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 (Monard et al., 2016; 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

Table 1: 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
Cyanobacteria	176790
Deferribacteres	108
Elusimicrobia	3744
Euryarchaeota	3414
FCPU426	20
Fibrobacteres	822

Phylum	Total Reads
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

Discussion

References

Li P, Yang SF, Lv BB, Zhao K, Lin MF, Zhou S, Song X, Tang XM. 2015. Comparison of extraction methods of total microbial DNA from freshwater. Genet Mol Res. 14(1):730-8.

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Sieber, G., Beisser, D., Bock, C., & Boenigk, J. 2020. Protistan and fungal diversity in soils and freshwater lakes are substantially different. Scientific reports, 10(1), 20025.

McMahon, K., S. Jones, A. Shade, R. Newton, E. Read, L. Beversdorf, R. Rohwer, B. Peterson, A. Linz, E. McDaniel, G. Wolf, and S. Schmitz. 2019. Microbial Observatory at North Temperate Lakes LTER High-resolution temporal and spatial dynamics of microbial community structure in freshwater bog lakes 2005 - 2009 original format ver 4. Environmental Data Initiative.
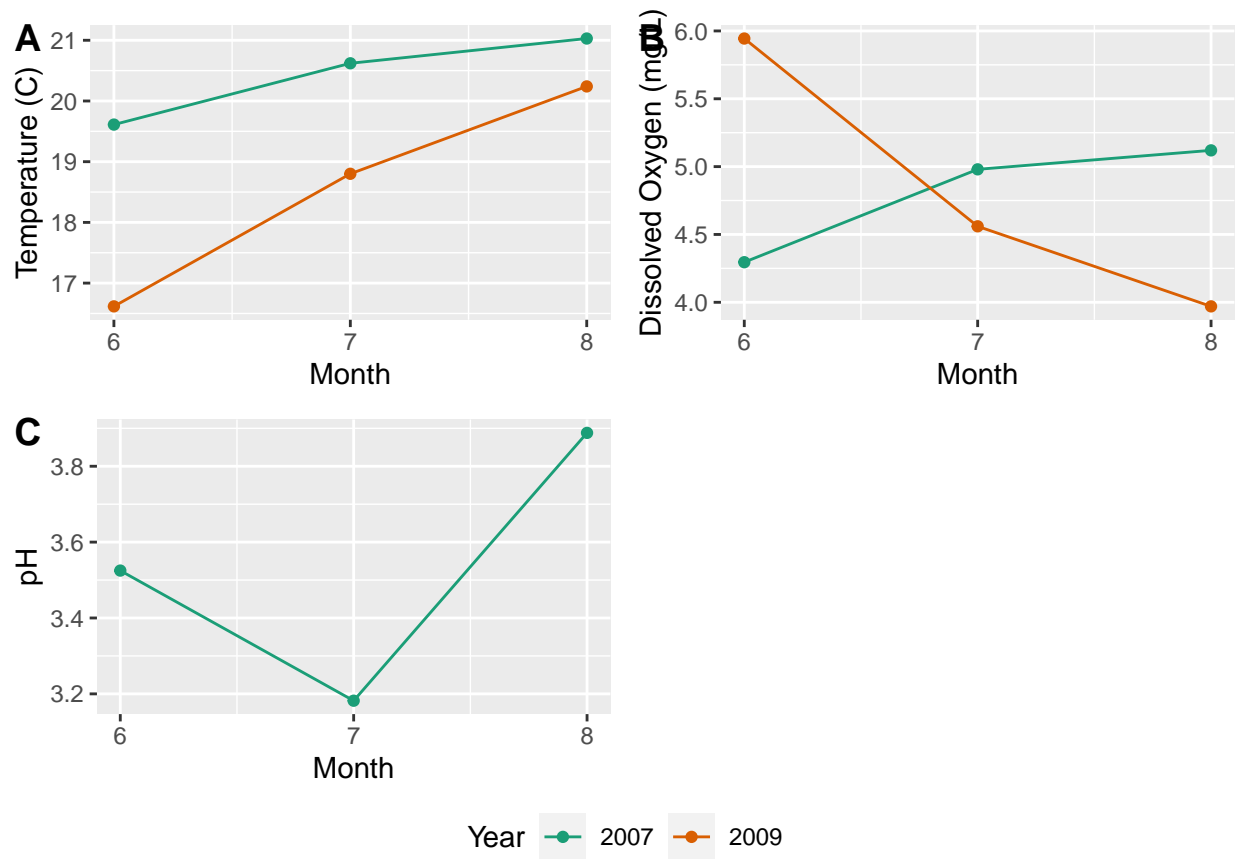
Figure 1: Average monthly temperature (A), dissolved oxygen (B), and pH (C) of Crystal Bog in 2007 and 2009. Time scale covers the Summer months: June (6), July (7), and August (8).
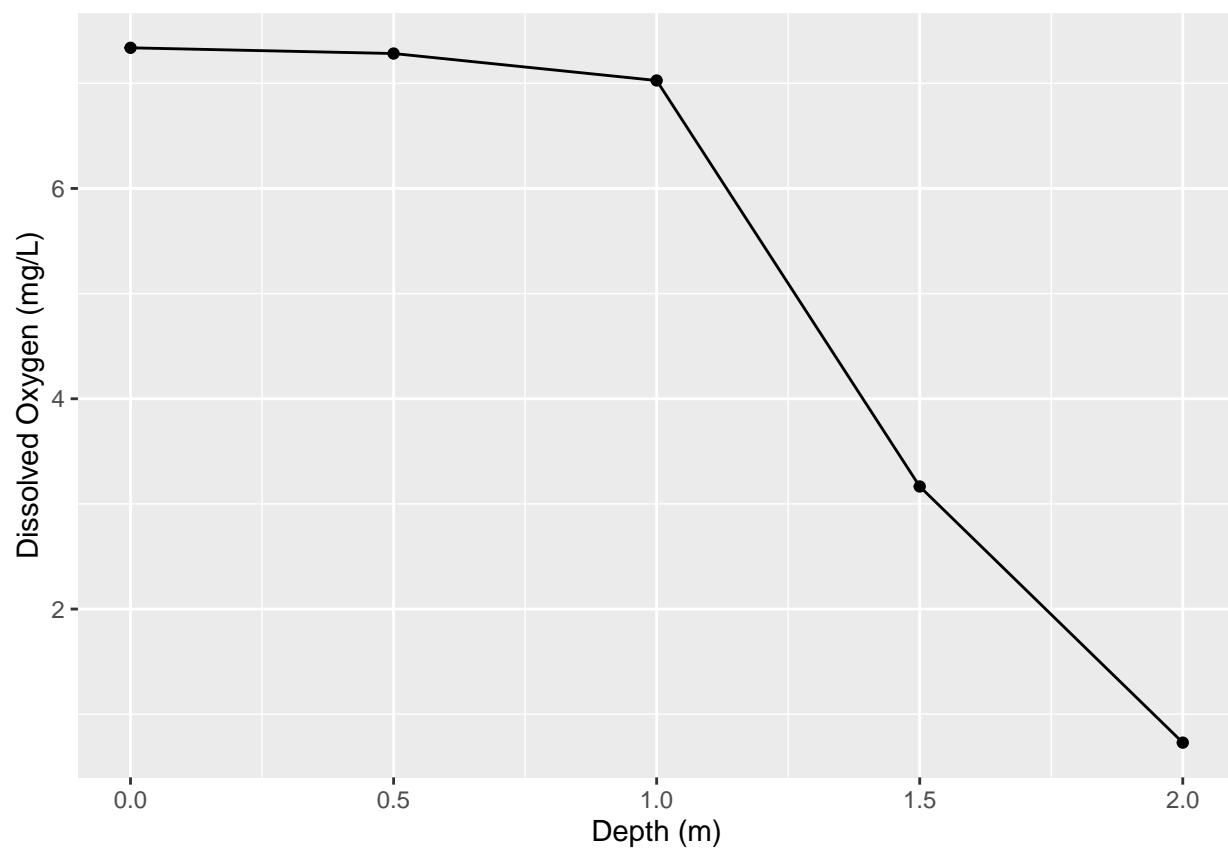
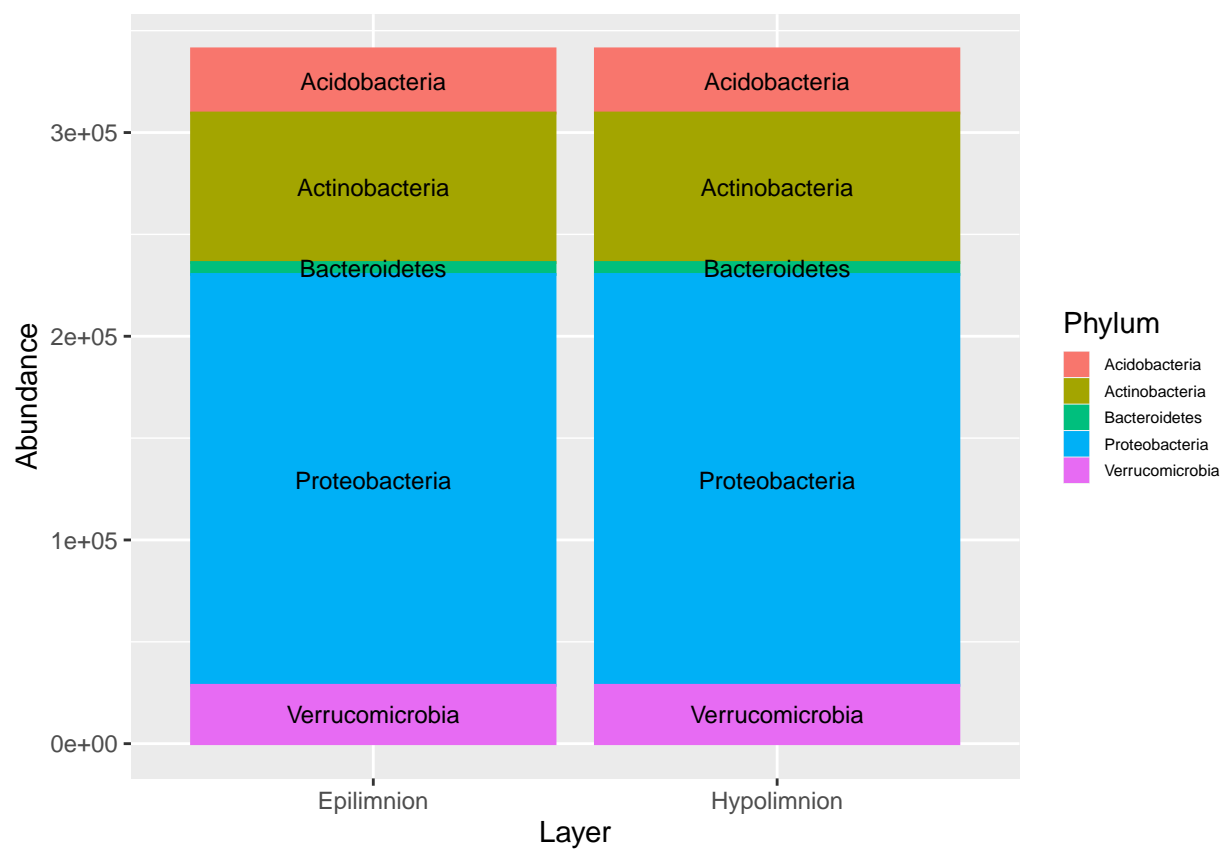Figure 2: Average dissolved oxygen content (mg/L) measured at increasing depth (m) in Crystal Bog.

Figure 3: Relative abundances of the most abundant phyla ($>$ 200 reads) identified at the upper (Epilimnion) and lower (Hypolimnion) layers of Crystal Bog.
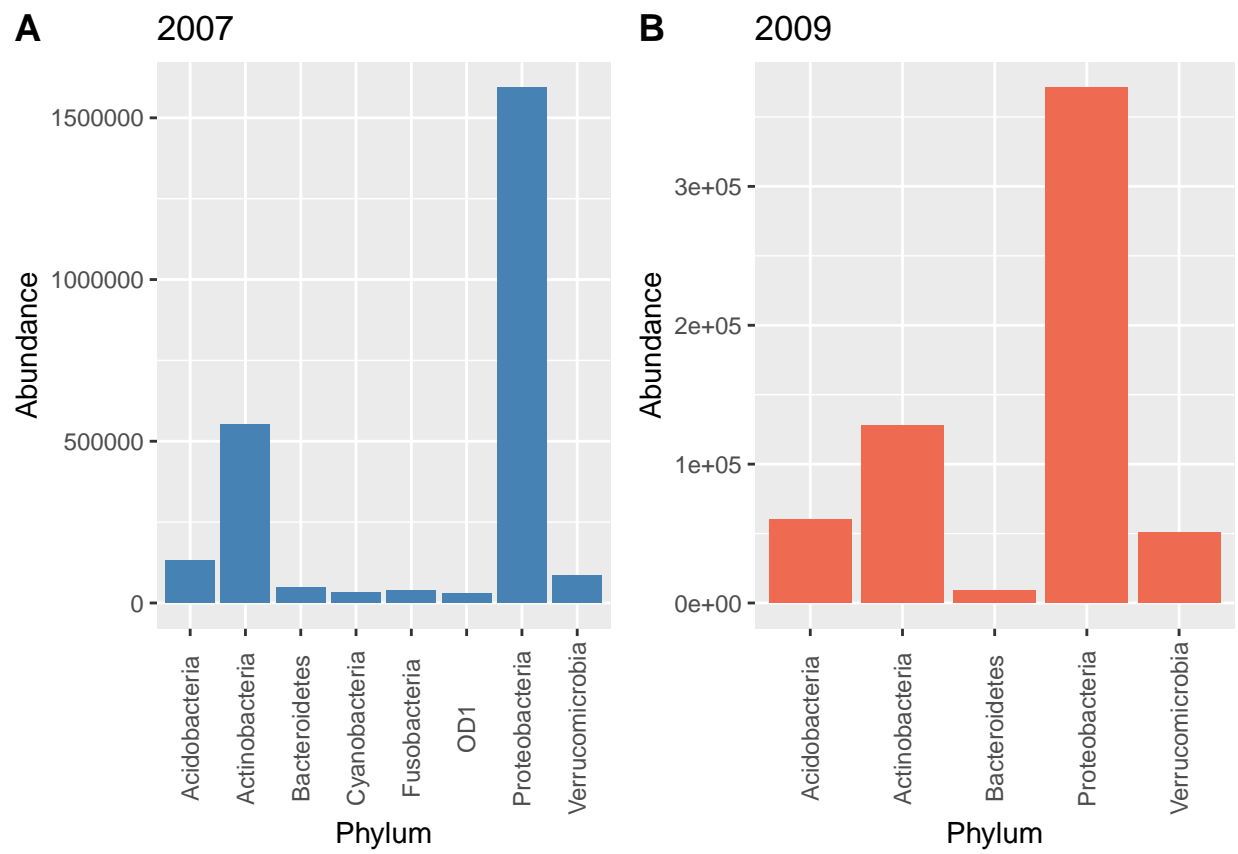
Figure 4: Relative abundances of the dominant phyla (>200 reads) in 2007 (A) and 2009 (B).