



The Microbial Diversity in Wet Soil and Dry Soil at Buffalo Creek



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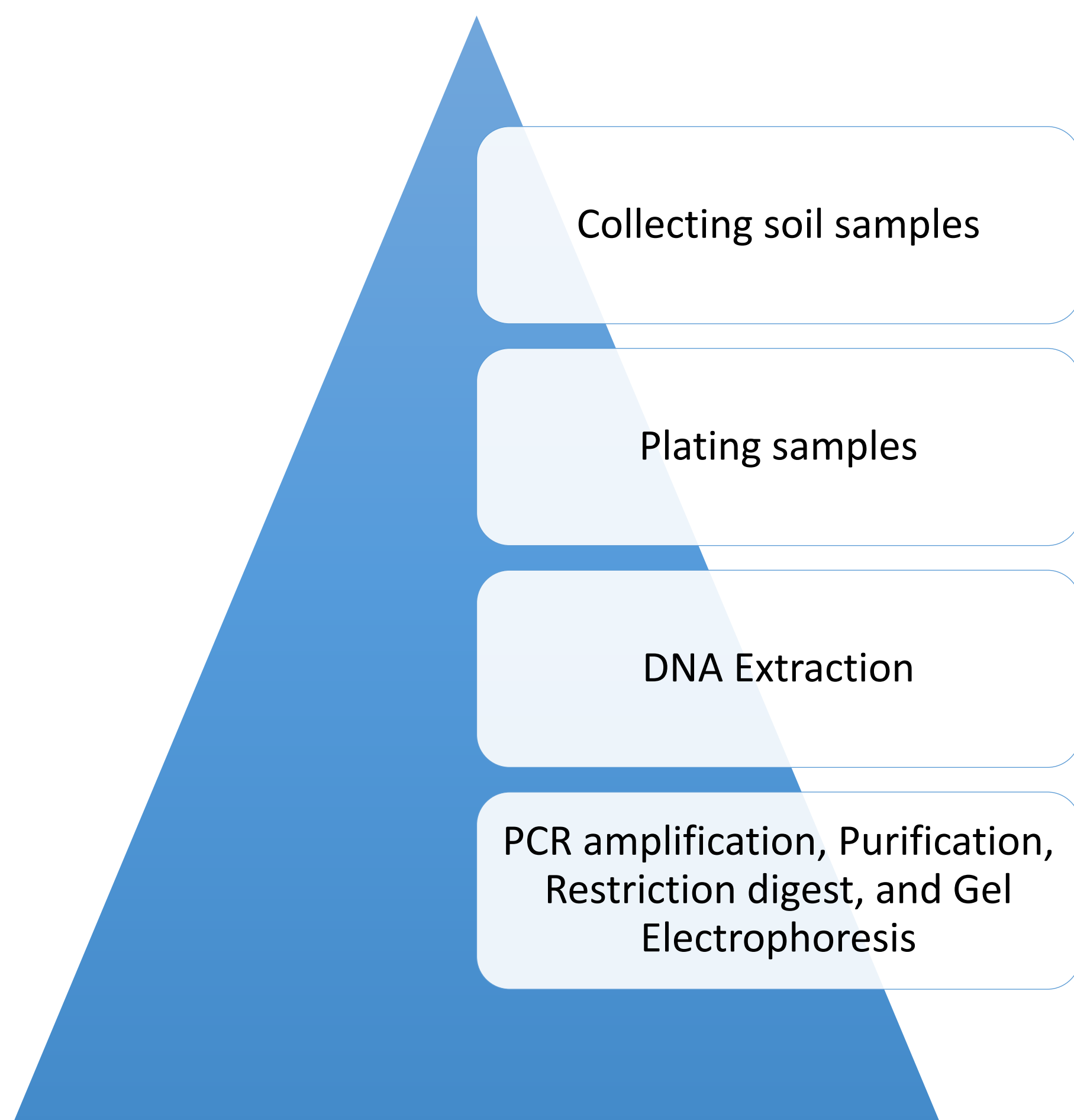
Background

In the article, Cross-biome metagenomic analyses of soil microbial communities and their functional attributes: The purpose of this study was to show how metagenomics can be used to understand microbial diversity across different terrestrial biomes.
In the article, Soil Microbial Community Responses to Multiple Experimental Climate Change Drivers, researcher found that changes in the climate can alter the overall abundance of the fungi and bacteria in the communities.
In the article, Responses of Soil Bacterial and Fungal Communities, researchers show how microbes react to extreme desiccation and rewetting. The researchers used three areas in California which had a larger amount of rain, and found that the "wet-up" caused an increase in the abundance of the bacteria, supporting the idea that the bacterial communities can be affected.

Specific Aim

Scientific Question: What is the microbial diversity between wet dirt versus the dry dirt at the creek?
Specific Aim: To sample and identify microbes that are living in Prince Edward County.
Hypothesis: The wet dirt would have more microbial diversity than the dry dirt.
Importance: Being able to identify the microbes will give us better understanding of the microbial community.

Methods



Data

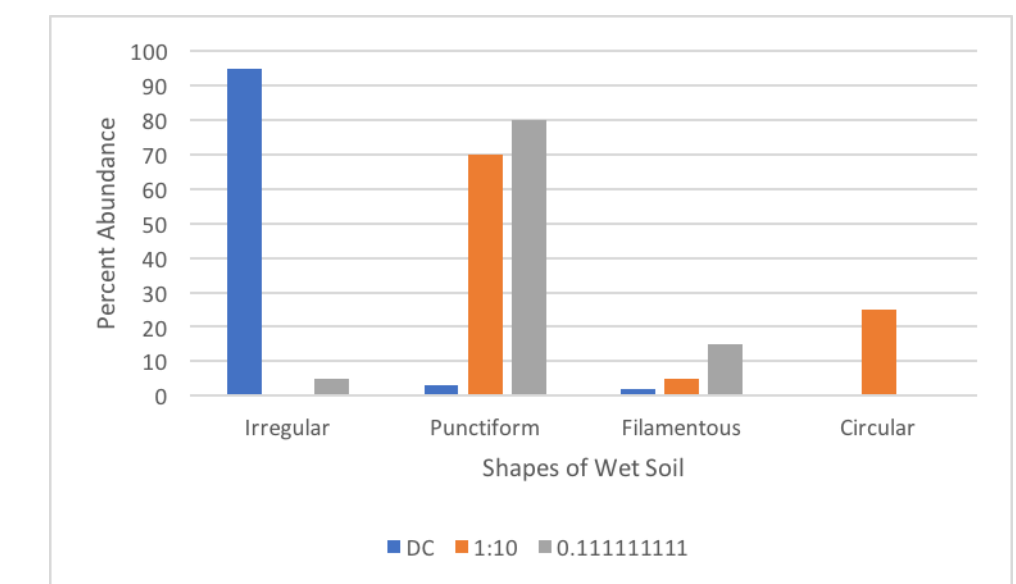
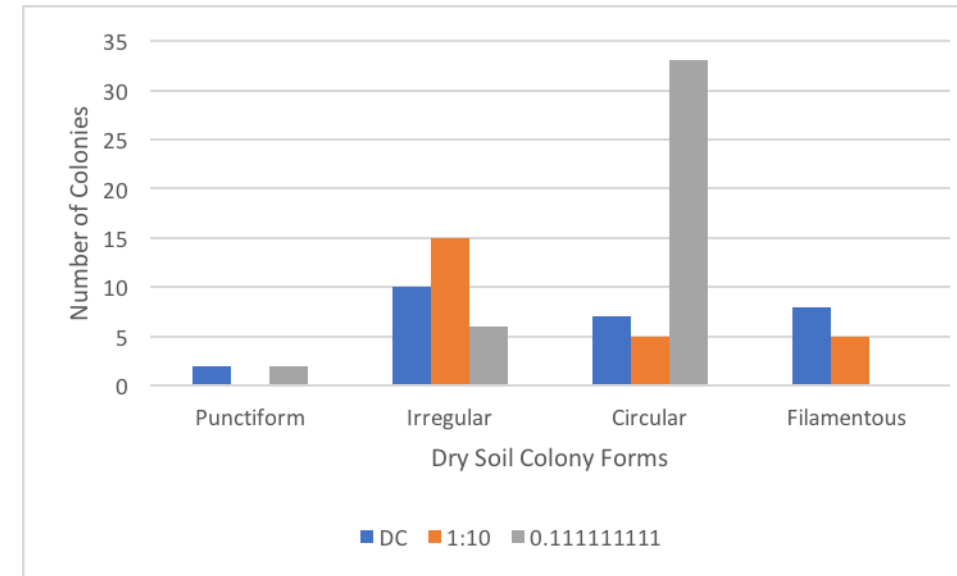


Figure 1. Number of colonies for dry soil. The data is shown for the different colony forms and plates. Irregular and circular formed colonies were the most common among all the plates. The largest difference is the amount of circular formed colonies in the 1:100 (.111111).

Figure 2. Percent of shaped colonies for wet soil. This data shows the percent abundance of the colony forms for the plates. The most common were irregular and punctiform shaped colonies. All of the plates had three different colony shapes



Figure 3. The plates shown is the number of colonies that were produced after being incubated for 2-3 days. The picture on the left is after 1 day of being incubated and the picture on the right is after 3 days. The plate allowed the colonies to rapidly produce and divide.

Conclusion

This experiment was conducted to compare the microbes in wet and dry soil from Buffalo Creek, located at the Environmental Center in Prince Edward County. The main concern was what is the microbial diversity in wet and dry soil surrounding Buffalo Creek? It was hypothesized that the wet soil would have a larger microbial difference than the dry soil because of the influence of the flowing water. The experiments hypothesis was rejected after the gel electrophoresis showed no results for the dry and wet soil. The site's DNA could not be sequenced because of an issue in the experiment and/or the sample collected was a yeast. Dr. Shanler ran the gel electrophoresis and managed to get a bacterium out of the wet soil sample, and which used for further analysis.
The genes and species of the bacteria is Pseudomonas koreensis Ps 9-14.

Citations

Fierer, N. (2012). Cross-biome metagenomic analyses of soil microbial communities and their functional attributes. PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA, 109(52), 21390-21395
Castro, H. F., Classen, A. T., Austin, E. E., & And, R. J. (2010). Soil Microbial Community Responses to Multiple Experimental Climate Change Drivers. American Society For Microbiology, 76(4), 999-1007
Barnard, R., Osborne, C. A., & Firestone, M. K. (2013). Responses of soil bacterial and fungal communities to extreme desiccation and rewetting. International Society for Microbial Ecology, 104(7), 2229-2241.