

Identification and Comparison of Arbuscular Mycorrhizal Fungi and Soil Microbiomes Between American Chestnuts and Surrounding Hardwoods

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Background/Questions/Methods

The introduction of the Chinese chestnut blight in 1904 decimated native American chestnut (*Castanea dentata* (Marshall) Borkh.) populations. In this study we aim to: 1) document the location of individual chestnuts in our vicinity; 2) document healthy versus blight infected individuals; 3) characterize putative differences in the soil microbiome between infected and non-infected individuals, as well as between chestnuts and hardwood neighbors. With this information we hope to provide new insights into mechanisms that may enhance blight and fungal resistance in American chestnuts through the understanding of the interactions between the trees and their surrounding soil microbiome.

Soil samples were collected 1 m north of the base of each of six of the chestnut trees located and 1m from the base of one hardwood tree within 5 m of each chestnut and aligned to one cardinal direction. Also, 2-3 root samples were collected approximately 5 m from the base of each individual chestnut. DNA was extracted from soil and root samples using extraction kits, replicated, confirmed using nanodrop dsDNA analysis and prepared for outsource sequencing.

Results/Conclusions

Thirty-two individual chestnut trees have been identified, with a subset of six mature trees used for this study. Only one is currently known to be infected with Chinese chestnut blight. We are in the process of DNA extraction from soil and root samples, after which samples will be sent off for analysis to examine the metagenomics of taxa present in the soil microbiome around the mature American chestnut trees. Thus far, nine samples from three different trees have successfully undergone extraction and have been analyzed for dsDNA content using a nanodrop.

Keywords

Microbiome

Arbuscular mycorrhizal fungi

Chinese chestnut blight

Castanea dentata

American chestnut

Metagenomics