

NSF RAPID

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Background

While endophytes can influence plant disease severity by several different mechanisms – including by producing antimicrobial compounds that antagonize pathogens, by parasitizing pathogens, and by modulating plant genetic resistance to pathogens (Busby et al. 2016a) – we know little about how plant genes and the microbiome interact to give rise to variation in disease severity. Answers to this question contribute to our basic understanding of plant-microbe interactions while addressing the global need to develop more sustainable disease management tools, and to promote ecosystem resilience in a changing climate (Vannier et al. 2019)

Study system

The recent introduction of a stem canker-causing pathogen in the Pacific Northwest, USA has created a unique opportunity to investigate how known plant resistance and susceptibility genes interact with the plant microbiome and modulate disease severity. The non-native, stem canker-causing pathogen *Sphaerulina musiva* was recently reported on *Populus trichocarpa* in a common garden planted with 1,075 re-sequenced *P. trichocarpa* trees (originating from wild populations) for which a 28 million SNP library exists (Evans et al. 2014). This is the first report of *S. musiva* on *P. trichocarpa* in the western USA (J. LeBoldus, unpub.); the pathogen's native host is the eastern cottonwood, *P. deltoides*. *P. trichocarpa* is a model tree in genomics and ecology, and its hybrids are grown worldwide for paper, pulp, and bioenergy. *S. musiva* is particularly devastating for poplar production because it degrades stem tissues.

Before the common garden was destroyed to eradicate *S. musiva*, we collected data on stem canker disease severity for the entire tree population (n=1,075) and sampled wood tissue for microbiome characterization for a subset of the population (n=430). Preliminary analysis of the disease severity scores indicates greater levels of resistance than have been previously reported for the same genotypes under controlled conditions (Muchero et al., 2018). Wood samples are being stored frozen until funds are available for processing and microbiome analysis.

Project summary

Our RAPID project will test the hypothesis that genetic resistance is modulated by variation in the composition of the stem microbiome, resulting in greater levels of resistance than would be expected based on the host genotype. We will specifically test whether loci previously associated with *S. musiva* resistance and susceptibility in a greenhouse study (Muchero et al. 2018) associate with disease severity in the common garden dataset. Additionally, we will characterize the wood microbiome of *P. trichocarpa* to associate community composition and the proportional abundance of individual

microbes with *S. musiva* disease phenotypes. Our ongoing work in the *P. trichocarpa* leaf microbiome has identified both fungal endophytes influencing foliar rust disease severity (Busby et al. 2016b), and candidate plant loci associated with the abundance of disease-modifying fungal endophytes (P. Busby, unpub.), indicating similar mechanisms may exist in woody tissues.

The specific aim of our RAPID is to identify microbiome characteristics (e.g., composition and abundance of individual microbes) under plant genetic control that modulate *S. musiva* disease phenotypes. To meet this aim we will: 1) conduct a genome wide association study (GWAS) to confirm plant SNPs/genes previously associated with stem canker disease severity, 2) characterize the fungal wood microbiome of *P. trichocarpa* using ITS metabarcoding and quantitative molecular approaches, and 3) conduct a GWAS of the stem microbiome. Results of this RAPID project will become key preliminary results in a full PBI proposal where we seek to explicitly test how plant allelic variation and the fungal wood microbiome individually and interactively contribute to disease resistance phenotypes.

References

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