



Table 1. Top Ten Taxa for Deep Samples	Ta
Genus	
unclassified Subgroup_6	ur
unclassified 67-14	N
Solirubrobacter	ur
unclassified Xanthobacteraceae	ur
Subgroup_10	R
unclassified Gaiellales	ur
unclassified Bacteria	ur
Gaiella	BI
unclassified Micromonosporaceae	ur
Nocardioides	P

Overall, there is not a large difference in the microbial communities between the winter and summer samples, but what difference they had could be due to shifting physicochemical properties that might be underlying due to seasonal changes (Wu et al., 2016). There is a difference in the microbial communities between the deep and shallow plots due to differences in the depth of green roof plots, agricultural differences, and 4x4modular boxes vs. a continuous green roof covering. We are continuing to analyze these data to gain additional insights into the factors that may influence green roof microbiome communities. Having a more thorough understanding of these green roof microbiomes will give the urban soils community and city planners improved strategies for maximizing the benefits of green roofs with hopes of mitigating urban heat island effects.



DISCUSSION & CONCLUSION

• The Shannon's α Diversity Index was higher in the shallow green roof plot architecture, as well as the seasonal winter samples.

• The three dominant phyla for both the seasons and green roof plot architecture were Actinobacteria, Acidobacteria, and Proteobacteria, which are common of most soil types.

 There was a higher commonality with the genus of the soil between the summer and winter compared to the deep and shallow plots.

• A larger amount of dissimilarity exists between the deep and shallow plots compared to the summer and

 Soil microbial communities are slightly influenced by seasonality, but more so by green roof plot architecture and other factors such as agriculture.

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• Oliveira FS, Brestelli J, Cade S, et al.; MicrobiomeDB: A Systems Biology Platform for Integrating, Mining and Analyzing Microbiome Experiments. Nucleic Acids Research 2018.

Oliveros, J.C. (2007-2015) Venny. An interactive tool for comparing lists Venn's diagrams. https://bioinfogp.cnb.csic.es/tools/venny/index.html

Shafique, M., Xue, X., & Luo, X. (2020). An overview of carbon sequestration of green roofs in urban areas. Urban Forestry & Urban Greening, 47, 126515. https://doi.org/10.1016/j.ufug.2019.126515126515. Weber N., et al. (2018) Nephele: a cloud platform for simplified, standardized and reproducible microbiome data analysis 1411–1413 https://doi.org/10.1093/bioinformatics/btx617

• Wu, Z., Lin, W., Li, J., Liu, J., Li, B., Wu, L., Fang, C., & Zhang, Z. (2016). Effects of seasonal variations on soil microbial community composition of two typical zonal vegetation types in the Wuyi Mountains. Journal of Mountain Science, 13(6), 1056–1065. https://doi.org/10.1007/s11629-015-3599-2

• Venn Diagrams and Methodology Created in Lucidchart