

**AGRICULTURAL RESEARCH FOUNDATION
INTERIM REPORT
FUNDING CYCLE 2017 – 2019**

TITLE: Identifying plant genes associated with beneficial microbes

RESEARCH LEADER: Posy Busby, Assistant Professor, Oregon State University

COOPERATORS: Shawn Brown, Postdoctoral Associate, Oregon State University

EXECUTIVE SUMMARY: We are conducting a genome-wide association study (GWAS) to discover plant genes associated with fungal leaf endophyte community structure, and particular beneficial endophytes within communities. To date, we have collected and processed field samples from >1000 tree genotypes in two contrasting locations. Our preliminary analyses reveal that endophyte communities vary significantly among tree genotypes and environments; our GWAS, which should identify the particular genes underlying the genetic effect, is ongoing.

OBJECTIVES: Our primary objective is to conduct a GWAS study to determine the relative influence of plant genes and the environment on fungal community structure, and particular beneficial fungi within communities.

PROCEDURES: In October 2016, we collected leaf samples from 1084 replicated genotypes in a common garden in Corvallis OR, and from 500 genotypes in a common garden in Westport OR. We used DNA metabarcoding techniques to characterize fungal community composition, and the abundance of individual fungi in leaf samples. We are using a 28-million SNP library to associate fungal community structure with plant genotypic variation. Genes associated with community composition will be determined by mapping the locations of the SNPs identified with GWAS to the *P. trichocarpa* genome.

SIGNIFICANT ACCOMPLISHMENTS TO DATE: Sample collection and processing is complete. In our preliminary analysis of metabarcode data, fungal endophyte communities varied significantly among plant genotypes originating from different populations throughout the tree's geographic range. This was true for both common garden environments. However, only in the Corvallis garden were patterns correlated with the mean annual temperature of the regions from which the genotypes originated. This suggests that plant traits affecting community composition may do so differently in the two environments. On our going GWAS is poised to elucidate these patterns by identifying specific genes/SNPs associated with endophyte community composition in the contrasting gardens.

ADDITIONAL FUNDING RECEIVED DURING PROJECT TERM: N/A

FUTURE FUNDING POSSIBILITIES: DOE-USDA Plant Feedstocks Genomics for Bioenergy