

## **BESC - Genetic Consortia Mediating Resistance to Septoria Pathogen**

### **Disclosure Number**

201603685

### **Technology Summary**

Invasive microbes, causing diseases such as sudden oak death and chestnut blight, negatively impact forest health, affecting ecosystems and economies around the world. Approaches for combating these introduced microbes typically rely on programs that can take decades to identify and breed resistant plants. To demonstrate how this process can be accelerated to rapidly identify host genes associated with resistance to emerging pathogens, we challenged ca. 1000 re-sequenced *Populus trichocarpa* genotypes with *Sphaerulina musiva*, an invasive fungal pathogen in western North America. We used genome-wide association mapping to identify loci associated with resistance and susceptibility. Three loci associated with resistance to *S. musiva* (Potri.005G012100, Potri.003G028200, Potri.009G036300) were identified and predicted to encode putative membrane-bound receptors. One locus associated with susceptibility (Potri.005G018000) was identified and predicted to encode a putative D-mannose receptor-like kinase. We also employed whole transcriptome analysis to show that patterns of differential expression are consistent with roles in resistance and susceptibility. Lastly, we used a population-wide characterization of these loci and found a disproportionately higher number of detrimental mutations in the genes encoding resistance receptors compared to the highly conserved susceptibility locus. These results suggest that the continued spread of *S. musiva* in western North America represents a danger to the riparian ecosystems where *P. trichocarpa* is a keystone species. The approach used herein demonstrates the power of using population-wide re-sequencing of undomesticated, non-model plant species to rapidly identify loci that influence host-pathogen interactions that could be used to help mitigate long-term impacts of emerging diseases in native ecosystems.

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