

Discovery and characterization of disease resistance loci in poplar

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Project Goals

1. Identification of genomic loci that control response to two damaging poplar diseases, leaf spot and leaf rust. In field trials and controlled infection experiments, genome-wide scans will identify poplar loci underlying qualitative (allelic) and quantitative (indels) parental loci affecting disease susceptibility.

2. Characterization of transcriptional networks governing the response of poplar to leaf pathogens. We will characterize major QTLs through integration of transcriptome data with developmental responses. We will develop quantitative models of co-expression networks of poplar genes, which will enable hypotheses testing regarding molecular mechanisms.

3. Identification of genes whose manipulation could result in sustainable, long-term tolerance to the target pathogens. Candidate genes will be evaluated based on gene expression, dosage sensitivity, functional annotations, and correlations with disease-related processes in objective 2. Individual candidate genes will be functionally characterized by transgenic validation and/or genome editing.

Abstract

Pathogenic fungi that colonize poplar leaves and stems reduce yield and can cause failure of industrial bioenergy plantations. Despite extensive study of poplar pathosystems, no durable resistance genes have been characterized from poplar, underscoring that new approaches are needed. With funding from the USDA/DOE Plant Feedstocks Genomics for Bioenergy program, we have developed an efficient functional genomics resource based on gene dosage changes in a *Populus nigra* x *P. deltoides* elite biomass hybrid. In this ~800 clone population, gene dosage variation is created by large-scale deletions and insertions that tile each chromosome. In clonally replicated field trials, we have successfully mapped dosage QTLs for key bioenergy traits, and recently have identified preliminary QTL influencing susceptibility of poplar to pathogens, demonstrating the utility of this resource for identifying loci affecting disease responses. The goal of this proposal is to exploit this unique resource to enable genomic-guided strategies for achieving durable resistance.

The approach is to first perform genome-wide scans using the previously developed poplar functional genomics resource to identify dosage-sensitive loci associated with disease susceptibility. Using field trials in California and Missouri, we will survey the most important diseases of poplar: leaf rust, leaf spot and stem canker. Together, these diseases not only cause extensive reductions in yields, but also severely limit the geographic range of key, high-yielding poplar interspecific hybrids. Greenhouse-based controlled inoculation screens will be performed for leaf rust isolates using the same genotypes. In addition to identification of QTL, correlations will be determined among disease QTL and previously

identified bioenergy QTL and traits for the same genotypes. Next, time-course analysis of gene expression during progression of disease symptoms will be performed for selected genotypes, and used to develop predictive models of transcriptional networks underlying disease susceptibility. A final set of experiments will use the information from the previous experiments to identify candidate genes for functional analysis by manipulation using CRISPR-Cas9. Such dosage-sensitive candidate genes with significant effects on disease susceptibility phenotypes could then be manipulated in breeding programs through selection of germplasm with naturally-occurring allelic variation or indels/copy number variation covering susceptibility or resistance loci.

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