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### Water Clarity Affects Microbial Diversity in Lakes at Longwood University

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### Background

- Many studies have demonstrated that water clarity plays a crucial role in aquatic systems.
- The build-up of sediment, and other particles, prevent sunlight from passing through, altering the temperature of the lake, changing the chemistry, and negatively impacting the biodiversity of the lake.
- A 2009 study found that littoral zooplankton population biomass saw a significant decrease in the presence of denser macrophyte beds, which often occurred in lakes with lower transparency.<sup>2</sup>
- Understanding how transparency effects lake and pond ecosystems has allowed scientists to gain better knowledge on the impacts of climate change at varying levels.<sup>6</sup>
- A 2016 study of bacterial diversity within lakes upon a glacier retreat found a great amount of bacterial diversity,<sup>4</sup> providing evidence that bacterial diversity has a positive correlation to clarity of water, which could be provided by a retreating glacier.

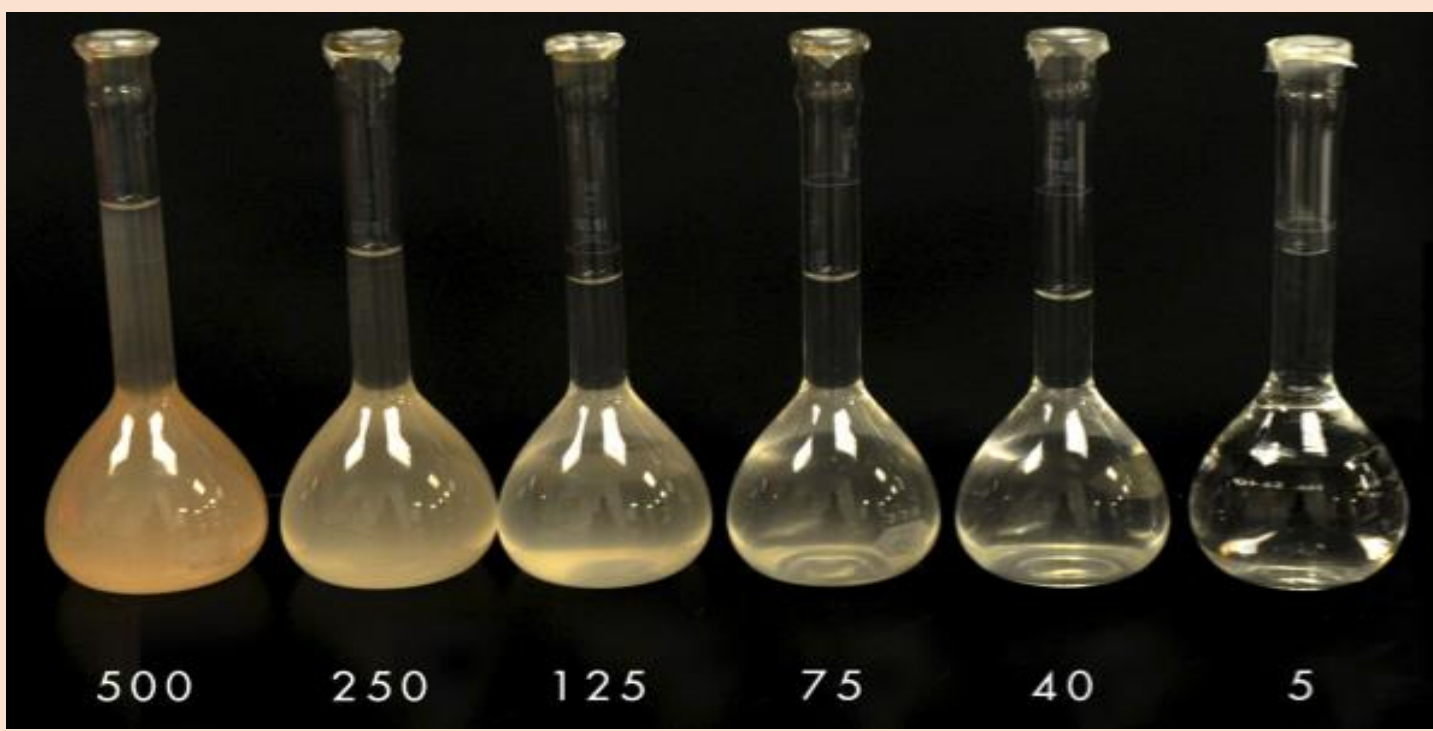


Figure 1: Scale of water clarity. A visual scale of different levels water turbidity/clarity.

### Specific Aim

- This study examines how water clarity affects the microbial diversity in Longwood Campus Pond and Lancer Park Pond.
- We hypothesized, based on previous secchi measurements for both ponds, that the average count and diversity of Longwood Campus Pond would be greater.



Figure 2: Sample collection sites. Longwood Campus Pond (left) and Lancer Park Pond (right).

### Methods

Lake water collection

Isolation and culture

16s Ribosomal RNA Amplification through PCR

Clean-up and Gel Electrophoresis

Sequence Analysis and Identification through BLAST sequencing

### References

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- Xu, Xuan; Huang, Xiaolong; Zhang, Yunlin; Yu, Dan. 2018. "Long-Term Changes in Water Clarity in Lake Liangzi Determined by Remote Sensing" *Remote Sensing* 10, no. 9 (2018).
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Water Clarity Image Source: Marine Geology Physics. 2021. Nephelometer. <https://www.marinegeophysics.com.au/nephelometer/>  
Special thanks to Dr. Amorette Barber for providing all required materials for this experiment.

### Results

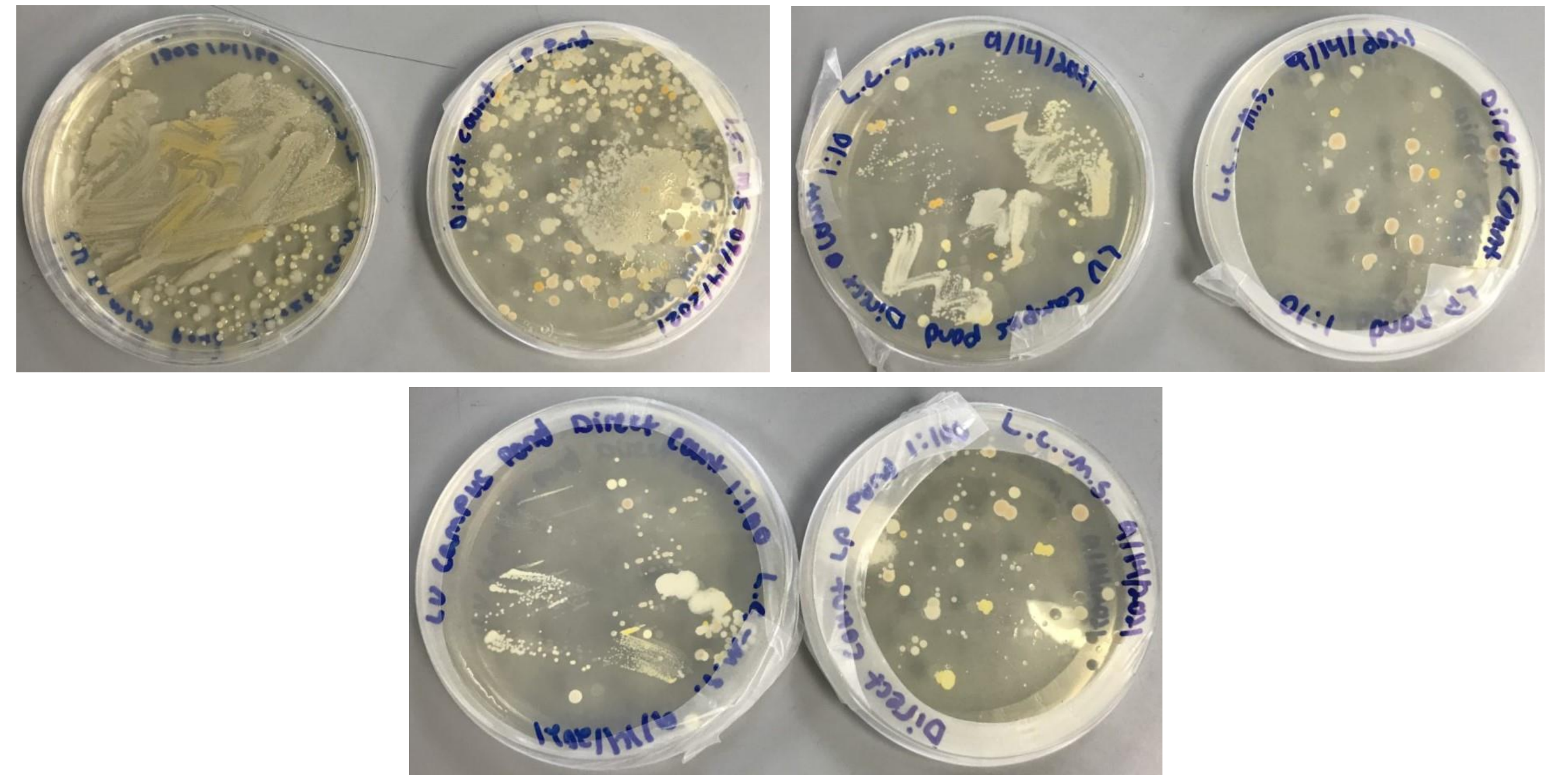


Figure 3A, B, C: Comparison of cultured bacterial colony plates. 2A. Direct Count "1:100" plates for both ponds. 2B. Direct Count "1:10" plates for both ponds. 2C. Direct Count "Full Count" plates for both ponds. All plates are shown upon first observation.

	Sample P	Sample Y	Sample O	Sample C
LUP 1-10	155	4	5	156
LUP 1-100	35	5	0	100
LP 1-10	24	2	1	29
LP 1-100	22	15	3	55

Table 1: Total plate counts. The distribution of each sample by plate. Each sample was labeled by color: Peach (P), Yellow (Y), Orange (O), and Cream (C).

**A**

**Pseudomonas frederiksbergensis strain JAJ28 16S ribosomal RNA, partial sequence**  
Sequence ID: [NR\\_028906.1](#) Length: 1503 Number of Matches: 1

Range 1: 66 to 1073 [GenBank](#) [Graphics](#) [Next Match](#) [Previous Match](#)

Score	Expect	Identities	Gaps	Strand
1631 bits(883)	0.0	992/1041(95%)	34/1041(3%)	Plus/Plus

```

Query 33  TGC-AGTCGAGCGGCAGCACGGGTACTTGTACCTGGTGGCGAGCGCGGACGGGTGAGTA 91
Sbjct 66  TGC AAGTCGAGCGGCAGCACGGGTACTTGTACCTGGTGGCGAGCGCGGACGGGTGAGTA 125
    
```

**B**

**Janthinobacterium rivuli strain FT68W 16S ribosomal RNA, partial sequence**  
Sequence ID: [NR\\_170540.1](#) Length: 1495 Number of Matches: 1

Range 1: 48 to 1146 [GenBank](#) [Graphics](#) [Next Match](#) [Previous Match](#)

Score	Expect	Identities	Gaps	Strand
1941 bits(1051)	0.0	1083/1102(98%)	7/1102(0%)	Plus/Plus

```

Query 6  ATGC-AGTCG-ACGGCAGCAGCGGAGCTTGTCTGGTGGCGAGTGGCGAACGGGTGAGTA 63
Sbjct 48  ATGCAAGTCGAAACGGCAGCAGCGGAGCTTGTCTGGTGGCGAGTGGCGAACGGGTGAGTA 106
    
```

**C**

**Pseudomonas lurida strain P 513/18 16S ribosomal RNA, partial sequence**  
Sequence ID: [NR\\_042199.1](#) Length: 1492 Number of Matches: 1

Range 1: 29 to 970 [GenBank](#) [Graphics](#) [Next Match](#) [Previous Match](#)

Score	Expect	Identities	Gaps	Strand
1607 bits(870)	0.0	928/955(97%)	15/955(1%)	Plus/Plus

```

Query 1  TGC-AGTCGAGCGGTAGAGAGAAGCTTGTCTTCTTGGAGACCGCGGACGGGTG-GTAAT 58
Sbjct 29  TGC AAGTCGAGCGGTAGAGAGAAGCTTGTCTTCTTGGAGACCGCGGACGGGTGAGTAAT 88
    
```

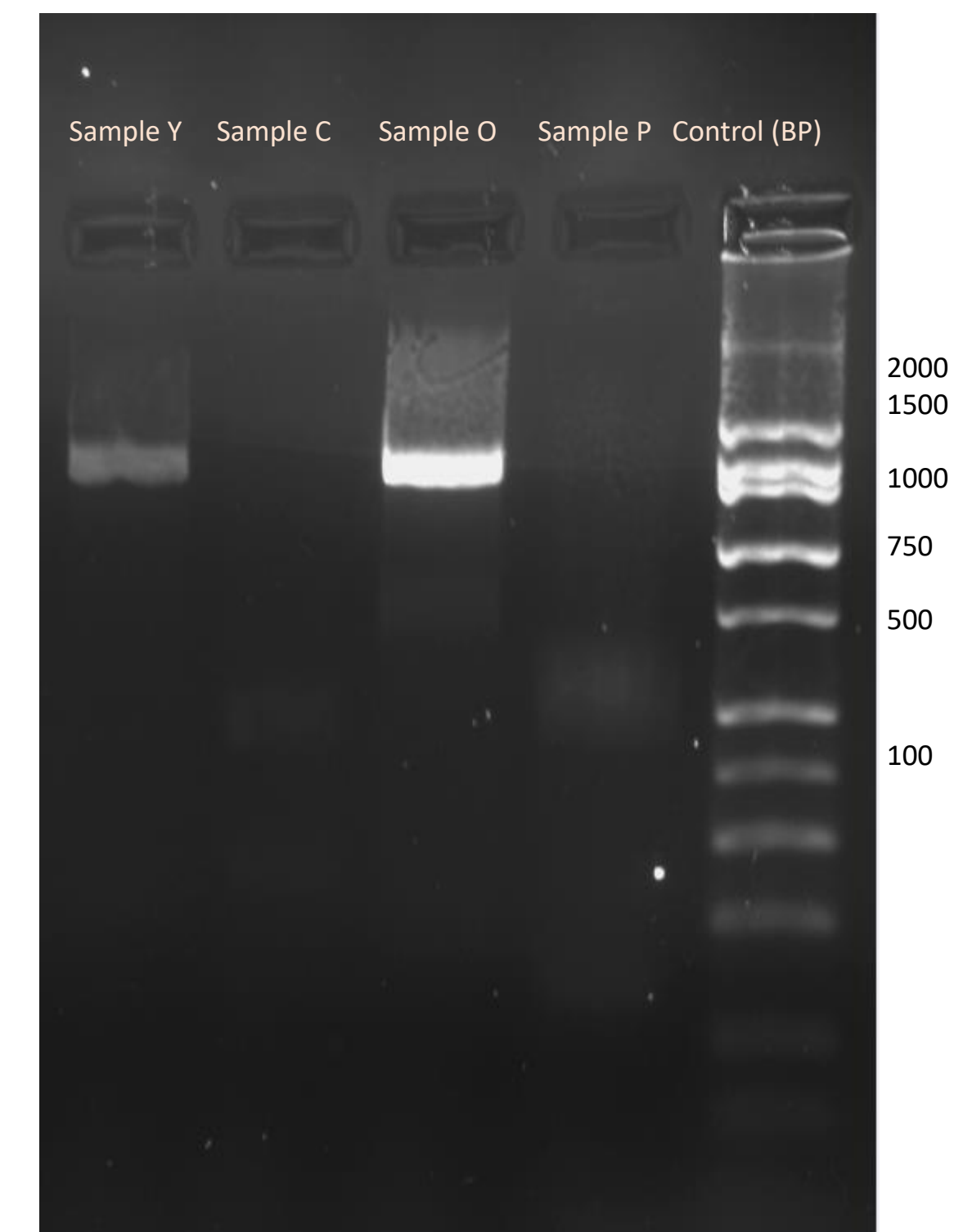


Figure 5: Gel Electrophoresis. Gel electrophoresis results for all four samples in comparison to the control.

Figure 4A, B, C: Top BLAST alignment sequences. The two sequences with the highest similarity percentage to Sequence O (3A), Sequence P (3B), and Sequence Y (3C). Sample C encountered issues in sequencing and was unable to be analyzed properly.

	Name (Scientific Name)	Query Cover	Identity Percent
Sample O	<i>Pseudomonas frederiksbergensis</i> (strain JAJ28)	89%	95.29%
Sample P	<i>Janthinobacterium rivuli</i> (strain FT68W)	99%	98%
Sample C	Unreadable	N/A	N/A
Sample Y	<i>Pseudomonas lurida</i> (strain P)	100%	97%

Table 2: Bacterium BLAST Identification. The closest matches for all bacterial colonies, chosen based off the comparison of the identity percent. Sample C was unreadable and could not be analyzed.

### Conclusions

- Based on the data presented, there is a negative correlation between water clarity and overall microbiome diversity.
- The importance of observing and preserving the ecological diversity of Longwood University, in addition Prince Edward County, can help contribute to the worldwide effort to study and preserve natural ecosystems in the face of a changing climate.
- Future possible studies on the biodiversity of the ponds' individual habitats include examinations of the implications of correlation between microbiome health and pollution, and examination of the habitats that depend on the ponds on university property.