contour.

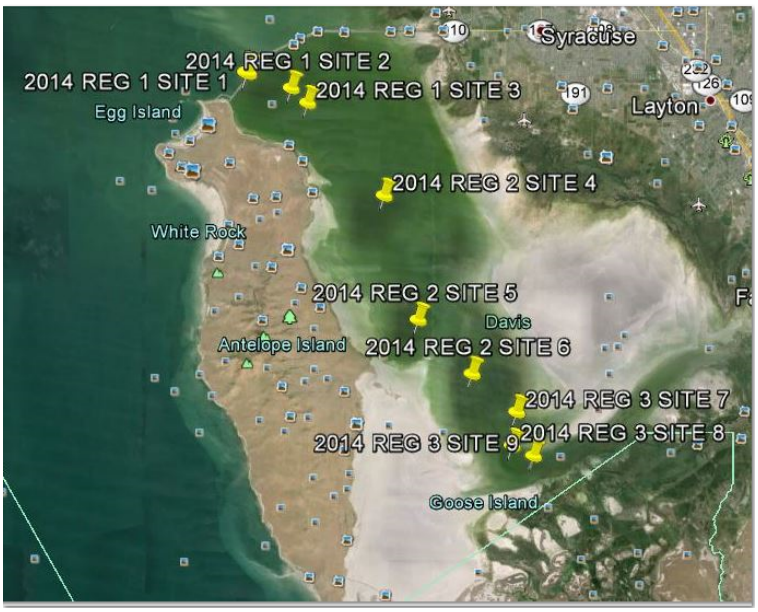

Figure 2. Sample site locations for the 2014 and 2015 Farmington Bay research program. Sample locations for these two program years were clustered based on broader geographical designations: north, central and south bay regions.

Routine Sample Site Procedures

- Routine Procedure:
  - Measure total depth
  - Secchi disk

  Measurements are taken at 25 cm depth include:
  - pH (YSI)
  - Temperature (YSI 550 temperature probe).
  - Salinity (refractometer)
  - Conductivity/TDS (Hach)
  - Dissolved oxygen (at intervals if depth is >50 cm)(YSI 550A)
  - In-vivo phytopigment measurement
    - Turner DataBank
      - Phycocyanin probe
  - Collect multiple 500 ml water samples for:
    - Nutrients
    - Complete algal assessment
    - Cyanobacteria
    - Chlorophyll-a
- Water samples treatment

  All water samples were pre-filtered through 500 or 125 micron sieves to remove zooplankton from the samples.
  - Nutrients
    - Preservative: none (samples are for immediate shipment)
    - Samples stored in HDPE bottle with eliminated head space.
    - Samples immersed in an ice bath and in the dark for transport to laboratory.

        - Samples transported to lab within 12h of completion of sampling program and shipped within 12 to 24 hours to analytical lab.
        - Samples were analyzed for NH_3, NO_3, NO_2, TKN, TP, Ortho-P
        - Samples were analyzed by Aquatic Research Inc.
        - Samples are prepared for nutrient analysis according to standard methods.
    - Algae (phytoplankton)
        - Preservative: concentrated Lugols solution.
        - Samples stored in HDPE bottle with eliminated head space. Samples immersed in an ice bath and in the dark for transport to laboratory.
        - Samples delivered to and analyzed by Rushforth Phycology.
    - Cyanobacteria
        - Preservative: none (samples are shipped overnight on same day of sampling)
        - Samples stored in HDPE bottle with eliminated head space. Samples immersed in an ice bath and in the dark for transport to Central Davis Sewer District for shipment or storage.
        - Samples shipped to GreenWater Laboratories within 12h of collection for immediate analysis.
    - Cyanotoxins
        - Preservative: None (samples are for immediate shipment)
        - Samples stored in HDPE bottle with eliminated head space. Samples immersed in an ice bath and in the dark for transport to Central Davis Sewer District for shipment.
        - Samples shipped to GreenWater Laboratories within 12h of collection for immediate analysis
    - Chlorophyll-a
        - Preservative: Magnesium Carbonate (lab).
        - Samples stored in HDPE bottle with eliminated head space.
        - Samples immersed in an ice bath and in the dark for transport to laboratory.
        - Samples shipped to laboratory within 24-48h.
        - Samples analyzed by Aquatic Research Inc.
- Net haul samples treatment:
    - Macroinvertebrates
        - Vertical net haul from bottom of water column using a 50 cm diameter plankton net with 65-micron mesh and affixed with detachable collection cup.
        - Entire contents were judiciously washed from net and into receiving collection cup.
        - Collection cup contents repeatedly rinsed with filtered Farmington Bay water into 4-liter sealed container.
        - Samples immersed in an ice bath and in the dark for transport to laboratory.
        - Zooplankton were then isolated from 4-liter container by filtration through 30-micron sieve and then rinsed into glass specimen jar.
        - Preservative: Buffered Formalin was added to the specimen jar to a final concentration of 2.5% buffered formaline.
        - Samples were then transported to the laboratory of Dr. Lawrence Gray, UVU for identification and enumeration.

- Sample identification and enumeration was carried out to the species level if possible. Enumeration includes population age class structure and fecundity assessments.

Analytical Methods

Cyanotoxin Measurements and Cyanobacteria Identification and Enumeration (GreenWater Laboratories)

Nodularins/Microcystins

- High performance liquid chromatography (HPLC) systems with photodiode array (PDA), fluorescence (FL), and mass spectrometry (M^{Sn}) detection.

Cyanobacteria Identification and Enumeration

- Samples were preserved with Lugols solution.
- Then Utermöhl counting chambers were constructed. Depending on the cell density of the sample settling towers of 5, 10 or 25 mL were used. Towers were secured to base using a thin film of high vacuum grease. Minimum settling times were 17 hours for 5 mL samples, 34 hrs for 10 mL samples and 74 hours for 25 mL samples.
- Enumerations were performed on a Nikon Eclipse TE200 inverted microscope equipped with phase contrast optics.
- A minimum of 400-600 natural units per slide were counted to give a 95% confidence interval of the estimate within +10% of the sample mean. QA/QC checks were performed at least once for every 10 samples counted and included a check for random distribution of cells (standard error among total number of natural units/field was calculated as the count was being performed with a goal of 15% or less) and a replicate count (goal being a difference between counts of 15% or less). New samples were prepared if samples failed to reach the QA/QC objectives.

Nutrients, Chlorophyll-a, pH, Salinity and Conductivity (Aquatic Research, Inc.)

- Ammonia: Automated Phenate, EPA# 350.1, Standard Method # 4500NH3H
- Nitrate/Nitrite: Automated Cadmium Reduction, EPA# 353.2, Standard Method # 4500NO3F
- Total Kjeldahl Nitrogen: micro-Kjeldahl, EPA # 351.1, Standard Method #4500NORGC
- Total Phosphorous: Automated Ascorbic Acid, EPA# 365.1, Standard Method #4500PF
- Soluble Reactive Phosphate: 0.45-micron filtration, EPA # 365.1, Standard Method #4500PF
- Salinity: Conductometric, Standard Method # 252OB
- pH: Potentiometric, EPA # 150.1, Standard Method #4500H+B
- Conductivity: Conductometric, EPA # 120.1, Standard Method #251OB

Analytical Laboratories

Nutrients, Chlorophyll-a, pH, Salinity and Conductivity

Aquatic Research, Inc.
3927 Aurora Avenue North
Seattle, WA

98103
Phone: 206.632.2715
http://www.aquaticresearchinc.com/contact.html
Certifications:

- Washington State Department of Ecology for the analysis of environmental and drinking water samples.
- State of California by the Department of Health Services Environmental Laboratory Accreditation Program (ELAP)

Cyanotoxins and Cyanobacteria Identification

GreenWater Laboratories
205 Zeagler Drive
Suite 302
Palatka, FL
32177
Phone: 386.328.0882
http://www.greenwaterlab.com/contactus.html

Phytoplankton Identification

Rushforth Phycology
4123 Bona Villa Drive
Ogden, UT
84403
801-376-3516
http://rushforthphycology.com/201.html

Zooplankton Identification

Dr. Lawrence Gray
Department of Biology
Utah Valley University
800 W. University Parkway
Orem, UT
84058
(801) 863-8558

Phytoplankton Identification and Enumeration

- Samples are filtered through a 1.2-micron pore filter
- Cells retained on the filter are resuspended in 5 ml of distilled water
- Subsamples are isolated placed in a Palmer Counting Chamber and viewed with a Nikon CF160 Infinity Optical System at 160X to 400X
- Identification is carried out to species level of taxa if possible and if species cannot be confirmed then identification is determined to genus level.
- Samples for diatom analysis are separately prepared using nitric acid digestion coupled with potassium dichromate staining.

- Diatoms are then slide mounted and identified using a Nikon Eclipse E200 microscope equipped with a Nikon CF160 optical system.
- Identification is to the lowest taxonomic level possible; species or genus level if possible, otherwise categorized according to centric or pinnate diatoms.
- Biovolume, relative abundance, and rank are determined or calculated along with cell counts.
- Detailed SOPs are available from Rushforth Phycology

Zooplankton Identification and Enumeration

- Samples are thoroughly mixed to ensure uniform distribution.
- Subsamples are then collected and dispensed into counting cells
- All zooplankton contained in subsamples are identified to lowest taxa possible.
- Age-class categories are identified, defined and enumerated according to standard procedures and distinctions.
- Gravid females are separately assessed.
- Biomass is calculated based on species composition and population size per liter.
-

Table 1. Sample collection method overview. Sample types are listed along with the details of the collection method, storage container, storage conditions, preservative method (if applicable), storage conditions, holding times, and analytical laboratories.

	Cyanotoxins	Chl-a	Macroinvertebrates	Algae	Cyanobacteria	Nutrients
Method for Sample Collection	25 cm depth sample	25 cm depth sample	Net Haul: 50cm, 160 um mesh, 30 um sample cup.	25 cm depth sample	25 cm depth sample	25 cm depth sample
Sample Container	HDPE Bottle	HDPE Bottle	Wide mouth glass specimen jar	HDPE Bottle	HDPE Bottle	HDPE Bottle
Container Volume in ml	500	500	250	500	500	500
Storage Conditions	Dark/Cold	Dark/Cold	Dark/Cold	Dark/Cold	Dark/Cold	Dark/Cold
Preservative	None	MgCO3	Formalin 5% or 60% Ethanol	Lugols /5ml per 500ml	None	None
Transit Storage Temperature	On-ice	On-ice	NA	On-ice	On-ice	On-ice
Long Term Storage Temperature	NA	NA	NA	+5ºC	+5ºC	NA
Holding Time Objectives	12h	24h	1-7d	12h (non-preserved) 1-3 days preserved	12h	<24h
Laboratory	GreenWater	Aq.Res. Inc.	Dr. Lawrence Gray	Rushforth Phycology	GreenWater	Aq. Res. Inc.

Statistical Methods

Spatial and Temporal Patterns of Phytoplankton and Zooplankton Assemblages: *Multivariate Models*

Non-metric multidimensional scaling (NMS) ordination was used to compare phytoplankton assemblages and zooplankton assemblages separately with several nutrients and chemistry variables between sites, months, and years. Ordination techniques are often more informative than hypothesis-testing approaches for exploring relationships between multivariate ecological assemblages or communities (McCune and Grace 2002). In general, ordination is the ordering of objects along axes according to their (dis)similarities; the main objective of ordination is to reduce many-dimensional relationships into a small number of more easily interpretable dimensions (i.e., axes on a plot). The strongest correlation structure in the data is extracted and is then used to position objects in ordination space. Objects that are close in the ordination space are more similar than objects distant in ordination space (McCune and Mefford 2011).

NMS was used in these analyses because it is widely used in community ecology and is often more broadly applicable than other ordination techniques because it does not require relationships among variables to be linear (McCune and Mefford 2011; Peck 2010). NMS has been shown to be highly informative for understanding chemical relationships including wetland pond sediment, pore water, and surface water chemistry in wetland ponds fringing Farmington Bay and other locations on the east front of GSL, (Carling et al. 2012) and for macroinvertebrate assemblages in impounded wetland ponds in Farmington Bay (Richards 2014), as local GSL examples. NMS ordination NMS ordination permits the visualization of the multidimensional relationships of nutrients and other chemical variables into a more easily visualized, lower dimensional space. Dimensional reduction obviously creates some distortion in relationships between samples. The level of reduction in distortion is measured as 'stress'; where lower stress values equal less distortion. NMS plots with stress values lower than 15% (0.15) are typically considered to be a good representation of the data and stress values lower than 10% (0.10) are considered excellent representations (McCune and Mefford 2011; Peck 2010).

Plankton data were condensed from the entire available dataset into a smaller set using only May to October data and by eliminating redundant variables prior to NMS analyses using PC-ORD Version 6.0 (2011). Phytoplankton cells/L were log+1 transformed and zooplankton counts/L were log generalized transformed prior to analysis. A Sorensen (Bray-Curtis) distance measure was used in the NMS analysis and run for 250 iterations using the real data and 250 iterations in randomized Monte Carlo simulations. The Sorensen distance measure is based on pairwise comparisons between all sample pairs, therefore NMS ordinations were rotated using varimax rotation to maximize variation along the axes and extracted as univariate scores. Consequently, the final ordinations can be rotated either vertically or horizontally without effecting the results. The best model was chosen based on scree plots and final stress values. Centroid labels of sites were added to the ordinations to aid in the interpret the relationships. Post hoc proportion of variance represented by each axis was calculated based on the R^2

value between distance in the ordination space and distance in the original space. Individual taxa and chemical/nutrient variable correlations with NMS axes were also calculated.

MRPP (multi-response permutation procedure), a non-parametric multivariate method was used to formally test the hypothesis of no differences in plankton assemblages between months, years, and sites. MRPP has the advantage of not requiring distributional assumptions such as multivariate normality and homogeneity of variance and thus is often preferred over MANOVA for analyzing multivariate ecological data (McCune and Grace 2002). A Sorensen (Bray-Curtis) distance measure was used in this MRPP analysis. The chance-corrected within-group test statistic, *A* (and associated p-value) was used to evaluate the hypothesis of no difference in the spatial and temporal groupings (McCune and Grace 2002).

Environmental Threshold Models

Phytoplankton and zooplankton assemblage and taxa thresholds were developed for several environmental variables including salinity using the R package: TITAN2 (Baker, King, and Kahle 2015, Baker and King 2011, 2013). This statistical method is relatively new and a detailed description of the model is provided in Appendix 4.

Random Forests (RF) and Regression Tree (RT) Models

Random Forest models were made for cyanobacteria, chlorophyte, and bacillariophyte densities in response to thirteen predictor environmental variables: salinity, temperature, SRP, TP, ammonia, TKN, TN:TP, DIN:TP, NO_3, NO_2, TN, and TN:SRP, TN molar, and TP molar. Random Forest is a statistical algorithm that is used to cluster points of data into functional groups and is considered unexcelled in accuracy among current machine learning algorithms (Breiman and Cutler 2016). When the data set is large and/or there are many variables it becomes difficult to cluster the data because not all variables can be considered, therefore the algorithm gives a certain chance that a data point belongs in a certain group. The algorithm clusters the data into groups and subgroups. If lines are drawn between the data points in a subgroup, and lines that connect subgroups into group etc. the structure would look somewhat like a tree. This is called a decision tree. At each split or node in this cluster/tree/dendrogram variables are chosen at random by the program to judge whether datapoints have a close relationship or not. The program makes multiple trees a.k.a. a forest. Each tree is different because for each split in a tree, variables are chosen at random. The Random Forest model used in our analyses was 'randomForest' R package (Breiman and Cutler 2015) run in RStudio (2016). We generated 500 trees. RF output was 'inclusive node purity', which was measured by mean square error (MSE), that averages cumulative reduction in node impurity due to splits by a variable over all trees or mean decrease in MSE. Higher node purity values indicate greater importance of the predictor variable.

Regression Trees (RT) were also developed using the same environmental predictor variables for dependent cyanobacteria densities used in our random forests models and simultaneous quantile regression. RTs are also machine learning decision trees where the variable is continuous as opposed to a finite set of values (classification trees), however they only produce one tree as opposed to Random Forests that select from hundreds of trees. We used the R statistical package 'rpart' for the RTs.

Structural Equation Models (SEM)

Ecologically based SEMs are designed to examine complex relationships and processes of the system 'as- a- whole', instead of just examining individual processes (Grace 2006). SEMs have been successfully used for many years in scientific fields outside of ecology and their utility is only now being appreciated and used in this discipline (Grace 2006). SEMs include a diverse set of mathematical models, computer algorithms, and statistical methods that fit networks of constructs to data (Kaplan 2007, Grace 2006). SEMs incorporate confirmatory factor analysis, path analysis, partial least squares path modeling, and latent growth modeling (Kline 2011, Grace 2006, Acock 2013). SEM is more of a confirmatory method and selection of interactions (dependencies, effects) were based on our a priori knowledge of the system. One of the more important aspects of SEMs is their ability to evaluate indirect effects ('dependencies') as opposed to other regression models that do not have this capability (Grace 2006). We used maximum likelihood with missing values algorithm in the SEM module in Stata/IC 14.2 for Mac (64-bit Intel) (StataCorp 2015) for all our SEM analyses to develop interaction models between nutrients/chemistry, phytoplankton groups, and zooplankton groups. We examined dozens of potential models and selected final models based on modification indices, overall model and equation level goodness of fit tests and then computed direct and indirect effects equations (Acock 2013, Stata 14.2).

RESULTS

Data collected from three years of field investigations of Farmington Bay were compiled and examined statistically and ecologically. The number of sites sampled and the frequency of sampling varied among the years. The most intensive survey program occurred during 2013, followed by lower frequency of programs and fewer sites examined in 2014 and 2015. The reduction in frequency and sites visited was primarily influenced by access—the decline in elevation of GSL during 2014 to 2015 resulted in extremely shallow conditions in Farmington Bay that precluded access to designated sampling locations. Other factors including a shift in research priorities and the allocation of limited funds altered the experimental design. Nonetheless, an abundance of useful information was gathered and provided the opportunity to explore in detail factors that influence cyanobacteria blooms. In addition to our focus on cyanobacteria blooms (i.e., harmful algal blooms—HABs) in Farmington Bay we devoted serious attention to documenting the remarkable biodiversity of Farmington Bay and their biotic response to nutrient availability.

ABIOTIC ASSESSMENTS

Salinity

Salinity varied both spatially and temporally across Farmington Bay throughout the course of each study period and showed differing yearly patterns. Within each sample program this north-south spatial gradient was observed (Figure 3). The southern region of received freshwater input from surface flow, transient stream contributions and from anthropogenic sources from POTWs located in Davis and Salt Lake Counties. Salinity was highest in the sites located in the northern region of the bay demonstrating influence from bidirectional flow of water from Gilbert Bay into Farmington Bay. The gradient was observed during all sampling programs, yet varied in the magnitude of the overall range. The southern region of Farmington Bay remained low in salinity throughout the summer months. Salinity in Farmington Bay decreased from 2013-2015 attributable to limited tributary inflow and subsequent declines in GSL elevation. The lower elevation of Gilbert Bay and diminished inflow greatly reduced the surface area of Farmington Bay, narrowed the flow channel, and reduced the salinity gradient. Farmington Bay was more like a broad slow moving river than a stagnant bay in 2015.

During 2013 salinity in the northern region of the bay near sites 1-3 was typically in the range of 10 ppt to 60 ppt. Sites 4, 5, and 6 exhibited some influence of salt influx from Gilbert Bay and showed salinity in the range of 5 to 30 ppt. Sites 6, 7 and 8 were essentially fresh water sites. These salinity levels are consistent with previous investigations that also documented consistent north-south gradient across the bay (Wurtsbaugh and Marcarelli 2004; Wurtsbaugh et al., 2012).

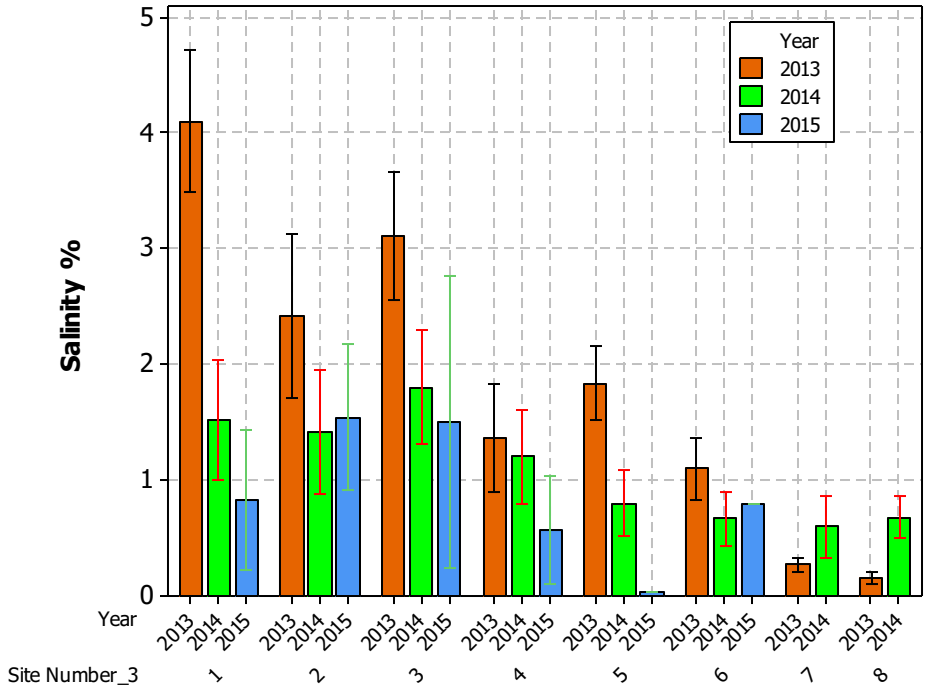

Figure 3. %Salinity at each year and site. Mean values and standard errors.

The highest salinity occurred at site 1 during 2013 with a measurement of 83 ppt while at the southern terminus of the bay the highest level recorded was 5 ppt. There was within year temporal influence on salinity in which evaporative loss during dry summer months resulted in a concentration of dissolved solutes and a concomitant increase in salinity. This was most evident during 2013 when the salinity of mid-bay sites showed a demonstrable increase (Fig 3). The collective salinity of Farmington Bay increased consistently from April through September in 2013. This same pattern of increased salinity was observed in the northern and mid-bay locations during 2014 but was not observed during 2015. During 2015 narrowing of the channel and a presumed decreased residence time in the bay may have diminished the net evaporative loss of water and in so doing maintained a lower salinity.

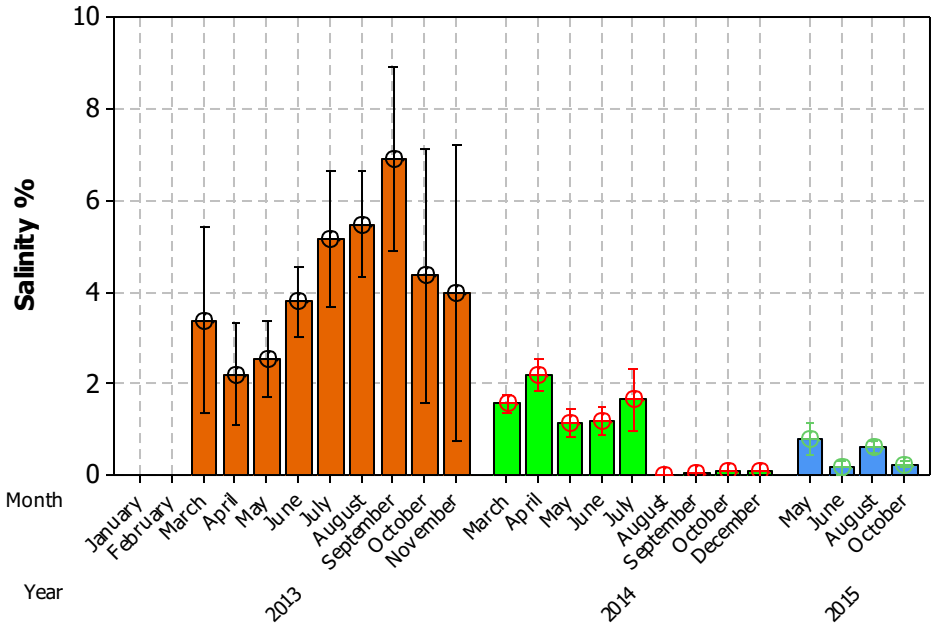

Figure 4. % Salinity by month and year.

Dissolved Oxygen

Dissolved oxygen levels in Farmington Bay did not show a distinct temporal and spatial pattern of variation as had been observed for other abiotic factors. Dissolved oxygen levels in the water column during the sampling program were generally adequate to support most oxygen dependent zooplankton (e.g., >2.0 mg/L) (Figure 5). Across all years of the study 98% of the DO readings were > 2 mg/L. This is a dissolved oxygen level which is known to support *Artemia* growth and development and that is generally supportive of other aquatic invertebrate biota.

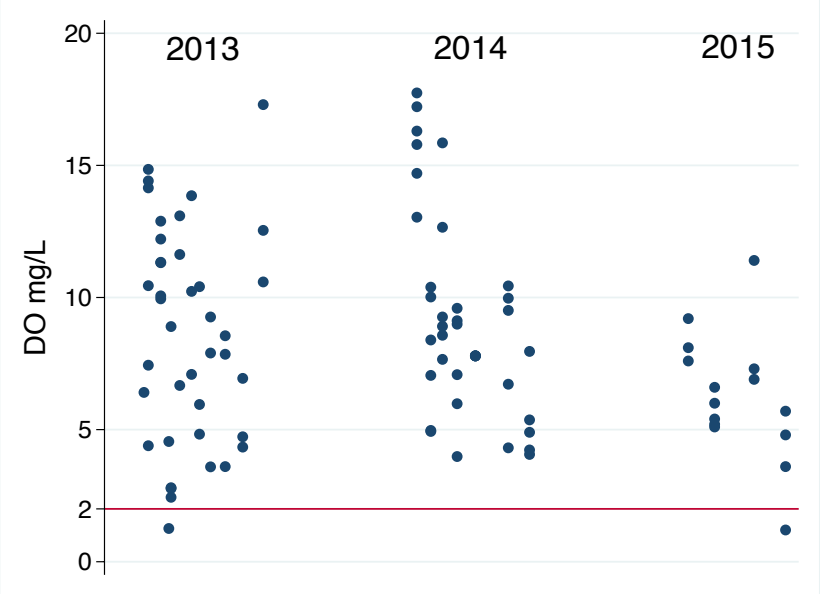

Figure 5. Dissolved oxygen (DO) levels (mg/L) from 2013 to 2015. Red horizontal line is threshold value for many taxa including Artemia.

However, there was a period of oxygen depletion, notably during the June 10-13, 2013 sampling programs. Average DO during this week was just 2.6 mg/L. This time frame followed the initial peak and subsequent decline in *Nodularia* abundance during 2013. Dissolved oxygen levels in the water column increased thereafter resulting in average dissolved oxygen levels across the bay that were between 2.6 and 10.7 mg/L. Peak levels were either in the early spring, at a time of low zooplankton biomass, or in November after grazing pressure from zooplankton had subsided.

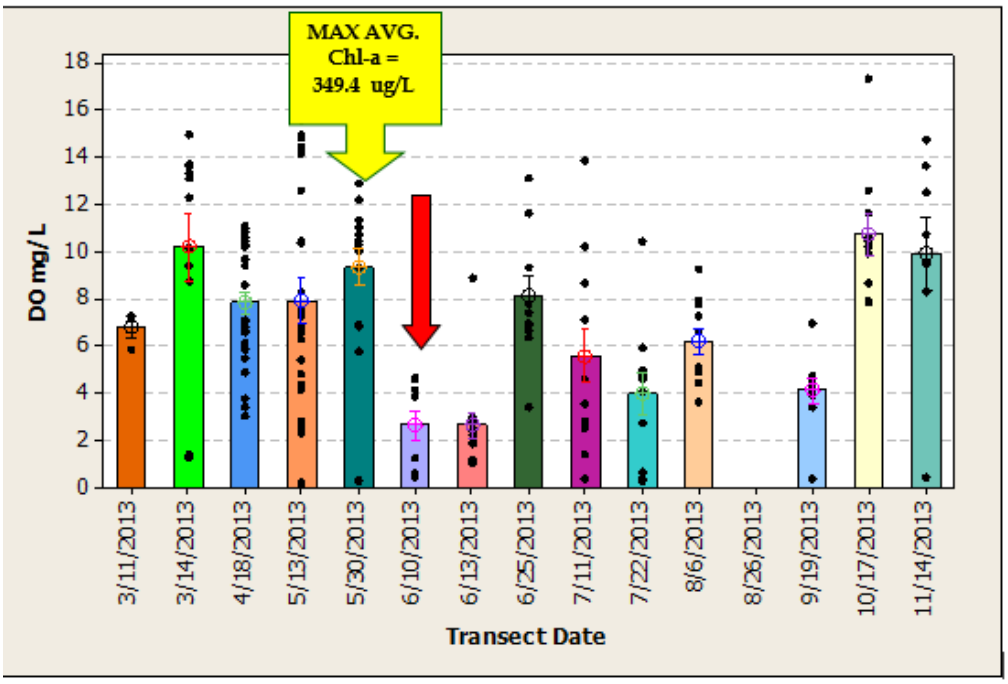

Figure 6. Dissolved oxygen measurements by sample program date for Farmington Bay. A distinct decrease in dissolved oxygen occurred in early June and occurred shortly after the initial peak and collapse of cyanobacteria.

Dissolved oxygen exhibited vertical stratification at sites that were greater than one meter in depth. For example, on March 13, 2013 the DO at 25 cm to 50 cm depth were all greater than 10 mg/L. At 75 cm depth this declined to 6.9 mg/L (i.e., 26% saturation) and at depths of 1 meter or more the dissolved oxygen declined to between 0.09 to 2.5 mg/L (i.e., $\leq$20 % saturation). Diel changes in DO were undoubtedly taking place, and may have exerted an influence on the observed pattern, yet such daily fluctuations were not documented. Observations during the study did not indicate lethal depletion of DO. Depletion of oxygen is one of the concerns often expressed regarding eutrophication of water bodies. Even though all mean daily values for the bay were above 2 mg/L there were isolated cases of hypoxia in which the oxygen levels dropped below 1 mg/L. Because all our measurements of dissolved oxygen took place during the day the perception of impairment is lessened and anoxic events could have taken place during the night but were unrecorded. When comparing zooplankton abundance with oxygen levels during the day there is no clear evidence of harm to the biota. Declines in oxygen during the night remains a concern though, especially when one considers the observations of Wurtsbaugh et al. (2012) who found that oxygen levels in the daytime could reach as high as 40 mg/L but would decline to 0 ug/L at night. In our study oxygen levels peaked at 17.3 mg/L while the lowest values were between 0.09 to 0.39 mg/L. The lowest levels coincided with the development and collapse of cyanobacteria blooms in May through July.

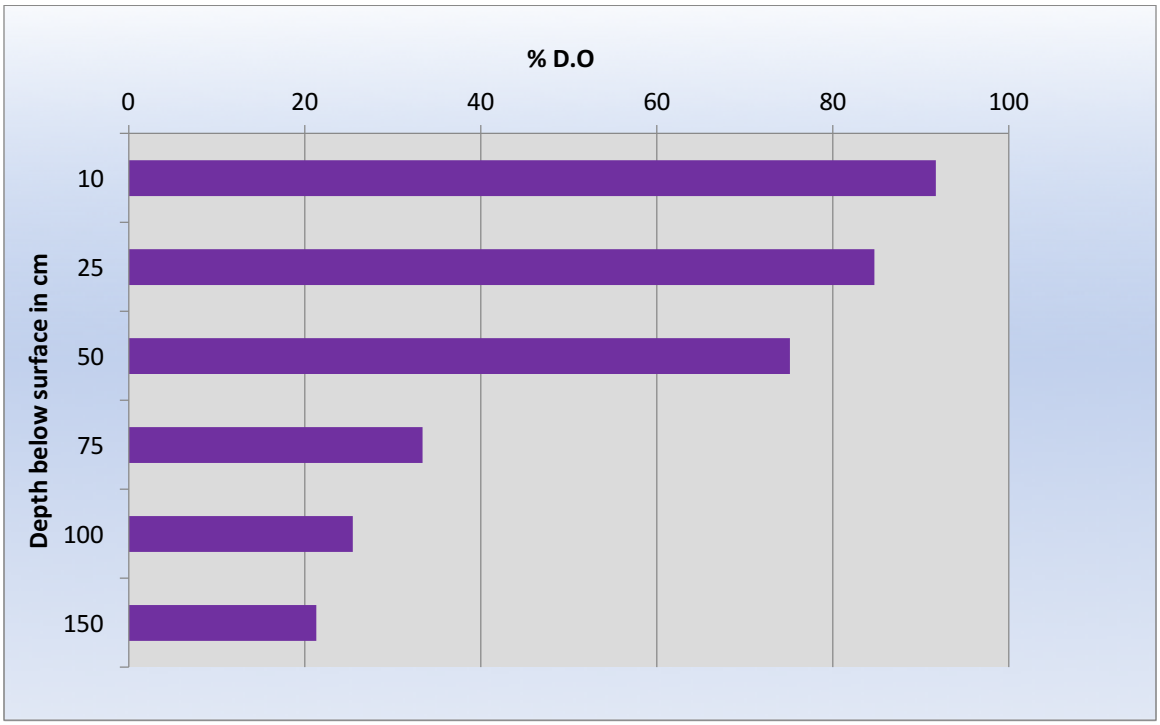

Figure 7. Vertical stratification of dissolved oxygen observed on May 13, 2014 at site #1. This location was one of the relatively deeper regions of the bay and was proximal to the Antelope Island causeway and breach. Stratification is likely the result of hypersaline water of Gilbert Bay forming a lens of denser water beneath the Farmington Bay water. This stratification may result in oxygen depleting reactions with hydrogen sulfide or methane found in sediments in this region of the bay.

Temperature

Over the course of the project, and during the months assessed, water temperature within Farmington Bay was between 1.5 and 30.6 degrees Celsius (Figure 8). The shallower sites located in the southern region of the bay warmed more quickly than the somewhat deeper sites in the northern region of the bay during April. Similarly, these shallow sites cooled off more quickly during September through November. The average water temperature peaked in July with an average temperature of 27.5 C. Water temperature was recorded only during transect sampling programs and diel temperatures were not recorded. The bay had warmed to over 20 C during May and cooled off rapidly each September. Due to reduced flow through Farmington Bay because of drought conditions during 2015 the bay exhibited more rapid increase in temperature and the June water temperature was well above that measured during 2013 and 2014. Maximum annual temperature usually occurs in July. Temperature is an important factor in growth and development of algae and zooplankton and in combination with salinity and nutrients

exerts a pronounced influence on population dynamics. Temperature also is known to be a significant factor in the cycling of nutrients and nutrient flux dynamics at the sediment/water interface.

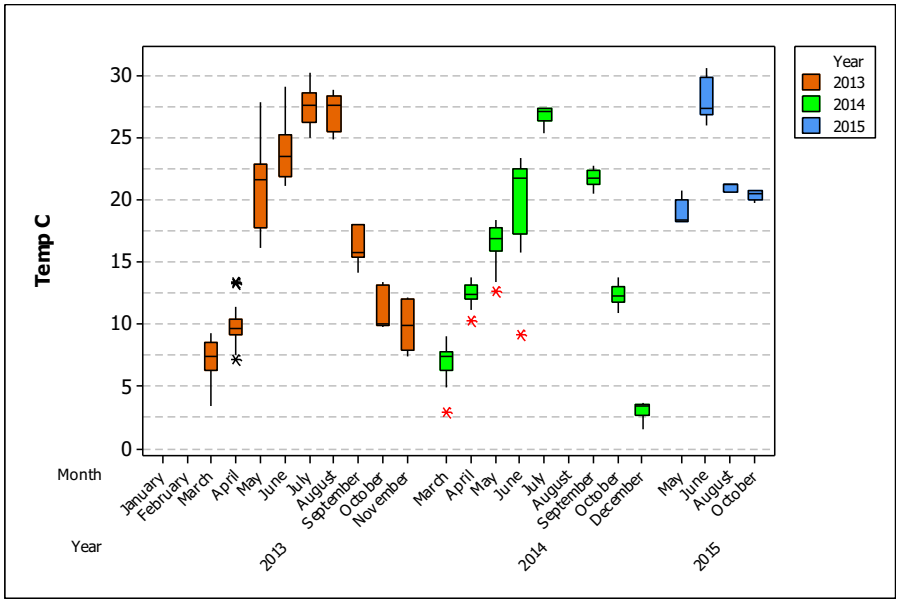

Figure 8.Variability of temperature (degrees C) by month and year in Farmington Bay.

BIOTIC ASSESSMENTS

Chlorophyll

Consistent with the oft-described character of Farmington Bay as eutrophic, or even hypereutrophic, chlorophyll-a levels in the water column varied substantially and achieved some extraordinarily high levels during periods of peak sunlight, temperature and cyanobacteria blooms. High levels of chlorophyll-a have been reported by multiple previous authors and have been in excess of 200—300 ug/L (Wurtsbaugh and Marcarelli, 2006; McCulley, 2014). These high levels of chlorophyll-a are the result of robust algal growth supported by readily available concentrations of P, a combination of N availability, N_2 fixation in N limited regions of the bay, and diminished grazing pressure on phytoplankton due to top-down control of zooplankton by invertebrate predators. While there is no dispute that chlorophyll-a levels in the bay routinely reached hypertrophic levels, there is much

uncertainty about whether it is indicative of any level of harm to the biota of the bay. A yearly comparison of chlorophyll-a is shown in Figure 9. Over the three-year period there was a collective decrease in chlorophyll levels. This decrease coincides with less frequent, smaller, or absent cyanobacteria blooms.

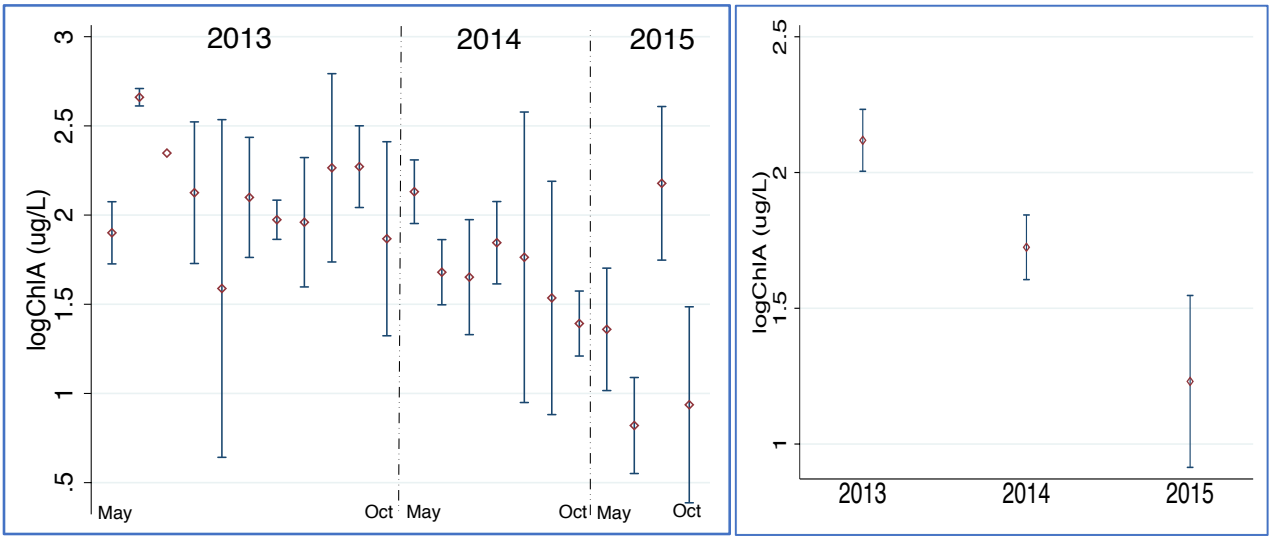

Figure 9.Variability of logChlA (ug/L) from 2013 to 2015 by sample date (May through October samples only). Second part of figure is combined logChlA values to further illustrate the decline from 2013 to 2015.

Chlorophyll-a concentrations in Farmington Bay were consistently high relative to values typically encountered in Gilbert Bay (peak values in Gilbert Bay are often ≤40 ug/L). Chlorophyll-a values for Farmington Bay differed from Gilbert Bay in that peak chlorophyll-a levels typically occur during late winter and early spring in Gilbert Bay, whereas in Farmington Bay peak levels occur during summer months (usually May) (Figure 10). On March 11, 2013, shortly after the melting of surface ice, the average concentration was only 9.01 ug/L. Coinciding with algal blooms in the bay, chlorophyll-a levels increased in a pronounced manner and by May 30, 2013 it reached the hypereutrophic level of 349.4 ug/L (average concentration for the entire bay). The site-specific peak level measured on this date was 506.0 ug/L. Algal production was taking place at an exponential growth rate during this time period and the primary algal group responsible for the Chl-a increase was cyanobacteria. The lowest dissolved oxygen levels recorded throughout the summer followed this maximum production of chlorophyll-a. The decline in dissolved oxygen occurred two-weeks later during the subsequent sampling programs on June 10-13th, thus exhibiting a classic pattern of eutrophication of a water body: exponential algal growth followed by a collapse of the population (*Nodularia* cells per liter declined by 72.5% between May 30th and June 13th) coupled with depletion of oxygen by bacterial degradation processes. It is notable that DO concentrations did recover from the depletion event quickly by July 11th and between July and October levels returned to between 4.0 mg/L and 10.7 mg/L.

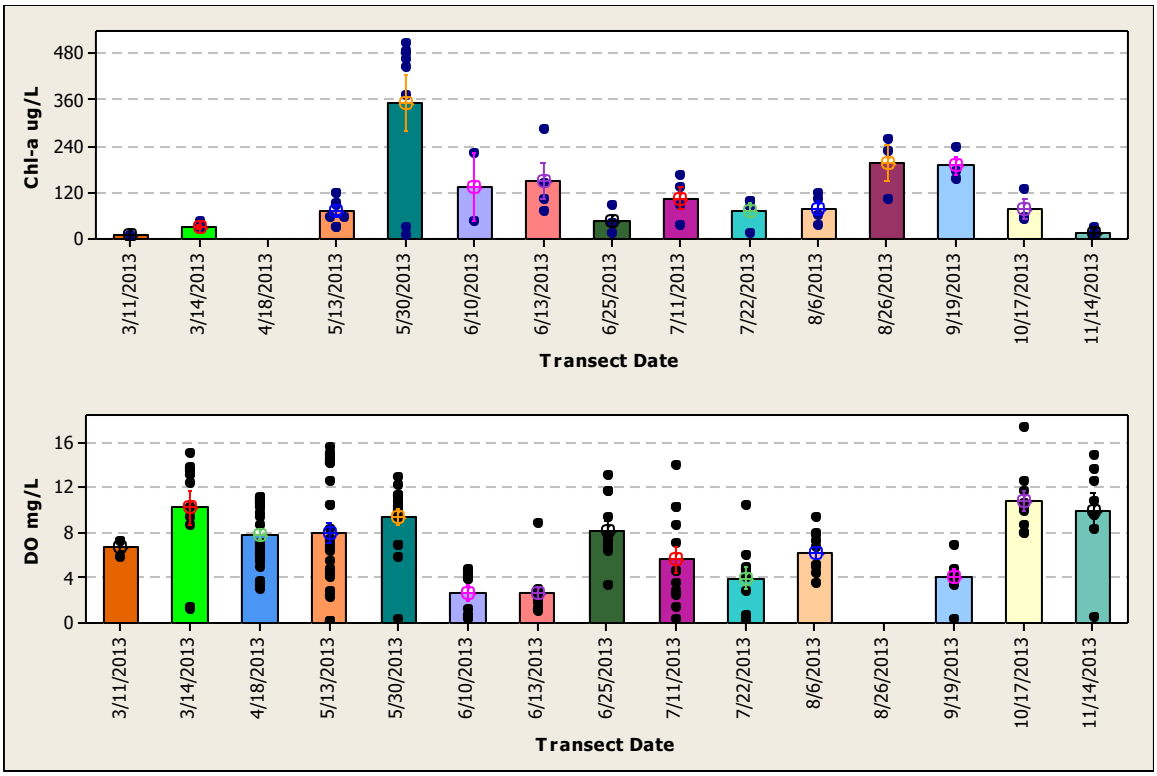

Figure 10. Comparison of chlorophyll-a values and dissolved oxygen from 2013 data set. The relationship between chlorophyll-a production and dissolved oxygen can be observed.

Comparing site specific chlorophyll-a values over the course of a three-year period shows a pattern of decreased chlorophyll-a production with each subsequent year—2013>2014>2015 (Figure 11). This pattern is evident in the sample locations in the central and northern regions of the bay. These are the regions that coincide with HABs indicating that the substantial variability between years is primarily a result of HABs rather than being attributable to other algal taxa. Additionally, the high chlorophyll counts were positively correlated with total numbers of *Nodularia* cells per liter ($R^2 = 0.48$). The relationship between Chl-a and other algal groups was not as evident.

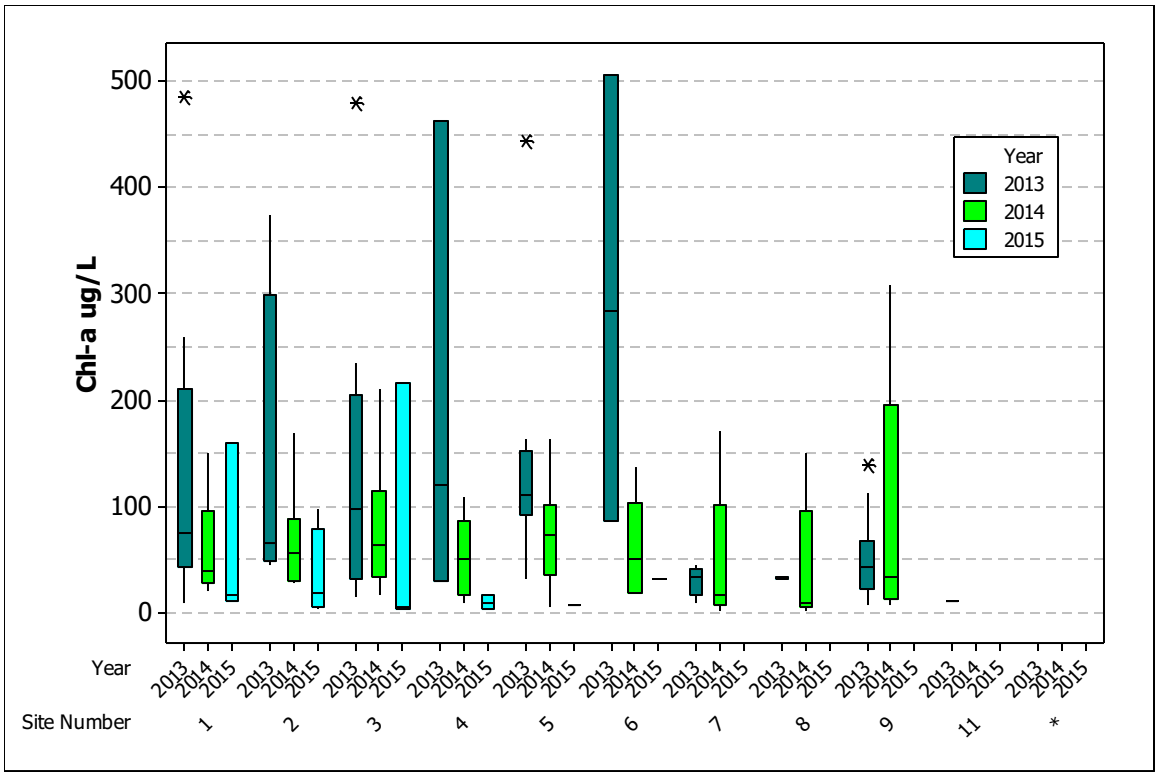

Figure 11.Chlorophyll-a levels are shown by year and site location. Among the sites in mid-bay (sites 4-6) or the northern region (sites 1-3) of Farmington Bay showed a general pattern of decreasing chlorophyll-a levels from 2013 to 2014 to 2015. Sample site 7-9 were not always accessible rendering comparisons less meaningful.

Chlorophyll-a and Secchi Depth

Transparency in the water column as measured by secchi disk showed consistently low light penetration into the water column. Average secchi depths measurements were between 20 and 43 cm. The maximum light penetration into the water column in Farmington Bay during the study was 150 cm at site #2 on March 11, 2013 shortly after the ice had cleared from the northern region of the bay. Sites 5 and 6 (mid-bay) had the lowest transparency measurements with an average depth of just 20 cm and 21 cm respectively. Secchi depth and chlorophyll-a levels exhibited a linked relationship (Figure 12 R^2 = 0.59) suggesting that diminished light penetration is attributable to chlorophyll producing algal cells rather than other sources of turbidity such as inorganic and organic particulate matter.

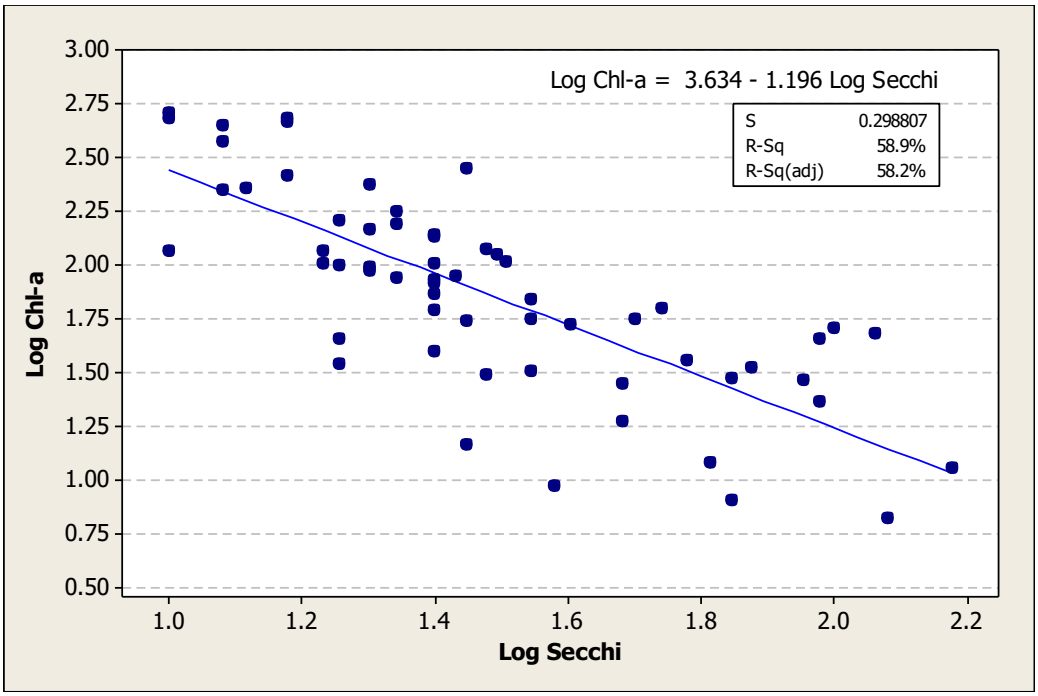

Figure 12.Chlorophyll-a concentration and secchi depth exhibit an inverse relationship; with increasing transparency chlorophyll-a values decrease in a log-linear manner.

NUTRIENTS

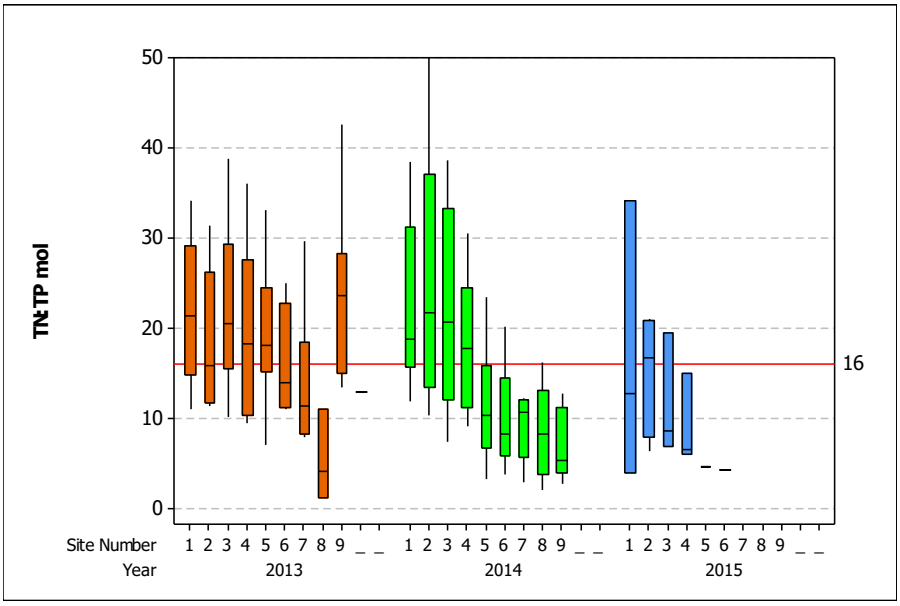

Figure 13. TN:TP by site and year.

PHYTOPLANKTON

The phytoplankton assemblage in Farmington Bay is exceedingly diverse. We found at least 23 Bacillariophyta (diatom) taxa; 97 Chlorophyta (green algae), and 29 Cyanobacteria (blue-green algae), as well as over a dozen other taxa including Chrysophytes (golden algae) and Euglenophytes.

Table 2. Phytoplankton Taxa List (2014 and 2015 data, all sites, all months).

Bacillariophyta	**Achnanthidium sp.**
	Amphiprora sp.
	Amphora sp.
	Asterionella formosa
	Aulacoseira distans
	Campylodiscus cf. bicostatus
	Chaetoceros sp.
	Cylindrotheca sp.
	Cymbella sp.
	Cymbella/Encyonema sp.
	Entomoneis sp.
	Gyrosigma sp.
	Navicula sp.
	Nitzschia acicularis
	Nitzschia closterium
	Nitzschia sp.
	pennate diatom sp.
	Phaeodactylum tricornatum
	Phaeodactylum tricornutum
	Plagiotropis sp.
	Stephanodiscus niagarae
	Surirella sp.
	Synedra cf. acus
Chlorophyta	**Actinastrum hantzschii**
	Actinastrum sp.
	Acutodesmus dimorphus
	Acutodesmus sp.
	Ankyra judayi
	Carteria sp.
	cf. Dictyosphaerium sp.
	cf. Dictyosphaerium sp./spp.
	Chlamydomonas sp.

Chlorogonium sp.
Closterium sp.
Closterium spp.
Coelastrum sp.
Coenochloris fottii
Cosmarium sp.
Crucigeniella sp.
Desmodesmus cf. bicaudatus
Desmodesmus cf. intermedius
Desmodesmus communis
Desmodesmus intermedius
Desmodesmus opoliensis
Desmodesmus sempervirens
Desmodesmus sp.
Desmodesmus spp.
Dichotomococcus sp.
Dictyosphaerium ehrenbergianum
Dictyosphaerium pulchellum
Dictyosphaerium sp.
Dictyosphaerium/Mucidosphaerium sp.
Didymocystis fina
Didymocystis sp.
Didymogenes palatina
Dunaliella sp.
Dunaliella sp./spp.
Hindakia tetrachotoma
Kirchneriella sp.
Kirchneriella/Monoraphidium sp.
Koliella sp.
Koliella/Monoraphidium sp.
Lobocystis sp.
Micractinium pusillum
Micratinium sp.
Monoraphidiium arcuatum
Monoraphidiium contortum
Monoraphidium arcuatum
Monoraphidium circinale
Monoraphidium contortum
Monoraphidium griffithii
Monoraphidium komarkovae

Monoraphidium minutum
Monoraphidium nanum
Monoraphidium sp.
Monoraphidium/Koliella sp.
Mucidosphaerium pulchellum
Mychonastes sp.
Nephrochlamys subsolitaria
Oocystis borgei
Oocystis pusilla
Oocystis sp.
Oocystis sp. (unicell)
Oocystis spp.
Pandorina morum
Paradoxia multiseta
Pediastrum boryanum
Pediastrum cf. boryanum
Pediastrum duplex
Pediastrum integrum
Pediastrum simplex
Pediastrum sp.
Pseudodidymocystis fina
Pseudodidymocystis sp.
Pseudopediastrum boryanum
Pseudopediastrum sp.
Scenedesmus acuminatus
Scenedesmus acutus
Scenedesmus cf. intermedius
Scenedesmus communis
Scenedesmus falcatus
Scenedesmus integrum
Scenedesmus linearis
Scenedesmus obliquus
Scenedesmus ovalternus
Scenedesmus sempervines
Scenedesmus sempervirens
Scenedesmus sp.
Scenedesmus sp. (unicell)
Scenedesmus spp.
Schroederia setigera
Sorastrum sp.

	Stauridium tetras
	Tetraedron minimum
	Tetraedron caudatum
	Tetraedron sp.
	Tetraselmis sp.
	Tetrastrum sp.
	Tetrastrum staurogeniaeforme
	Treubaria triappendiculata
Chrysophyta	**Chrysococcus sp.**
	Mallomonas sp.
Cryptophyta	**Chroomonas/Rhodomonas sp.**
	Cryptomonas sp.
Cyanobacteria	**Anabaenopsis elenkinii**
	Anabaenopsis sp.
	Aphanocapsa delicatissima
	Aphanocapsa sp.
	Aphanocapsa/Chroococcus sp.
	Aphanothece sp.
	cf. Eucapsis sp.
	cf. Romeria sp.
	Chroococcus sp.
	Coelosphaerium sp.
	Cyanodictyon sp.
	Dactylococcopsis irregularis
	Dolichospermum sp.
	Komvophoron sp.
	Merismopedia punctata
	Merismopedia sp.
	Merismopedia tenuissima
	***Nodularia* spumigena**
	nostocalean filament sp.
	Oscillatoria sp.
	Oscillatoria/Phormidium sp.
	Phormidium sp.
	Planktothrix sp.
	Pseudanabaena catemata
	Pseudanabaena sp.
	Sphaerospermopsis aphanizomenoides

	Spirulina meneghiniana
	Spirulina sp.
	Synechococcus sp.
Euglenophyta	**Colacium sp.**
	Euglena sp.
	Lepocinclis sp.
	Lepocinclis/Phacus sp.
	Phacus megalopis
	Phacus sp.
	Trachelomonas sp.
Eustigmatophyta	**eustigmatophyte unicell sp.**
Haptophyta	**Chrysochromulina cf. parva**
	Chrysochromulina sp.
Prasinophyta	**Tetraselmis sp.**
Pyrrhophyta	**dinoflagelate sp.**
Xanthophyta	**Goniochloris sp.**

Phytoplankton Assemblages

MRPP analyses showed that phytoplankton assemblages differed significantly between years (A=0.10, p <<0.01) and months (A=0.35, p <<0.01) but not sites (A=-0.02, p = 0.96) (Sites 1-6 included in analyses). Assemblages likely differed significantly between each month (Appendix 2). Our best NMS model was a 3-dimensional model with final stress = 12.68, instability = 0.00, at 43 iterations. Cumulative R^2 = 0.85, Axis 1 R^2=0.53, Axis 2 R^2= 0.20, and Axis 3 R_2 = 0.12. Differences in assemblages by years are illustrated in Figure 14, Axis 1 and 2.

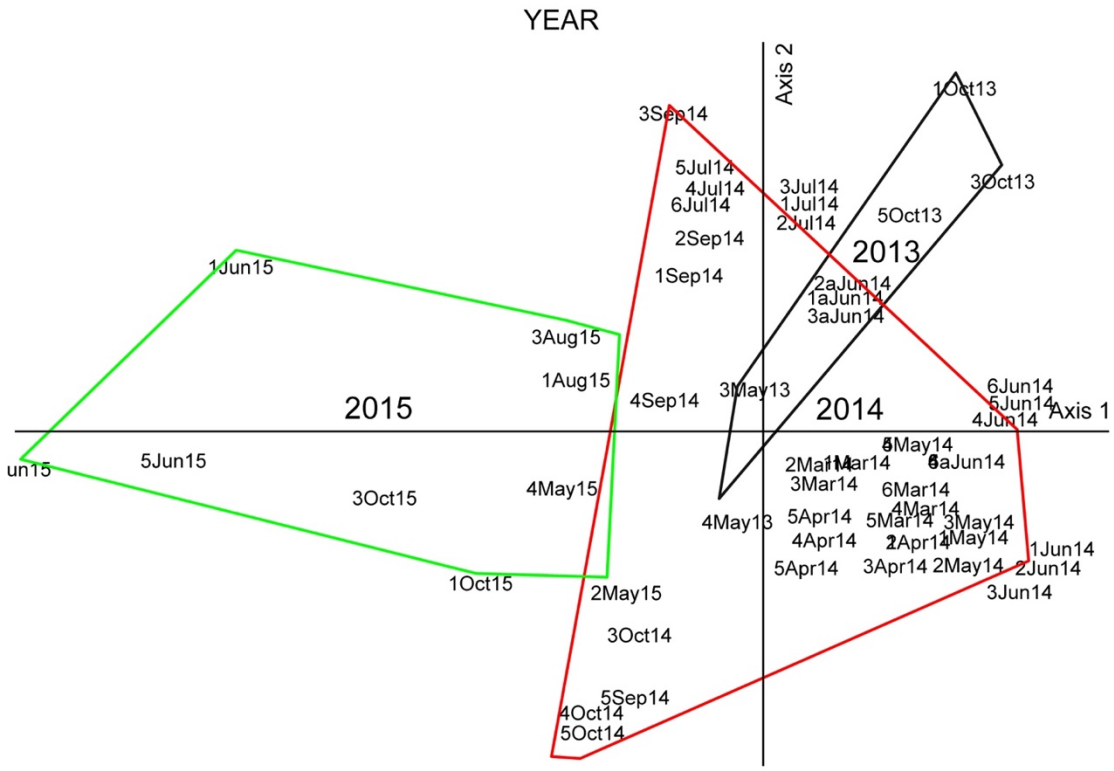

Figure 14.NMS ordination showing relationships between phytoplankton assemblages in Farmington Bay by year (April-October, 2013-2014 data). Axis 1 R^2 = 0.53; Axis 2 R^2 = 0.20. Phytoplankton assemblages differed significantly between years (see MRPP results, Appendix X)

Differences in phytoplankton assemblages by month are illustrated in Figure 15. In addition, taxa and chemistry/nutrients that had correlation coefficients >0.5 with each axis are shown. The general pattern is that assemblages tended to group by season; spring (March, April, and May), summer (July, August, and September) and autumn (October and November)(Figure 15). Conductivity was generally higher in spring and SRP, TP, TN, and NH_3 lower and conversely conductivity lower, and SRP, TP, TN and NH3 higher in summer and autumn. *Dictyospherium*, *Nodularia*, *Chaetocerous*, and *Oocystis* sp. also tended to be more abundant in spring than in summer and autumn. Microflagellates, *Amphora* sp., and euglenophytes appeared to dominate in late summer and autumn (Axis 1, Figure X) and *Nitzchia closterium*, *Spirulina* sp. and *Navicula* sp. were generally more common in summer than in spring and autumn (Axis 2, Figure 15).

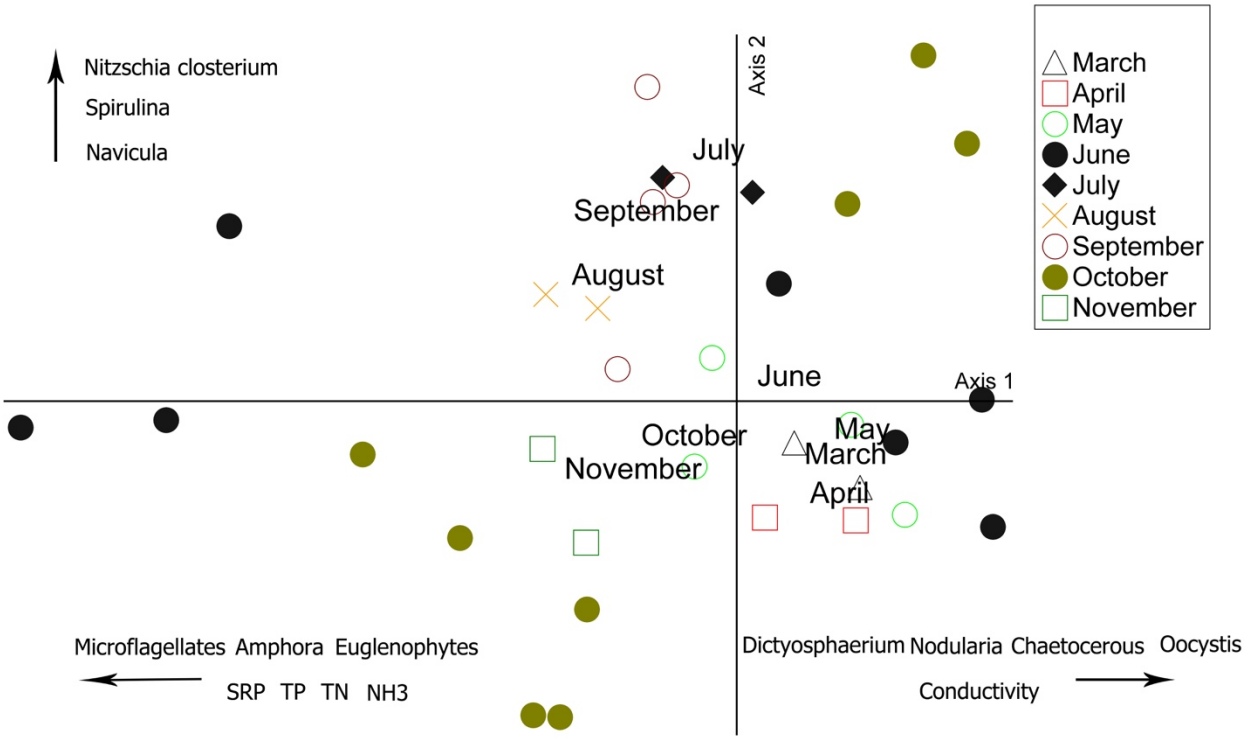

Figure 15. NMS ordination showing relationships of phytoplankton assemblages in Farmington Bay between months (April-October, 2013-2014 data). Axis 1 R^2 = 0.53; Axis 2 R^2 = 0.20. Phytoplankton assemblages differed significantly between months (see MRPP results, Appendix X). Individual taxa and chemistry/nutrients along axes are those with correlations $\geq$ 0.5. (see MRPP results, Appendix 1)

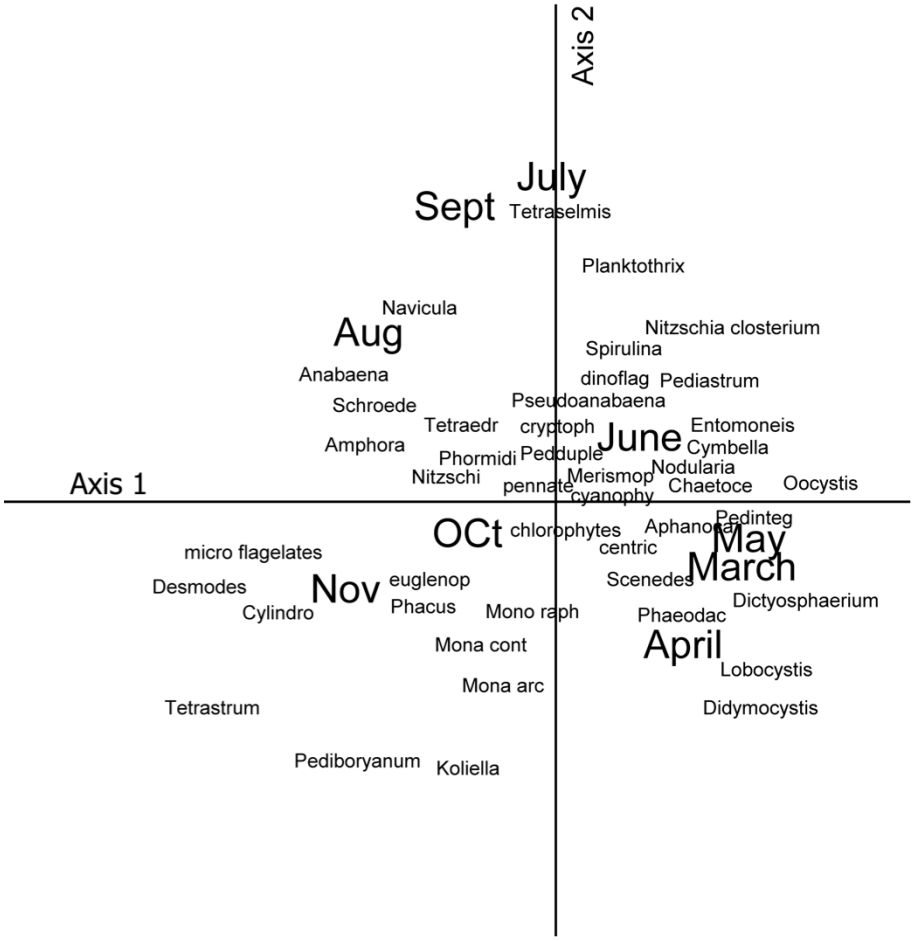

Figure 16. NMS ordination showing relationships of phytoplankton assemblages in Farmington Bay between months illustrating individual taxa relationships (April-October 2013-2014). Axis 1 R^2 = 0.53; Axis 2 R^2 = 0.20. (see MRPP results, Appendix 1).

Major phytoplankton groups also varied by month with peak cyanobacteria and chlorophytes occurring in August and bacillariophytes in July (Figure 17).

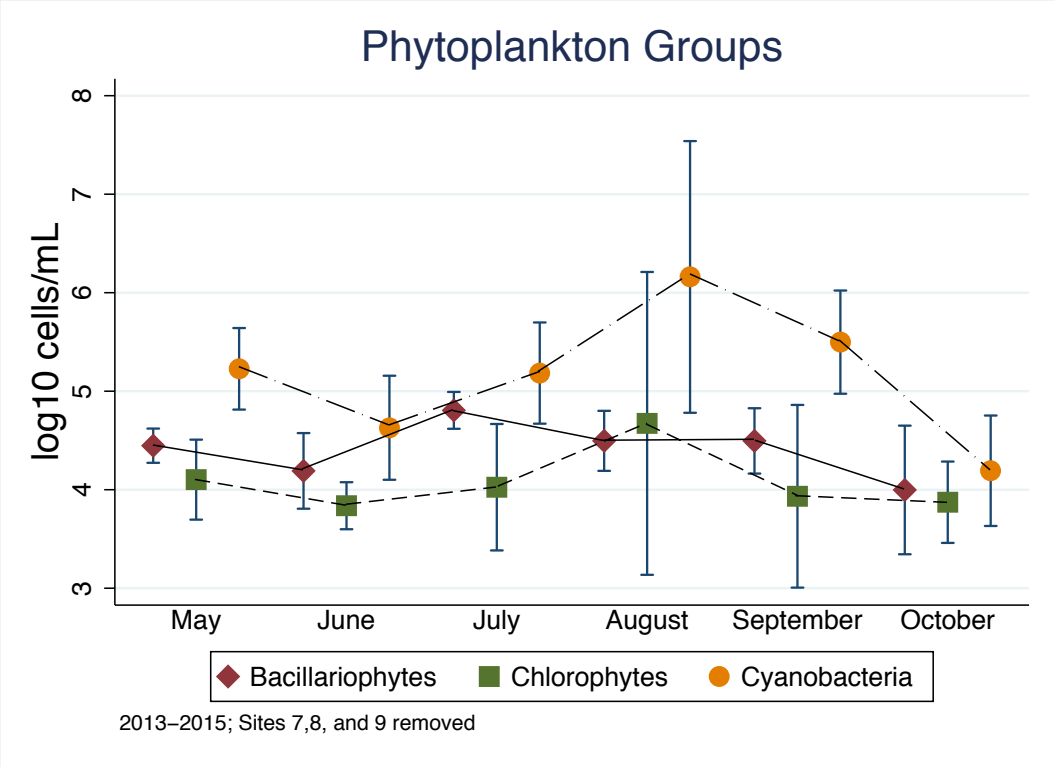

Figure 17. The three major phytoplankton groups densities (log10 cells/L) from April to October (all years and sites except 7, 8, and 9 combined). Mean and 95% CIs.

Phytoplankton assemblage and taxa salinity thresholds

Because salinity is a predominant factor determining community structure and function in saline lakes, we examined salinity driven modifications in biodiversity, composition and abundance of phytoplankton in Farmington Bay—especially the role that salinity has on cyanobacteria growth and development. Our inquiry is based on extensive previous research on fresh water, marine and saline lakes that demonstrates that as salinity increases from fresh water to marine concentration, or slightly above marine levels, algal growth, nutritional quality, community structure and biological diversity are impacted. Williams (1998) found that although salinity is an important factor in the structure of biological communities it is less influential as a determinant of community structure than is often thought, yet Williams does support the observation that increasing salinity coincides with a decrease in species richness. Salinity becomes a major influence at high levels but at lower levels the various salinity tolerances of zooplankton and phytoplankton, and the predator/prey relationships that emerge, serve a similarly important role in determining the overall biotic structure. Changes along the lower end of the salinity spectrum result in the greatest changes in community structure. As salinity increases further (i.e., 5% to >15%) there is less of an effect on richness and diversity, though an effect on community structure still is present. In hypersaline systems, there is excess osmotic regulatory stress coupled with increased energetic demands that in combination result in decreased individual fitness. A variety of algal taxa that have desirable

nutritional features for upper trophic predators decline in abundance and diversity as salinity increase (Clavero et al., 2000).

Nodularia have tolerate a salinity range that begins around 5 ppt and has an upper limit of 70 ppt with a reported optimal range of 12-24 ppt (Blackburn et al., 1996). Most algal taxa typically represented in Farmington Bay demonstrate progressive declines in growth, abundance and photosynthesis as salinity increases above 50 ppt (Sudhir and Murthy, 2004; Mazur-Marzec et al. 2005; Moisander et al. 2001). Among the cyanobacteria that can tolerate higher salinity there is often an impact on N_2 fixation rates with increased salinity (Allkhverdiev and Murata, 2008). Another impact of elevated salinity is a decrease in dissolved oxygen with associated hypoxic stress on cells, tissues and individuals (Williams, 1998). In the combined salinity and nutrient enrichment experiments conducted by Marcarelli, Wurtsbaugh, and Griset (2006) these investigators found that when the salinity was 70g/L nitrogen fixation ceased. Under such conditions nitrogen can become limited rather than phosphorous. In their policy forum paper Conley et al., (2009) commented that significant planktonic nitrogen fixation is not observed at salinities in excess of 8% even in circumstances of severe nitrogen limitation. These experiments illustrate that when considering nutrient effects on a waterbody salinity is clearly a controlling factor. Collectively these direct and indirect effects of salinity exert their influence on algal communities found in Farmington Bay.

Wurtsbaugh et al. (2012) expressed concern about the impact that the Antelope Island causeway has had on Farmington Bay and they supported the idea that greater exchange between Farmington Bay and Gilbert Bay would have multiple beneficial outcomes. They state that the causeway has increased residence time in the bay thereby capturing and containing high nutrient loads and preventing them from entering Gilbert Bay. The reduced exchange between bays has clearly lowered the salinity in Farmington Bay into a range that favors cyanobacteria blooms. An additional benefit of improving the exchange between the bays would be increased primary productivity in Gilbert Bay and as a result greater production of forage items for birds, such as the phalaropes or grebes, hence an improvement in the beneficial uses of the lake although this would not likely benefit waterfowl and shorebirds which have been found to primarily utilize freshwater/brackish water macroinvertebrates and seeds from various species of submergent and emergent vegetation (Cavitt 2007, Wilson 2011).

Salinity did in fact turn out to be one of the most influential environmental gradients in the bay, particularly from May to October. Farmington Bay phytoplankton assemblages and individual taxa responded to this gradient by either increasing or decreasing in abundance (cells/L) with increased salinity (Figures 18, 19). The overall phytoplankton assemblage salinity threshold change point, CP was 15.1 ppt for taxa that decreased in abundance with increased salinity and the CP for taxa that increased in abundance with increased salinity was 3.7 (Appendix 4). Fourteen taxa met purity and reliability criteria as designated “decreasers” (decreased in abundances with increased salinity) (Figure 18) and five taxa met criteria as increasers (increased in abundances with increased salinity) (Figure 19).

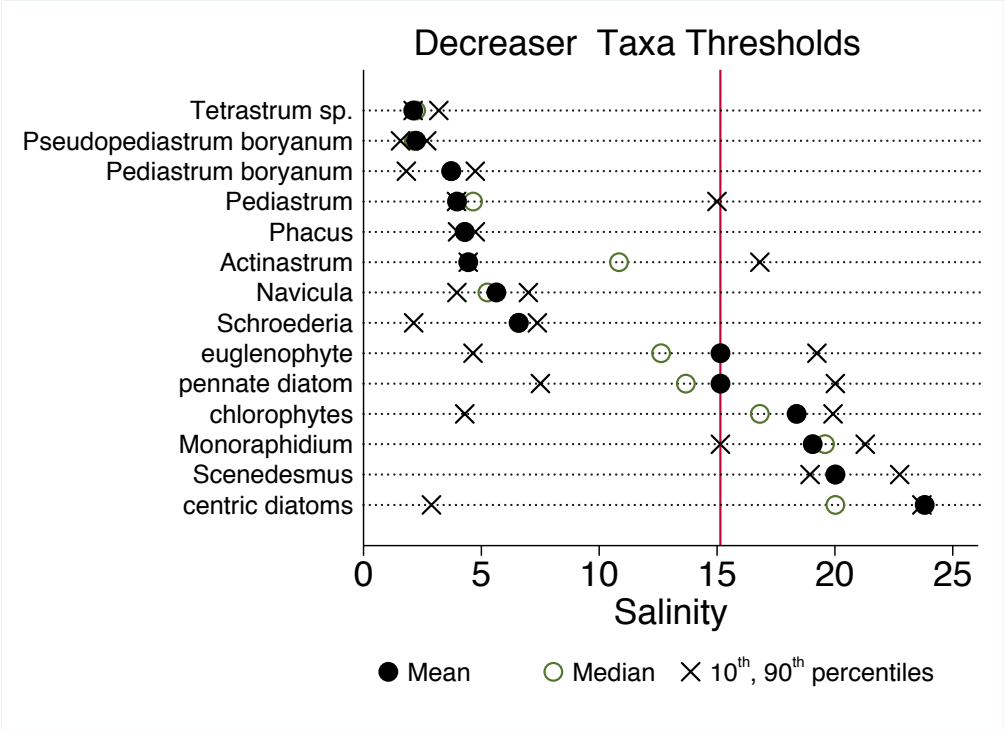

Figure 18.Mean (solid circles), median (hollow circles) and 10th and 90th percentile (x's) CPs for phytoplankton taxa that decreased in abundances with increased salinity (decreaser z-) and met purity and reliability criteria (see Appendix 4 for details). The phytoplankton assemblage filtered mean z-CP threshold was 15.2 (red vertical line).

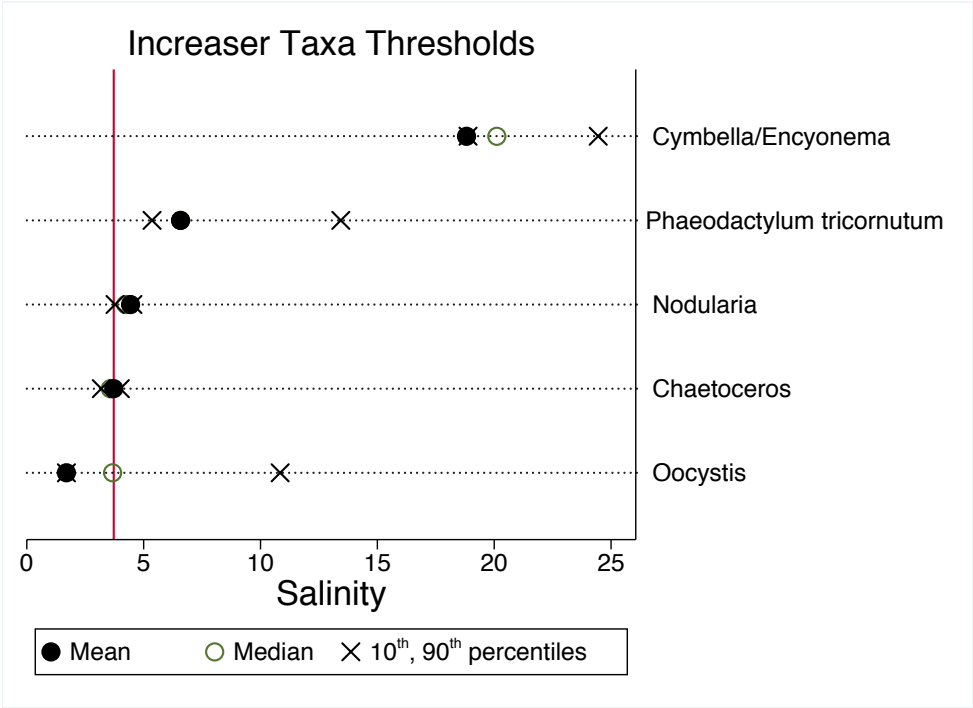

Figure 19.Mean (solid circles), median (hollow circles), and 10th and 90th percentile (x's) CPs for phytoplankton taxa that increased in abundances with increased salinity (increaser z-) and met purity

and reliability criteria (see Appendix 4 for details). The phytoplankton assemblage filtered mean z-CP threshold was 15.2 (red vertical line).

Some of the taxa identified as "decreasers" such as pennate and centric diatoms, chlorophytes, euglenophytes, and Scenedesmus do have species that are tolerant of higher salinity than thresholds identified herein. Yet, the particular species present during our study did exhibit decreased abundances as salinity increased above these thresholds. It is instructive to note that *Nodularia* increased in abundance as salinity increased above 4 ppt. This is slightly below the lower salinity limit identified by McCulley (2014) where he reports that *Nodularia* was most pronounced in Farmington Bay between 7 and 50 ppt. In the Baltic Sea Lehtimaki et al. (1997) observed an optimal range for *Nodularia* between 7 and 20 ppt. This bracket of salinity tolerance confers *Nodularia* some advantages over other algal taxa that are less tolerant of salinity and it offers a sound explanation for one of the factors that favors HABs development in the mid-bay to northern regions of Farmington Bay and, in contrast, it helps to understand why HABs are seldom if ever found in the southern region of the bay where the water is essentially fresh or hyposaline. Clearly salinity is one of the main factors that adjusts algal community structure in Farmington Bay and a role player in HAB development.

Other environmental gradients such as temperature, DO, nutrient concentrations and ratios or biological interactions such as competition, predation, and facilitation or combinations most likely also affected relative abundances of the phytoplankton assemblage and individual taxa. Therefore, the salinity threshold results presented here should be interpreted as specifically derived from conditions that occurred during collection of the data used in these analyses. Salinity thresholds for these assemblages and individual taxa may vary somewhat under different locations or future conditions.

Cyanobacteria

Cyanobacteria densities (log10 cells/L) were significantly greater than average in August and September and lower in October and June (Figure 20) but on average didn't vary significantly between Sites 1-6 (Figures 20 and 21).

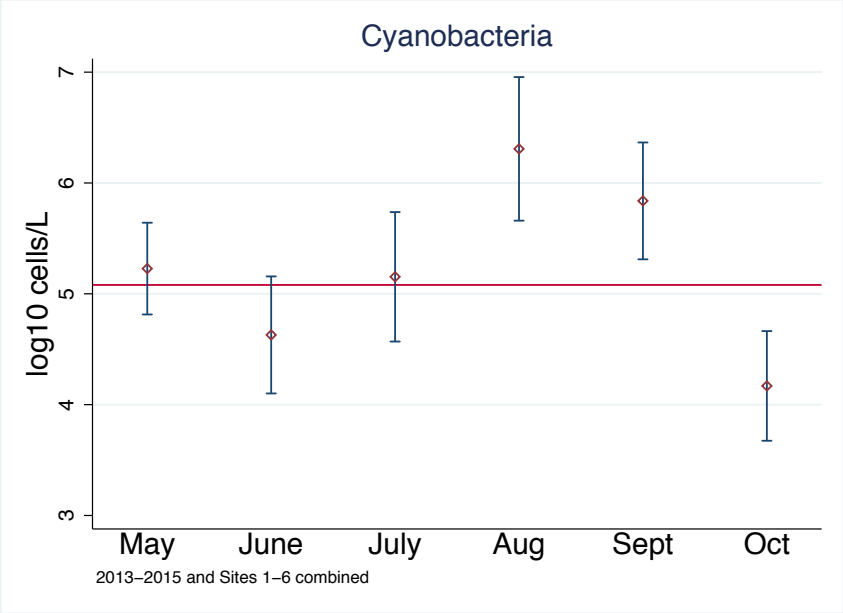

Figure 20.Cyanobacteria density (log10 cells/L) by months (May through October; 2013-2015; Sites 7, 8, and 9 removed). Mean and 95% CIs.

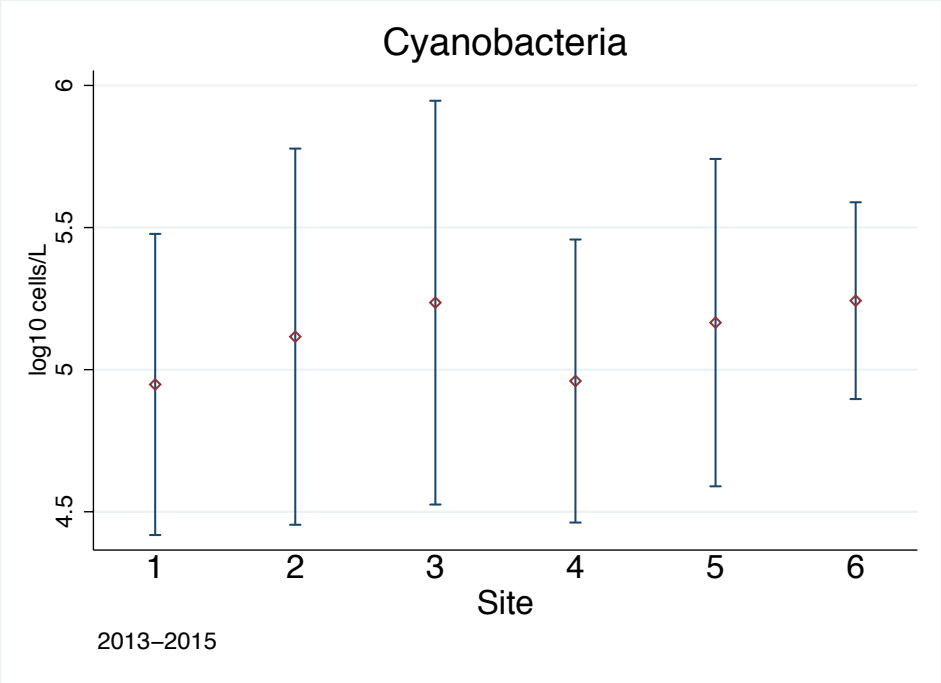

Figure 21.Cyanobacteria density (log10 cells/L) by sites. (May through October; 203-2015; Sites 7, 8, and 9 removed). Mean and 95% CIs.

Cyanobacteria in relation to chemistry/nutrients: Bottom-Up effects

Random Forest (RF) models showed that of the eleven chemistry/nutrient variables modeled; salinity and SRP were the best predictors of log Cyanobacteria (Mean of squared residuals: 0.466, % Var explained: 51.63)(Table 3).

Table 3. Random Forest IncNodePurity values for logCyanobacteria vs. variable in the table. The higher the value the more important the predictor.

	IncNodePurity
Salinity	**12.98**
TN:SRP	**9.16**
SRP	**8.57**
TP	**5.27**
PTN:PTP	**5.08**
TKN	**4.73**
N03+N02	**4.01**
Temperature	**3.59**
Ammonia	**3.31**
TN:TP	**2.65**
TN molar	**2.03**
DIN:TP	**1.93**
TP molar	**0.08**

Regression Tree (RT) analyses also showed that out of all predictor variables listed in Table 3, salinity and TN:SRP were the two best predictors of cyanobacteria density (log 10 cells/L)(Figure 22). These results support other previous findings by us and those that are presented in this report that cyanobacteria mostly consume SRP and as cyanobacteria densities increase, TN:SRP increases. The RT model suggested that there was a major threshold change point in cyanobacteria densities of at least an order of magnitude increase that occurred when TN:SRP was > 31, from about 13,000 cells/L to at least 250,000 cells/L (Figure 22). There was then a major change point in cyanobacteria densities of again more than an order of magnitude, when salinity was > 48.5 ppt resulting in an estimated change in abundance of cyanobacteria (cells/L) from about 250,000 to well over 4,000,000 (cells/L)(Figure 22).

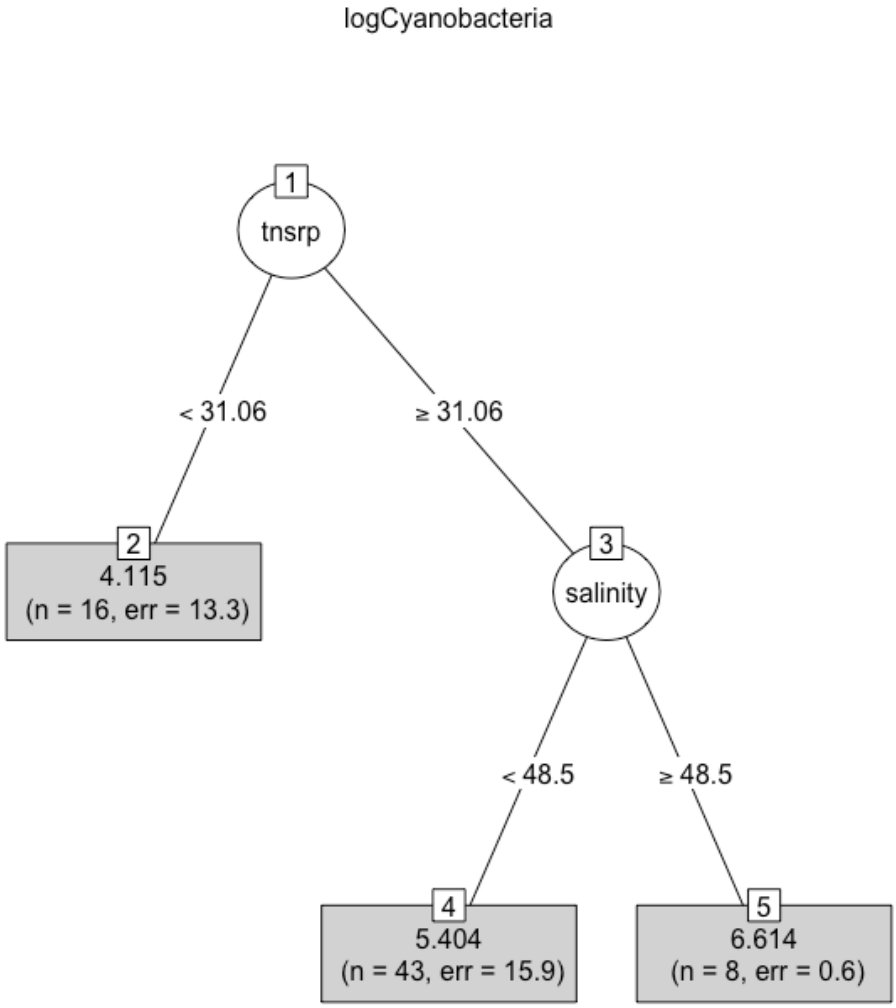

Figure 22. Regression Tree results of log10Cyanobacteria relationships to environmental variables from Table X. Only TN:SRP and salinity were determined to be useful predictors of cyanobacteria in these models.(Inverse log10 of 4.115 = 13,032; 5.404 = 253,513; 6.6114 = 4,111,497)).

We also conducted simultaneous quantile regression on logCyanobacteria vs. the predictor variables in Table X using 25th, 50th, and 75th percentiles (bootstrapped replications = 500). Only salinity was a significant predictor of cyanobacteria and was significant at all three percentiles (Table 4).

Table 4. Simultaneous quantile regression (25th, 50th, and 75th quantiles) of cyanobacteria (log10) vs thirteen predictor variables in Table x.

Simultaneous quantile regression — Number of obs = 66
bootstrap(500) SEs — .25 Pseudo R2 = 0.5482
.50 Pseudo R2 = 0.4800
.75 Pseudo R2 = 0.4751

logCyanoba~a	Coef.	Bootstrap Std. Err.	t	P>|t|	[95% Conf.	Interval]
q25						
salinity	.0185617	.0084165	2.21	0.032	.0016648	.0354586
tempc	.0420821	.0306548	1.37	0.176	-.0194601	.1036242
tp	.1340645	1.704771	0.08	0.938	-3.288406	3.556535
srp	-3.615758	2.119571	-1.71	0.094	-7.870974	.6394587
ammonia	-50.90132	33.88825	-1.50	0.139	-118.9348	17.13218
n03n02	-48.67277	34.15253	-1.43	0.160	-117.2368	19.89129
tkn	-51.39351	33.95206	-1.51	0.136	-119.5551	16.76809
tntknamnos	51.47964	33.92352	1.52	0.135	-16.62466	119.584
tntp	-.0275346	.0685922	-0.40	0.690	-.1652393	.1101701
tnmolar	-1606.377	4431.69	-0.36	0.718	-10503.37	7290.612
tpmolar	24929.31	21281.3	1.17	0.247	-17794.68	67653.3
ptnptp	-.0002996	.0178166	-0.02	0.987	-.0360678	.0354686
dintp	-.0722121	.4221573	-0.17	0.865	-.9197283	.775304
tnsrp	-.0001311	.0007016	-0.19	0.853	-.0015397	.0012775
_cons	4.310149	.8310048	5.19	0.000	2.641837	5.97846
q50						
salinity	.0246182	.008802	2.80	0.007	.0069474	.042289
tempc	.0268883	.024068	1.12	0.269	-.0214302	.0752068
tp	2.101819	1.700448	1.24	0.222	-1.311973	5.51561
srp	-2.878127	1.806722	-1.59	0.117	-6.505273	.7490194
ammonia	-16.01533	31.0231	-0.52	0.608	-78.29681	46.26615
n03n02	-16.34202	31.31549	-0.52	0.604	-79.21048	46.52644
tkn	-16.55317	31.03212	-0.53	0.596	-78.85275	45.74641
tntknamnos	16.25847	31.02323	0.52	0.602	-46.02326	78.5402
tntp	.0349931	.0681231	0.51	0.610	-.1017696	.1717559
tnmolar	1001.893	4131.114	0.24	0.809	-7291.665	9295.451
tpmolar	-1402.301	20566.9	-0.07	0.946	-42692.07	39887.47
ptnptp	-.0003371	.0140745	-0.02	0.981	-.0285929	.0279187
dintp	-.2429412	.3085828	-0.79	0.435	-.862447	.3765646
tnsrp	.0004261	.0006189	0.69	0.494	-.0008164	.0016686
_cons	4.049787	.7985805	5.07	0.000	2.44657	5.653004
q75						
salinity	.0249092	.008978	2.77	0.008	.006885	.0429333
tempc	.0238875	.0262559	0.91	0.367	-.0288234	.0765983
tp	.1569814	2.075735	0.08	0.940	-4.010232	4.324194
srp	-1.435921	2.232682	-0.64	0.523	-5.918218	3.046375
ammonia	-5.724404	28.04775	-0.20	0.839	-62.03262	50.58381
n03n02	-6.520539	28.19108	-0.23	0.818	-63.1165	50.07542
tkn	-5.683685	28.05962	-0.20	0.840	-62.01573	50.64836
tntknamnos	5.134092	28.07929	0.18	0.856	-51.23743	61.50562
tntp	-.0336339	.080346	-0.42	0.677	-.1949353	.1276675
tnmolar	7253.021	4263.898	1.70	0.095	-1307.111	15813.15
tpmolar	7955.936	22108.59	0.36	0.720	-36428.91	52340.78
ptnptp	-.0010386	.0181686	-0.06	0.955	-.0375137	.0354364
dintp	-.0091825	.3832113	-0.02	0.981	-.7785113	.7601462
tnsrp	.0001652	.000586	0.28	0.779	-.0010113	.0013417
_cons	5.2252	.8498589	6.15	0.000	3.519038	6.931363

Simultaneous quantile regression of only cyanobacteria vs salinity was significant at all three quantiles although salinity was slightly better at predicting cyanobacteria at the 75th quantile (pseudo $R^2 = 0.24$) than at the 25th and 50th quantiles (Table 5). This supports the regression tree model that showed that TN:SRP also played a role in cyanobacteria densities particularly at lower densities.

Table 5. Simultaneous quantile regression (25th, 50th, and 75th quantiles) of cyanobacteria (log10) vs salinity.

```
Simultaneous quantile regression                  Number of obs =         70
  bootstrap(500) SEs                              .25 Pseudo R2 =     0.1627
                                                  .50 Pseudo R2 =     0.1706
                                                  .75 Pseudo R2 =     0.2351
```

logCyanoba~a	Coef.	Bootstrap Std. Err.	t	P>|t|	[95% Conf.	Interval]
q25						
salinity	.031114	.0134972	2.31	0.024	.0041808	.0580472
_cons	3.967774	.3011889	13.17	0.000	3.366761	4.568787
q50						
salinity	.0316208	.0104401	3.03	0.003	.010788	.0524536
_cons	4.659094	.3036008	15.35	0.000	4.053268	5.26492
q75						
salinity	.027252	.0055483	4.91	0.000	.0161806	.0383233
_cons	5.144807	.1445075	35.60	0.000	4.856447	5.433168

Relationships between Cyanobacteria cell counts, PTOX cell counts, and Nodularin

Results in this section are primarily a summary of findings that we presented in a technical memo to WFWQC in 2016 (Richards 2016) and are important to our understanding of Farmington Bay cyanobacteria ecology. Ordinary least squares (OLS) regression results of 2013 to 2015 data showed small to moderate significant relationships between: nodularin concentration vs. PTOX cell counts (Figure 24); nodularin concentration vs. cyanobacteria cell counts (Figure 25); and PTOX cell counts vs. cyanobacteria cell counts (Figure 26).

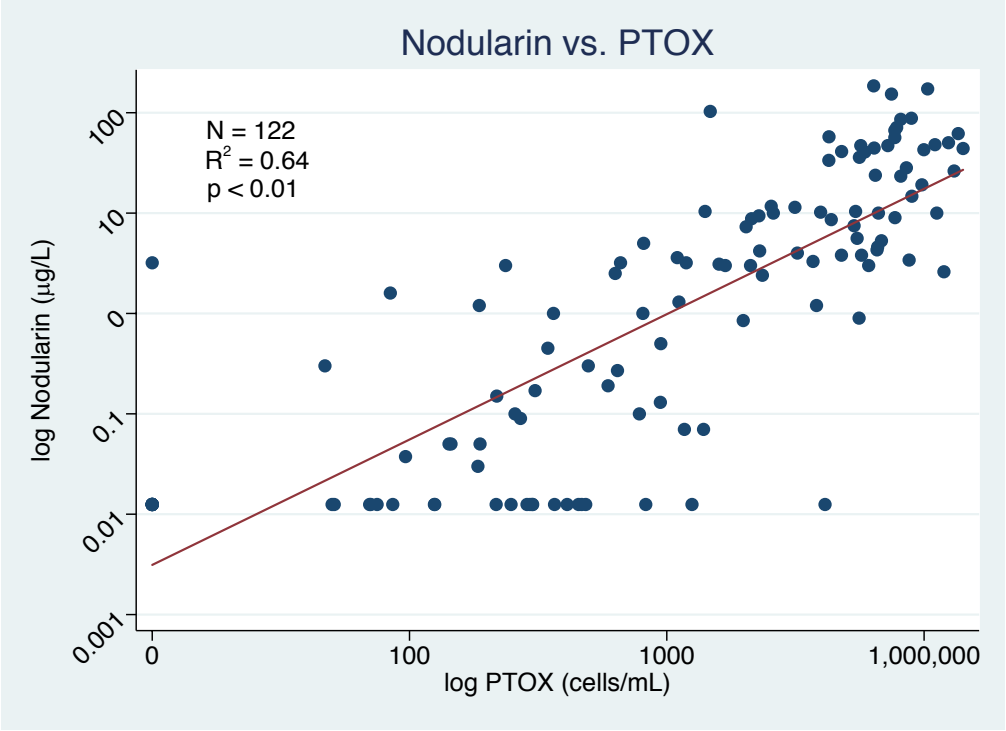

Figure 23. Relationship between nodularin (ug/L) and PTOX (cells/mL) in Farmington Bay, Great Salt Lake (from Richards 2016).

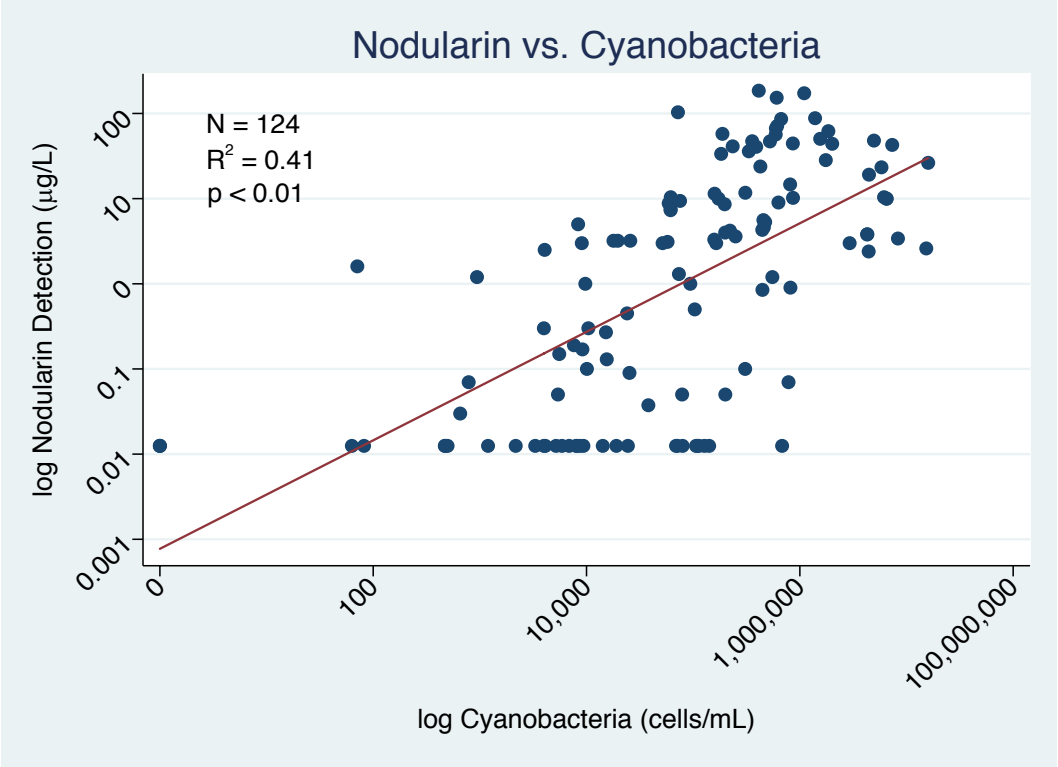

Figure 24.Relationship between nodularin (ug/L) and cyanobacteria (cells/mL) in Farmington Bay, Great Salt Lake (from Richards 2016).

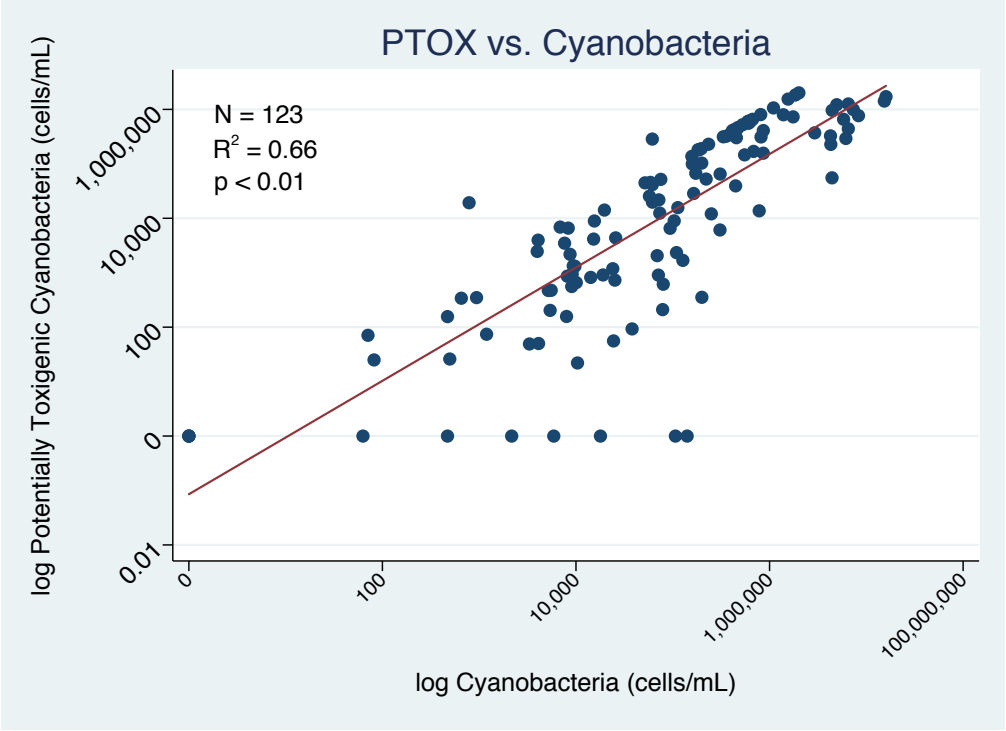

Figure 25.Relationship between PTOX (cells/mL) and cyanobacteria (cells/mL) in Farmington Bay, Great Salt Lake (from Richards 2016).

PTOX and Cyanobacteria varied seasonally and there was a slight but significant decreasing trend from 2013 to 2015 (Figure 27).

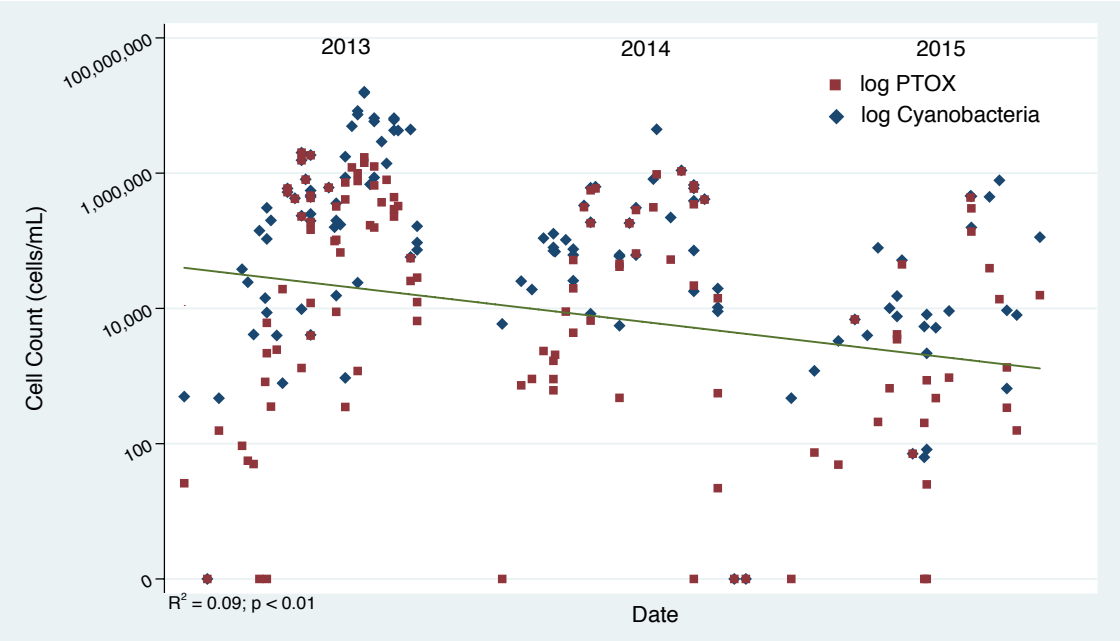

Figure 26.Changes in PTOX and cyanobacteria over time (2013-2015) in Farmington Bay, Great Salt Lake (from Richards 2016).

Nodularin non-detect values

Nodularin non-detect values (< 0.025ug/L) (N = 30 or 24% of data) occurred under a wide range of cyanobacteria and PTOX values (Figure 28). Therefore, in many instances nodularin concentration was not related to cyanobacteria or PTOX cell counts.

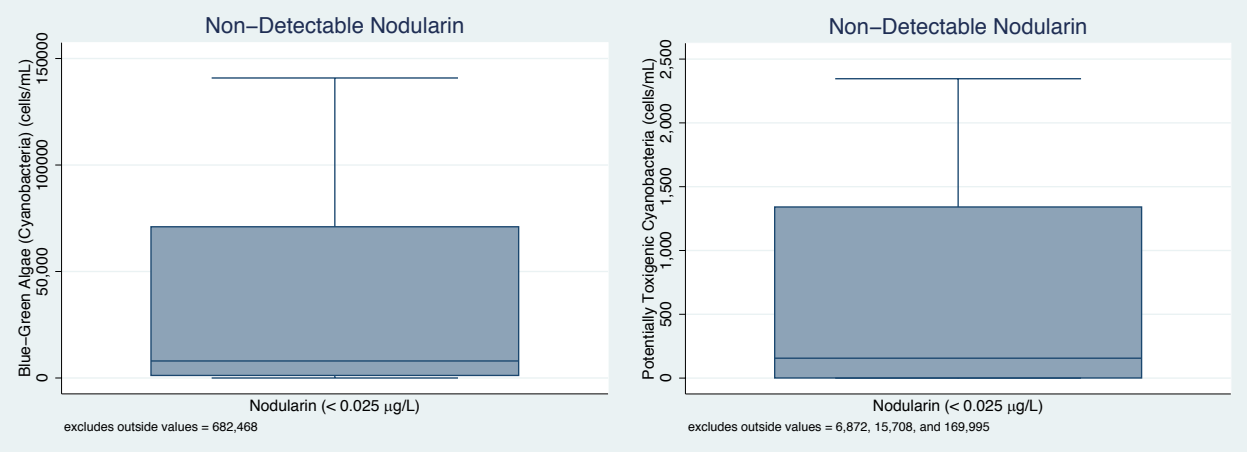

Figure 27.Range of cyanobacteria cell counts to non-detectable nodularin concentrations and range of PTOX cell counts to non-detectable nodularin concentrations (< 0.025 ug/L) (from Richards 2016).

Nodularin values recorded as non-detect suggests a poor relationship between nodularin and the other variables at low levels and likely contributed to the relatively mediocre OLS regression fits.

Quantile Regression

Nodularin vs. Cyanobacteria

There were no significant differences between OLS regression model and any of the three quantile regressions for log Nodularin vs. log Cyanobacteria (Table 6) however, the OLS regression model was not useful for predicting the intercept at low and high quantiles and nodularin concentrations near the non- detect levels (Figure 29).

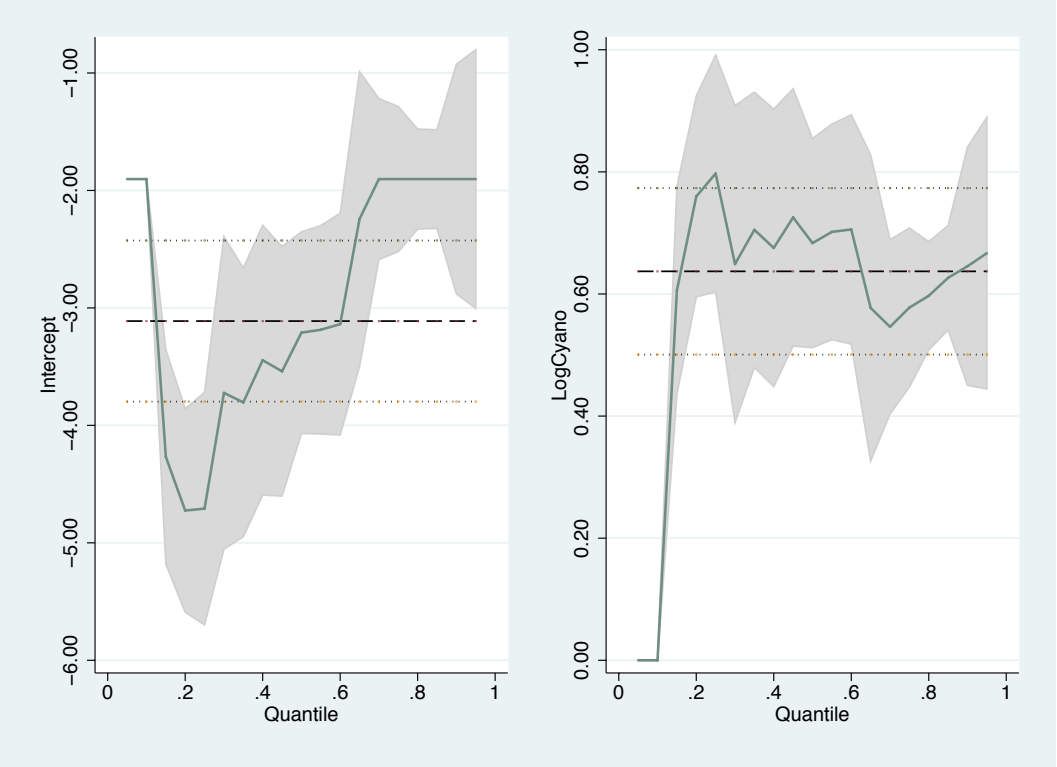

Figure 28. Figure 29.Quantile regression diagnostic plots for log Nodularin vs. log Cyanobacteria. Dashed parallel lines are OLS fit line with 95% CIs and solid line with gray shading is quantile regression fit lines and 95% CIs. (from Richards 2016).

Table 6. OLS Regression and Simultaneous Quantile Regression results for logNodularin vs logCyanobacteria (from Richards 2016).

OLS regression

```
. regress logNodularin LogCyano
```

Source	SS	df	MS	Number of obs	=	124
				F(1, 122)	=	85.52
Model	98.1189224	1	98.1189224	Prob > F	=	0.0000
Residual	139.978228	122	1.14736252	R-squared	=	0.4121
				Adj R-squared	=	0.4073
Total	238.09715	123	1.93574919	Root MSE	=	1.0712

logNodularin	Coef.	Std. Err.	t	P>|t|	[95% Conf.	Interval]
LogCyano	.6370475	.0688883	9.25	0.000	.5006761	.7734188
_cons	-3.112014	.3463567	-8.98	0.000	-3.797662	-2.426366

Simultaneous quantile regression

```
Simultaneous quantile regression                    Number of obs =        124
  bootstrap(1000) SEs                               .25 Pseudo R2 =     0.2182
                                                    .50 Pseudo R2 =     0.2710
                                                    .75 Pseudo R2 =     0.2463
```

logNodularin	Coef.	Bootstrap Std. Err.	t	P>|t|	[95% Conf.	Interval]
q25						
LogCyano	.7973322	.1083959	7.36	0.000	.5827517	1.011913
_cons	-4.708829	.5723678	-8.23	0.000	-5.841888	-3.57577
q50						
LogCyano	.6833206	.1046454	6.53	0.000	.4761646	.8904766
_cons	-3.210838	.5498299	-5.84	0.000	-4.299282	-2.122395
q75						
LogCyano	.5776766	.0959882	6.02	0.000	.3876584	.7676948
_cons	-1.90309	.4980563	-3.82	0.000	-2.889042	-.9171377

Nodularin vs. PTOX

There were no significant differences between OLS regression model and any of the three quantile regression models for log nodularin vs. log PTOX (Table 7). The OLS regression model over predicted the intercept up to about the 0.4 quantile and underestimated the intercept above approximately the 0.6 quantile (Figure 31). The OLS model also was a poor fit for nodularin values below the 0.2 quantile (Figure 31).

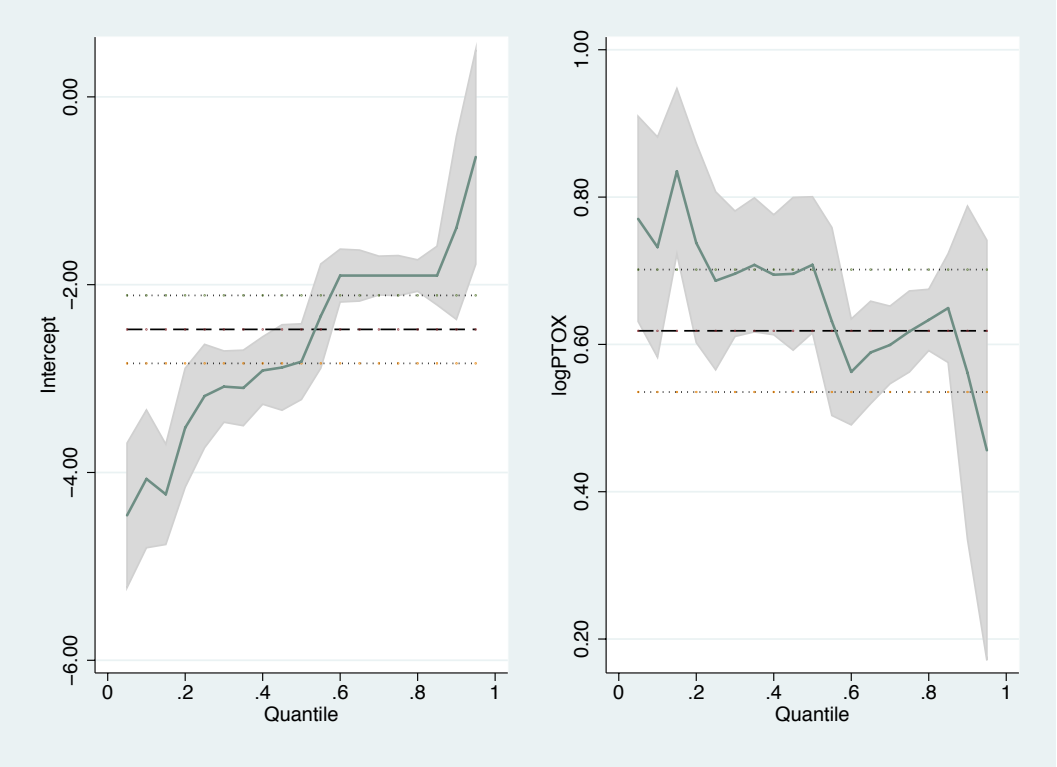

Figure 30. Quantile regression diagnostic plots for log Nodularin vs. log PTOX. Dashed parallel lines are OLS fit line with 95% CIs and solid line with gray shading is quantile regression fit lines and 95% CIs. (from Richards 2016).

Table 7. OLS and quantile regression results for log Nodularin vs. log PTOX(from Richards 2016).

OLS regression

```
. regress logNodularin logPTOX
```

Source	SS	df	MS	Number of obs	=	123
				F(1, 121)	=	216.98
Model	150.598808	1	150.598808	Prob > F	=	0.0000
Residual	83.980474	121	.694053504	R-squared	=	0.6420
				Adj R-squared	=	0.6390
Total	234.579282	122	1.922781	Root MSE	=	.8331

logNodularin	Coef.	Std. Err.	t	P>|t|	[95% Conf.	Interval]
logPTOX	.6184521	.0419848	14.73	0.000	.5353321	.701572
_cons	−2.476271	.1828946	−13.54	0.000	−2.838359	−2.114183

Simultaneous quantile regression results

```
Simultaneous quantile regression                    Number of obs =        123
  bootstrap(1000) SEs                               .25 Pseudo R2 =     0.4312
                                                    .50 Pseudo R2 =     0.4670
                                                    .75 Pseudo R2 =     0.4454
```

logNodularin	Coef.	Bootstrap Std. Err.	t	P>|t|	[95% Conf.	Interval]
q25						
logPTOX	.6863908	.07956	8.63	0.000	.5288808	.8439008
_cons	-3.186113	.4128743	-7.72	0.000	-4.003507	-2.36872
q50						
logPTOX	.7080812	.0849294	8.34	0.000	.539941	.8762215
_cons	-2.819815	.4242681	-6.65	0.000	-3.659765	-1.979864
q75						
logPTOX	.6175137	.0241815	25.54	0.000	.5696402	.6653873
_cons	-1.90309	.0955353	-19.92	0.000	-2.092227	-1.713953

PTOX vs. Cyanobacteria

There were no significant differences between OLS regression model and any of the three quantile regressions for log PTOX and log cyanobacteria (Table 8). The OLS regression model over predicted the intercept up to about the 0.2 quantile (Figure 32). The OLS model also underestimated PTOX values below the 0.2 quantile (Figure 32).

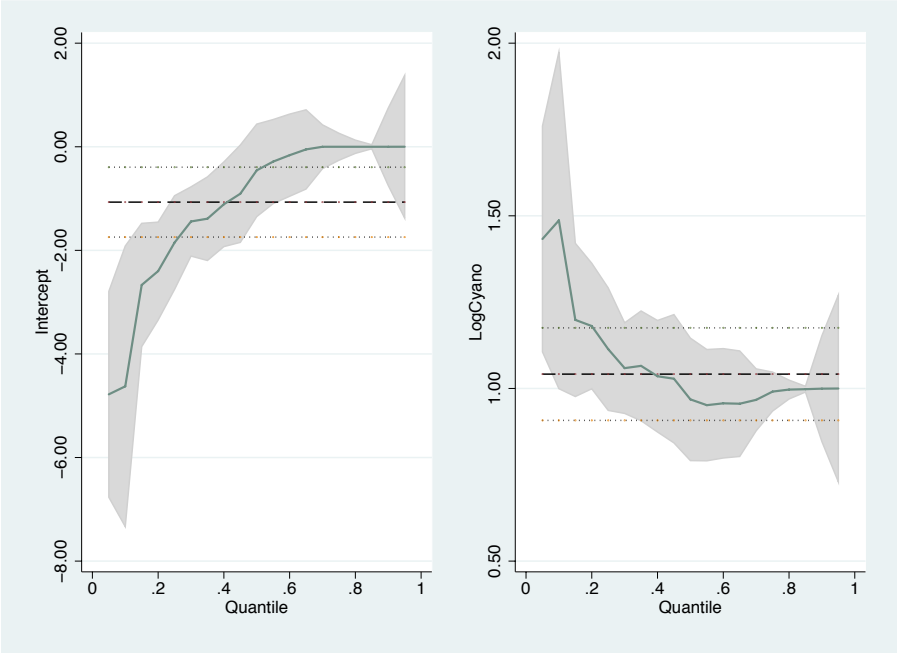

Figure 31.Quantile regression diagnostic plots for log PTOX vs. log cyanobacteria. Dashed parallel lines are OLS fit line with 95% CIs and solid line with gray shading is quantile regression fit lines and 95% CIs. (from Richards 2016).

Table 8. OLS regression and simultaneous quantile regression logPTOX vs logCyanobacteria (from Richards 2016).

```
. regress logPTOX LogCyano
```

Source	SS	df	MS	Number of obs	=	123
				F(1, 121)	=	236.87
Model	260.610081	1	260.610081	Prob > F	=	0.0000
Residual	133.129849	121	1.10024669	R-squared	=	0.6619
				Adj R-squared	=	0.6591
Total	393.739931	122	3.22737648	Root MSE	=	1.0489

logPTOX	Coef.	Std. Err.	t	P>|t|	[95% Conf.	Interval]
LogCyano	1.04151	.0676726	15.39	0.000	.9075339	1.175485
_cons	-1.069074	.3409171	-3.14	0.002	-1.744009	-.3941388

```
Simultaneous quantile regression                Number of obs =       123
  bootstrap(1000) SEs                           .25 Pseudo R2 =    0.4532
                                                .50 Pseudo R2 =    0.5015
                                                .75 Pseudo R2 =    0.5100
```

logPTOX	Coef.	Bootstrap Std. Err.	t	P>|t|	[95% Conf.	Interval]
q25						
LogCyano	1.113839	.0783115	14.22	0.000	.9588007	1.268877
_cons	-1.849789	.4858849	-3.81	0.000	-2.811727	-.8878521
q50						
LogCyano	.9684	.1116398	8.67	0.000	.7473796	1.18942
_cons	-.4553972	.5930191	-0.77	0.444	-1.629435	.7186405
q75						
LogCyano	.9909636	.0494586	20.04	0.000	.8930473	1.08888
_cons	-8.88e-16	.259706	-0.00	1.000	-.5141564	.5141564

Cyanobacteria cell counts were a moderate metric for estimating nodularin concentrations, except at lower and upper nodularin concentrations. This was also mostly the case for PTOX as a predictor of nodularin concentration and for cyanobacteria as a predictor of PTOX, particularly at lower concentrations and cell counts. However, there was a solid positive relation with *Nodularia* (cells/L) and nodularin (ug/L) (Figure 33).

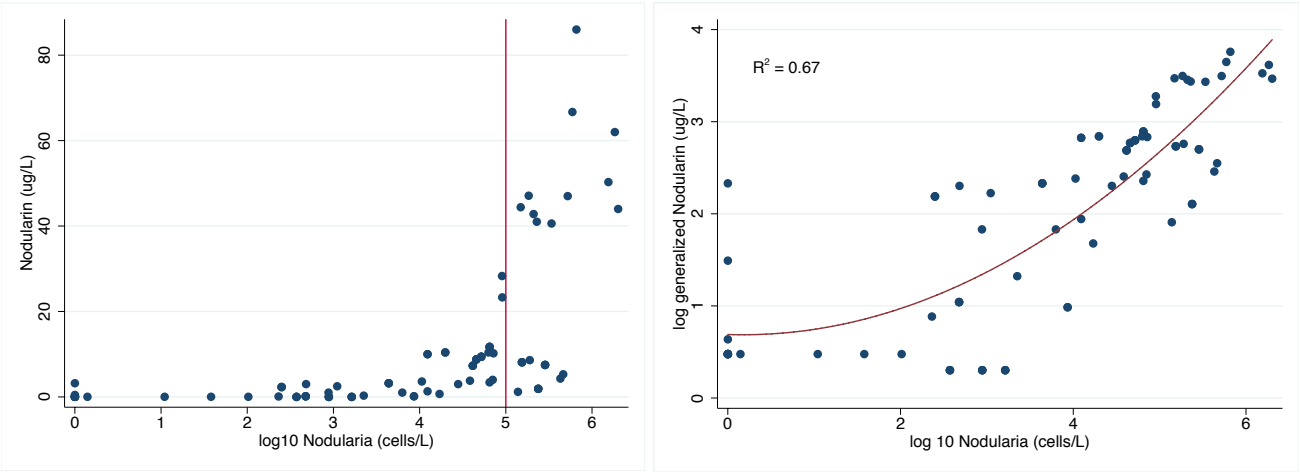

Figure 32.Relationship between Nodularia sp.(cells/L) and nodularin (ug/L). The graph on left is without nodularin transformed showing a rapid increase at approximately 100,000 Nodularia cells/l. The graph on the right is a typical log/log scale but with nodularin log generalized transformed as opposed to log10 transformed (see Appendix 1 for description of log generalized transformations).

Table 9.OLS quadratic regression of nodularin (ug/L) (log generalized transformed) as a function of Nodularia sp. (cell/L)(log 10 transformed).

```
. regress logGenNodularin logNodularia logNodularia2
```

Source	SS	df	MS	Number of obs	=	90
				F(2, 87)	=	88.85
Model	69.7248238	2	34.8624119	Prob > F	=	0.0000
Residual	34.1378762	87	.392389381	R-squared	=	0.6713
				Adj R-squared	=	0.6638
Total	103.8627	89	1.16699663	Root MSE	=	.62641

logGenNodul~n	Coef.	Std. Err.	t	P>|t|	[95% Conf.	Interval]
logNodularia	-.0294845	.129846	-0.23	0.821	-.2875675	.2285984
logNodularia2	.085235	.0207738	4.10	0.000	.0439448	.1265253
_cons	.6893353	.1918068	3.59	0.001	.3080985	1.070572

In 2013, there was evidence of a threshold limit of *Nodularia* cells that corresponded with a substantial increase in the concentration of nodularin observed in water samples (Figure 34).

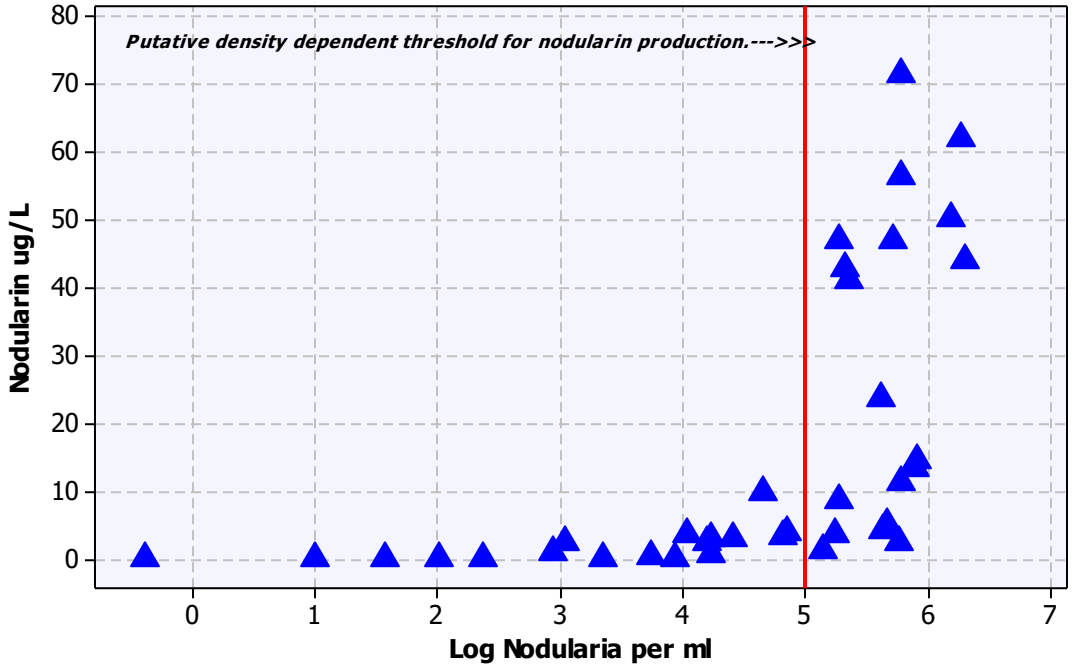

Figure 33.The concentration of nodularin in Farmington Bay water samples is a non-linear relationship with the number of Nodularia cells per ml. There appears to be a density dependent production of nodularin occurring when Nodularia is >100,000 cells per ml.

Green Algae (Chlorophyta): Bottom Up Effects

Chlorophyte density (log10 cells/L) were best predicted by N03+N02 using Random Forest and Regression Tree analyses (Table 10, Figure 35). Predicted chlorophyte densities were about 7000 cells/L at N03+N02 < 0.04 and increased dramatically up to more than 75,000 cells/L when N03+N02 > 0.04.

Table 10.Random Forest IncNodePurity values for logChlorophyta vs. variables listed in the table. The higher the value the more important the predictor. DIN:TP

	IncNodePurity
n03n02	**10.12**
salinity	**4.82**
tp	**3.77**
ptnptp	**3.25**
tkn	**2.85**
tntp	**2.62**
tnsrp	**2.508**
dintp	**2.47**
tempc	**2.17**
ammonia	**2.03**
srp	**1.63**
tnmolar	**1.45**
tpmolar	**0.053**

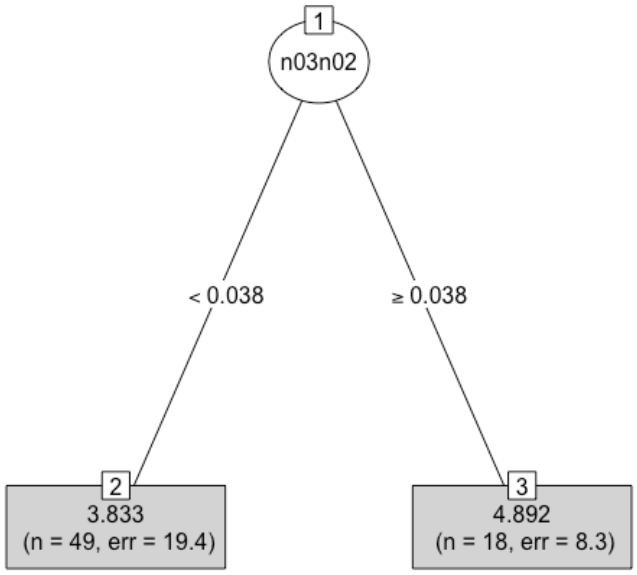

Figure 34. Regression tree of logChlorophyta (green algae) as predicted by nitrate & nitrite concentrations.

Diatoms (Bacillariophytes): Bottom Up Effects

Several variables were good predictors of diatoms using Random Forest models including: N03+N02, salinity, temperature, and TP (Table 11).

Table 11. Random Forest model IncNodePurity results for diatoms (log10 Bacillariophytes) vs predictors. The higher the IncNodePurity the greater the importance in predicting diatom abundance (biomass).

Variable	IncNodePurity
N03+N02	**49.31**
Salinity	**32.20**
Temperature	**17.55**
TP	**17.03**
DIN:TP	**12.80**
TN:SRP	**10.57**
TKN	**8.47**
Ammonia	**7.36**
PTN:PTP	**7.35**
TN:TP	**6.58**
SRp	**5.67**
TN molar	**2.12**
TP molar	**0.344**

Regression Tree analysis suggested that when N03+N02 was > 0.03 ug/L and salinity > 25 ppt diatom density was only about 3 cells/L. When salinity was < 25 ppt and N03+N02 was > 0.03 ug/L diatoms occurred at about 2400 cells/L. However, when N03+N02 was < 0.03 ug/L diatom density was about 33,000 cells/L (Figure 36). Therefore, diatoms in FB appear to do better at low levels of nitrate/nitrite and low concentrations of salinity.

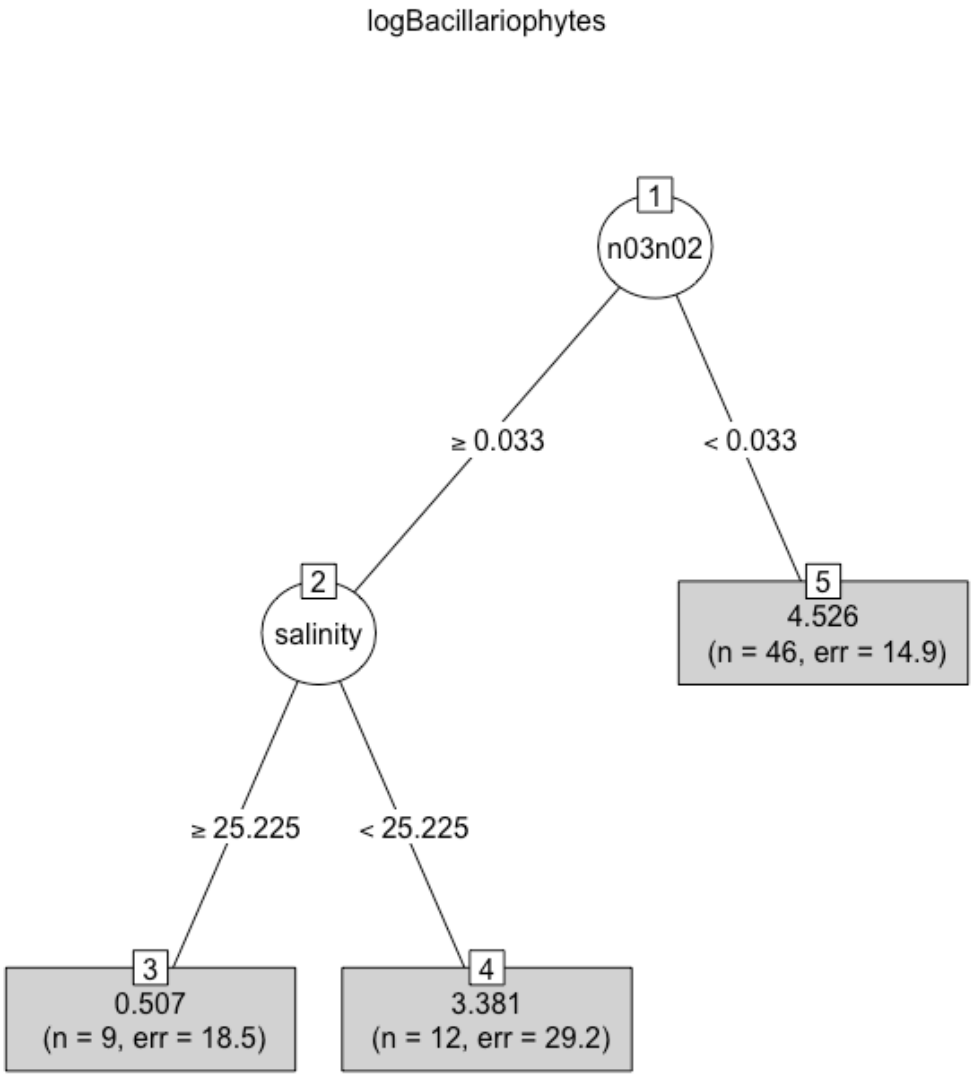

Figure 35. Regression tree of logBacillariophyta (diatoms) as predicted by nitrate+nitrite and salinity concentrations (ppt).

Zooplankton

We found 25 Copepoda, Rotifera, and Cladocera zooplankton taxa to date (Table 12).

Table 12. Preliminary Zooplankton taxa list from Farmington Bay, Great Salt Lake found in this study.

Phylum	Subphylum	Class	Subclass	Order	Suborder	Family	Species
Arthropoda	**Crustacea**	Branchiopoda	Phylipoda	Diplostraca	Cladocera	Bosminidae	*Bosmina longirostris*
						Chydoridae	*Chydorus sphaericus*
							Leydigia sp.
							Pleuroxus aduncus
							Pleuroxus striatus
						Daphniidae	Ceriodaphnia quadrangula
							Daphnia dentifera
							Daphnia pulex
							Simocephalus vetulus
						Moinidae	*Moina macrocarpa*
			Sarcostraca	Anostraca	Artemina	Artemiidae	*Artemia franciscana*
		Malacostraca	Eumalaconstraca	Amphipoda	Gammaridea	Hyalellidae	*Hyalella* sp.
		Maxillopoda	Copepoda	Cyclopoida	NA	Cyclopidae	*Acanthocyclops robustus*
							Diacyclops sp.
							Eucyclops agilis
						Canthocamptidae	*Cletocamptus* sp.
						Diaptomidae	*Leptodiaptomus connexus*
		Ostracoda					Undetermined
	Hexapoda	Insecta	Pterygota	Diptera		Chironomidae	(undetermined)
						Ephydridae	(undetermined)
				Hemiptera	Heteroptera	Corixidae	*Corisella decolor*
							Trichocorixa verticalis
Rotifera	NA	Monogonta	Monogononta	Ploima	NA	Brachionidae	*Brachionus plicatilis*
							Notholca acuminata
							Keratella quadrata

Trichocorixa verticalis dominated by biomass along with *Moina macrocarpa*, *Leptodiaptomus connex,* and *Artemia franciscana* (Figures 37 and 38).

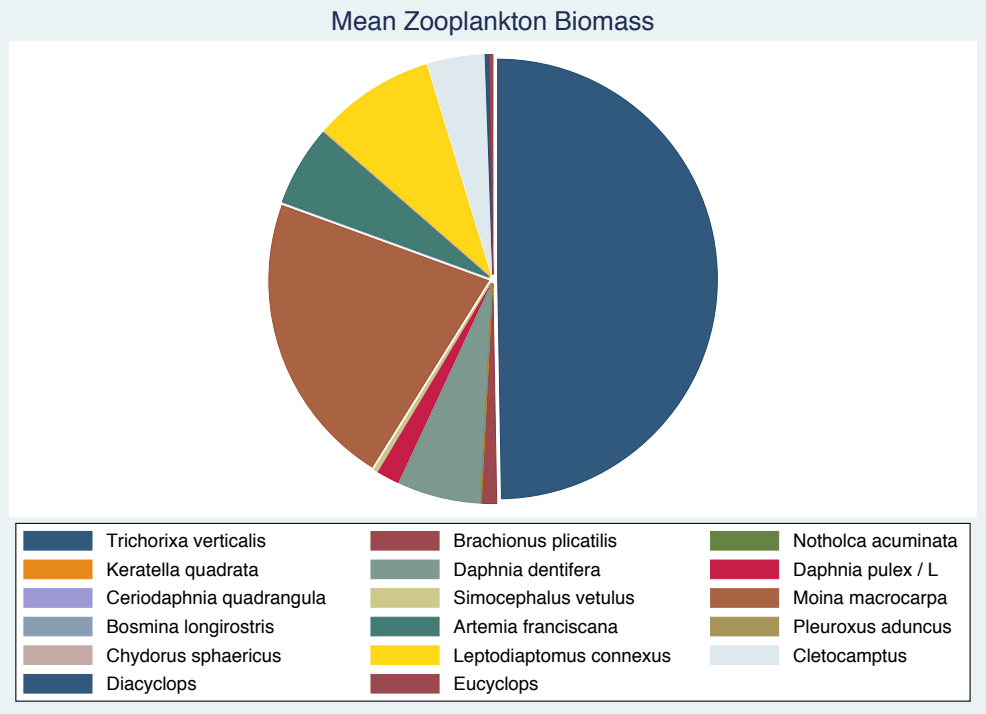

Figure 36. Mean zooplankton taxa biomass (ug/L) for all sites and dates, including Trichocorixa verticalis.

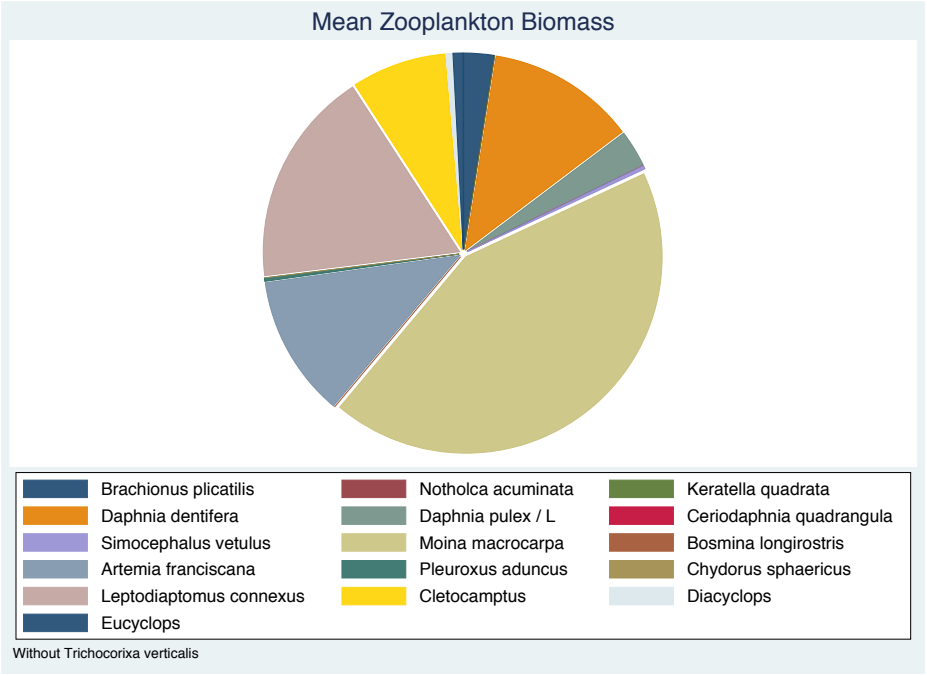

Figure 37. Mean zooplankton taxa biomass (ug/L) for all sites and dates, excluding Trichocorixa verticalis.

Zooplankton assemblages differed significantly by site (MRPP: A=0.03, P = 0.002), month (A=0.27, p <<0.01, and year (A=0.03, p < 0.01) as illustrated in Figure 39 (see MRPP results for multiple comparisons in Appendix 2).

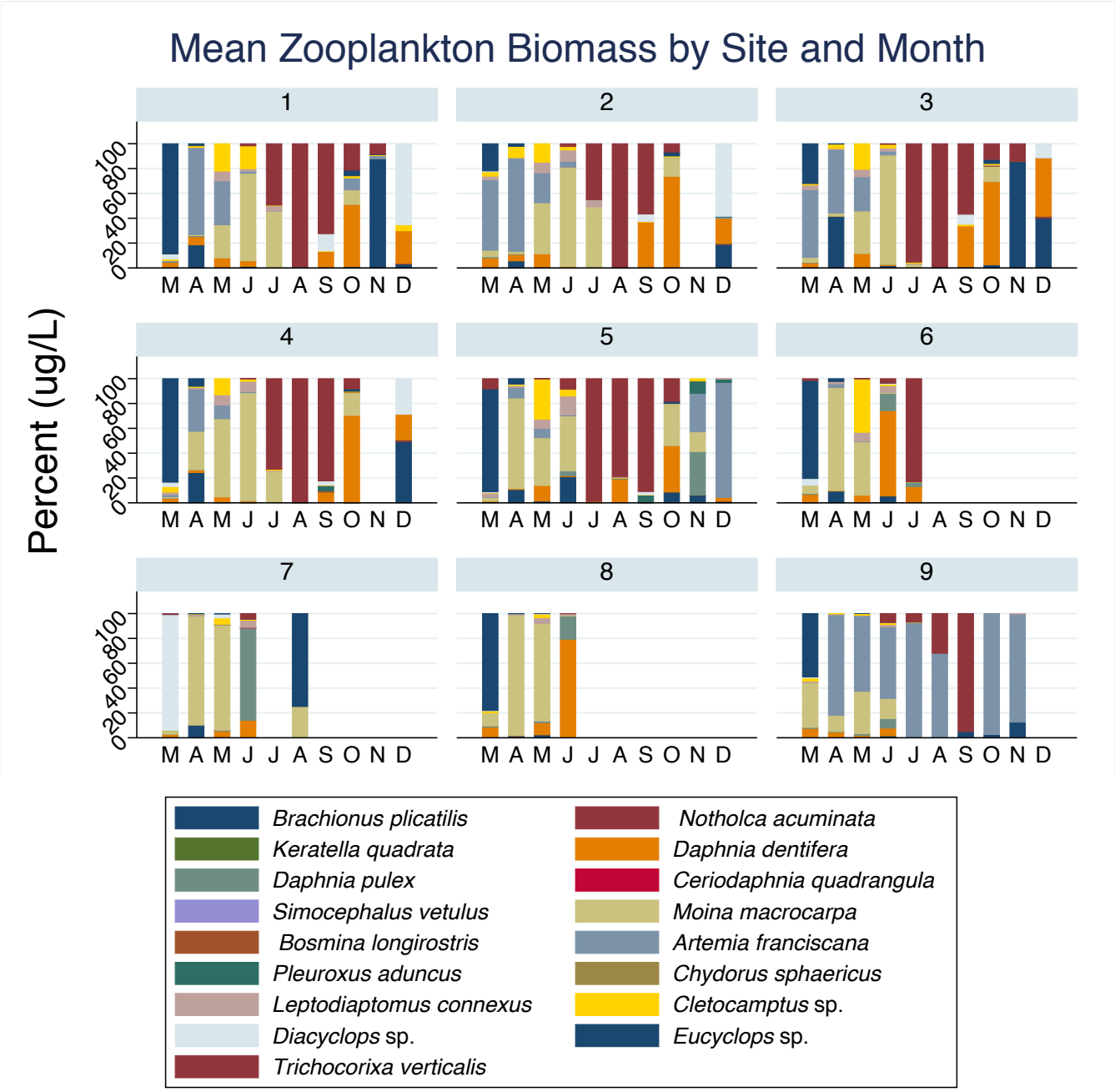

Figure 38. Mean zooplankton taxa biomass (ug/L) by site and month.

Zooplankton taxa richness generally increased from north to south likely due to salinity gradients, whereas, evenness and diversity didn't vary much between sites except Site 2 where evenness and diversity were higher and Site 9, which had the lowest diversity (Figure 40).

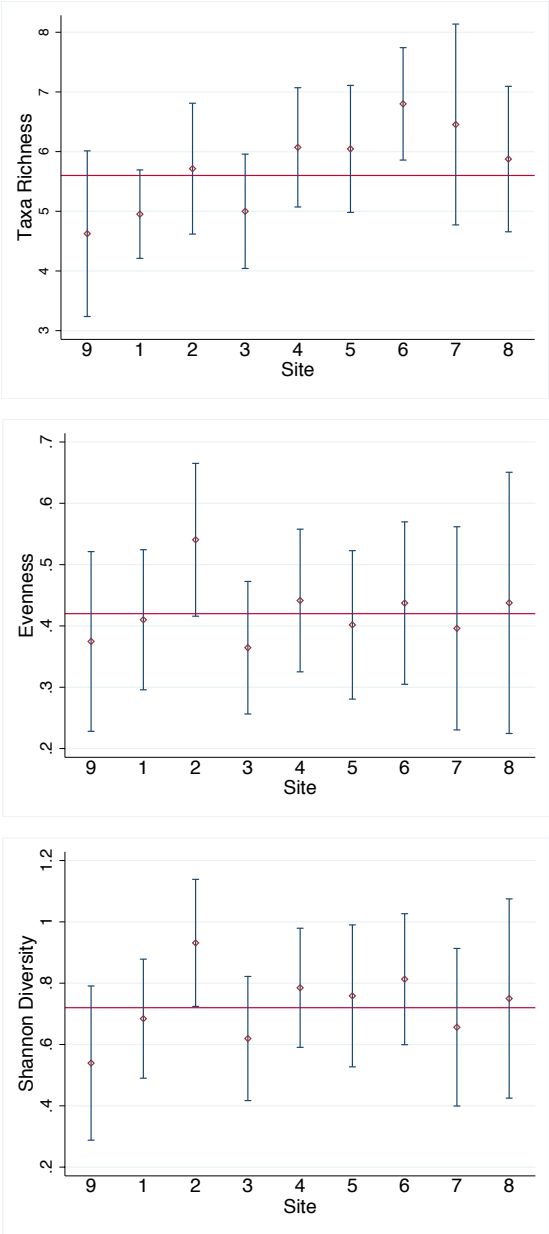

Figure 39. Zooplankton taxa richness, evenness, and diversity by sites (mean and 95%CIs).

Zooplankton groups showed monthly biomass (ug/L) trends with corixids dominating July-September and rotifers typically showing the lowest biomass as well as *Artemia* in July.

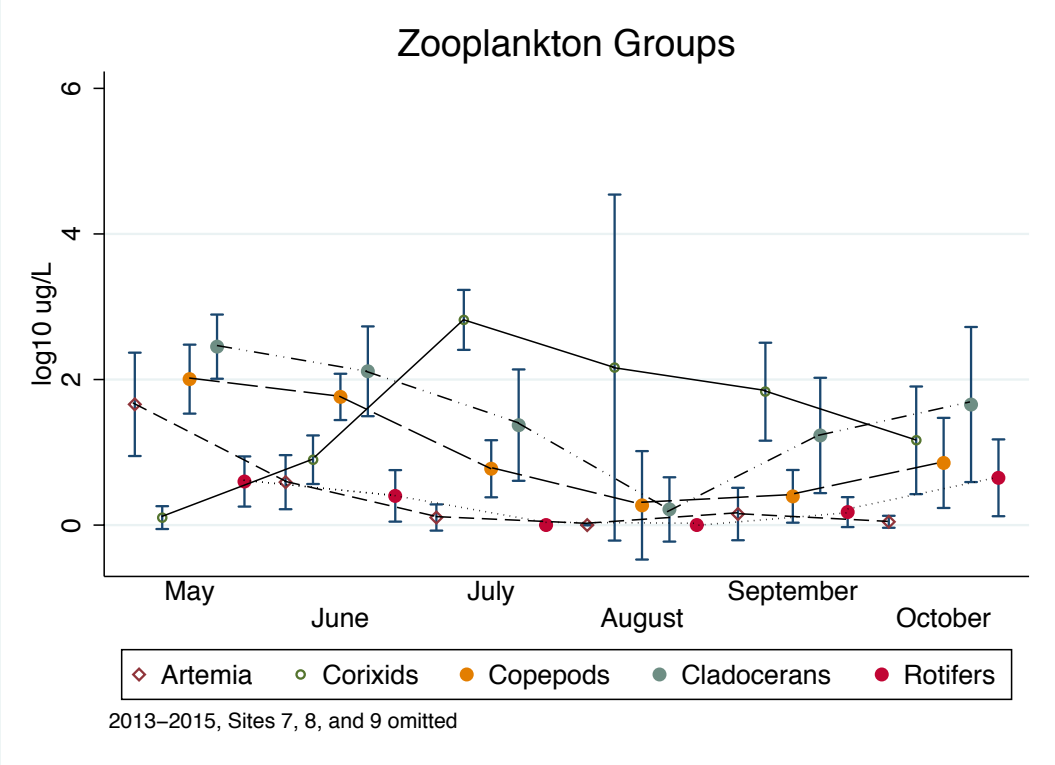

Figure 40. The five major zooplankton groups densities (log10 cells/L) from April to October (all years and sites except 7, 8, and 9 combined). Mean and 95% CIs.

Zooplankton taxa and environmental thresholds

Salinity

There was a zooplankton assemblage threshold change point (CP) at salinity = 8.2 ppt for taxa that decreased in abundance with increased salinity and a salinity CP = 6.6 ppt for taxa that increased in abundances with increased salinity (Figure X). Eight taxa met purity and reliability criteria for decreasers (taxa that decreased in abundance with increased salinity), two taxa met purity and reliability for increaser taxa (Figures 42 and 43).

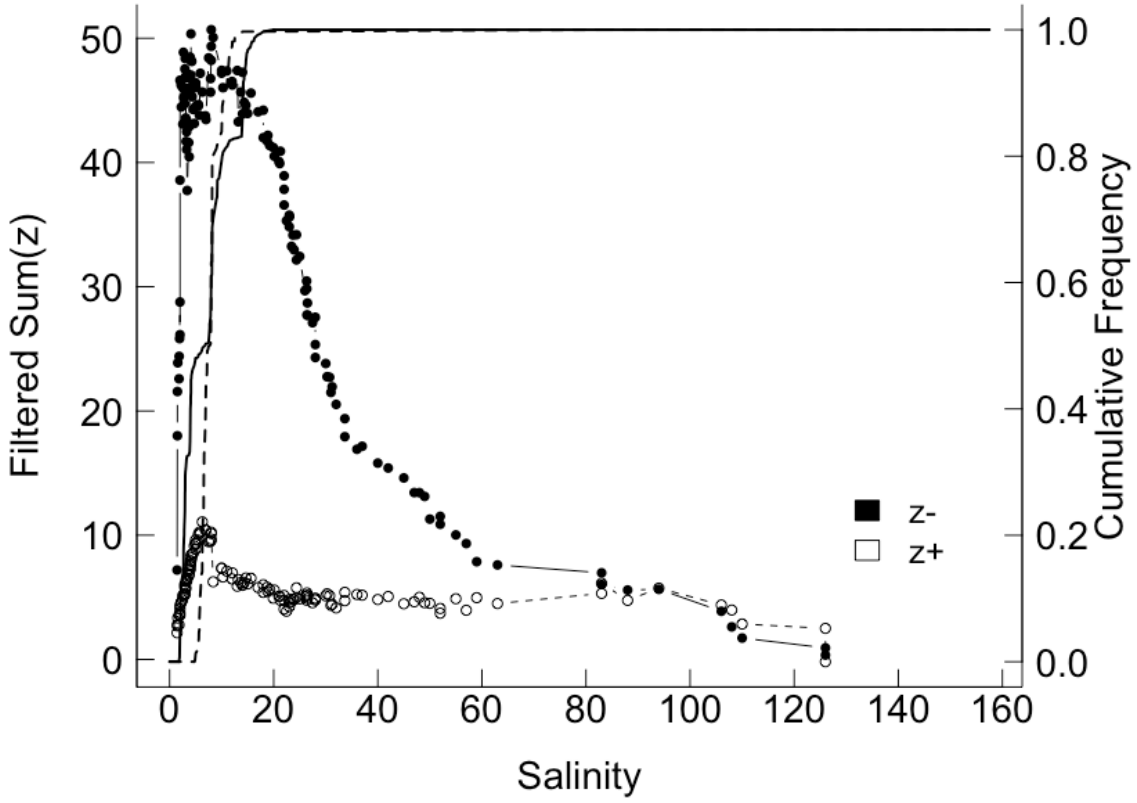

Figure 41. Filtered zooplankton assemblage level summed z scores. The filled circles denote the magnitude of the summed z – scores for decreasing taxa abundances with increasing salinity and the hollow symbols are for z+ taxa with increasing abundances with increasing salinity. Peaks in the values indicate points along the salinity gradient that produced large amounts of change in assemblage composition and/or structure. Plateaus denote regions of change. Solid and dashed lines without circles are the cumulative frequency distributions (CFDs) of sum(z-) and sum(z+) maxima across bootstrap replicates. (Baker, King, and Kahle 2015).

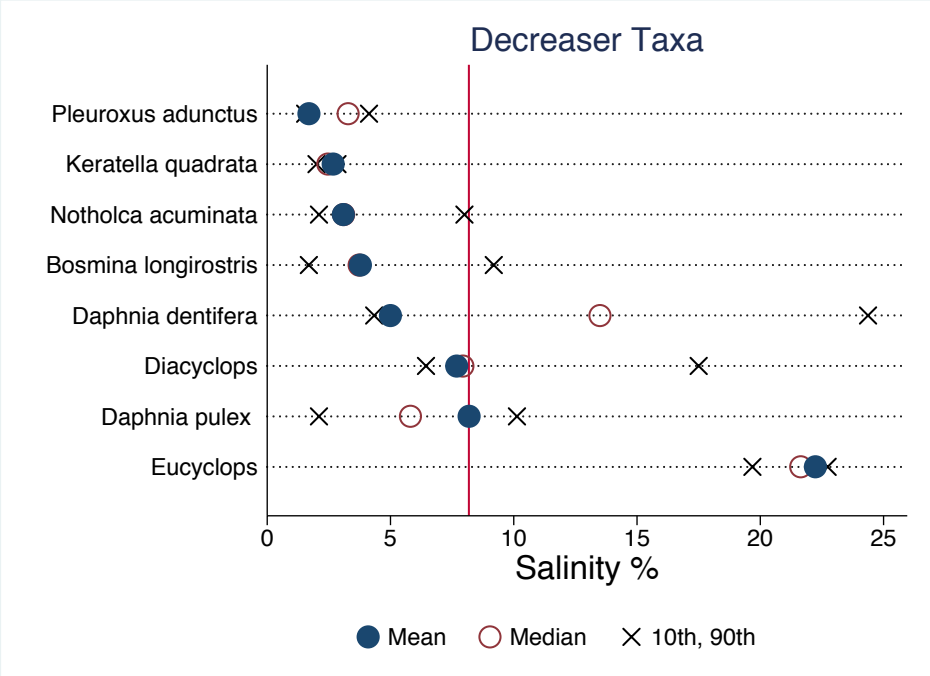

Figure 42. Mean (solid circles), median (hollow circles) and 10th and 90th percentile (x's) CPs for zooplankton taxa that decreased in abundances with increased salinity (decreaser z-) and met purity and reliability criteria. The zooplankton assemblage filtered mean z- CP threshold was 8.2 (red vertical line).

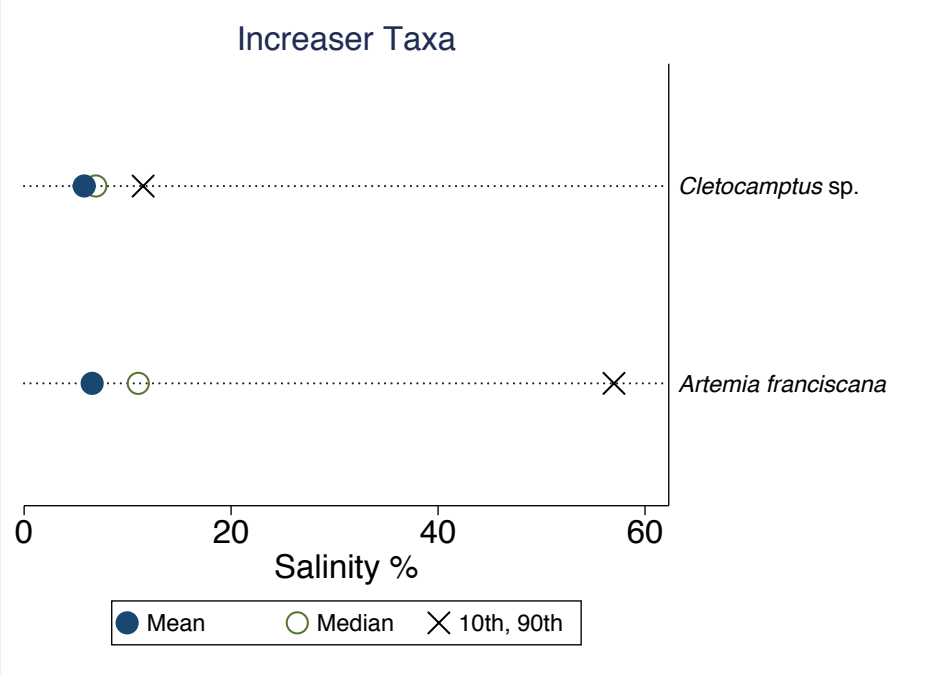

Figure 43. Mean (solid circles), median (hollow circles) and 10th and 90th percentile (x's) CPs for the two zooplankton taxa, Artemia franciscana and Cletocamptus sp. that increased in abundances with increased salinity (increaser z-) and met purity and reliability criteria. The zooplankton assemblage filtered mean z- CP threshold was not meaningful due to only two increaser taxa.

The thresholds indicated for zooplankton taxa found in Farmington Bay provide details of the potential impact that elevated salinity can have on the biodiversity of Farmington Bay. Among the zooplankters observed eight taxa exhibited physiological constraints at less than one percent salinity (<10 ppt) while only a couple of well-known halophilic zooplankter (i.e., *Artemia*) demonstrated an increase in abundance as salinity increased. The importance of these threshold observations is that it shows the potential harm to Farmington Bay should salinity increase dramatically. Salinity has long been proposed to be useful as a mechanism to disfavor HABs in Farmington Bay and the level proposed to accomplish this is 70 ppt (Marcarelli, Wurtsbaugh, and Griset (2006). Although this level may be effective at reducing HABs it would have the converse effect of causing widespread impacts among diverse zooplankton populations. Thus, a management quandary evolves in which there are divergent and mutually exclusive outcomes that would arise because of salinity modifications in the bay, especially since the proposed level to control HABs is 7-fold higher than the tolerance level of many of the zooplankton taxa. It is worth noting that Herbst (2006) found that evaporation ponds of intermediate salinity (112 g/L) produced the best combination of zooplankton diversity and nutritional quality in terms of foraging opportunities for shorebirds. He observed greater usage of these ponds by birds and found that the lower salinity (98 g/L) and higher salinity ponds (173 g/L) were suboptimal in terms of food quality and quantity for birds. Salinity has been proposed as a means of moderating predation by corixids on zooplankton (Van De Neutter, Trekels, Green and Stoks, 2010). Although corixids deplete other zooplankters Miller, Hoven and Cavitt (2009) found corixids to be a dominant prey item in shorebirds feeding in Farmington Bay and other GSL wetlands. Corixids have been studied in detail for decades and have been known to be top level carnivores in some alkaline systems but that they also are omnivores capable of exploiting a variety of resources (Reynolds, 1975). Corixids gut contents often contain cyanobacteria, diatoms, and assorted amorphous detritus content. Yet when algal sources are depleted and zooplankton prey are abundant corixids can shift their foraging preference and rapidly denude the water column of prey items. Diets of corixids if FB need to be examined using DNA barcoding if we are to understand their dynamics and influence on HABs (see Recommendation section).

Temperature effects on zooplankton

Three zooplankton taxa, *Notholca acuminata* (Rotifera), *Diacyclops* sp. (Copepoda), and *Eucyclops* sp. (Copepoda) decreased in abundances with increased temperatures (Figure 45). *Cletocamptus* sp. (copepod)was the only zooplankter that was a pure and reliable increaser with increasing temperature (Median 13.45°C; 10^{th} = 11.9°C, 90^{th} = 15.9°C)

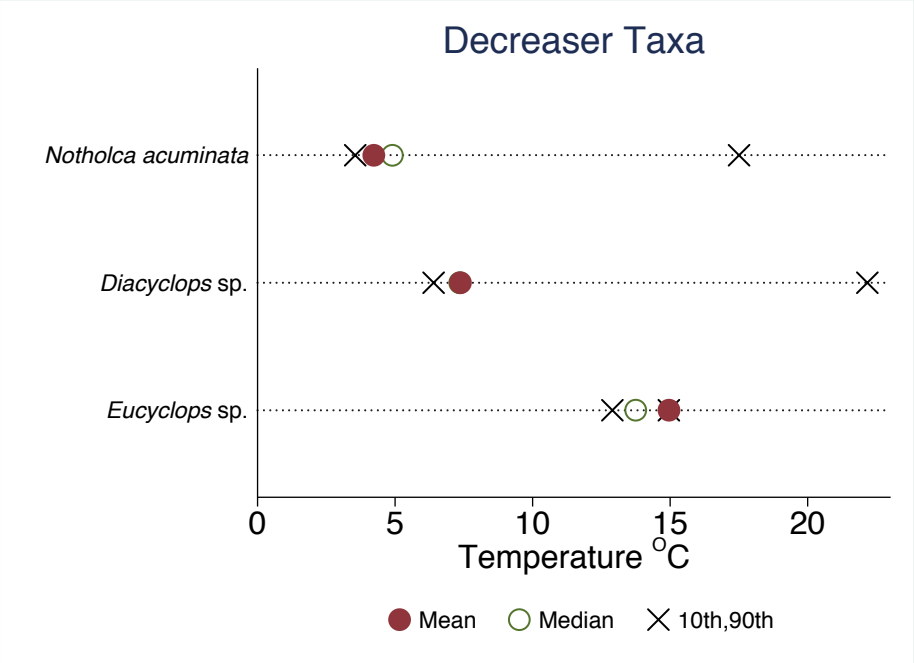

Figure 44. Mean (solid circles), median (hollow circles) and 10th and 90th percentile (x's) CPs for the three zooplankton taxa that decreased in abundances with increased temperature (decreaser z-) and met purity and reliability criteria

Ecological Interactions and the Foodweb

The relationships between phyto- and zooplankton groups varied seasonally (April –October) and between years (2013 vs. 2014)(Figures 46-53). In general, the algal groups varied more in 2013 particularly early in the season and the zooplankton groups decreased in summer except corixids that tended to increase in summer. Abundances for the three algal groups tended to remain steady after mid-July and through September in 2014 even though rotifers, cladocerans, and copepods tended to decrease or fluctuate during this time suggesting that something other than food resource availability was regulating these zooplankton groups. Corixids increased in biomass during this time almost mirror imaging the other zooplankton strongly suggesting that corixids had a major top down effect on these populations (Figures 54-59). Our SEM analysis confirms this substantial predation effect on other zooplankters by corixids (Figure 62).

***Artemia* vs algal groups**

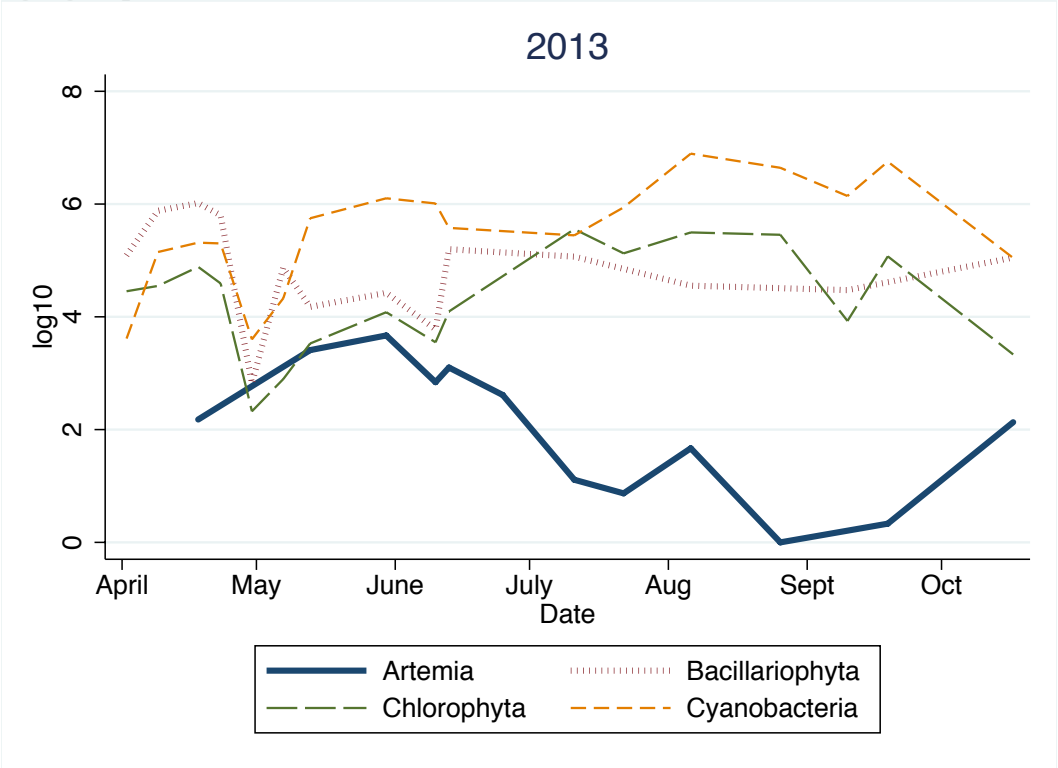

***Figure 45. Artemia* vs. phytoplankton groups, 2013**

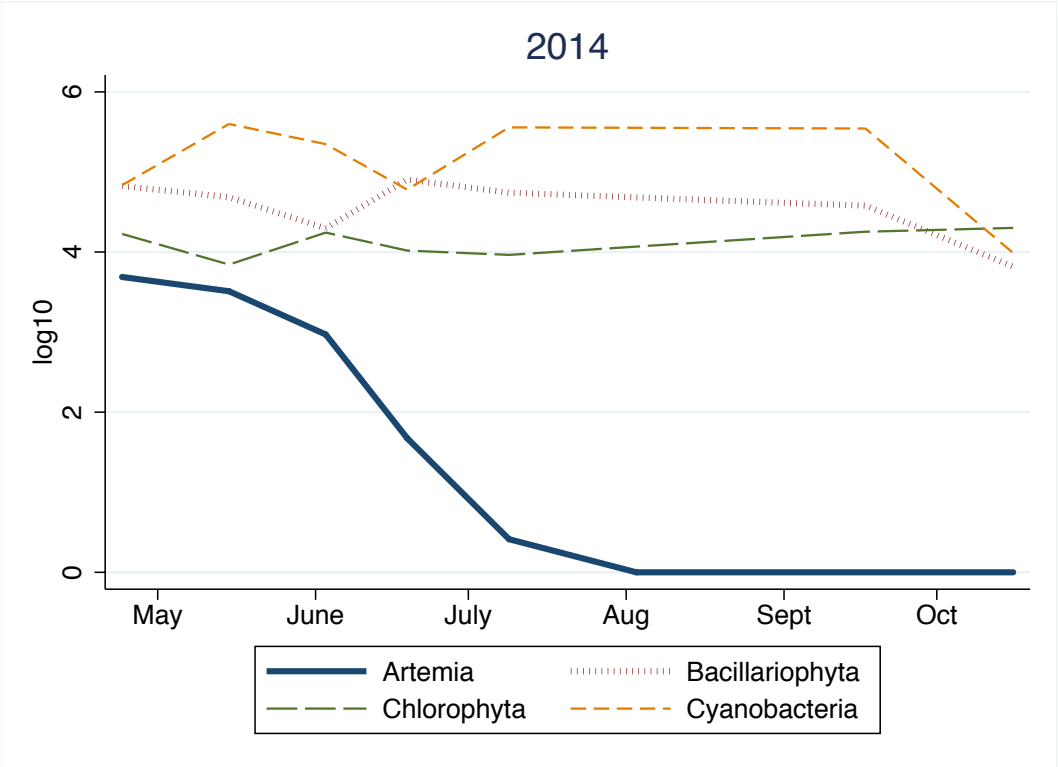

***Figure 46. Artemia* vs. phytoplankton groups, 2014**

Cladocera vs algal groups

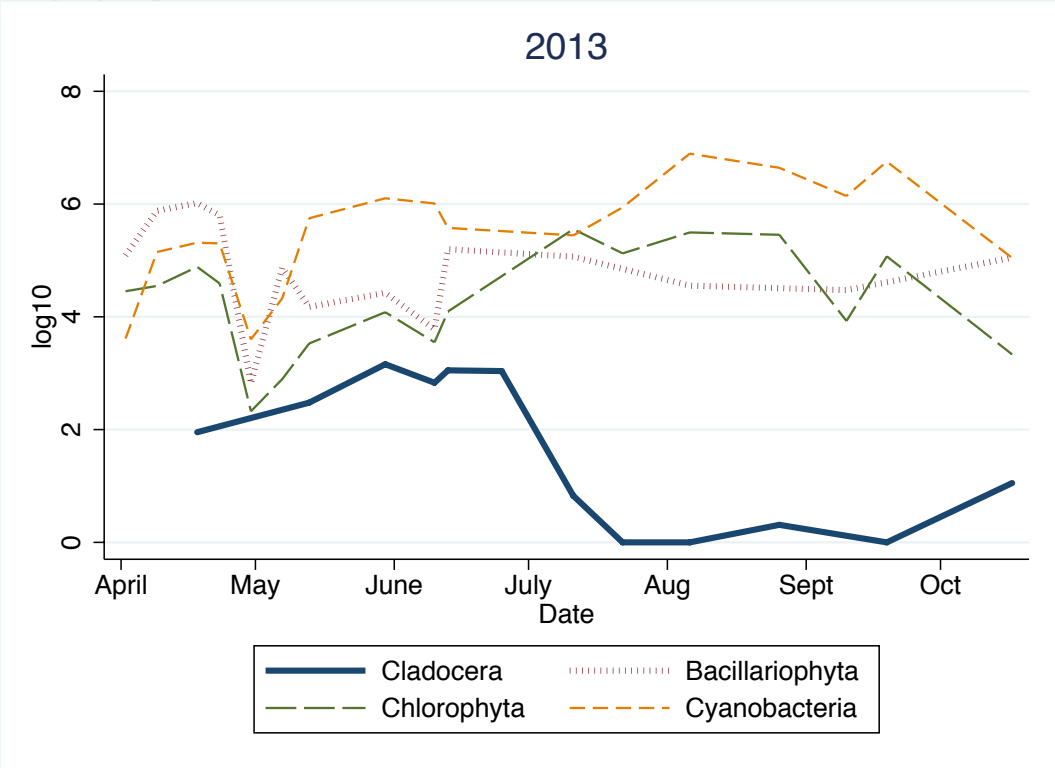

***Figure 47*. Cladocera vs. phytoplankton groups, 2013**

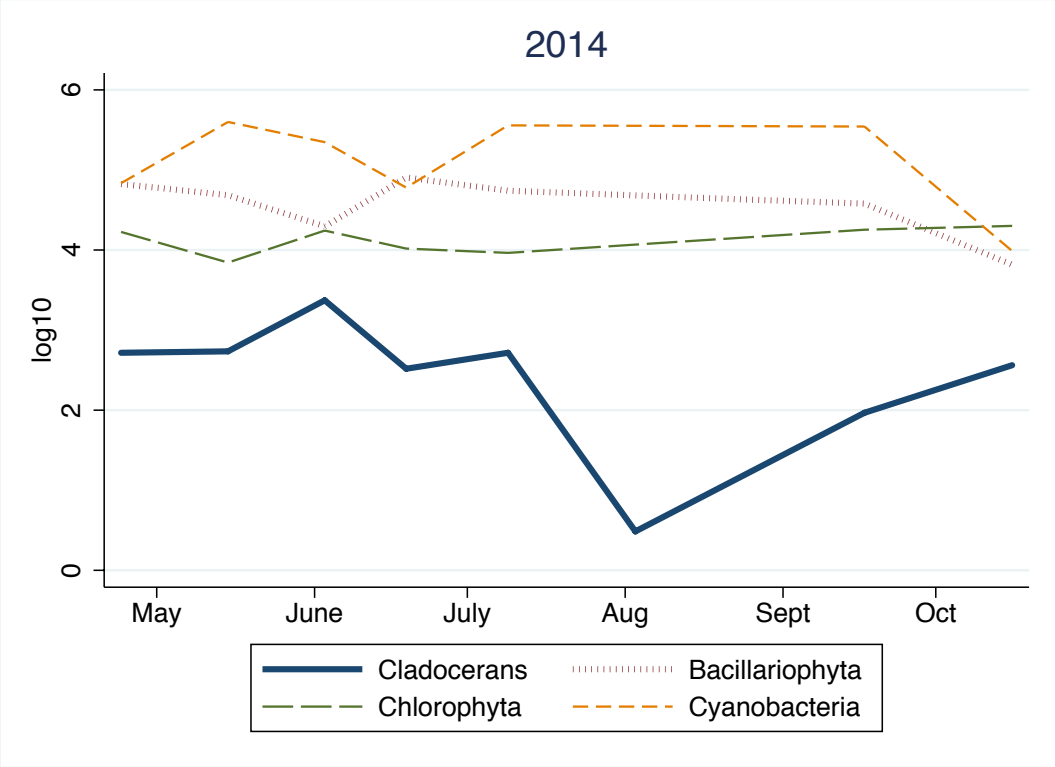

***Figure 48*. Cladocera vs. phytoplankton groups 2014**

Copepods vs algal groups

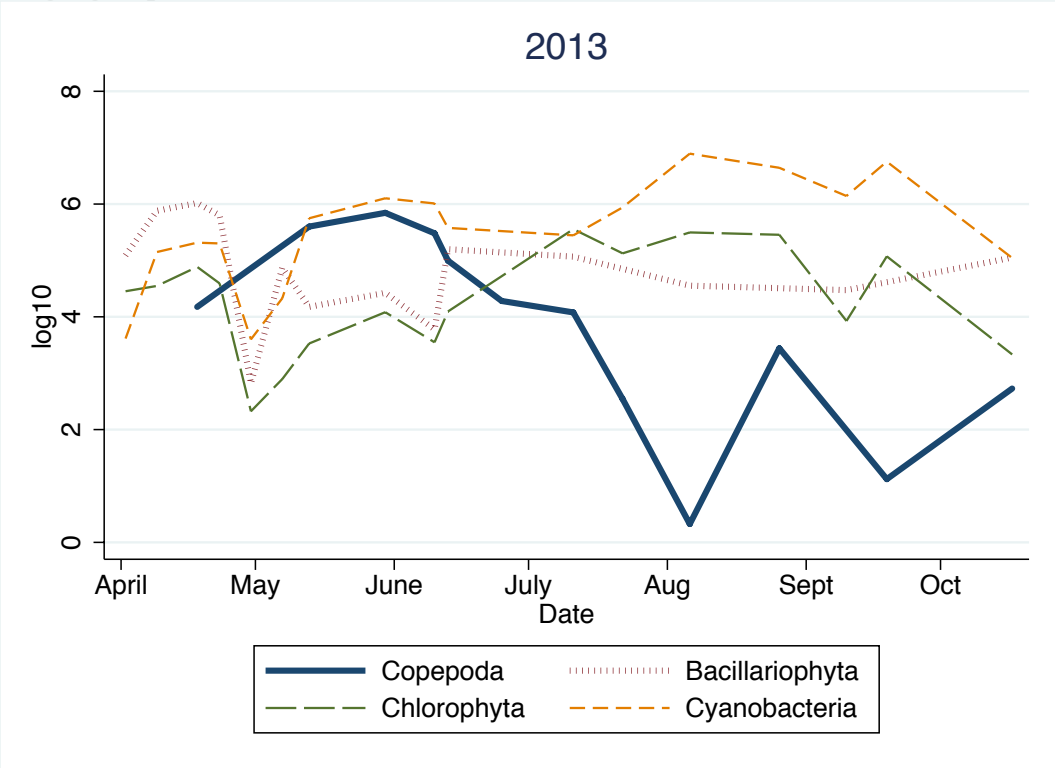

***Figure 49*. Copepods vs phytoplankton groups, 2013**

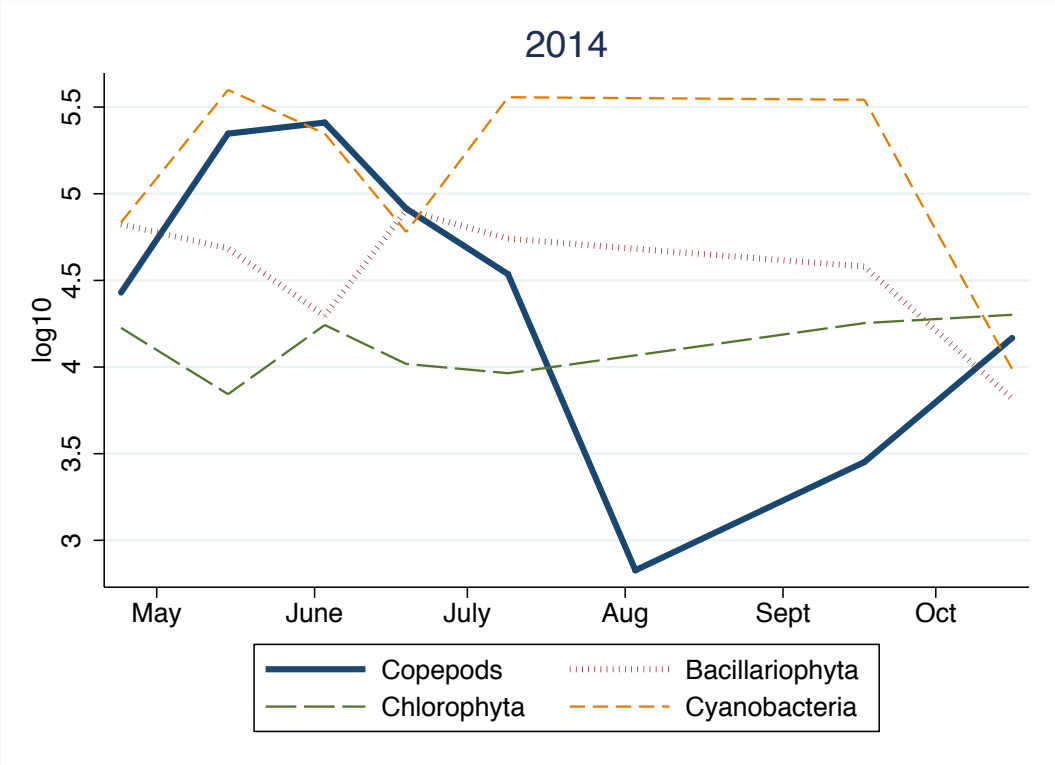

***Figure 50*. Copepods vs phytoplankton groups, 2014**

Rotifers vs algal groups

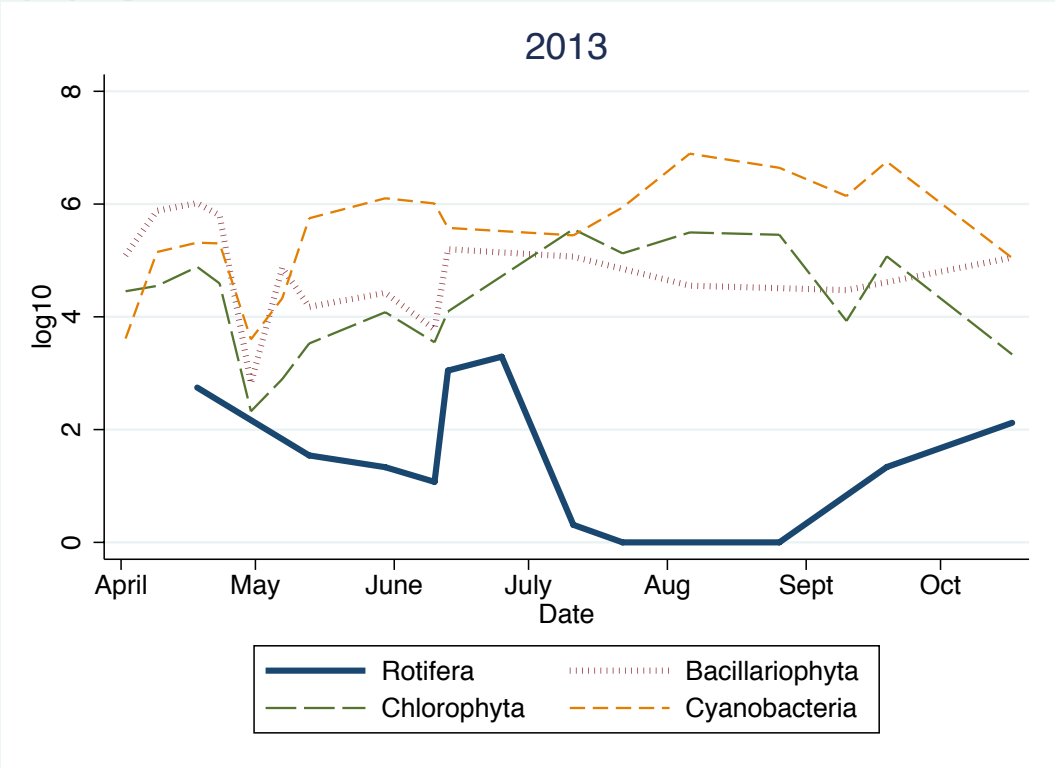

Figure 51. **Rotifers vs phytoplankton groups, 2013**

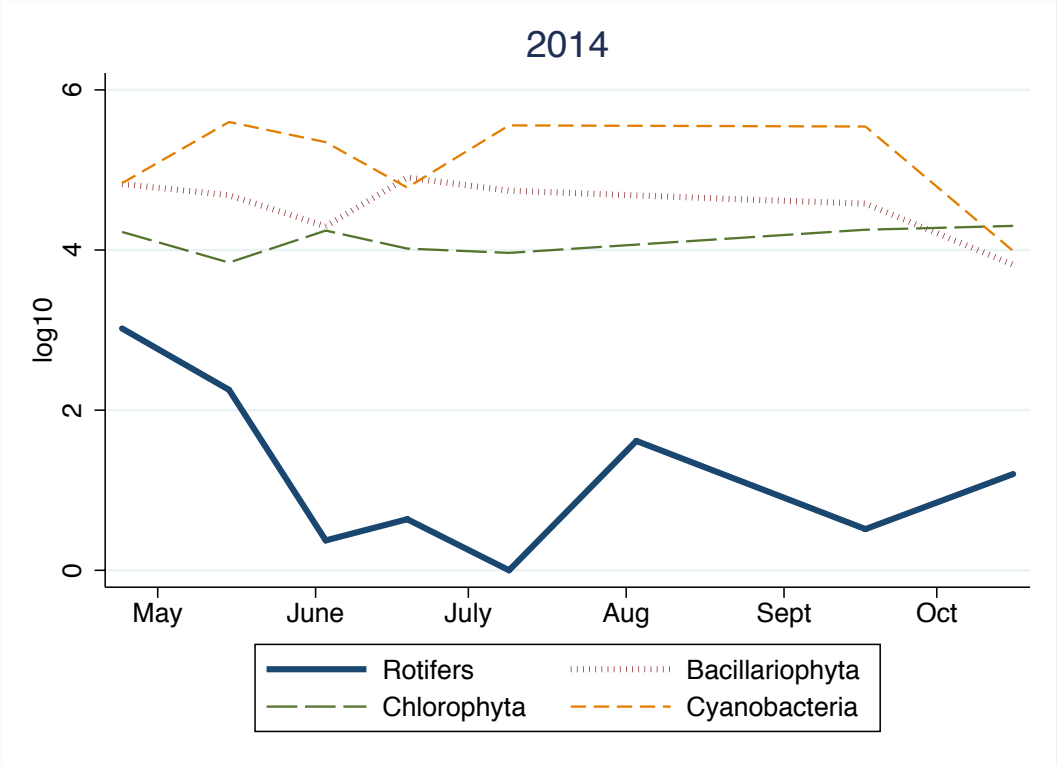

Figure 52. **Rotifers vs phytoplankton groups, 2014**

Zooplankton groups vs Corixids

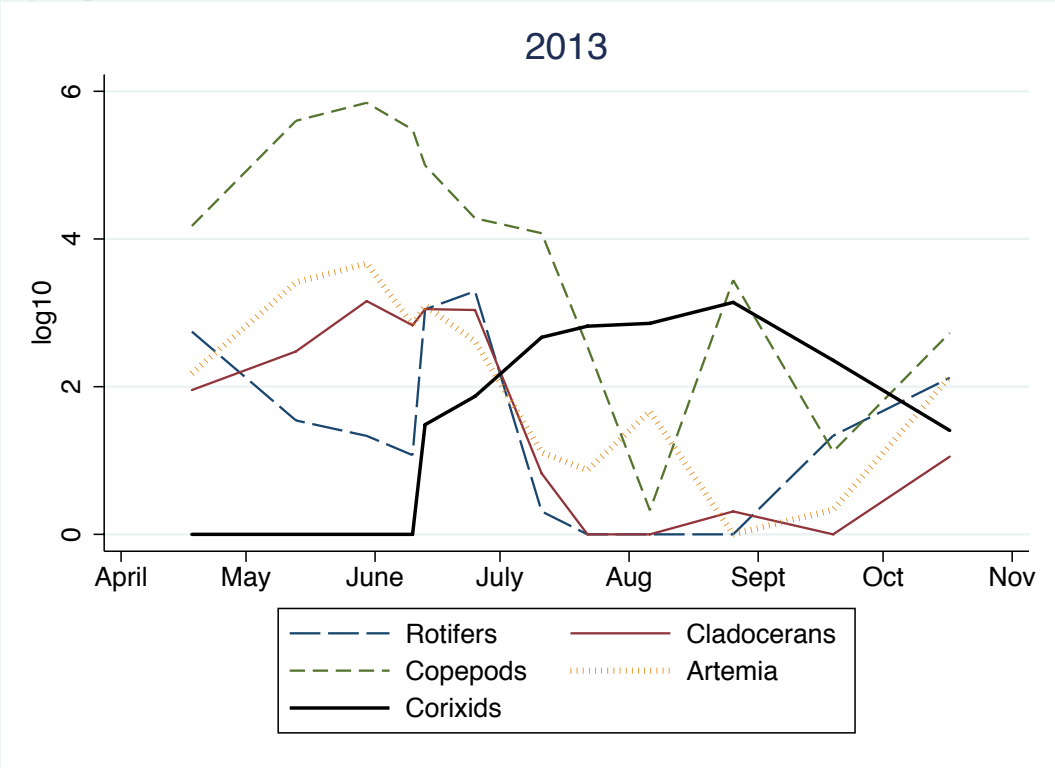

***Figure 53*. Zooplankton groups vs. corixids, 2013**

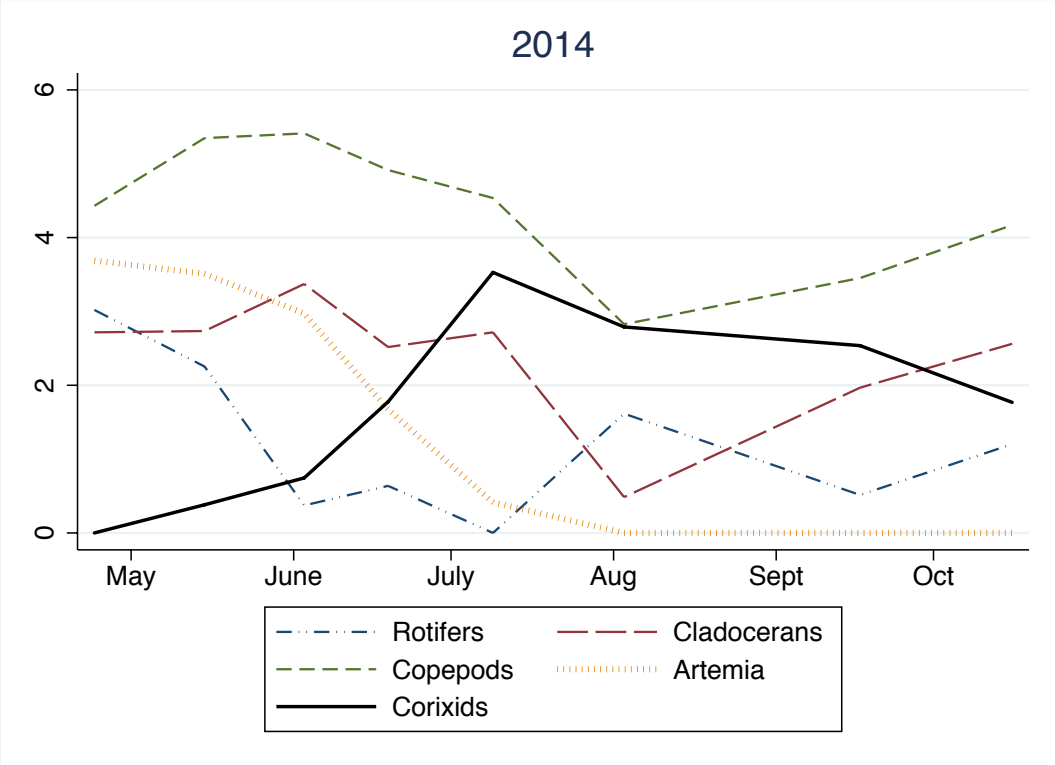

***Figure 54*. Zooplankton groups vs. corixids, 2014**

Zooplankton vs algal groups

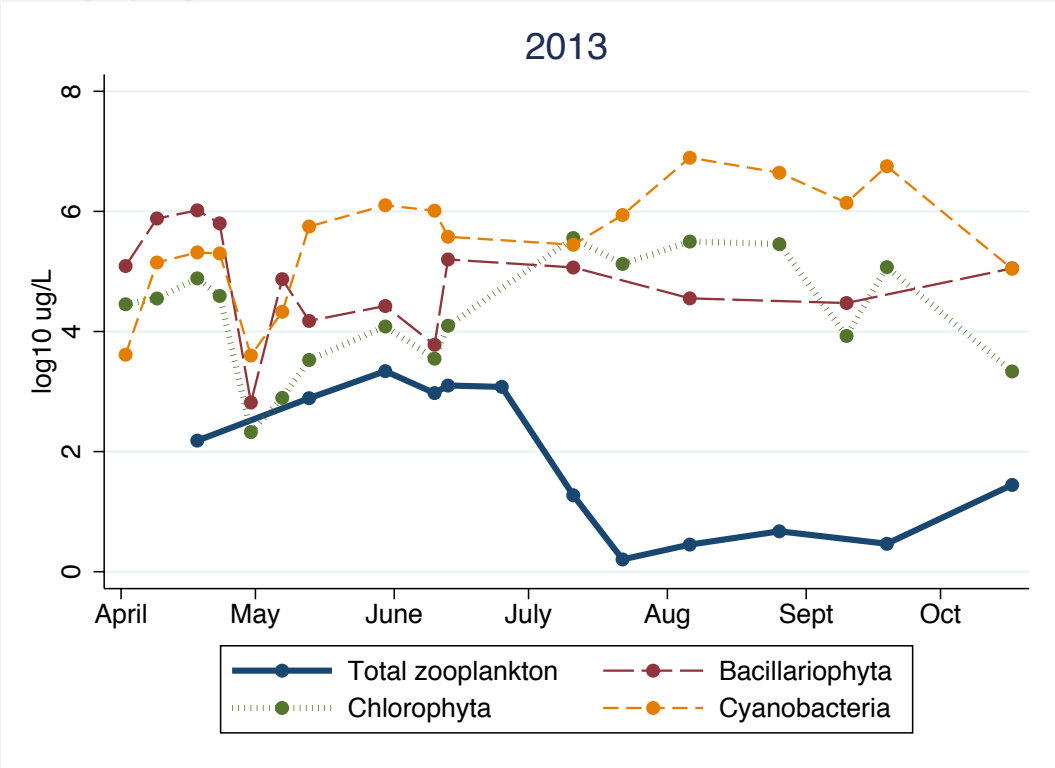

***Figure 55*. Zooplankton vs. algal groups, 2013**

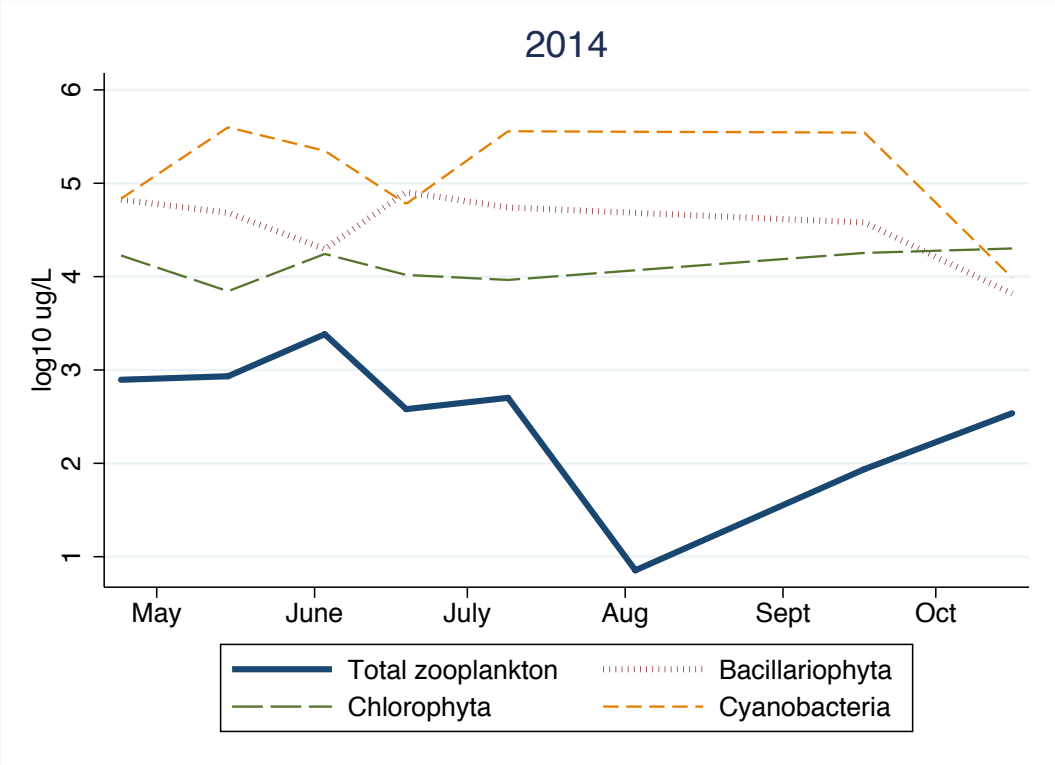

***Figure 56*. Zooplankton vs. algal groups, 2014**

Zooplankton vs Corixids

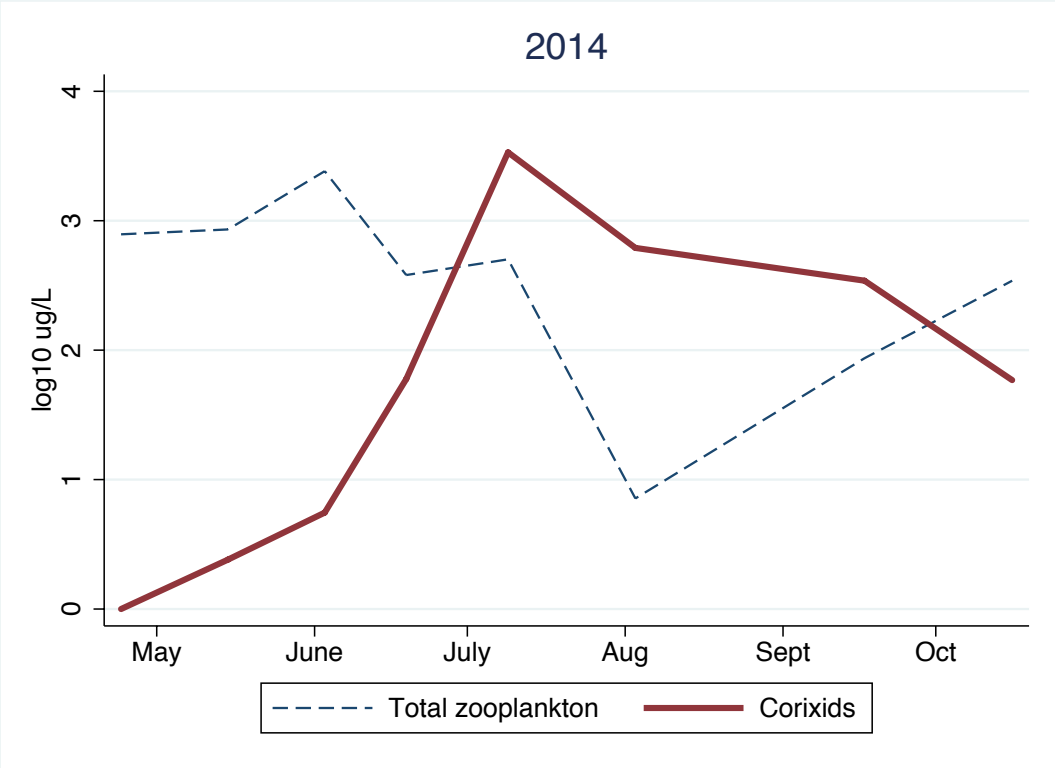

***Figure 57*. Zooplankton vs corixids, 2013**

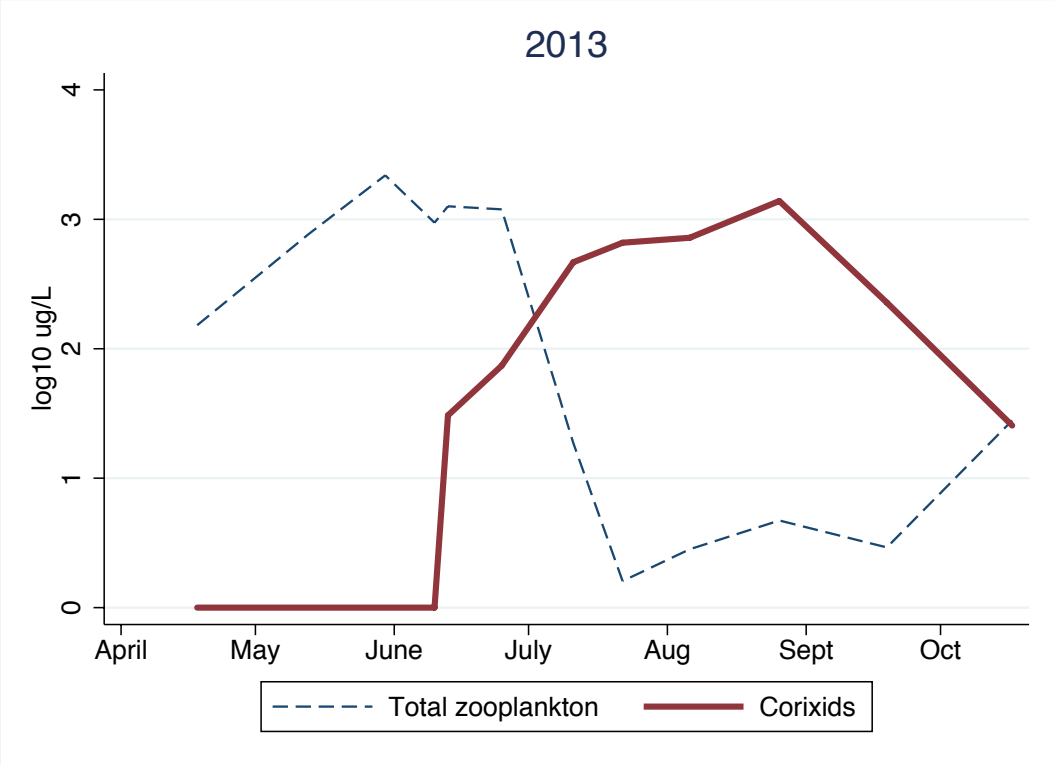

***Figure 58*. Zooplankton vs corixids, 2014**

The temporal and spatial distribution of corixids and Moina from the 2013 sampling season are shown in Figure 60. Comparing the patterns of abundance between these two taxa illustrates the characteristic top-down predation exerted by Corixids on other zooplankters. As the abundance of Corixids increases their prey items subsequently collapse. There is little doubt that this predatory effect of Corixids is one of the main driving forces behind zooplankton population dynamics and indirectly phytoplankton populations in the Bay.

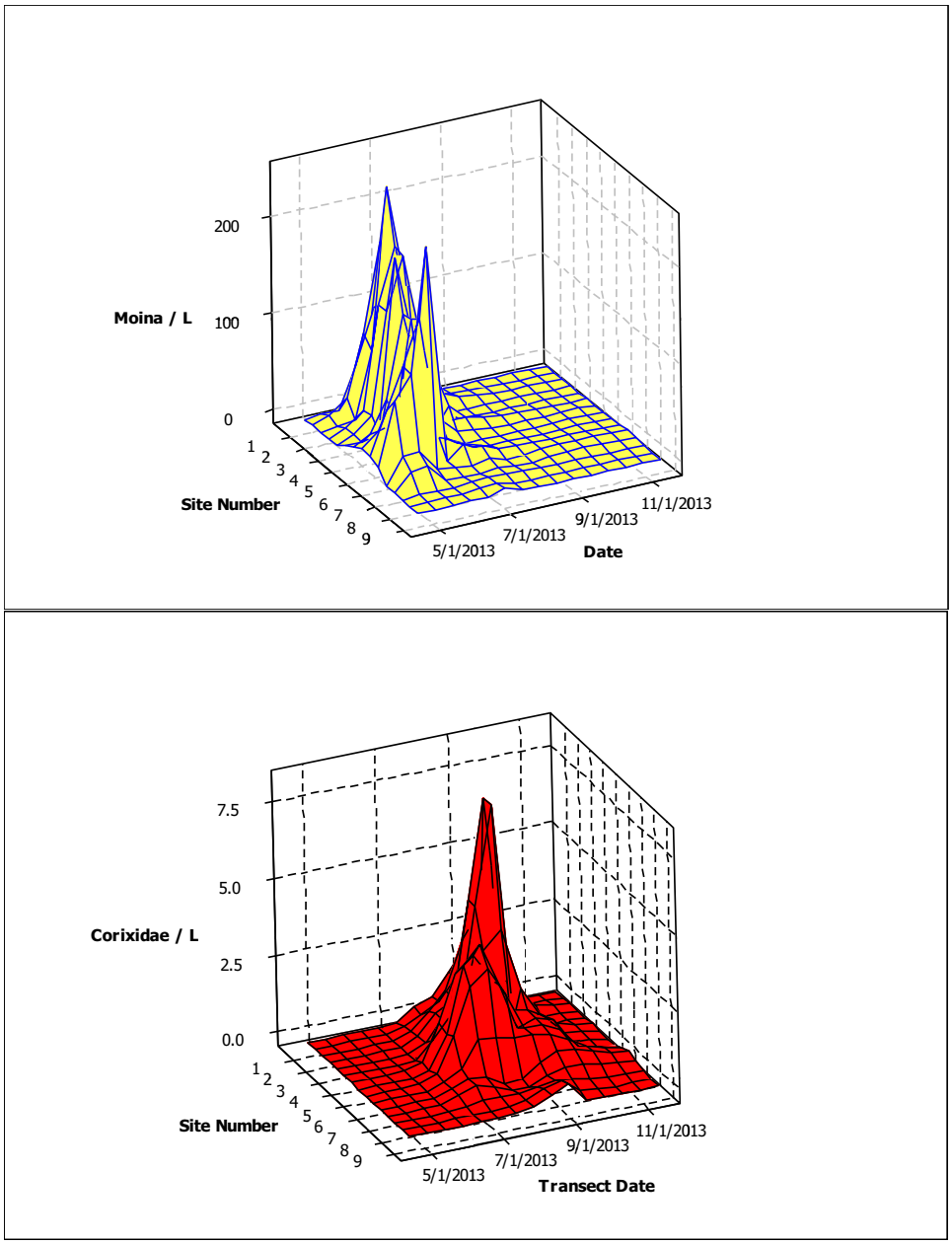

Figure 59. The spatial and temporal abundance of Moina and Corixids are shown in figures 60a and 60b. Moina emerge in the spring and reach robust abundance by May. Coinciding with a dramatic increase in Corixid abundance in June, July and August Moina abundance decreases substantially.

This is one example of Corixid prey depletion that occurs as the Corixid population expands in size and distribution across the Bay.

Nodularin and DO vs zooplankton groups

Correlations between nodularin (log10) and zooplankton groups (log10) showed only weak positive relationships suggesting that nodularin did not have a negative effect on these populations (Table X). Simiarly, DO was not correlated with the zooplankton groups except for copepods that had a weakly significant positive correlation (Table 13).

Table 13..Correlations between zooplankton groups and nodularin (ug/L) and DO, all log10 transformed (N = 93 pairs). * = p<0.05.

	nodularin	**DO**
Zooplankton Group	***r***	***r***
Rotifers	**0.12**	**-0.06**
Cladocerans	**0.33***	**-0.08**
Copepods	**0.19***	**0.18***
Artemia	**0.24***	**0.06**
Corixids	**0.37***	**-0.04**

This is only a preliminary analysis and we need much more research and analysis as time permits. However, nodularin and DO did not seem to have any effect on zooplankton groups.

Table 14.Correlations between algal groups and zooplankton groups

	logCya~a	logChl~a	logBac~s	logArt~a	logCor~s	logCop~s	logCla~s
logCyanoba~a	**1.0000**						
logChlorop~a	**0.2102**	**1.0000**					
logBacilli~s	**0.6670**	**0.0167**	**1.0000**				
logArtemia	**0.1127**	**-0.2520**	**-0.0520**	**1.0000**			
logCorixids	**0.2173**	**0.2023**	**0.2362**	**-0.4774**	**1.0000**		
logCopepods	**-0.1380**	**-0.3271**	**-0.0473**	**0.6348**	**-0.5116**	**1.0000**	
logCladoce~s	**-0.2729**	**-0.3045**	**-0.2485**	**0.3799**	**-0.3810**	**0.7771**	**1.0000**
logRotifers	**-0.0560**	**-0.0344**	**0.1644**	**-0.0035**	**-0.1781**	**0.0977**	**-0.0136**

There were only very weak correlations between all groups except moderate correlations between Cyanobacteria and bacillariophytes, cladocerans and copepods, and *Artemia* and copepods (Table 14 and

Figure 61). Consequently, any regression analyses would have shown poor fits resulting in less informative and possibly misleading interpretations.

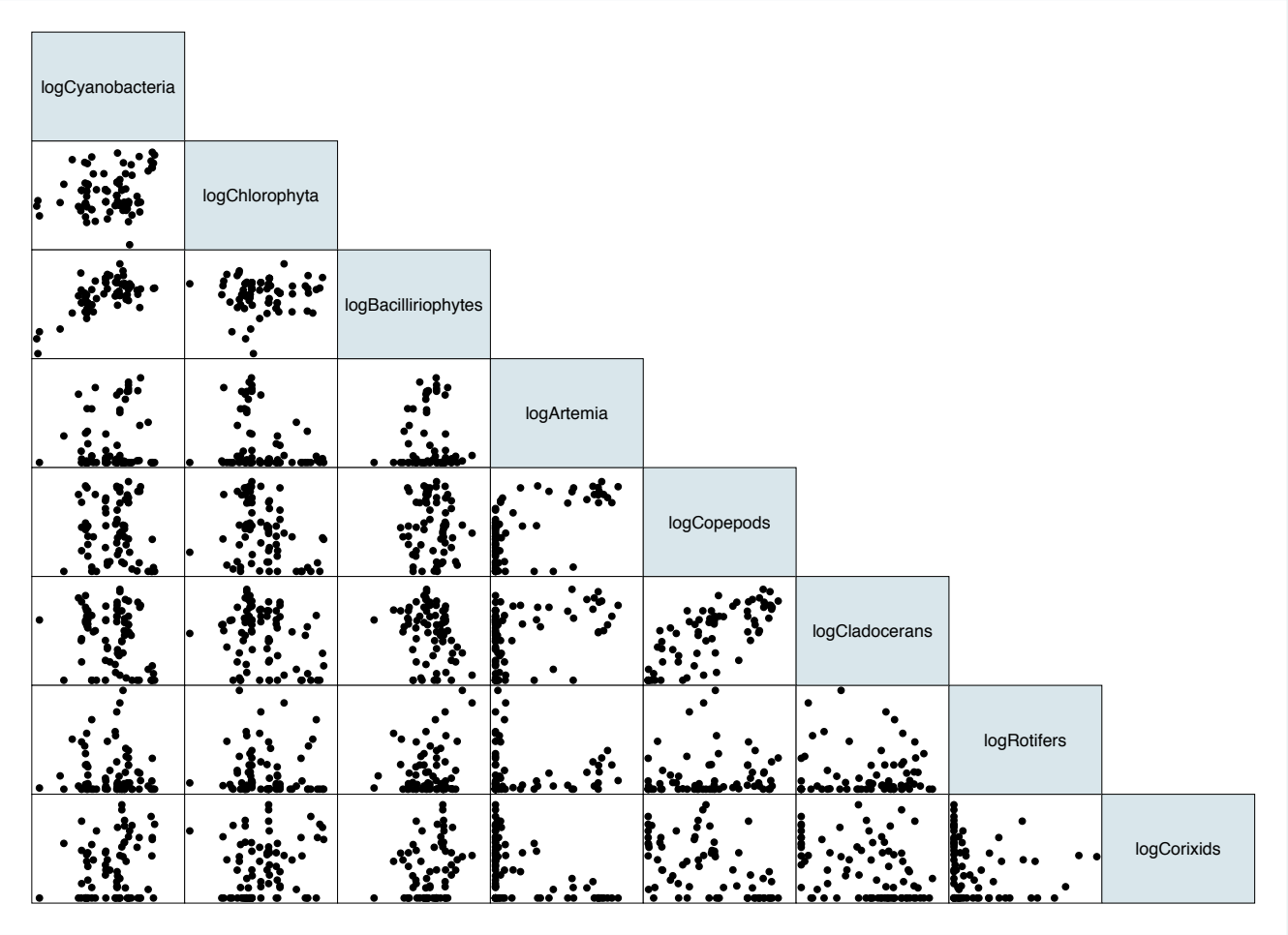

Figure 60. Scatterplots showing bivariate relationships between phytoplankton and zooplankton groups.

SEM Model of Trophic Relationships

Because correlations shown in Table 14 and Figure 61 are bivariate (i.e. two way interactions), they cannot show all the complexities in the FB food web. Subsequently, reliance on bivariate relationships to understand the food web can be misleading. A more informative modeling method for determining direct and indirect direction interactions between these groups (and nutrients) was structural equation models or SEM. We examined and compared dozens of SEM models based on our *a priori* knowledge of FB ecology and general limnological/ecological known interactions and examining all possible combinations. The following model met our ecological criteria and was statistically the best fit model (Figure 62).

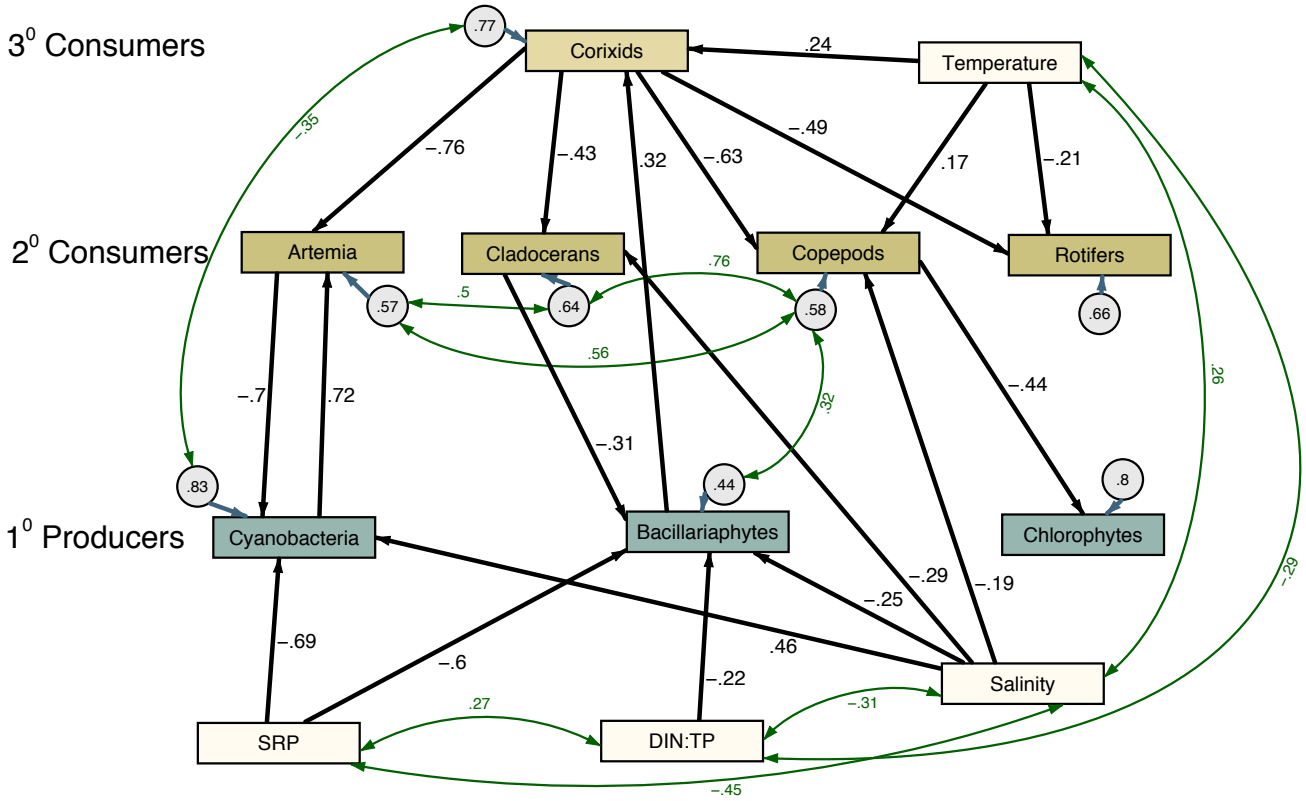

Figure 61. Final standardized structural equation model (SEM) showing significant interactions and covariables of chemistry/nutrients, phytoplankton groups (primary producers), zooplankton groups (secondary consumers), and the predaceous corixids (tertiary consumers). Straight black lines with one arrowhead are dependencies; green lines with double arrowheads are covariates (correlations) and circles with values inside are unexplained variability for the endogenous variables. Artemia, Cladocerans, Copepods, and Corixids were modeled as log generalized biomass (ug/L). Cyanobacteria, Bacillariophytes, and Chlorophytes were modeled as log10 cells/L. 2013-2015, May-October, Sites 7, 8, and 9 omitted.

All structural 'dependencies' and covariates shown in Figure 62 were significant ($p < 0.05$) (Table 16). This SEM had a $X^2 = 24.93$, p value = 0.92, with 36 df (X^2 p-values need to be greater than 0.05 to be significant). RMSEA (Root Mean Square Error) was 0.00, signifying an excellent fit and CFI (Comparative Fit Index) was 1.00 which also signified an excellent fit. All equation slopes were significantly different than 0 (Table 20). The SEM overall goodness of fit was very good at $R^2 = 0.68$. The SEM explained 0.66 variability of diatoms but explained < 0.50 variability for all the other endogenous variables.

Our interpretation of the SEM (Figure 62) starting from nutrients and moving upward through the foodweb is as follows: The four most important and significant nutrients/chemistry variables selected from thirteen candidate variables that had dependencies (effects) with phyto- and zooplankton were; SRP, DIN:TP, salinity, and temperature. These four were also correlated with each other. SRP positively covaried with DIN:TP. SRP and DIN:TP negatively covaried with salinity. Temperature negatively covaried with DIN:TP and positively covaried with salinity. Bacillariophytes, cladocerans, and copepods were less tolerant of salinity and decreased with increased salinity whereas, cyanobacteria were more tolerant of salinity. Cyanobacteria and bacillariophytes quickly incorporated SRP. Bacillariophytes negatively interacted with DIN:TP. The SEM suggested that three zooplankton groups, *Artemia*, cladocerans, and copepods selectively grazed on different phytoplankton groups and had significant top down effects on the phytoplankton groups. Rotifers were not dependent on any phytoplankton group nor were they important grazers but decreased in biomass with increased temperatures. *Artemia* and cyanobacteria appeared to have had a strong bidirectional feedback loop on each other. *Artemia*, cladocerans, and copepods positively covaried, which was likely due to phytoplankton food resource availability or possibly facilitation. Copepods and bacillariophytes also covaried; consequently, cladocerans and *Artemia* indirectly covaried with bacillariophytes. There was a major top down predation effect of corixids on *Artemia*, copepods, rotifers, and cladocerans, which indirectly positively affected the three phytoplankton groups. Corixids and copepods also had higher biomass with increased temperatures. Corixids and cyanobacteria negatively covaried possibly due to grazing but this effect certainly needs further investigation.

Indirect and total effects (indirect + direct) were numerous and somewhat unexpected and the SEM was far superior in explaining these than any other model used in this report (Tables 17, 18 and 19). The myriad of dependencies and covariates that caused indirect effects between the variables and the total over all effects need to be more closely examined and described in subsequent reports and will likely be modified after the 2017 field season. Suffice it to say, indirect effects are far more numerous and important than appear by casual examination of the SEM.

Table 15. Final SEM for Farmington Bay foodweb (2013-2015, May through October, sites 7, 8, and 9 omitted).

Structural equation model Number of obs = **93**
Estimation method = **mlmv**
Log likelihood = **-1620.5261**

	OIM Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
Structural						
logCyanobacteria <-						
logArtemia	-.5771961	.1700538	-3.39	0.001	-.9104953	-.2438968
salinity	.0210762	.0052228	4.04	0.000	.0108397	.0313128
srp	-1.640095	.2926145	-5.60	0.000	-2.213609	-1.066581
_cons	5.707561	.2530284	22.56	0.000	5.211635	6.203488
logArtemia <-						
logCyanobacteria	.8750767	.12119	7.22	0.000	.6375486	1.112605
logCorixids	-.8384861	.100002	-8.38	0.000	-1.034486	-.6424858
_cons	-2.544226	.6173981	-4.12	0.000	-3.754304	-1.334148
logCladocerans <-						
logCorixids	-.4926183	.1045267	-4.71	0.000	-.6974868	-.2877498
salinity	-.0170127	.0044943	-3.79	0.000	-.0258213	-.0082041
_cons	3.285037	.1831432	17.94	0.000	2.926083	3.643991
logBacillariophyts <-						
logCladocerans	-.1401846	.0497447	-2.82	0.005	-.2376823	-.0426868
salinity	-.0063837	.0026844	-2.38	0.017	-.0116449	-.0011224
srp	-.8031928	.1203846	-6.67	0.000	-1.039142	-.5672433
dintp	-.1626243	.0633682	-2.57	0.010	-.2868238	-.0384249
_cons	5.202158	.1646543	31.59	0.000	4.879442	5.524875
logCopepods <-						
logCorixids	-.8165582	.1165664	-7.01	0.000	-1.045024	-.5880922
salinity	-.0125706	.0050396	-2.49	0.013	-.022448	-.0026931
tempc	.0509787	.016357	3.12	0.002	.0189196	.0830378
_cons	3.198781	.3459876	9.25	0.000	2.520658	3.876904
logChlorophyta <-						
logCopepods	-.2413817	.0628345	-3.84	0.000	-.364535	-.1182284
_cons	4.824093	.2109595	22.87	0.000	4.41062	5.237566
logCorixids <-						
logBacillariophyts	.6290096	.20935	3.00	0.003	.2186911	1.039328
tempc	.0548792	.0202822	2.71	0.007	.0151269	.0946316
_cons	-2.869214	1.067612	-2.69	0.007	-4.961694	-.7767331
logRotifers <-						
logCorixids	-.7409011	.1320404	-5.61	0.000	-.9996955	-.4821067
tempc	-.0703203	.0298955	-2.35	0.019	-.1289143	-.0117263
_cons	4.635149	.6385792	7.26	0.000	3.383556	5.886741
mean(salinity)	22.85796	2.321494	9.85	0.000	18.30791	27.408
mean(srp)	.2173056	.0454321	4.78	0.000	.1282603	.3063509
mean(tempc)	21.1129	.5251474	40.20	0.000	20.08363	22.14217
mean(dintp)	.6021776	.0828048	7.27	0.000	.4398833	.764472
var(e.logCyanobacteria)	.876397	.282843			.4655747	1.649728
var(e.logArtemia)	.9002057	.1685418			.6236986	1.299298
var(e.logCladocerans)	1.083303	.1610179			.809526	1.44967
var(e.logBacillariophyts)	.1497668	.027858			.1040122	.2156487
var(e.logCopepods)	1.281516	.2065633			.9343755	1.757625
var(e.logChlorophyta)	.5189025	.0889813			.3707848	.7261889
var(e.logCorixids)	1.002945	.1564914			.7386902	1.361732
var(e.logRotifers)	1.932152	.2848803			1.447233	2.579552
var(salinity)	501.2082	73.50074			376.0036	668.1046
var(srp)	.1897415	.0280441			.1420213	.2534959
var(tempc)	25.64752	3.761135			19.24062	34.18784
var(dintp)	.6241213	.0933468			.4655419	.8367181
cov(e.logCyanobacteria,e.logCorixids)	-.3301574	.1722029	-1.92	0.055	-.6676688	.007354
cov(e.logArtemia,e.logCladocerans)	.4901662	.1208956	4.05	0.000	.2532152	.7271171
cov(e.logArtemia,e.logCopepods)	.6019444	.1421599	4.23	0.000	.3233161	.8805727
cov(e.logCladocerans,e.logCopepods)	.8935921	.158093	5.65	0.000	.5837354	1.203449
cov(e.logBacillariophyts,e.logCopepods)	.142303	.0439923	3.23	0.001	.0560797	.2285263
cov(salinity,srp)	-4.364805	1.188249	-3.67	0.000	-6.69373	-2.035879
cov(salinity,tempc)	29.42116	12.14622	2.42	0.015	5.615003	53.22731
cov(salinity,dintp)	-5.517573	2.216685	-2.49	0.013	-9.862196	-1.172951
cov(srp,tempc)	.2805452	.2337763	1.20	0.230	-.177648	.7387383
cov(srp,dintp)	.0925689	.0373773	2.48	0.013	.0193108	.1658271
cov(tempc,dintp)	-1.157614	.4428187	-2.61	0.009	-2.025522	-.289705

LR test of model vs. saturated: chi2(**36**) = **24.93**, Prob > chi2 = **0.9175**

Table 16. Equation level goodness of fit for the final SEM for Farmington Bay foodweb (2013-2015, May through October, sites 7, 8, and 9 omitted).

Equation-level goodness of fit

depvars	Variance fitted	Variance predicted	Variance residual	R-squared	mc	mc2
observed						
logCyanoba~a	**1.061565**	**.9953555**	**.876397**	**.1744295**	**.5742253**	**.3297346**
logArtemia	**1.57216**	**1.225807**	**.9002057**	**.4274085**	**.6835216**	**.4672017**
logCladoce~s	**1.697344**	**.5156544**	**1.083303**	**.3617657**	**.6037637**	**.3645306**
logBacilla~s	**.3398091**	**.1764404**	**.1497668**	**.559262**	**.7483538**	**.5600335**
logCopepods	**2.192216**	**.9289942**	**1.281516**	**.4154245**	**.6445662**	**.4154656**
logChlorop~a	**.6466322**	**.1277297**	**.5189025**	**.1975307**	**.4444443**	**.1975307**
logCorixids	**1.301571**	**.2075382**	**1.002945**	**.2294353**	**.4869438**	**.2371142**
logRotifers	**2.916178**	**.9840256**	**1.932152**	**.3374367**	**.5808931**	**.3374367**
overall				**.6822246**		

Table 17. Direct effects for the final SEM for Farmington Bay foodweb (2013-2015, May through October, sites 7, 8, and 9 omitted).

Direct effects

	OIM Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
Structural						
logCyanobacteria <-						
logCyanobacteria	**0**	(no path)				
logArtemia	**-.5771961**	**.1700538**	**-3.39**	**0.001**	**-.9104953**	**-.2438968**
logCladocerans	**0**	(no path)				
logBacillariophyts	**0**	(no path)				
logCorixids	**0**	(no path)				
salinity	**.0210762**	**.0052228**	**4.04**	**0.000**	**.0108397**	**.0313128**
srp	**-1.640095**	**.2926145**	**-5.60**	**0.000**	**-2.213609**	**-1.066581**
tempc	**0**	(no path)				
dintp	**0**	(no path)				
logArtemia <-						
logCyanobacteria	**.8750767**	**.12119**	**7.22**	**0.000**	**.6375486**	**1.112605**
logArtemia	**0**	(no path)				
logCladocerans	**0**	(no path)				
logBacillariophyts	**0**	(no path)				
logCorixids	**-.8384861**	**.100002**	**-8.38**	**0.000**	**-1.034486**	**-.6424858**
salinity	**0**	(no path)				
srp	**0**	(no path)				
tempc	**0**	(no path)				
dintp	**0**	(no path)				
logCladocerans <-						
logCladocerans	**0**	(no path)				
logBacillariophyts	**0**	(no path)				
logCorixids	**-.4926183**	**.1045267**	**-4.71**	**0.000**	**-.6974868**	**-.2877498**
salinity	**-.0170127**	**.0044943**	**-3.79**	**0.000**	**-.0258213**	**-.0082041**
srp	**0**	(no path)				
tempc	**0**	(no path)				
dintp	**0**	(no path)				
logBacillariophyts <-						
logCladocerans	**-.1401846**	**.0497447**	**-2.82**	**0.005**	**-.2376823**	**-.0426868**
logBacillariophyts	**0**	(no path)				
logCorixids	**0**	(no path)				
salinity	**-.0063837**	**.0026844**	**-2.38**	**0.017**	**-.0116449**	**-.0011224**
srp	**-.8031928**	**.1203846**	**-6.67**	**0.000**	**-1.039142**	**-.5672433**
tempc	**0**	(no path)				
dintp	**-.1626243**	**.0633682**	**-2.57**	**0.010**	**-.2868238**	**-.0384249**
logCopepods <-						
logCladocerans	**0**	(no path)				
logBacillariophyts	**0**	(no path)				
logCorixids	**-.8165582**	**.1165664**	**-7.01**	**0.000**	**-1.045024**	**-.5880922**
salinity	**-.0125706**	**.0050396**	**-2.49**	**0.013**	**-.022448**	**-.0026931**
srp	**0**	(no path)				
tempc	**.0509787**	**.016357**	**3.12**	**0.002**	**.0189196**	**.0830378**
dintp	**0**	(no path)				
logChlorophyta <-						
logCladocerans	**0**	(no path)				
logBacillariophyts	**0**	(no path)				
logCopepods	**-.2413817**	**.0628345**	**-3.84**	**0.000**	**-.364535**	**-.1182284**
logCorixids	**0**	(no path)				
salinity	**0**	(no path)				
srp	**0**	(no path)				
tempc	**0**	(no path)				
dintp	**0**	(no path)				
logCorixids <-						
logCladocerans	**0**	(no path)				
logBacillariophyts	**.6290096**	**.20935**	**3.00**	**0.003**	**.2186911**	**1.039328**
logCorixids	**0**	(no path)				
salinity	**0**	(no path)				
srp	**0**	(no path)				
tempc	**.0548792**	**.0202822**	**2.71**	**0.007**	**.0151269**	**.0946316**
dintp	**0**	(no path)				
logRotifers <-						
logCladocerans	**0**	(no path)				
logBacillariophyts	**0**	(no path)				
logCorixids	**-.7409011**	**.1320404**	**-5.61**	**0.000**	**-.9996955**	**-.4821067**
salinity	**0**	(no path)				
srp	**0**	(no path)				
tempc	**-.0703203**	**.0298955**	**-2.35**	**0.019**	**-.1289143**	**-.0117263**
dintp	**0**	(no path)				

Table 18. Indirect effects for the final SEM for Farmington Bay foodweb (2013-2015, May through October, sites 7, 8, and 9 omitted).

Indirect effects

	OIM Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
Structural						
logCyanobacteria <-						
logCyanobacteria	-.3355883	.08583	-3.91	0.000	-.503812	-.1673646
logArtemia	.1937002	.1053123	1.84	0.066	-.0127081	.4001085
logCladocerans	-.0296415	.0143101	-2.07	0.038	-.0576888	-.0015942
logBacillariophyts	.2114466	.0835566	2.53	0.011	.0476787	.3752144
logCorixids	.3361579	.0759129	4.43	0.000	.1873713	.4849445
salinity	-.0079185	.0030606	-2.59	0.010	-.013917	-.0019199
srp	.3805643	.1882708	2.02	0.043	.0115603	.7495683
tempc	.0184481	.0078766	2.34	0.019	.0030103	.0338859
dintp	-.0343864	.0183372	-1.88	0.061	-.0703265	.0015538
logArtemia <-						
logCyanobacteria	-.2936655	.1091381	-2.69	0.007	-.5075722	-.0797588
logArtemia	-.3355883	.08583	-3.91	0.000	-.503812	-.1673646
logCladocerans	.0513544	.0238304	2.15	0.031	.0046477	.0980611
logBacillariophyts	-.366334	.1345235	-2.72	0.006	-.6299953	-.1026727
logCorixids	.256088	.0887393	2.89	0.004	.0821623	.4300137
salinity	.0137188	.0031879	4.30	0.000	.0074706	.019967
srp	-.6593328	.2205381	-2.99	0.003	-1.09158	-.2270861
tempc	-.0319616	.0129549	-2.47	0.014	-.0573527	-.0065705
dintp	.0595748	.03041	1.96	0.050	-.0000277	.1191774
logCladocerans <-						
logCladocerans	.0454104	.0194953	2.33	0.020	.0072003	.0836204
logBacillariophyts	-.3239326	.1183343	-2.74	0.006	-.5558635	-.0920017
logCorixids	-.02237	.0112549	-1.99	0.047	-.0444292	-.0003108
salinity	.0012953	.0010141	1.28	0.201	-.0006922	.0032829
srp	.2601803	.1009766	2.58	0.010	.0622698	.4580908
tempc	-.0282622	.0120787	-2.34	0.019	-.0519359	-.0045884
dintp	.0526793	.0271169	1.94	0.052	-.0004689	.1058276
logBacillariophyts <-						
logCladocerans	-.0063658	.0044425	-1.43	0.152	-.0150729	.0023412
logBacillariophyts	.0454104	.0194953	2.33	0.020	.0072003	.0836204
logCorixids	.0721934	.0273057	2.64	0.008	.0186751	.1257117
salinity	.0022033	.0010731	2.05	0.040	.0001	.0043067
srp	-.0364733	.0165001	-2.21	0.027	-.068813	-.0041336
tempc	.0039619	.0020368	1.95	0.052	-.0000302	.007954
dintp	-.0073848	.0040561	-1.82	0.069	-.0153346	.000565
logCopepods <-						
logCladocerans	.0752717	.0329221	2.29	0.022	.0107454	.1397979
logBacillariophyts	-.5369468	.1951142	-2.75	0.006	-.9193636	-.15453
logCorixids	-.0370802	.0172043	-2.16	0.031	-.0708	-.0033604
salinity	.0021471	.0016592	1.29	0.196	-.0011048	.005399
srp	.4312718	.1661948	2.59	0.009	.105536	.7570075
tempc	-.046847	.0187773	-2.49	0.013	-.0836499	-.0100442
dintp	.0873206	.0442622	1.97	0.049	.0005683	.174073
logChlorophyta <-						
logCladocerans	-.0181692	.0091467	-1.99	0.047	-.0360964	-.000242
logBacillariophyts	.1296091	.0574973	2.25	0.024	.0169165	.2423018
logCopepods	0	(no path)				
logCorixids	.2060527	.0609704	3.38	0.001	.0865529	.3255525
salinity	.002516	.0013993	1.80	0.072	-.0002265	.0052586
srp	-.1041011	.0480212	-2.17	0.030	-.198221	-.0099812
tempc	-.0009973	.0055569	-0.18	0.858	-.0118886	.0098939
dintp	-.0210776	.0120319	-1.75	0.080	-.0446597	.0025045
logCorixids <-						
logCladocerans	-.0921816	.041791	-2.21	0.027	-.1740904	-.0102728
logBacillariophyts	.0285636	.0190993	1.50	0.135	-.0088704	.0659975
logCorixids	.0454104	.0194953	2.33	0.020	.0072003	.0836204
salinity	-.0026295	.0019924	-1.32	0.187	-.0065345	.0012756
srp	-.528158	.1935905	-2.73	0.006	-.9075884	-.1487277
tempc	.0024921	.0014308	1.74	0.082	-.0003122	.0052964
dintp	-.1069374	.0526443	-2.03	0.042	-.2101184	-.0037564
logRotifers <-						
logCladocerans	.0682975	.0332695	2.05	0.040	.0030905	.1335044
logBacillariophyts	-.4871967	.1883661	-2.59	0.010	-.8563874	-.118006
logCorixids	-.0336446	.0156392	-2.15	0.031	-.0642968	-.0029924
salinity	.0019482	.0015165	1.28	0.199	-.0010241	.0049204
srp	.3913129	.1594866	2.45	0.014	.0787248	.7039009
tempc	-.0425065	.0174782	-2.43	0.015	-.0767631	-.0082498
dintp	.07923	.0414814	1.91	0.056	-.002072	.1605321

Table 19. Total effects for the final SEM for Farmington Bay foodweb (2013-2015, May through October, sites 7, 8, and 9 omitted).

Total effects

	OIM Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
Structural						
logCyanobacteria <-						
logCyanobacteria	−.3355883	.08583	−3.91	0.000	−.503812	−.1673646
logArtemia	−.3834958	.0675962	−5.67	0.000	−.5159819	−.2510098
logCladocerans	−.0296415	.0143101	−2.07	0.038	−.0576888	−.0015942
logBacillariophyts	.2114466	.0835566	2.53	0.011	.0476787	.3752144
logCorixids	.3361579	.0759129	4.43	0.000	.1873713	.4849445
salinity	.0131578	.0036064	3.65	0.000	.0060893	.0202262
srp	−1.259531	.1899375	−6.63	0.000	−1.631801	−.8872601
tempc	.0184481	.0078766	2.34	0.019	.0030103	.0338859
dintp	−.0343864	.0183372	−1.88	0.061	−.0703265	.0015538
logArtemia <-						
logCyanobacteria	.5814112	.0546438	10.64	0.000	.4743114	.688511
logArtemia	−.3355883	.08583	−3.91	0.000	−.503812	−.1673646
logCladocerans	.0513544	.0238304	2.15	0.031	.0046477	.0980611
logBacillariophyts	−.366334	.1345235	−2.72	0.006	−.6299953	−.1026727
logCorixids	−.5823981	.0897874	−6.49	0.000	−.7583782	−.406418
salinity	.0137188	.0031879	4.30	0.000	.0074706	.019967
srp	−.6593328	.2205381	−2.99	0.003	−1.09158	−.2270861
tempc	−.0319616	.0129549	−2.47	0.014	−.0573527	−.0065705
dintp	.0595748	.03041	1.96	0.050	−.0000277	.1191774
logCladocerans <-						
logCladocerans	.0454104	.0194953	2.33	0.020	.0072003	.0836204
logBacillariophyts	−.3239326	.1183343	−2.74	0.006	−.5558635	−.0920017
logCorixids	−.5149883	.1109373	−4.64	0.000	−.7324214	−.2975552
salinity	−.0157174	.0048173	−3.26	0.001	−.0251592	−.0062756
srp	.2601803	.1009766	2.58	0.010	.0622698	.4580908
tempc	−.0282622	.0120787	−2.34	0.019	−.0519359	−.0045884
dintp	.0526793	.0271169	1.94	0.052	−.0004689	.1058276
logBacillariophyts <-						
logCladocerans	−.1465504	.0536355	−2.73	0.006	−.251674	−.0414268
logBacillariophyts	.0454104	.0194953	2.33	0.020	.0072003	.0836204
logCorixids	.0721934	.0273057	2.64	0.008	.0186751	.1257117
salinity	−.0041803	.0028829	−1.45	0.147	−.0098307	.0014701
srp	−.8396661	.1265657	−6.63	0.000	−1.08773	−.5916019
tempc	.0039619	.0020368	1.95	0.052	−.0000302	.007954
dintp	−.1700092	.0659946	−2.58	0.010	−.2993561	−.0406622
logCopepods <-						
logCladocerans	.0752717	.0329221	2.29	0.022	.0107454	.1397979
logBacillariophyts	−.5369468	.1951142	−2.75	0.006	−.9193636	−.15453
logCorixids	−.8536384	.1242508	−6.87	0.000	−1.097166	−.6101113
salinity	−.0104235	.0051652	−2.02	0.044	−.0205471	−.0002998
srp	.4312718	.1661948	2.59	0.009	.105536	.7570075
tempc	.0041317	.023024	0.18	0.858	−.0409944	.0492578
dintp	.0873206	.0442622	1.97	0.049	.0005683	.174073
logChlorophyta <-						
logCladocerans	−.0181692	.0091467	−1.99	0.047	−.0360964	−.000242
logBacillariophyts	.1296091	.0574973	2.25	0.024	.0169165	.2423018
logCopepods	−.2413817	.0628345	−3.84	0.000	−.364535	−.1182284
logCorixids	.2060527	.0609704	3.38	0.001	.0865529	.3255525
salinity	.002516	.0013993	1.80	0.072	−.0002265	.0052586
srp	−.1041011	.0480212	−2.17	0.030	−.198221	−.0099812
tempc	−.0009973	.0055569	−0.18	0.858	−.0118886	.0098939
dintp	−.0210776	.0120319	−1.75	0.080	−.0446597	.0025045
logCorixids <-						
logCladocerans	−.0921816	.041791	−2.21	0.027	−.1740904	−.0102728
logBacillariophyts	.6575732	.2256192	2.91	0.004	.2153676	1.099779
logCorixids	.0454104	.0194953	2.33	0.020	.0072003	.0836204
salinity	−.0026295	.0019924	−1.32	0.187	−.0065345	.0012756
srp	−.528158	.1935905	−2.73	0.006	−.9075884	−.1487277
tempc	.0573713	.0212596	2.70	0.007	.0157033	.0990393
dintp	−.1069374	.0526443	−2.03	0.042	−.2101184	−.0037564
logRotifers <-						
logCladocerans	.0682975	.0332695	2.05	0.040	.0030905	.1335044
logBacillariophyts	−.4871967	.1883661	−2.59	0.010	−.8563874	−.118006
logCorixids	−.7745457	.13879	−5.58	0.000	−1.046569	−.5025222
salinity	.0019482	.0015165	1.28	0.199	−.0010241	.0049204
srp	.3913129	.1594866	2.45	0.014	.0787248	.7039009
tempc	−.1128268	.0332781	−3.39	0.001	−.1780507	−.0476029
dintp	.07923	.0414814	1.91	0.056	−.002072	.1605321

Table 20. Equation level Wald test for SEM

Wald tests for equations

	chi2	df	p
observed			
logCyanobacteria	**62.46**	**3**	**0.0000**
logArtemia	**93.61**	**2**	**0.0000**
logCladocerans	**39.78**	**2**	**0.0000**
logBacillariophyts	**66.69**	**4**	**0.0000**
logCopepods	**55.13**	**3**	**0.0000**
logChlorophyta	**14.76**	**1**	**0.0001**
logCorixids	**14.90**	**2**	**0.0006**
logRotifers	**44.18**	**2**	**0.0000**

DISCUSSION

Zooplankton: Predator-prey relationships, trophic interactions: top-down and bottom-up effects.

Food web direct and indirect interactions and relations to cyanobacteria are clearly complex. For example, there were clear spatial and temporal changes in the zooplankton abundance. Although salt-tolerant *Artemia* were recorded in the northern portion of the bay near the Antelope Island causeway, meso-haline-adapted invertebrates dominate the remainder of the bay. Rotifers were the dominant zooplankter in June and then again in November. Their population decline was followed by an increase in cladocerans, which yielded dominance to copepods in some locations—primarily in the north-central region of the bay; the region that often had the highest cyanobacteria counts. The temporal and spatial pattern observed in this study corresponded to previous studies on zooplankton on FBay in which cladocerans (primarily *Moina* sp. and *Daphnia* sp.) were found in substantial concentrations in May, but showed a diminished presence in the bay thereafter (Wurtsbaugh et al., 2010). These authors also recorded depletion in zooplankton abundance during mid-summer once the number of corixid adults started increasing and eventually reached densities of 0.5 per liter or higher. Corixid eggs are known to hatch between 20-36^{o} C (Kelts, 1979) and this may indicate why the emergence of corixids as a dominant zooplankter began in June when water temperature was sustained at or above 20^{o} C. Corixid adults appeared in meaningful densities in mid-June and remained until the end of September. Corixids have four advantages over other zooplankton: 1) they are air-breathers and are therefore not harmed by anoxic or hypoxic events; 2) they are predators of most other zooplankton; 3) they are omnivorous and can exploit a variety of food sources; and 4) they have piercing mouth parts that can be used to pierce filamentous algae, that are too large for most other zooplankton to consume, and ingest the contents (Cheng, 1976). It is not surprising then that throughout the period of corixid abundance other

zooplankton were found in low numbers. It was clear from the population dynamics and SEM analysis that corixids were a major influence on other zooplankton population abundances.

Other invertebrates, such as the chironomids, were occasionally identified but were quite patchy in their distribution and were found in substantially lower abundance numbers. Their presence nevertheless represents an additional and potentially important alternative food source for shorebirds and waterbirds. For example, Miller, Hoven and Cavitt (2009) found that corixids and midges (Chironomidae) were the main prey items identified in the stomach contents of shorebirds such as American avocets and black-necked stilts. Clearly the diversity of invertebrates found in FBay is a highly important element included in the beneficial use of "support for waterfowl and shorebirds and the aquatic life in their food chain". In addition, benthic macroinvertebrates are a critical component of the ecology and ecosystem functioning of FBay. They are a major link between sediment chemistry, water column chemistry, nutrient cycling, benthic algae, phytoplankton, and the Bay's food web. Midges (chironomids) are an underappreciated but likely major driving force in HABs in the Bay (Richards 2017, Baranov et al. 2016, Molot et al. 2014, Holker et al. 2015). Our field sampling methods were not conducive for chironomid collection or for other benthic invertebrates so they are likely underrepresented in the data. In 2017, we will intensively sample benthic invertebrates in the Bay.

The early (i.e., pre-Corixid period) dynamics of cladocerans and copepods may be a function of their selective or generalist grazing habits. Cladocerans, especially the large-bodied ones like *Daphnia,* are generalist feeders and may encounter foraging stress sooner in the presence of filamentous algal blooms, whereas many of the copepods are selective grazers and have been shown to have a greater capacity to exploit alternative phytoplankton, or protists, during times of cyanobacteria dominance (Ger, Hansson and Lurling, 2014). Other investigators such as Fulton and Paerl, (1988) and Hansson et al. (2007) have observed shifts in zooplankton population composition because of adaptations among the zooplankters. The copepods exhibit selective feeding capabilities that allow them to forage for alternative food sources during a cyanobacteria bloom. These authors additionally commented that cyanobacteria blooms did not favor dominance by rotifers—an observation somewhat consistent with rotifer population dynamics in FBay during our study in which peak rotifer abundance occurred prior to and after peak cyanobacteria blooms.

In the present study, cladocerans, such as *Moina*, were disproportionately abundant relative to other species, which may be a function of their tolerance of cyanobacteria. *Moina* population size remained relatively stable throughout May and June--months over which *Nodularia* densities were at their peak. In contrast, the larger-bodied, and generally more sensitive species, *Daphnia dentifera* was identified in plankton net hauls in notable numbers (0.2 to 38.7 individuals per liter) only during April and May. They declined in number well in advance of the presence of corixids, but consistent with the progression of cyanobacteria blooms in May, thereby suggesting vulnerability to conditions dominated by filamentous algae. In contrast, *Moina* abundance was in the range of 17 to 243 individuals per liter throughout May and June 2013 despite tremendous growth of the cyanobacteria population. Numbers of

Moina did not coincidentally decline with the emergence of cyanobacteria dominance, but instead appeared to be more influenced by corixid predation. Other authors support this relative tolerance of cyanobacteria by Moina compared to Daphnia (Guo and Xie, 2006) who found that the smaller cladocerans like *Moina* and *Ceriodaphnia* develop tolerance to cyanobacteria better than the larger bodied *Daphnia*. In more recent research Sarnelle, Orlando, Gustabsson and Hansson (2010) did in fact observe that Daphnia previously exposed to cyanotoxins not only developed resistance to it but demonstrated positive population growth even at high concentrations of cyanotoxins.

Depletion of algal species, such as diatoms, coinciding with increases in known phytoplanktivorous species suggests important predator-prey or grazing relationships that shape the temporal and spatial abundance and population structure of phytoplankton. Evidence of grazing pressure caused by the zooplankters was indicated by the phytoplankton population fluctuations and responses. Zooplankton grazers such as the cladocerans and *Artemia* have the capacity to graze near 100% of the water column per day according to studies conducted by Wurtsbaugh (2012). In the current study the results were consistent with "top-down" control of algal dominance in the presence of substantial grazing pressure: when algal grazers such as the cladocerans and *Artemia* were present the densities of "edible" algae were held in check. However, once the grazing pressure of these zooplankters diminished, for example during July, the densities of "edible" phytoplankton, such as the chlorophytes, showed signs of resurgence in abundance.

Predation of other zooplankton by corixids was anticipated based on observations of previous investigations (Wurtsbaugh, 1992; Tanner, Glen and Moore, 1999; Cheng, 1976; Reynolds, 1975) and from our own laboratory studies demonstrating predator-prey relationships between corixids and *Artemia*. Of importance are the observations of Simonis (2013a) that all instars of *Trichocorixa verticalis* preferentially prey on *Moina* in food preference studies and that prey by corixids creates a top-down cascade releasing phytoplankton from grazing pressure. Additionally, Wurtsbaugh and Berry (1989) reported that *Trichocorixa verticalis* invaded the pelagic region of the GSL when the salinity dropped from around 100 g/L to 50 g/L and as a result initiated a cascading trophic shift in the food web structure by depleting the phytoplanktivore *Artemia*. In an investigation of rock-pool communities Simonis (2013b) found that *Moina* population density is the primary factor influencing emigration of *Trichocorixa verticalis*—at certain low abundances of *Moina* the corixids will leave their current ponds and exploit other ponds with greater abundance of *Moina*. They further found that *T. verticalis* are "voracious predators" of *Moina macrocapa*. In our study there was a definitive progression of depletion of cladocerans, copepods, rotifers, and *Artemia* when corixids were in an adult abundance of more than 1 mature adult/L. This progression of population decline was observed both temporally, beginning in June, and spatially, with corixids reaching maturity first in the southern region of the bay and then over time moving in a south-northward expansion of dominance in zooplankton assemblage. Although the evidence indicates pronounced top-down control by corixids, the decline in the abundance and diversity of zooplankton may not be solely attributed to corixid predation as it may be a combined function of predation coupled with intra- and interspecific competition, normal life-cycle sequences of development,

growth and mortality, food limitation, temperature tolerances, dissolved oxygen levels or the presence of cyanotoxins. Yet the combination of controlled laboratory experiments that documented corixid predation rates, coupled with the correlation between corixid presence and the decline of other zooplankton, followed by recovery of other zooplankton once corixid numbers were in decline, all strongly support top-down control mechanism of zooplankton abundance in FBay by corixids. Our SEM further provides statistical evidence of the important top-down control of Corixids on other aquatic macroinvertebrates and it also shows that cyanobacteria blooms are not exerting a direct adverse impact on aquatic invertebrate population size or structure.

The trophic transfer of energy, nutrients, carbon and other essential elements and compounds is most certainly influenced by phytoplanktivory rates among the various zooplankton species. It is well established in the scientific literature that the type of algae available exerts an influence on grazing rates and digestibility of consumed food by zooplankton (Gibor, 1956). While there are substantial differences in grazing rates and digestibility among the various divisions of algae—for example cyanobacteria (division Cyanophyta) compared to diatoms (division Chrysophyta) and green algae (division Chlorophyta)—there are even differences within the families or genera of phytoplankton (Tanner et al., 1999). For example, Gibor (1956) found that differences existed even within the same genera of green algae: he observed that *Dunaliella viridis* was superior over *D. salina when grazed by Artemia*. He also found that *Artemia* could selectively graze one type of green algae in preference to other less desirable and less digestible species. In his study the *Artemia* grazed selectively on *D. viridis* over *Stichococcus*. Gibor also reported that *Stichococcus* cells that passed through the digestive system of the *Artemia* remained viable. In similar studies Tanner et.al. (1999) observed that equivalent populations of *Artemia* in salt ponds had very different impacts on the abundance of algae; they found that *Artemia* grazed diatoms down to low densities (only 1,250 cells per mL), whereas when the cyanobacteria *Synechococcus* was present more than 4.2 million cells per mL remained despite the same density of adult *Artemia*. They also found that when *Artemia* were not present the salt ponds contained high numbers of diatoms, thereby supporting the hypothesis that selective algal grazing by *Artemia* can determine the algal species composition of salt ponds. These and other studies illustrate the importance of food quality on zooplankton and the pressure that they exert on competition, growth and survival among the invertebrate grazers. In FBay this has relevance because phytoplankton of presumed high quality, such as diatoms and green algae, require a dependable supply of nutrients to FBay and without nutrient availability there may be declines in these favorable algal taxa—an impact that would be vectored throughout the GSL food web.

Artemia were found primarily in the central to northern regions of FBay and their distribution was influenced by salinity. It is well known that *Artemia* are classic extremeophiles (Hengherr, Schill and Clegg, 2007) that exhibit a remarkable capacity to withstand hypoxia and a vast range of salinities, ranging from marine water to saturated brines. It is in this capacity that they derive a competitive advantage over other zooplankters. They are known to demonstrate selective feeding capacities and can survive given a wide range of phytoplankton options if the size of algal cells is sufficiently small (i.e., 4-

8 microns for metanauplii and <20 microns for adults) to pass their feeding apparatus (Makridis, P., & Vadstein, O., 1999). In our 2013 study there were periodic periods of high abundance in the northern regions of the bay (20.6/L to 27.9/L) while peak abundance in sites 6, 7& 8 (southernmost sites in our study) the *Artemia* only achieved a maximal value of 1.73, 0.18, and 0.00/L respectively. The low salinity of this region of FBay did not support *Artemia* growth and development likely due to interspecific competition and predation pressure. In contrast, at site #9 (GB), just on the north side of the Antelope Island causeway breach abundant *Artemia* were observed.

Within the northern section of FBay (defined as sites 1, 2, & 3) the mean salinity during 2013 ranged from 0.2% to 4.1% and the highest observed at site #1 was 8.2%. These are well below values for the Gilbert Bay site where the average salinity was 11.1% and the high was 14.0%. Clearly the salinity of the Gilbert Bay site conferred some advantage for *Artemia* over other zooplankton as well as relieving the *Artemia* from the predation pressure of corixids—the average number of corixids per liter at this site was a mere 0.09/L and the maximum value was 0.69/L. In previous work on FBay by Wurtsbaugh and Marcarelli (2004) they found that corixid abundance of just 0.28/L was sufficient to control *Artemia* population size, whereas the lower corixid abundance they observed in 2003 (0.06/L) did not control the *Artemia* population size.

Artemia abundance in sites 1- 5 were comparable to reports in the literature of *Artemia* abundance in Farmington and Gilbert Bay. In our 2013 study *Artemia* mean values for these sites were between 1.84 and 6.64 individuals/L with a peak abundance range of 8.81 to 27.91/L. These peak values are more than were reported by Stephens and Gillespie (1976) for Gilbert Bay in which they found that 12-15 individuals per liter was the upper limit for *Artemia*. Wurtsbaugh and Gliwicz (2001) present a mean value for adult *Artemia* in Gilbert Bay of 3.1/L and compare this to a more productive Mono Lake that boasts 6-8/L. These values, and the average abundance we observed for site #9 (GB) in our study (4.62/L) are well above the mean values for *Artemia* abundance even in the northern zone of FBay (0.75/L to 0.85/L). Collectively this indicates that a variety of conditions in FBay such as competition, predation, and food availability maintain the *Artemia* population below more productive levels observed when salinity is higher and *Artemia* have an ecological advantage, such as in Gilbert Bay.

Phytoplankton and Chlorophyll-a

There was a remarkable diversity of algal taxa observed in the current study: 10 major taxa, 81 genera and more than 50 species of algae were collected and identified in 2013 alone. This is greater diversity than some of the previously reported values for FBay (Wurtsbaugh, Marcarelli, and Boyer, 2012) and may be a result of the thoroughness and frequency of the sampling program and area of the bay that was sampled. It is also greater diversity than was found in the other more saline bays of the GSL. The decrease in diversity of species observed in the other bays of the GSL is an expected outcome of the diminishing effect that increases in salinity has on algal and zooplankton species diversity (but not necessarily on the bacterial populations). One of the factors that favored species richness during our

study was the low level of the GSL (elevation between 4194 and 4197 and approaching the lowest level ever recorded—4191 feet above sea level). This low elevation of Gilbert Bay results in most of FBay being in the lower range of salinity (i.e., 0%-6%). Previous studies of FBay that reported less diversity also recorded higher salinity across the bay—with salinities ranging from 4% to 10% (Wurtsbaugh and Marcarelli, 2006), 1% to 9% (Wurtsbaugh, Marcarelli, and Boyer, 2012). The low elevation and therefore low salinity of FBay during 2013 favored the growth of cyanobacteria. In contrast, in 2015 the continued decline in GSL elevation and depleted water input into FBay resulted in fresh or hyposaline conditions through FBay that disfavored cyanobacteria blooms. The contrasting scale of HABs among the years illustrates the lower and upper limits of salinity optima for cyanobacteria.

Farmington Bay is a highly dynamic water body characterized by constant production, movement, mixing, grazing, and growth and decline of algal populations. During this perpetual change, there are patterns that emerge and that can be identified and characterized. Clearly the most apparent pattern is the emergence and dominance of the cyanobacteria bloom that begins in May and results in pronounced dominance of the algal assemblage that continues well into September. This is consistent with a variety of earlier studies that are reviewed in detail in Wurtsbaugh, Marcarelli, and Boyer (2012). In this publication, they cite multiple earlier investigations of FBay that also recorded cyanobacteria blooms starting in May and extending into the fall. One difference in our study from some of the previously reports is that while *Nodularia* was the early and dominant cyanobacteria it was displaced in dominance by *Pseudanabaena* in August. In most of the studies reported by Wurtsbaugh this dramatic increase in *Pseudanabaena* is not reported, yet *Aphanothece* does show up in some of the studies at high abundances. In a thorough investigation of FBay by Wurtsbaugh in 2009 (cited in Wurtsbaugh et al., 2012) *Nodularia* represented 91% of the total cyanobacteria and 86% of the total algae in FBay. In this same publication Wurtsbaugh et al., had similar results to our study in which the southern locations in the bay, with salinities in the range of 1% to 3%, did not support cyanobacteria blooms. Their interpretation of the cause is consistent with ours: exclusion of cyanobacteria from this region of the bay is due to available nitrogen from input sources (mainly discharges by POTWs) that create an environment which favors other algal groups and not nitrogen fixing filamentous algae. Another consistent finding is that there is a salinity threshold for *Nodularia*: both in our study and in a summary of findings from 2002, 2003, 2005 and 2009: the upper threshold limit for *Nodularia* at approximately 6% salinity (Wurtsbaugh et al., 2012). Roney (2009) also reported on the exclusion of specific cyanobacteria species because of salinity.

As a point of clarification, the generally accepted definition of the term “algal bloom” indicates the emergence of a particular algal group that represents >50% of the total algal population. Throughout this report the term “bloom” is used to reference the rapid appearance of a particular algal group, and of a magnitude approaching or exceeding 50% of all represented algae. Among the algal groups that were documented during this study only the cyanobacteria and diatoms demonstrated “large algal blooms” that resulted in dominance of a particular group of more than 50%. Hence these two taxa are the predominant algal groups in FBay during our study. Chlorophytes never achieved this degree of

dominance, but they did show a pattern of pronounced resurgence once grazing pressure was diminished in July through September.

In the early spring the bay supports the growth and development of edible and desirable algal groups for zooplankton grazers. Among these are the diatoms and chlorophytes. Other algal groups such as the cryptophytes, chrysophytes, pyrrhophytes, and flagellates that periodically make notable appearances in the bay, albeit at far lower abundance than the three main algal groups: cyanophytes, bacillariophytes, and chlorophytes. Scrutiny of the dynamics of each of the algal groups provides some insight into the relationship between nutrients, algae and zooplankton grazers and the patterns of abundance. There is evidence that grazing pressure coupled with nutrient availability, salinity, and temperature all interact to select patterns of algal dominance. Tanner et al. (1999) found *Artemia* to selectively graze chlorophytes and diatoms in preference to cyanobacteria. The conditions that favor cyanobacteria are readily available in FBay: abundant phosphorous, nitrogen limitation, salinity below 6%, water temperature over 20C, and a reduction in grazing pressure by zooplankton. In a separate experiment, Wurtsbaugh and Marcarelli (2004) did controlled studies of nitrogen-fixing bacteria growth under differing conditions of nutrients and salinity. They found that growth of nitrogen-fixing algae occurs below 7% salinity. Our field research does not provide a definitive range of factors that favor the presence of diatoms or green algae over the nitrogen fixing algae, but some general observations are that nitrogen availability (and the bioavailable forms of nitrate or nitrite and ammonia), fresh water or salinity of >6%, and reductions in grazing pressure, encourages the growth of these non-cyanobacteria algal divisions. Additionally, reductions in the shading effects caused by the extensive cyanobacteria blooms—an event which happens when the blue-green algae "scums" settle to the bottom of the bay—also confer some advantage to other algal groups.

Farmington Bay is quite different from Gilbert Bay and the wetlands that border the eastern, northern and southern margins of the GSL. In this study of the phytoplankton flora of GSL wetlands Rushforth and Rushforth (2004) found the order of importance was pinnate diatoms>centric diatoms>chlorophytes>cyanophytes. In their study of ten different wetlands these authors attributed 83% of the summed index of importance to diatoms. It is noteworthy when making comparisons among regions of the bay to include temporal effects; in the Rushforth study the wetlands were only sampled in October and November—months in which the cyanobacteria were already in their decline in FBay. In our study clearly the dominance pattern differed from the surrounding wetlands and was cyanophytes>diatoms>chlorophytes.

Algal assemblages differ in very profound ways in FBay compared to the other bays of the GSL. For example, during 1972 and 1973 Stephens and Gillespie found that the algal flora of Gilbert Bay was essentially limited to just two species: *Dunaliella viridis* and an unidentified green alga. In a 1998 paper Stephens reports only 6 species of algae in Gunnison Bay and 15 species of algae in Gilbert Bay. This low level of diversity in Gilbert Bay during times of high salinity reveals one of the very important aspects of FBay—its remarkable diversity of algae and zooplankton serve demonstrable benefits to the

GSL ecosystem. A broad variety of conditions that supports an array of zooplankton in turn provides much greater diversity of prey choices for the tens-of-thousands of waterbirds and shorebirds that utilize FBay and its surrounding environs.

Chlorophyll-a levels reached exceedingly high values at various times and locations during this study. The mean yearly chlorophyll for the entire study was 114.6 ug/L, 63.9 and 40.7 ug/L for 2013, 2014 and 2015 respectively and the highest value recorded was 506.0 ug/L. This is quite similar to previous studies in which the mean chlorophyll level from 2002 to 2009 was 141 ug/L (Wurtsbaugh et al., 2012). During 2013 and 2014 the average chlorophyll levels were above the generally accepted value for hypereutrophic conditions of 56 ug/L (Carlson and Simpson, 1996). An exception to this occurred at sites 7 and 8 where peak values were 45.4 and 32.7 ug/L respectively. The mean values at these locations were: 29.8 and 32.4 ug/L. These are well below the mean values for sites 1-6 that had mean values of 131 to 291 ug/L and maximum values that were between 373.8 and 506.0 ug/L. These are extremely high values for chlorophyll and are associated with robust primary production and in particular, cyanobacteria blooms. In contrast chlorophyll-a levels observed during 2015 were much lower with a range of 2.7 to 216 and an overall mean of 40.7. Of the limited number of sampling programs undertaken in 2015 there was no evidence of the magnitude nor scale of cyanobacteria blooms observed in 2013 and 2014. It is inferred that this was partially attributable to the low salinity recorded in the Bay during 2015.

Cyanotoxins

Cyanotoxins are a huge concern in association with cyanobacteria blooms. The presence of cyanotoxins is well known to accompany blue-green algae blooms; for example, Antoniou, de la Cruz and Dionysiou (2005) state that up to 50% of all recorded cyanobacteria blooms contain cyanotoxins. Cyanotoxins are known to harm resident biota, contaminate ground water, and can be toxic to humans via dermal or ingestion exposure (Funari and Testai, 2008). The two main modes of toxicity of cyanotoxins are either via neurological or hepatic disruption. In our study, the hepatotoxin nodularin was observed in substantial concentrations when *Nodularia* abundance exceeded 10,000 cells per ml and when the cell density exceeded 100,000 cells per ml. We also analyzed for the neurotoxin Anatoxin-a, but did not detect elevated levels. Nodularin, on the other hand, was first observed in May and later reached a maximum value of 88.0 ug/L in early June 2013. Over the study the mean concentration was 13.4 ug/L and according to the distribution of *Nodularia* across the bay nodularin was highest in the mid to northern regions of the bay and quite low among the southern sites. Nodularin continued to be found in water samples until November. Concentrations recorded during 2013 were lower than some of the previous reported values. In 2009 Wurtsbaugh et al. documented a bay-wide average of 41 ug/L and they report an astonishing value of 600 ug/L at one site. Over a 3-year period (including 2006, 2007 and 2009), and for the period May to August, they reported mean values of 20, 24, and 104 ug/L respectively. In contrast to our threshold model for nodularin these authors documented a linear relationship between microcystins and *Nodularia*. It should be noted that an investigation by Goel

(2007) did not arrive at the same conclusions regarding cyanotoxins in FBay as were reported in some of the publications by Wurtsbaugh et al. Neither direct nor indirect impacts of nodularin on the biota of FBay were evident from our field study.

The presence of cyanotoxins in the water of FBay raises some concerns about direct harm to GSL biota. In our controlled studies of nodularin impacts on *Artemia* we did not identify any adverse impacts at environmentally realistic concentrations. Various studies have demonstrated adverse impacts on zooplankton such as *Artemia* because of cyanotoxin exposure (Lee, Chen, and Chen 1999; Kiviranta et al., 1991). In the study by Kiviranta eta al., (1999), exposure of *Artemia* to 29 toxic bloom samples, they found that only 4 out of the 29 were nontoxic to *Artemia*. In an investigation of detoxication mechanisms of *Artemia* Beattie et al. (2003) found that *Artemia* have phase II conjugation enzyme systems (i.e., glutathione S-transferase) that afford the *Artemia* some limited capacity to withstand nodularin exposure. Although Anatoxin-a was not found in our study, it is a neurotoxin of potential concern. It is produced by Anabaena flos-aquae strain NRC 525-17 and has a LD50 of a mere 20-50 ug/kg body weight in mice; and at this level of toxicity is included in the class of potent toxins (Patocka, Gupta and Kuca, 2011). It exerts its toxic potential via the inhibition of cholinesterase which includes it alongside some of the well-known neurotoxins, such as Sarin gas, used in chemical warfare. However, Anatoxin-a apparently does not cross the blood-brain barrier and is unable to disrupt central nervous system neurons. It causes its harm to the individual through impairment in peripheral nervous system tissues and neuromuscular junctions. Because of their known toxicity it is prudent to continue to monitor FBay for elevated levels of Anatoxin-a and nodularin. Yet, as described above, we could not find any significant relationship between *Nodularia* densities and changes in the zooplankton community. Additional monitoring and research should be conducted to elucidate the potential for toxicity due to cyanobacteria blooms in FBay.

Dissolved oxygen and Salinity

Depletion of oxygen is one of the concerns often expressed regarding eutrophication of water bodies. In our study, all mean daily values for the bay were above 2 mg/L. There were isolated cases of hypoxia or anoxia in which the oxygen levels dropped below 1 mg/L. Because all our measurements of dissolved oxygen took place during the day the perception of impairment is lessened and anoxic events could have taken place during the night but were unrecorded. When comparing zooplankton abundance with oxygen levels during the day there is no clear evidence of harm to the biota. Yet, declines in oxygen during the night remains a concern, especially when one considers the observations of Wurtsbaugh et al. (2012) who found that oxygen levels in the daytime could reach as high as 40 mg/L but would decline to 0 ug/L at night. In our study oxygen levels peaked at 19.5 mg/L while the lowest values were between 0.09 to 0.83 mg/L. The lowest levels coincided with the development and collapse of cyanobacteria blooms in May through July.

Salinity is clearly a major influential factor determining community structure in the Bay. During all our research programs there was a south-north gradient in salinity across the Bay. This was most pronounced during 2013 when the difference between the maximum level in the southern region of the Bay was compared to the maximum level in the northernmost sample location—the difference was 8.1%. During 2014 and 2015 this gradient was diminished, especially during 2015 when the northern region of the Bay did not exceed 2%. Our statistical analysis of salinity effects on cyanobacteria indicates a salinity range in which cyanobacteria are favored when salinity is approximately 0.5% and that there is an upper threshold of 6%. This range is similar to values reported in the scientific literature for cyanobacteria, and in particular for *Nodularia.* Knowledge of this range affords resource managers the ability to use salinity as a tool to favor desirable algal taxa and to influence the magnitude, distribution and duration of cyanobacteria blooms in FBay.

Nutrients: sources, gradients, and evidence of limitation.

The nutrients that were thoroughly documented during the study included various molecular forms of nitrogen (N) and phosphorous (P). Other nutrients or essential elements were not evaluated. The results show evidence of site-specific loading of nutrients into FBay. The primary source location is the Northwest Oil Drain that transports the Salt Lake City POTW effluent to a discharge point located near sample site #7. Both phosphorous and nitrogen were elevated in this area well above most other sites. All assessments of nutrients varied temporally and spatially across the bay and some sites were consistent with ratios expected from eutrophic systems that are demonstrating N limitation. Molar TN:TP ratios showed annual mean values of 20.49, 16.68 and 12.22 for 2013, 2014 and 2015 respectively. This decreasing trend of average TN:TP coincides with diminished HABs size and occurrence in the Bay. Although a collective TN:TP measurement is of interest, pooling the TN:TP ratios is problematic because it obfuscates important spatial and temporal differences among the sites.

Previous studies have found Gilbert Bay to be N limited and FBay to vary spatially in terms of N or P limitation. Wurtsbaugh and Marcarelli (2004) did a series of week-long bioassays using FBay water and found that in all cases algal growth was N limited. Marcarelli, Wurtsbaugh and Griset (2006) demonstrated that in N-limited FBay water N_2 fixing cyanobacteria are selectively favored and P additions caused demonstrable increases in cyanobacteria blooms. Wurtsbaugh, Marcarelli and Boyer (2012) found that in regions of FBay where robust cyanobacteria blooms were taking place the algal population was, not surprisingly, P limited. In one report, Wurtsbaugh et al. (2012) found that all bays of the GSL had TN:TP ratios of 25 or higher—indicating that, under the circumstances and timing of those assessments, all bays of the GSL, nitrogen would be adequate while phosphorous would in fact be the limiting nutrient. However, when one compiles a full history of studies of nutrient limitation in GSL, including Wurtsbaugh's own studies, nitrogen is consistently shown to be the rate limiting nutrient and P is in abundance. This is particularly true for Gilbert Bay, whereas FBay the TN:TP ratio is very much a function of location and time- period. For example, the TN:TP molar ratio increased from south to north

from 5.45 to 25.20 in 2013 and 7.09 to 22.43 in 2014. This site-specific average increase in TN:TP is indicative of N limitation in southern regions and the higher values are a result of N_2 fixation by heterocystic cyanobacteria in the mid to northern regions. In 2015, the TN:TP ratio did not increase along a south to north transect as was observed in 2013 and 2014 and corresponded to a lack of HABs in 2015. In 2013 and 2014 low initial values for TN:TP were present in the spring and then showed a notable increase in May and June that continued to be maintained until fall. This increase resulted from nitrogen fixing capacities of cyanobacteria blooms that began in May but that reached their peak in June and July. The spatial differences in TN:TP are a result of substantial inputs of nitrogen and phosphorous from the Northwest Oil Drain outlet near sites 7 & 8 followed by rapid uptake of bioavailable forms of N (nitrate and ammonia) and P (SRP) by algae. Assimilation of bioavailable N and P depletes dissolved levels and causes partitioning into particulate and organic forms. N is apparently depleted more readily than P and results in N limitation. When water quality conditions, such as nutrients, salinity and temperature are in the optimal ranges for cyanobacteria they afford a competitive advantage to the cyanobacteria and cause a rapid formation of blooms and along with it a remedy to N limitation.

The mean concentration of bioavailable forms of N and P near site #7 were higher than other sites by almost an order of magnitude: SRP at sites #7 and #8 had a multi-year average of 0.668 to 0.923 to mg/L and a maximum value of 1.64 to 2.61 mg/L. During 2013 and 2014 the other sites had mean values between 0.02 to 0.14 mg/L and maximum values of 0.04 to 1.14 mg/L. However, SRP remained high across the bay in 2015 with all sites having an average of 0.56 to 1.83. Uptake of SRP appeared to be substantially less in 2015 than in 2013 and 2014.

Similarly, ammonia near site #7 had a peak mean value of 3.95 mg/L (with a high of 16.29 mg/L) in 2013 while all other sites were between 0.22 to 0.54 mg/L. Nitrate and nitrite also showed the same type of pattern: the mean value at site #7 was 3.77 compared to a range of 0.03 to 0.28 mg/L during 2013. Consistently this was the case near site #7—soluble bioavailable forms of N or P were at their highest in this region. Based on these results it is quite evident that this source is one the major contributors to nutrient input into FBay. It should also be pointed out that two additional POTWs discharge to FBay, the Central Davis and North Davis Sewer Districts' discharges. However, under such low lake elevations (as during the last several years), the Central Davis discharge evaporates before it reaches the open water of the bay. The North Davis discharge occurs approximately 500 meters from the Antelope Island causeway. While it is a substantial flow (approximately 30 cfs), our sampling, even at site 1, did not identify any chemical, nutrient or biological differences that could be associated with this discharge. It likely flows parallel to the causeway until it is reaches the breach where it is immediately discharged to Gilbert Bay.

There is an abundance of information in the scientific literature evaluating the roles of N and P in eutrophication of water bodies. Classic long-term, lake-scale, studies done by Schindler et al., (2008) found that P was the dominant nutrient controlling eutrophication in lakes. This, and other studies, ushered in the "Phosphorous Paradigm" in which it was recognized that implementation of P controls

could effectively reduce deleterious impacts of eutrophication on fresh water lakes and streams. Success stories, such as was encountered in Lake Washington, following P controls bolstered the awareness of the value of P controls for improving water quality of lakes and streams. However, there has also been much debate about the applicability of this approach to other water bodies, especially marine or estuary systems (Smith and Schindler, 2009; Genkai-Kato and Carpenter, 2005; Lewis and Wurtsbaugh, 2008; Sondergaard, Jensen and Jeppesen, 2003; Sondergaard, Jensen and Jeppesen, 2001; Schindler et al., 2008; Sterner, 2008; Lewis, Wurtsbaugh and Paerl, 2011). A synthesis of the minutiae of these investigations is beyond the scope of this paper, but a distillation of ideas and observations suggests that in FBay initial reductions in P coupled with unchanged N inputs may reduce the dominance advantage of cyanobacteria over other algal species. However, one should recognize that changes in either N or P or the combination of them causes a shift in the pattern or status of limitation and may also introduce unintended consequences. Furthermore, it is known from a variety of studies (Sondergaard, Jensen and Jeppesen, 2003) that years of nutrient loading into lakes, internal cycling of nutrients, and other biogeochemical processes can continue to supply biota with nutrients for years, or even decades, even if dramatic reductions in nutrient loading was implemented. The processes of remineralization, nitrogen fixation or denitrification all contribute to either depletion or liberation of N for assimilation into biological systems and legacy accumulations of P in the sediments of FBay could continue to provide sufficient P for robust algal and cyanobacteria growth for years even with substantial reductions in P input.

Field observations can only provide a glimpse into the relative limitation, or co-limitation, of nutrients in the bay. It is imperative to conduct laboratory and mesocosm studies of algal responses to enrichment to understand the spectrum of likely outcomes of either P or N or N&P limitation on the ecological processes in FBay. Proposed reductions of nutrient input into FBay must consider the possible impacts on other bays of the GSL and their resident biota. Resource management of the Bay needs to accurately interpret and anticipate the broader implications of changes in nutrient input and connectivity between bays. It is possible that dramatic reductions in nutrient input into FBay could result in diminished primary and secondary productivity of Gilbert and Gunnison Bays. An unintended consequence of this could be reduced food available for avian predators that rely upon sizeable zooplankton populations. Such a change would violate a primary beneficial use of GSL—namely support of aquatic wildlife and avifuana that depend upon the ecosystem services of GSL.

Based on our three years of study in FBay it is evident that the factors controlling HAB formation are intricate and complex. There are many subtle interactions, indirect and direct effects of various factors. However, among the many contributing factors salinity, SRP and various N:P ratios stand out as being highly influential. It is evident that under conditions of fresh water or hyposaline conditions HABs are not favored. In addition, low SRP and sufficient bioavailable forms of N (e.g., ammonia and nitrate) will favor non-cyanobacteria over cyanobacteria. Of course, there are many other factors such as temperature and grazing pressure that exert an influence on the occurrence of HABs, but salinity and SRP remain strongly influential. This knowledge can assist resource managers in reducing the

occurrence of HABs (if deemed necessary) meanwhile providing sufficient nutrient input to support robust growth of other GSL biota.

Eutrophication of FBay has indeed been identified as a matter of some concern, however our research, and that of many other previous investigators of FBay, have recognized that there is not a straightforward relationship between cyanobacteria blooms and harm to the Bay. In fact, there are multilayered trophic relationships that demonstrate remarkable biotic production in the Bay under current nutrient input regimes and algal growth cycles. Despite cyanobacteria blooms there is little to no evidence of demonstrable harm from the cyanobacteria blooms to the biota of FBay. Furthermore, the GSL ecosystem integrity is a functional outcome of nutrient and biotic exchanges among the various bays in which N limitation and constraints on biotic production in Gilbert Bay is in part remedied by N_2 fixation in FBay and the export of both environmental and anthropogenic N into Gilbert Bay. Because of the critical interconnections among the bays of GSL changes in nutrient input into FBay must consider a wide array of potential consequences and need to be based on rigorous science that couples field observations with carefully designed and executed laboratory studies that can simulate the variety of possible outcomes from alterations in nutrient input. Management of the Bay needs to be an iterative, systematic process that judiciously considers both short and long term goals and outcomes and that understands the interconnectivity of FBay with the rest of the GSL. The goal of all our past, present and future research on FBay has been, and will continue to be, to understand complex ecological networks of FBay and to use this information to suggest best possible management decisions for the long-term health and integrity of the entire GSL ecosystem.

RECOMMENDATIONS FOR FURTHER RESEARCH ON FBAY

DNA Food web Studies

- Use DNA barcoding techniques to specifically identify the algal dietary preferences of zooplankton and identify prey items of Corixids.
- Identify isotopic profiles of algal and zooplankton taxa to identify sources of C and N and to tract their trophic pathway through the food web.

Nutrient Enrichment and Salinity Studies

- Conduct both laboratory and mesocosm experiments. Laboratory studies have the advantage of being able to control many of the variables.
- Mesocosms have perhaps more practical applied relevancy, but they are prone to disruption by the vicissitudes of the weather or demonic interventions.
- Conduct experiments on both FBay and Gilbert Bay water sources collected at various times of the year.
- Add N, P, N&P
- Alter salinity and track outcomes—especially within and outside of the preferred salinity range for cyanobacteria.

N_2 Fixation Studies

- Determine rates of nitrogen fixation in FBay.

Toxicity Testing of Cyanotoxins on Relevant Zooplankton from FBay

- Test the impacts of nodularin on *Daphnia* and *Artemia* collected from FBay
- Test nodularin on other cladocerans, rotifers, or copepods
- When using *Artemia* do hatching, growth, development and survival tests

Nutrient Balance Study

- Conduct detailed studies of the input sources and then fate and effects of nutrients that enter FBay.
- Devote attention to the role that the Salt Lake City POTW drain imposes on FBay

Ecological Studies of Farmington Bay

- Continue with monthly or bi-monthly investigations of the biota and abiotic characteristics of FBay (essentially continue the baseline ecological work that has already been underway for two years)
- Initiate an intensive benthic invertebrate study designed to understand the role of the benthos, particularly chironomids on HABs and their importance to the food web.

- Increase monitoring intensity of waterfowl and shorebirds that use Farmington for resting and feeding including the use of drone-mounted cameras.

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APPENDICES

Appendix 1.*Log generalized transformations*

A log transformation is often useful when there is a high degree of variation within attributes or when there is a high degree of variation among attributes within a sample. **Log generalized transformation** is best if the data contain zeros and the smallest positive value is not close to 1 (for example, smallest x = 0.02 or smallest x = 200). The formula for the generalized log transform is:

$$b = \log(x+xmin) - \log(xmin)$$

where xmin is the smallest positive value in the data set or individual variable. If data are count data with the smallest positive value = 1, the results will be the same as choosing log(x + 1).

Appendix 2. MRPP results for phytoplankton taxa by year, month, and site.

Year

Chance-corrected within-group agreement, A = 0.09561422

A = 1 - (observed delta/expected delta)

Amax = 1 when all items are identical within groups (delta=0)

A = 0 when heterogeneity within groups equals expectation by chance

A < 0 with more heterogeneity within groups than expected by chance

Probability of a smaller or equal delta, p = 0.00000000

PAIRWISE COMPARISONS

Note: p values not corrected for multiple comparisons.

Groups (identifiers)
Compared T A p

2013 vs. 2014 -5.28863947 0.04326526 0.00052755

2013 vs. 2015 -4.80342010 0.13473193 0.00088260

2014 vs. 2015 -10.49097674 0.07212830 0.00000009

Month

Test statistic: T = -18.844013

Observed delta = 0.30111896

Expected delta = 0.46236217

Variance of delta = 0.73217698E-04

Skewness of delta = -0.51868804

Chance-corrected within-group agreement, A = 0.34873790

A = 1 - (observed delta/expected delta)

Amax = 1 when all items are identical within groups (delta=0)

A = 0 when heterogeneity within groups equals expectation by chance

A < 0 with more heterogeneity within groups than expected by chance

Probability of a smaller or equal delta, p = 0.00000000

PAIRWISE COMPARISONS

Note: p values not corrected for multiple comparisons.

Groups (identifiers)

Compared	T	A	p
5 vs. 10	6.36547630	0.18076389	0.00007091
5 vs. 11	3.00772417	0.25419663	0.01296860
10 vs. 9	3.89034016	0.15696955	0.00402938
3 vs. 9	5.34598500	0.51425621	0.00115220
4 vs. 11	3.02249834	0.38446096	0.01420368
7 vs. 9	2.85941955	0.23594716	0.01607878
5 vs. 3	6.85147925	0.36133983	0.00007069
5 vs. 8	3.44121374	0.29506010	0.00900022
10 vs. 11	1.58157220	0.09292352	0.07546680
3 vs. 11	3.03941772	0.39424445	0.01409476
4 vs. 8	3.50109120	0.47161633	0.01024193
7 vs. 11	2.95861319	0.40408940	0.01501919
5 vs. 4	7.20588606	0.37878875	0.00005485
10 vs. 3	5.66259006	0.20274747	0.00027452
10 vs. 8	1.55977226	0.09311679	0.07608775
3 vs. 8	3.07281869	0.40921412	0.01366459
6 vs. 7	6.21456193	0.16990823	0.00013447
7 vs. 8	2.37161172	0.33148725	0.02700120
5 vs. 6	4.74642002	0.10147218	0.00077467
10 vs. 4	6.27305047	0.22798120	0.00011077
3 vs. 4	5.39517880	0.40629737	0.00040275
4 vs. 6	7.32072434	0.19424040	0.00001611
6 vs. 9	4.16570513	0.12441752	0.00270018
9 vs. 11	2.73628347	0.38315168	0.01819622
5 vs. 7	7.01577810	0.38507357	0.00008087
10 vs. 6	4.88055497	0.09178332	0.00094361
3 vs. 6	7.26552881	0.19349225	0.00001781
4 vs. 7	6.24362791	0.50571544	0.00031250
6 vs. 11	2.15184569	0.09349152	0.03986193
9 vs. 8	2.60821606	0.31258871	0.02014238
5 vs. 9	5.70970398	0.34312014	0.00045997
10 vs. 7	5.64075503	0.21044989	0.00034988
3 vs. 7	6.25468599	0.49993537	0.00029693
4 vs. 9	5.41074479	0.52414058	0.00117270
6 vs. 8	2.01732928	0.08831675	0.04640448
11 vs. 8	1.41264000	0.33680473	NaN

Site

Chance-corrected within-group agreement, A = -0.02089586

A = 1 - (observed delta/expected delta)

Amax = 1 when all items are identical within groups (delta=0)

A = 0 when heterogeneity within groups equals expectation by chance

A < 0 with more heterogeneity within groups than expected by chance

Probability of a smaller or equal delta, p = 0.96080761

PAIRWISE COMPARISONS

Note: p values not corrected for multiple comparisons.

Groups (identifiers)

Compared	T	A	p
3 vs. 4	0.28225307	-0.00313152	0.56597487
3 vs. 2	1.43794127	-0.02457181	0.96454076
4 vs. 5	2.03196302	-0.03792766	0.99684321
3 vs. 1	2.34747746	-0.03348822	0.99998749
3 vs. 6	-0.88240214	0.01218720	0.17679001
4 vs. 2	0.19948454	-0.00312402	0.52879588
1 vs. 5	0.16889740	-0.00221668	0.50733340
1 vs. 6	-0.36149029	0.00592431	0.30409144
5 vs. 6	1.49530431	-0.03806817	0.95576264
3 vs. 5	-0.02498831	0.00029995	0.43051121
4 vs. 1	0.31325670	-0.00376501	0.57034636
4 vs. 6	1.55823588	-0.04049816	0.95962694
1 vs. 2	1.54639246	-0.03225558	0.98461370
5 vs. 2	-0.63052275	0.00962631	0.23866739
2 vs. 6	0.18643733	-0.00432965	0.51002653

Appendix 3. Zooplankton assemblage relations to site, month, and year.

MRPP by site

Chance-corrected within-group agreement, A = 0.02861281
A = 1 - (observed delta/expected delta)
Amax = 1 when all items are identical within groups (delta=0)
A = 0 when heterogeneity within groups equals expectation by chance
A < 0 with more heterogeneity within groups than expected by chance

Probability of a smaller or equal delta, p = 0.00168929

PAIRWISE COMPARISONS
Note: p values not corrected for multiple comparisons.

Groups (identifiers)

Compared	T	A	p
1 vs. 2	0.66451539	-0.00903636	0.71203462
1 vs. 3	0.90279134	-0.01006134	0.87190171
1 vs. 4	0.08227173	-0.00105543	0.42622630
1 vs. 5	0.72588526	-0.00719855	0.75062924
1 vs. 6	-2.16100150	0.02870505	0.03871459
1 vs. 7	-1.50513240	0.01803999	0.08262937
1 vs. 8	-3.26829141	0.04274121	0.00943338
1 vs. 9	-1.49556042	0.01727391	0.08351823
2 vs. 3	-0.53895528	0.00739090	0.22835313
2 vs. 4	1.16633861	-0.01860022	0.94584800
2 vs. 5	-0.77981713	0.00908145	0.17894887
2 vs. 6	-1.09029124	0.01742444	0.13420590
2 vs. 7	-1.08860505	0.01555983	0.13572363
2 vs. 8	-2.44582153	0.03799207	0.02216491
2 vs. 9	-1.63837770	0.02308530	0.07068948
3 vs. 4	-0.44537739	0.00591011	0.24975247
3 vs. 5	1.03929462	-0.01057227	0.96536206
3 vs. 6	-1.86721848	0.02593420	0.05495319
3 vs. 7	-2.23369911	0.02692027	0.03593372
3 vs. 8	-3.27078680	0.04397113	0.00980164
3 vs. 9	-3.36412024	0.03779073	0.00881194
4 vs. 5	-0.26932732	0.00314844	0.29948418
4 vs. 6	0.11027891	-0.00169778	0.45974655
4 vs. 7	-0.42600595	0.00575057	0.28112262
4 vs. 8	-1.36316826	0.01990707	0.09726833
4 vs. 9	-2.82400592	0.03918638	0.01824041
5 vs. 6	-0.97475112	0.01231512	0.14888365
5 vs. 7	-0.87044043	0.00953678	0.16855027
5 vs. 8	-2.62043998	0.03100178	0.02168572
5 vs. 9	-4.10805947	0.04355516	0.00344871
6 vs. 7	0.07766124	-0.00124226	0.46837827
6 vs. 8	0.33030854	-0.00606085	0.57095493
6 vs. 9	-3.95588002	0.07084910	0.00602676
7 vs. 8	0.87900504	-0.01400171	0.80863020
7 vs. 9	-3.65851746	0.05782118	0.00806973
8 vs. 9	-3.52202685	0.06784785	0.01026887

MRPP by Month

Chance-corrected within-group agreement, A = 0.27140477
A = 1 - (observed delta/expected delta)
Amax = 1 when all items are identical within groups (delta=0)
A = 0 when heterogeneity within groups equals expectation by chance
A < 0 with more heterogeneity within groups than expected by chance

Probability of a smaller or equal delta, p = 0.00000000

PAIRWISE COMPARISONS
Note: p values not corrected for multiple comparisons.

Groups (identifiers)
Compared T A p
4 vs. 5 -10.67526166 0.09423475 0.00000069
4 vs. 6 -10.96898891 0.08283440 0.00000007
4 vs. 7 -14.46910479 0.21727533 0.00000001
4 vs. 8 -15.45328348 0.27769893 0.00000005
4 vs. 9 -14.07236995 0.24274191 0.00000003
4 vs. 10 -4.97181221 0.08237870 0.00118877
4 vs. 11 -2.17410547 0.04354276 0.03490016
4 vs. 3 -7.76124760 0.11342299 0.00001702
4 vs. 12 -6.46870897 0.12294021 0.00009252
5 vs. 6 -8.27821254 0.05618524 0.00002177
5 vs. 7 -18.31317623 0.22461940 0.00000000
5 vs. 8 -21.06862685 0.31818751 0.00000000
5 vs. 9 -17.55439554 0.25263503 0.00000000
5 vs. 10 -10.79032393 0.13469587 0.00000129
5 vs. 11 -8.60423626 0.12727648 0.00000786
5 vs. 3 -14.01882087 0.19146729 0.00000013
5 vs. 12 -10.98481336 0.16505639 0.00000098
6 vs. 7 -11.51095460 0.11060413 0.00000025
6 vs. 8 -18.09286693 0.20602929 0.00000000
6 vs. 9 -14.00006910 0.15997395 0.00000002
6 vs. 10 -7.69708430 0.07737238 0.00001386
6 vs. 11 -5.55071535 0.07271062 0.00028582
6 vs. 3 -15.10651060 0.15092547 0.00000000
6 vs. 12 -11.62367017 0.13586063 0.00000006
7 vs. 8 -2.10707246 0.03290800 0.03904137
7 vs. 9 -4.80905583 0.08463257 0.00077231
7 vs. 10 -6.02218275 0.12290657 0.00014997
7 vs. 11 -5.55756929 0.15299430 0.00044490
7 vs. 3 -11.62110291 0.24777606 0.00000102
7 vs. 12 -8.94509879 0.24971471 0.00001019
8 vs. 9 -2.93920814 0.05767227 0.01703754
8 vs. 10 -7.32242064 0.17812848 0.00009974
8 vs. 11 -5.76847041 0.17406864 0.00036348
8 vs. 3 -10.55573747 0.29705395 0.00001712
8 vs. 12 -8.30728424 0.27436306 0.00005677
9 vs. 10 -5.52645080 0.14317115 0.00034668
9 vs. 11 -4.78935191 0.18924936 0.00139437
9 vs. 3 -8.95482173 0.25919148 0.00002338
9 vs. 12 -6.06040447 0.21284775 0.00027940
10 vs. 11 -2.07432432 0.10811104 0.04396236
10 vs. 3 -5.31921277 0.13442857 0.00059506
10 vs. 12 -4.81789764 0.19809364 0.00157419
11 vs. 3 -5.40683946 0.19642256 0.00031763
11 vs. 12 -2.75237704 0.16248662 0.01714291
3 vs. 12 -5.38841377 0.17470601 0.00068176

MRPP by Year

Chance-corrected within-group agreement, A = 0.03234463
A = 1 - (observed delta/expected delta)
Amax = 1 when all items are identical within groups (delta=0)
A = 0 when heterogeneity within groups equals expectation by chance
A < 0 with more heterogeneity within groups than expected by chance

Probability of a smaller or equal delta, p = 0.00000023

Appendix 4.Taxa Thresholds

2a. Description of TITAN2
Threshold Indicator Taxa (R package, "TITAN2")(Baker, King, and Kahle 2015, Baker and King 2011, 2013)

TITAN2 which may be new to some readers, was used to detect changes in phytoplankton and zooplankton taxa distributions along several environmental gradients (i.e. salinity, temperature, nodularin) and to assess synchrony among taxa change points to determine assemblage temperature thresholds (Baker, King, and Kahle 2015, Baker and King 2011, 2013). TITAN2 used indicator species scores to integrate occurrence, abundance and directionality of taxa responses (Baker, King, and Kahle 2015). The model then identified the optimum environmental gradient value, which partitioned the samples while maximizing taxon-specific scores. Indicator z scores standardized the original scores relative to the mean and standard deviation of 250 permuted samples along the environmental gradient emphasizing the relative magnitude of change and increasing the contributions of taxa with low occurrence frequencies but with high sensitivity to the gradient (Baker, King, and Kahle 2015). TITAN2 distinguished negative (z−) and positive (*z*+) taxa responses and tracked cumulative responses of declining [sum(z−)] and increasing [sum(*z*+)] taxa in the community (Baker, King, and Kahle 2015). Bootstrapping was used to estimate indicator '*reliability*' and '*purity*' as well as uncertainty of individual taxa and community change points (Baker, King, and Kahle 2015).

> "Indicator *purity* is the proportion of change-point response directions (positive or negative) among bootstrap replicates that agree with the observed response. Pure indicators (e.g., purity >= 0.95) are consistently assigned the same response direction, regardless of abundance and frequency distributions generated by resampling the original data.
> If bootstrap resampling substantially alters the probability of obtaining an equal or larger IndVal based on 250 random permutations of the data, then that particular taxon is not a reliable indicator. Indicator *reliability* is estimated by the proportion of bootstrap change points whose IndVal scores consistently result in P-values below one or more pre-determined probability levels (e.g., P <=0.05). Reliable indicators (>= 0.95 of the bootstrap replicates achieving P <=0.05) were those with repeatable and consistently large IndVal maxima." (Baker and King 2010)

Default settings for TITAN2 were used, except we bootstrapped the data 1000 times. We used the filtered z scores for all reported results that met default purity and reliability criteria cutoff values of 0.95 (see Baker, King, and Kahle 2015).

2b. Phytoplankton assemblage thresholds

	cp	0.05	0.1	0.5	0.9	0.95
sumz-	15.14	2.10	3.28	14.33	19.68	20.02
sumz+	3.52	3.11	3.38	3.57	4.54	5.73

fsumz-	15.14	4.40	4.64	15.14	19.40	19.68
fsumz+	3.72	3.35	3.52	3.72	5.82	7.88

2c. Individual taxa thresholds to salinity

Salinity

Decreasers MaxGroup =1

Pure and reliable Filter = 1

Taxon	ienv.cp	zenv.cp	freq	IndVal	obsiv.prob	zscore	5%	10%	50%	90%	95%	purity	reliability	z.median
Tetrastrum sp.	2.10	2.10	6	43.51	0.004	8.32	1.89	2.10	2.23	3.19	3.38	1.00	0.96	8.44
Pseudopediastrum boryanum	2.10	2.23	9	48.46	0.004	8.24	1.32	1.57	2.13	2.68	5.26	1.00	0.98	8.59
Pediastrum boryanum	1.69	3.72	9	34.94	0.004	6.92	1.69	1.82	3.72	4.74	4.87	1.00	1.00	6.96
Pediastrum	3.96	3.96	50	69.62	0.012	3.8	3.33	3.95	4.64	15.00	19.58	1.00	0.98	4.40
Phacus	4.30	4.30	17	44.03	0.004	6.96	3.97	3.99	4.30	4.74	4.93	1.00	1.00	6.83
Actinastrum	15.14	4.44	12	23.33	0.004	3.82	4.40	4.44	10.84	16.81	18.00	1.00	0.97	4.36
Navicula	5.26	5.64	31	55.82	0.004	4.27	3.94	3.96	5.26	6.99	10.61	0.96	0.97	4.71
Schroederia	2.10	6.58	9	23.08	0.004	4.28	2.10	2.13	6.58	7.37	7.76	1.00	0.98	4.95
euglenophyte	16.81	15.14	45	76.95	0.004	8.48	4.25	4.64	12.62	19.24	19.58	1.00	1.00	8.42
pennate diatom	30.50	15.14	69	74.94	0.008	4.49	6.29	7.50	13.68	20.02	21.22	1.00	1.00	4.65
chlorophytes	20.02	18.37	69	82	0.008	2.61	2.59	4.30	16.81	19.92	20.44	0.98	0.98	2.98
Monoraphidium	20.02	19.06	47	71.16	0.004	5.94	5.90	15.14	19.58	21.28	21.64	1.00	1.00	6.31
Scenedesmus	26.97	20.02	51	64.55	0.004	5.16	15.55	18.95	20.02	22.75	23.44	0.98	1.00	5.71
centric diatoms	26.97	23.80	60	78.95	0.004	2.92	1.91	2.88	20.02	23.69	24.14	0.99	0.95	3.53

Decreasers MaxGroup =1

Did not meet purity and reliability Filter = 0

Taxon	ienv.cp	zenv.cp	freq	IndVal	obsiv.prob	zscore	5%	10%	50%	90%	95%	purity	reliability	z.median
Amphora	1.87	1.87	31	70.88	0.004	3.69	1.51	1.72	2.00	13.93	23.80	0.92	0.89	4.01
Anabaenopsis elenkinii	6.58	6.93	9	19.53	0.012	2.61	4.86	5.26	6.87	14.33	14.81	0.97	0.86	2.97
Chrysochromulina parva	3.19	3.33	6	20.71	0.004	4.39	1.91	3.11	3.33	7.94	9.97	1.00	0.92	4.99
Cylindrotheca	5.26	5.26	10	23.79	0.008	2.99	2.06	2.36	5.28	14.33	14.81	0.99	0.95	3.84
Desmodesmus	2.10	2.23	7	24.78	0.012	4.16	2.10	2.10	2.24	14.16	14.49	0.92	0.80	4.06
Koliella/Monoraphidium	1.69	3.02	8	13.61	0.056	1.16	1.69	1.87	4.18	20.02	24.88	0.75	0.58	2.30
microflagellate	1.69	1.69	12	55.19	0.012	6.19	0.92	1.15	2.00	30.74	31.96	0.74	0.77	5.27
Pediastrum duplex	1.87	1.87	19	28.44	0.084	0.61	1.87	1.87	3.97	25.36	26.35	0.66	0.52	2.01
Pediastrum integrum	1.87	23.23	34	44.84	0.044	1.9	2.10	2.23	10.19	22.75	23.04	0.78	0.77	2.48
Phormidium	1.69	16.81	19	26.83	0.02	2.58	0.40	1.20	16.00	22.23	22.52	0.93	0.86	3.16
Planktothrix	1.69	22.00	5	8.33	0.324	0.57	0.92	1.44	7.69	21.15	22.00	0.50	0.45	2.08
Tetraedron	2.10	2.10	11	25.98	0.032	2.27	2.10	2.10	2.95	25.35	25.35	0.79	0.77	3.40

Increasers MaxGroup =2
Pure and Reliable Filter = 2

Taxon	ienv.cp	zenv.cp	freq	IndVal	obsiv.prob	zscore	5%	10%	50%	90%	95%	purity	reliability	z.median
Cymbella/Encyonema	26.37	18.81	18	46.27	0.004	7.55	17.18	18.88	20.11	24.45	26.37	1.00	1.00	8.37
Phaeodactylum tricornutum	6.58	6.58	28	49.28	0.004	4.44	4.33	5.36	6.58	13.44	13.84	0.99	0.98	4.44
Nodularia	2.59	4.44	66	87.86	0.004	6.97	3.58	3.78	4.23	4.54	4.67	1.00	1.00	6.98
Chaetoceros	1.69	3.72	71	85.98	0.004	5.03	3.10	3.19	3.57	4.00	4.22	0.97	1.00	5.13
Oocystis	1.69	1.69	69	88.36	0.004	4.06	1.63	1.69	3.67	10.84	13.69	0.95	0.98	4.54

Increasers MaxGroup =2

Did not meet purity and reliability Filter = 0

Taxon	ienv.cp	zenv.cp	freq	IndVal	obsiv.prob	zscore	5%	10%	50%	90%	95%	purity	reliability	z.median
Aphanocapsa	2.91	3.33	16	22.46	0.144	1.16	2.91	3.38	5.00	22.23	23.56	0.70	0.52	2.01
cryptophyte	7.94	7.94	8	15.05	0.064	1.57	2.10	2.10	7.94	30.99	32.45	0.69	0.73	2.93
cyanophytes	1.69	3.52	73	64.23	0.012	2.68	1.44	2.76	4.52	32.45	32.45	0.75	0.86	3.73
Dictyosphaerium	3.52	3.52	32	45.06	0.008	3.67	3.02	3.38	5.00	13.70	25.36	0.92	0.99	4.11
Didymocystis	2.10	19.06	19	21.58	0.12	1.31	2.10	2.59	11.04	22.75	25.35	0.58	0.69	2.58
dinoflagellates	1.69	3.52	32	36.18	0.12	1.38	2.00	2.24	4.40	26.34	26.97	0.85	0.66	2.45
Entomoneis	26.97	3.72	29	40.13	0.024	2.62	3.38	3.52	4.64	22.23	22.52	0.59	0.92	3.21
Lobocystis	3.72	3.72	19	32.2	0.024	2.63	3.33	3.43	3.73	10.03	18.00	0.94	0.95	3.26
Merismopedia	4.87	4.87	6	12.77	0.064	2.08	4.43	4.55	5.00	18.37	18.75	0.62	0.55	2.26
Nitzschia	3.52	3.52	69	75.5	0.032	1.96	2.87	3.27	5.00	26.97	32.20	0.78	0.75	2.43
Pseudanabaena	1.69	3.52	42	46.89	0.024	2.67	1.87	3.28	3.86	26.34	28.86	0.88	0.82	3.14
Spirulina	1.69	1.69	37	48.51	0.12	0.7	1.87	1.91	3.52	25.35	25.35	0.72	0.58	2.20
Tetraselmis	28.86	28.86	11	47.11	0.004	5.14	3.38	4.55	28.32	28.86	29.10	0.79	0.91	4.61

Appendix 5. Zooplankton assemblage salinity thresholds

	cp	0.05	0.1	0.5	0.9	0.95
sumz-	4.109359	2.103741	2.453668	5	11.015245	14.327564
sumz+	6.578697	4	4.054359	6.294325	6.984944	7.431816
fsumz-	8.185	2.102835	2.128116	6.871195	14.164943	14.673068
fsumz+	6.578697	5.717048	5.896203	7.722142	11	11.5

Appendix 6. Individual zooplankton thresholds for salinity

	ienv.cp	zenv.cp	freq	maxgrp	IndVal	obsiv.prob	zscore	5%	10%	50%	90%	95%	purity	reliability	z.median	filter
Brachionus plicatilis	3.99	4.05	115	2	72.01	0.00	3.92	3.95	3.98	4.54	28.00	41.08	0.746	1.000	4.30	0
Notholca acuminata	1.54	3.09	17	1	34.40	0.00	9.27	1.88	2.10	3.10	8.00	10.00	1.000	1.000	9.48	1
Keratella quadrata	2.10	2.68	12	1	49.82	0.00	16.55	2.00	2.00	2.46	2.85	2.94	1.000	1.000	17.36	1
Daphnia dentifera	1.50	5.00	83	1	74.25	0.00	9.60	4.11	4.34	13.50	24.37	25.35	1.000	1.000	10.40	1
Daphnia pulex / L	2.37	8.19	50	1	55.62	0.00	7.70	2.00	2.10	5.81	10.13	16.31	1.000	1.000	9.23	1
Ceriodaphnia quadrangula	2.51	3.28	5	1	12.85	0.00	7.02	2.10	2.25	2.91	5.00	5.28	0.995	0.932	7.66	0
Simocephalus vetulus	1.50	2.23	6	1	12.18	0.04	3.91	1.50	1.54	4.00	9.00	10.00	0.998	0.938	5.41	0
Moina macrocarpa	100.00	46.00	101	1	66.06	0.00	4.04	2.63	2.68	32.64	49.00	52.00	0.522	1.000	4.57	0
Bosmina longirostris	1.69	3.78	8	1	13.41	0.00	4.90	1.50	1.69	3.73	9.19	10.13	0.998	0.960	5.56	1
Artemia franciscana	73.00	6.58	81	2	76.72	0.00	8.24	6.29	6.87	11.03	57.00	73.00	1.000	1.000	8.84	2
Pleuroxus aduncus	1.54	1.69	11	1	36.88	0.00	9.68	1.54	1.54	3.28	4.13	4.30	1.000	1.000	10.83	1
Chydorus sphaericus	2.51	3.22	4	1	9.53	0.02	4.63	2.21	2.51	3.28	5.54	5.73	0.986	0.869	5.57	0
Leptodiaptomus connexus	52.00	52.00	99	1	65.35	0.03	1.62	2.00	2.00	5.00	26.60	32.83	0.658	0.462	-2.31	0
Cletocamptus	1.69	5.81	103	2	68.18	0.01	3.26	4.33	5.26	6.93	11.50	11.55	0.969	0.993	3.76	2
Diacyclops	7.69	7.69	36	1	43.74	0.00	7.12	5.00	6.44	7.94	17.50	19.44	1.000	1.000	7.91	1
Eucyclops	21.64	22.23	37	1	34.27	0.00	4.15	18.36	19.68	21.64	22.73	23.24	0.999	1.000	4.71	1
Trichorixa verticalis	1.47	73.00	72	1	46.35	0.14	1.01	1.50	1.50	2.76	26.40	28.00	0.743	0.509	1.88	0

Appendix 7. Decreaser taxa temperature thresholds

taxon	ienv.cp	zenv.cp	freq	maxgrp	IndVal	obsiv.prob	zscore	5%	10%	50%	90%	95%	purity	reliability	z.median
Notholca acuminata	4.225	4.225	17	1	63.23	0.004	9.29	3.475	3.55	4.9	17.505	20.7	0.992	0.968	8.230692
Diacyclops	7.375	7.375	36	1	83.46	0.004	11.24	6.3	6.4	7.35	22.17	22.475	0.997	1	10.426637
Eucyclops	13.775	14.95333	37	1	63.63	0.004	11.58	11.9475	12.9	13.75	14.95333	15.225	1	1	12.717538
Cletocamptus	11.9375	13.35	103	2	69.64	0.004	3.5	11.8	11.9375	13.45	15.9	16.77125	0.991	1	3.970352

Appendix 8. Nodularin thresholds

Nodularin

No useful results for **nodularin and zooplankton groups**

Proportion of pure and reliable taxa = 0"

"Warning: low number of pure and reliable taxa, sum(z) output should be interpreted with caution"

[1] "Number of z- taxa = 0, Number of z+ taxa = 0"

Decreasers MaxGroup =1

Did not meet purity and reliability Filter = 0

	ienv.cp	zenv.cp	freq	IndVal	obsiv.prob	zscore	5%	10%	50%	90%	95%	purity	reliability	z.median
Rotifera	1.63	0.67	25	49.39	0.128	1.16	0.13	0.13	0.67	1.57	1.63	0.83	0.64	2.45

Increasers MaxGroup =2

Did not meet purity and reliability Filter = 0

	ienv.cp	zenv.cp	freq	IndVal	obsiv.prob	zscore	5%	10%	50%	90%	95%	purity	reliability	z.median
Corixidae	0.30	0.45	21	62.74	0.012	2.86	0.25	0.30	0.44	1.53	1.65	0.89	0.91	3.05
Moina	0.69	0.69	26	55.9	0.092	1.64	0.57	0.66	1.23	1.65	1.67	0.90	0.68	2.56
Cladocera	1.50	1.39	26	54.96	0.1	1.44	0.60	0.69	1.39	1.66	1.67	0.90	0.69	2.62
Copepoda	1.65	1.39	29	64.96	0.036	2.68	0.25	0.32	1.22	1.65	1.65	0.98	0.92	3.53
Artemiidae	1.65	1.42	23	64.56	0.004	2.93	0.62	0.69	1.40	1.66	1.67	0.95	0.86	3.39

Appendix 9. *Descriptions of TITAN2 results*

ienv.cp—environmental change point for each taxon based on IndVal maximum (used if imax = TRUE)

zenv.cp—environmental change point for each taxon based on z maximum (default, imax = FALSE)

freq—number of non-zero abundance values per taxon

maxgrp—1 if z- (negative response); 2 if z+ (positive response)

IndVal-Dufrene and Legendre 1997 IndVal statistic, scaled 0-100%

obsiv.prob—the probability of obtaining an equal or larger IndVal score from random data; (number of random IndVals > = observed IndVal)/ numPerm

zscore—IndVal z score

5%, 10%, 50%, 90%, 95%—change point quantiles among bootstrap replicates

purity—proportion of replicates matching observed maxgrp assignment
and is the proportion
of change-point response directions (positive or negative) among
bootstrap replicates that agree with the observed response. Pure indicators
(e.g., purity >=0.95) are consistently assigned the same response
direction, regardless of abundance and frequency distributions
generated by resampling the original data.
From Baker and King 2010

reliability—proportion of replicate obsiv.prob values < = 0.05
If bootstrap resampling substantially alters the probability of
obtaining an equal or larger IndVal based on 250 random permutations
of the data, then that particular taxon is not a reliable indicator.
Indicator reliability is estimated by the proportion of bootstrap
change points whose IndVal scores consistently result in P-values
below one or more user-determined probability levels (e.g., P<=0.05).
Reliable indicators (e.g., >=0.95 of the bootstrap replicates achieving
P <=0.05, or some other user-defined proportion of replicates) are
those with repeatable and consistently large IndVal maxima.
From Baker and King 2010

z.median—median score magnitude across all bootstrap replicates

filter—logical (if >0) indicating whether each taxa met purity and reliability criteria, value indicates maxgrp assignment.

TITAN Literature Cited

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