Investigating Microbial Diversity Between Water and Gravel in Prince Edward County

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Background

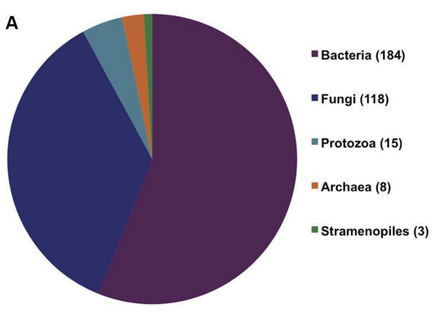
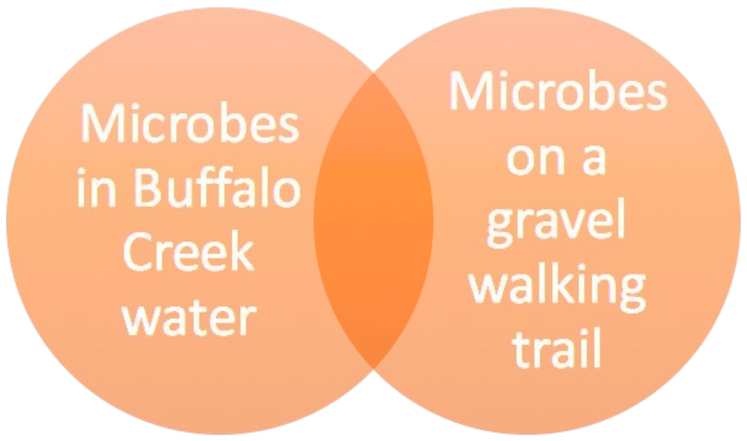


Figure 1. Overall diversity of organisms found in a stream.[4]

- Microbes are mainly composed of bacteria, archaea, algae, protozoa, fungi and small metazoa, representing the most abundant and diverse group across ecosystem.[1]
- Some microbes can be found in sediments 500-600 meters in a lake.[3]
- In river ecosystems, microbial communities are driven by many interacting factors and processes:
  - Temperature
  - Climate
  - Environmental factors[1]
- Numerous DNA- and lipid-based investigations of soil microbial communities have suggested high spatial and seasonal variability.[2]

Specific Aim



- The purpose of the experiment was to collect and grow microbes from two sampling spots from Lancer Park in Prince Edward County and compare them.
- It was thought that there would be interesting microbes in these locations due to the different environmental interactions they encounter every day.
- It is hypothesized that both sampled areas will have many microbes, though their classifications will be very diverse.

Methods

Figure 2. Buffalo Creek collection site.

Figure 3. Gravel walking trail collection site.

Figure 4. The gravel site tube for collection and growth of bacteria.

Results

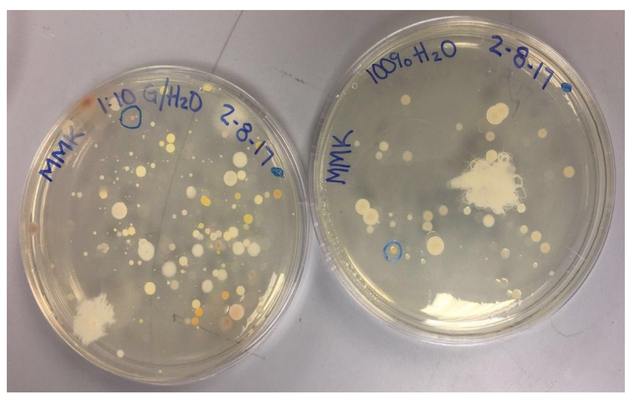


Figure 5. Colony growth on two chosen samples. The figure shows actual colonies that grew on two of the six plates. The plates shown in the figure are the 1:10 diluted gravel sample (right) and the 100% undiluted creek water sample.

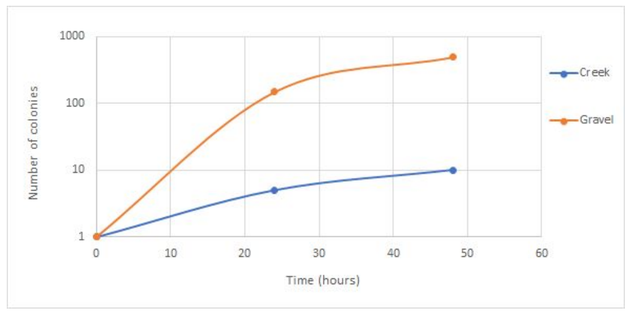


Figure 6. Progressive colony growth over a 48-hour period. The data shown represents the growth in the amount of colonies from the time samples were plated until 48-hours later. Data was collected 24-hours after the samples were plated and again at 48-hours after.

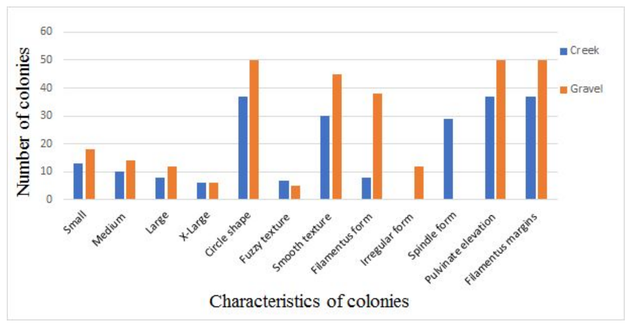


Figure 7. Characteristics of colonies. The data shown represents the differences in characteristics between the different samples. Data observed from the colonies includes sizes, shapes, textures, forms, and margins. Colonies were viewed from a 1:10 gravel sample and 100% creek water sample.

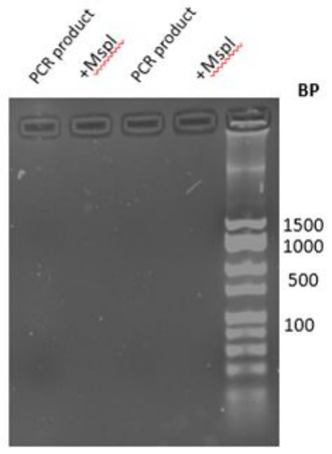


Figure 8. Gel electrophoresis for MspI and PCR product. The figure shows that our product was not pure enough to show any migration.

Bacterial alignment	Percent identity	Number of gaps
Janthinobacterium lividum strain	99	2
Janthinobacterium svalbardensis strain	98	6
Janthinobacterium agaricidamnosum strain	98	11
Herminiimonas glaciei strain	97	12
Herminiimonas saxobsidens strain	97	15

Figure 9. Top 5 bacterial alignments. The figure shows the top five bacterial alignments according to the percent identity and number of gaps in the DNA sequence. *Janithobacterium lividum strain* was the top matched bacteria with 99% identity and 2 gaps.

Conclusions

- The gravel site showed a higher growth rate than the creek site as well as more bacterial diversity according to the observed characteristics.
- The bacteria collected was *Janithobacterium lividum strain DSM 1522 16S Ribosomal.*
- It is found on the skin of amphibians and protects against fungal pathogens.
- Finding this bacterium could help to multiply it and therefore help the amphibians fight off the diseases
- Also to further study *Janthinobacterium lividum,* studies could be done to see the interaction of the *Janthinobacterium lividum* and other bacteria, and the interaction with the amphibians.
- Knowing more about the bacteria can help the massive decline in amphibians around Prince Edward county and ultimately around the world.

Acknowledgements

1. Liu, Lemian, Jun Yang, Xiaoqing Yu, Guangjie Chen, and Zheng Yu. 2013. "Patterns in the Composition of Microbial Communities from a Subtropical River: Effects of Environmental, Spatial and Temporal Factors." *PLoS One* 8 (11). doi:http://dx.doi.org/10.1371/journal.pone.0081232.
2. Yarwood, S., Brewer, E., Yarwood, R., Lajtha, K., & Myrold, D. (2013). Soil Microbe Active Community Composition and Capability of Responding to Litter Addition after 12 Years of No Inputs. *Applied and Environmental Microbiology*, *79*(4), 1385–1392.
3. Vuillemin A, Friese A, Alawi M, Henny C, Nomosatryo S, Wagner D, Crowe SA, Kallmeyer J, et al. 2016. Geomicrobiological Features of Ferruginous Sediments From Lake Towuti, Indonesia. [Web]; Frontiers in Microbiology 7:1007.
4. Zeglin, L. H. (2015, May 18). Stream microbial diversity in response to environmental changes: review and synthesis of existing research. *Frontiers in Microbiology.*
5. We would like to acknowledge Dr. Amorette Barber for all of her guidance and help along with all of the materials and protocols she provided throughout this research project.