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Towards the identification of the soil fungal microbiome community associated with Longleaf Pine

This project is part of a larger study looking at the restoration of the Longleaf Pine (LLP) ecosystem in certain Wildlife Management Areas (WMA) in Northwest Georgia. Our long-term aim is to look for potential associations between the aboveground and belowground community structures as the complex system of feedback mechanisms between the soil microbiome, the rhizosphere, and the plant communities is not yet understood.

Soil samples were collected from a total of six plots in the Sheffield WMA located in Paulding County. The samples were collected from north or south facing hillside plots except for in the savanna sites (an area actively being restored for longleaf pine), where samples were collected on east or west facing slopes. Soil was sampled at three locations per plot (at the center, and 10 m below and above the center of each plot). A total of 18 soil samples were collected, each in sterile tubes with screw tops. DNA was extracted from five subsamples per tube using a commercially available kit.

We hypothesized that the soil microbiome would differ significantly in north versus south facing areas, as well as between the savanna LLP and other plots due to the difference in aboveground plant communities. Analysis shows that the fungal phyla of Ascomycota and Basidiomycota are predominant in all plots of sampled. Basidiomycota shows its greatest predominance in the center of each plot. The most diverse results were found in the savanna plots showing a significant amount of unclassified fungi present as well as Zygomycota.

Key Words: Longleaf pine, fungal soil microbiome, restoration.