Abiotic and Biotic Characteristics of Crystal Bog, Wisconsin in 2007 and 2009

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Introduction

Microbial communities are responsible for carrying out crucial ecosystem functions and processes, and are therefore essential to life on Earth (Li et al. 2015). Specifically, in aquatic systems, bacterial communities play vital roles in biogeochemical cycling (Monard et al. 2016). Knowledge of the composition, structure, and distribution of microbial communities can be utilized to predict how an ecosystem may respond to environmental changes over time Sieber et al. (2020).

The North Temperate Lakes Long Term Ecological Research (LTER) program located in Vilas County, Wisconsin has collected a myriad of data from lakes and bogs in the area. In 2007 and 2009, data on pH, dissolved oxygen (DO), and temperature were collected from Crystal Bog. Additionally, samples were collected and analyzed to identify members of the microbial community by 16S rRNA sequencing (McMahon et al. 2019). This dataset was analyzed using R v. 4.1.1 to gain an understanding of the influence these environmental factors (pH, DO, temperature) may have had on microbial community composition between Summer 2007 and Summer 2009.

Methods

Data was collected by researchers through the North Temperate Lakes LTER in Vilas County, Wisconsin. Freshwater samples were collected from Crystal Bog in 2007 and 2009 and 16S rRNA sequencing was performed. Data was analyzed using R v. 4.1.1.

Results and Discussion

Abiotic characteristics of Crystal Bog measured in Summer 2007 and Summer 2009 were temperature (C) and DO content (mg/L). Measurements of pH were recorded only in 2007. Between June and August of 2007 and 2009, the temperature of Crystal Bog increased consistently (Figure 1A). The overall average temperature across the Summer months of 2009 was lower than those in 2007, which was unexpected due to trends of warming in northern lakes (Cavaco et al. 2019). In 2007, the DO content increased between June and August, while it decreased over the same time span in 2009 (Figure 1B). However, average DO content plotted against depth (m) showed a decreasing amount of oxygen as depth increased (Figure 2). This trend helps to explain the contrasting patterns of DO content observed in 2007 vs. 2009, as there were variations in the depth that DO was measured by year. The pH of Crystal Bog in 2007 became more acidic between June and July, and increased between July and August (Figure 1C). The average pH of Crystal Bog remained acidic, with no measurements recorded over a pH of 4.0. Freshwater microbes are frequently exposed to changes in pH conditions, therefore there was unlikely to be a significant correlation found between changes in pH and microbial community composition Low-Décarie et al. (2016).

16S rRNA sequencing of samples resulted in the recognition of 45 unique phyla that had more than five reads across all samples in 2007 and 2009. The total abundance of each phylum ranged from 20 (FCPU426) to 5,597,312 (Proteobacteria) reads (Table 1). Samples were collected at varying depths, including both the upper (Epilimnion) layer and lower (Hypolimnion) layer of Crystal Bog. When compared, the same five major phyla (Acidobacteria, Actinobacteria, Bacteroidetes, Proteobacteria, and Verrucomicrobia) were found to dominate both layers (Figure 3). Relative abundances of the major phyla (>200 reads) were calculated separately for 2007 and 2009 due to varying numbers of samples collected per year. In 2007, eight phyla were found to make up the majority of the microbial community. In order of abundance, the eight phyla were: Proteobacteria, Actinobacteria, Acidobacteria, Verrucomicrobia, Bacteroidetes, Fusobacteria, Cyanobacteria, and OD1 (Figure 4A). In 2009, only five phyla were found to dominate the microbial community. In order of abundance, the five phyla were: Proteobacteria, Actinobacteria, Acidobacteria, Verrucomicrobia, and Bacteroidetes (Figure 4B).

Microbial sampling of freshwater lakes is important for determining the associations microbes may have with major processes such as stratification, which leads to significant decreases in oxygen availability in lower lake layers, and biogeochemical cycling Joint, Doney, and Karl (2011). Though the stages of these processes have been well documented, the impact they may have on microbial community stability over time is less clear (Morrison et al. 2017). Further study of abiotic characteristics associated with freshwater lakes and their coexisting microbial communities should be performed over extended periods of time to gain a better understanding of the variability that may be caused by these processes.

References

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Figures

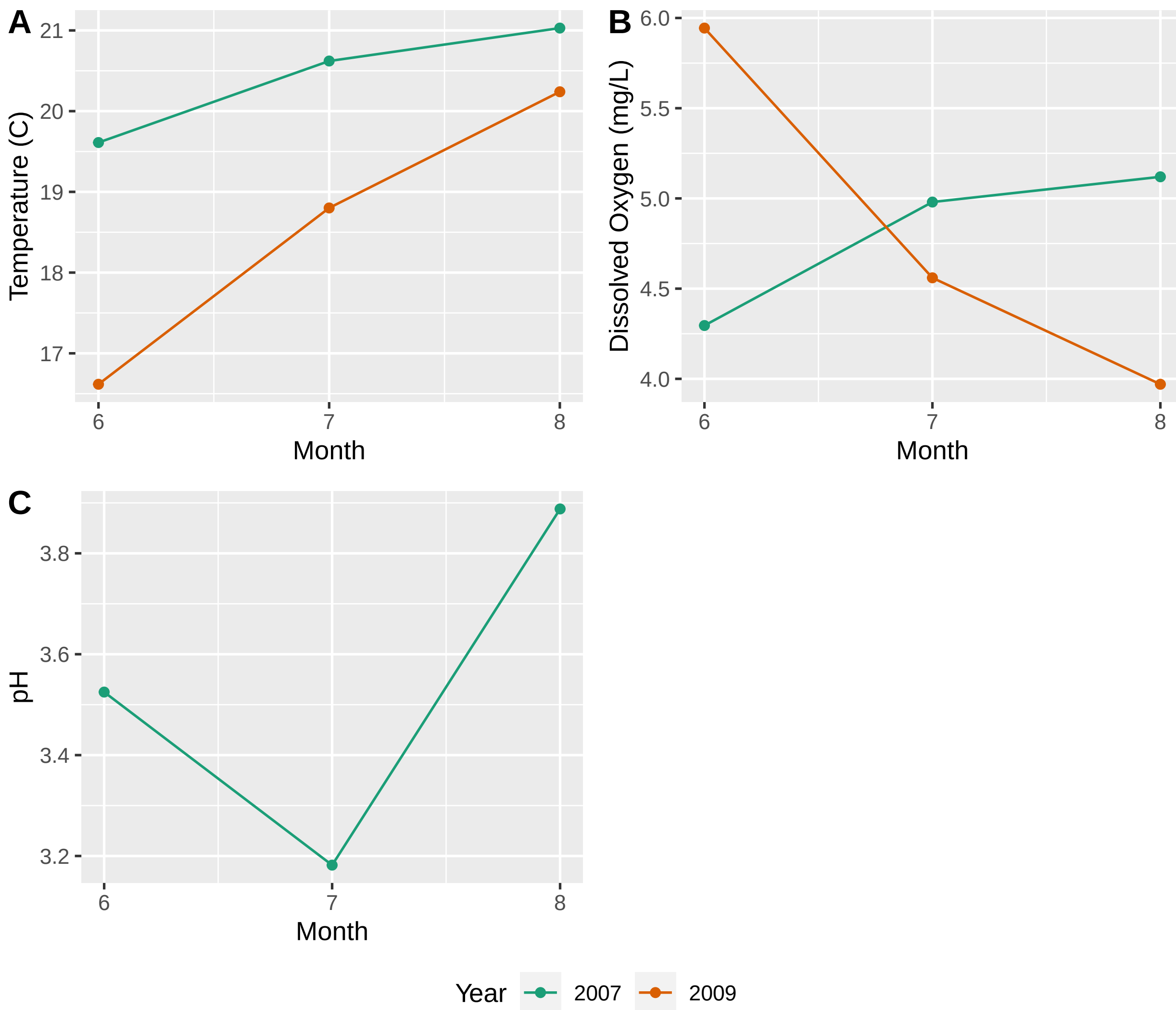

Figure 1: Average monthly temperature (A), dissolved oxygen content (B), and pH (C) of Crystal Bog in 2007 and 2009. Time scale covers the Summer months: June (6), July (7), and August (8).

Table 1: Total abundances of each phyla in Crystal Bog

Phylum	Total Reads
AC1	148
Acidobacteria	397690
Actinobacteria	2500358
Armatimonadetes	21954
Bacteroidetes	1009954
Caldiserica	36
Chlamydiae	8138
Chlorobi	65958
Chloroflexi	11856
Crenarchaeota	48

Phylum	Total Reads
Cyanobacteria	176790
Deferribacteres	108
Elusimicrobia	3744
Euryarchaeota	3414
FCPU426	20
Fibrobacteres	822
Firmicutes	35652
Fusobacteria	64380
GN02	276
LD1	330
Lentisphaerae	7666
NC10	298
Nitrospirae	686
NKB19	396
OD1	79780
OP11	3538
OP3	20190
OP8	2326
Parvarchaeota	2826
Planctomycetes	30058
Proteobacteria	5597312
Spirochaetes	7732
SR1	21218
Tenericutes	100
Thermi	222
TM6	4654
TM7	2224
Verrucomicrobia	1133370
WPS-2	196
WS1	466
WS3	494
WS4	72
WS5	2808
WWE1	64
ZB3	320

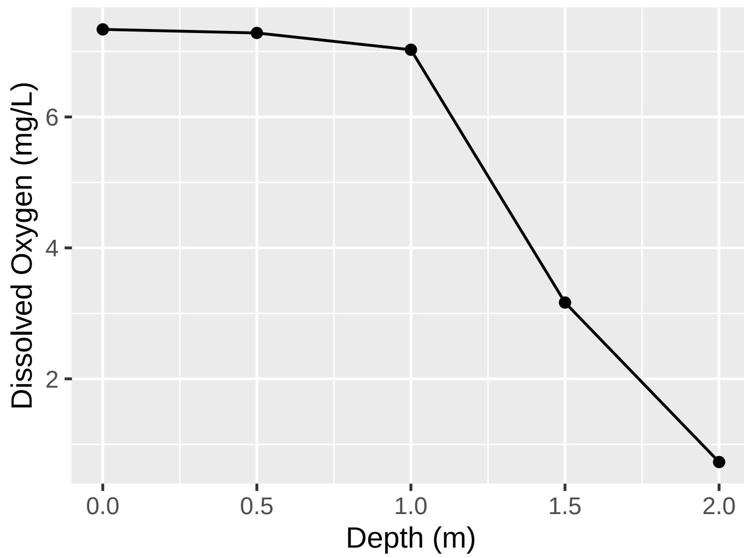

Figure 2: Average dissolved oxygen content (mg/L) measured at increasing depth (m) in Crystal Bog.

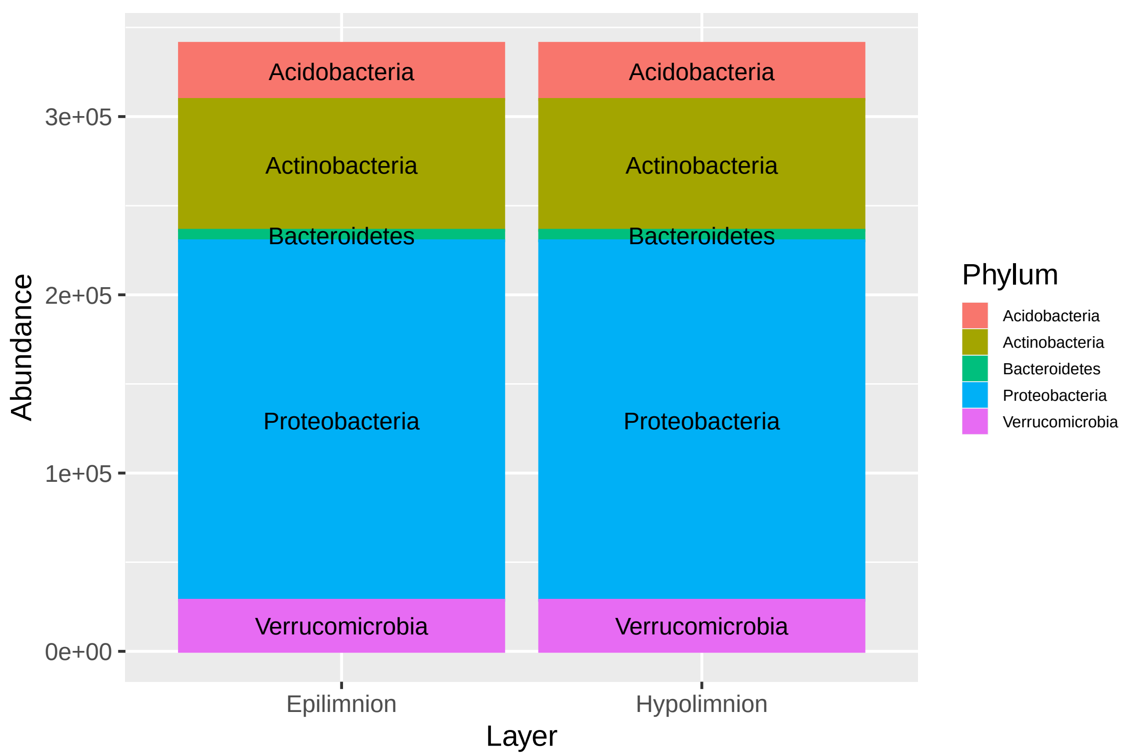

Figure 3: Relative abundances of the most abundant phyla (> 200 reads) identified at the upper (Epilimnion) and lower (Hypolimnion) layers of Crystal Bog.

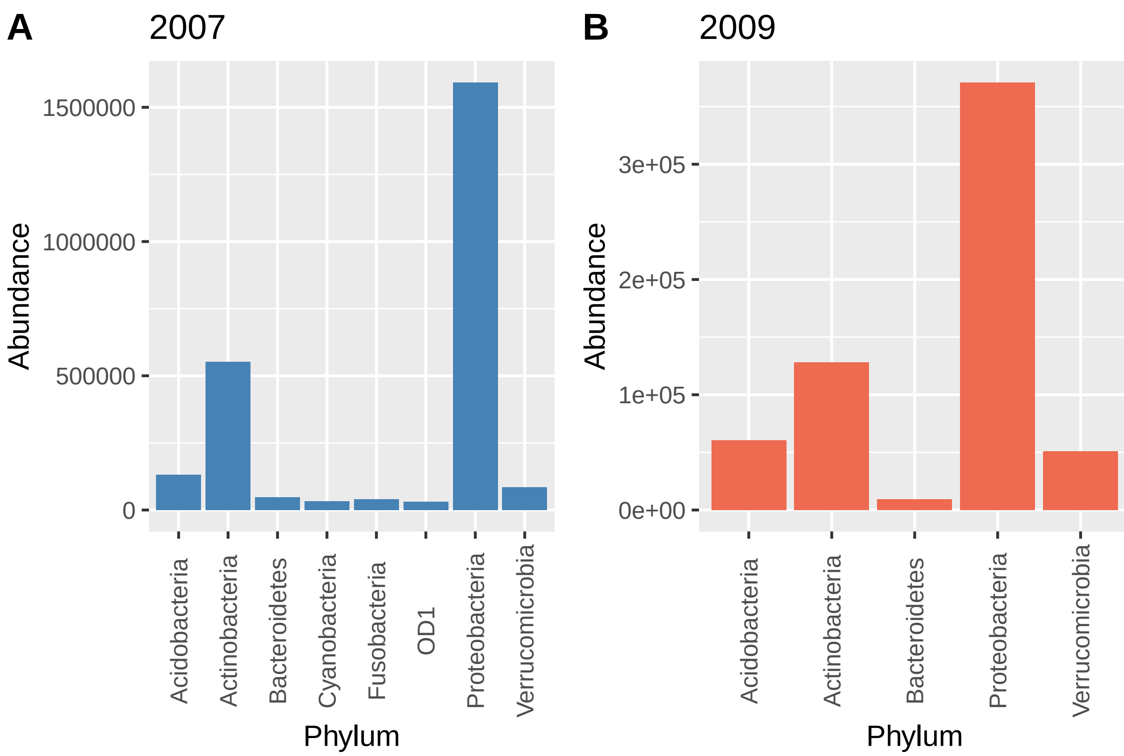

Figure 4: Relative abundances of the dominant phyla (>200 reads) in 2007 (A) and 2009 (B).