

Discovery and characterization of disease resistance loci using a unique gene copy number variant population

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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, the genetic control of poplar resistance to pathogens is still poorly understood, underscoring the need for new approaches. We developed a unique functional genomics resource based on gene dosage variation in an elite biomass poplar hybrid. We pollinated *Populus deltoides* with gamma irradiated *P. nigra* pollen to produce ~ 800 F1 seedlings. These contain large-scale deletions and insertions that together tile each chromosome multiple times. Under natural infection in the field, as well as under controlled inoculations in the greenhouse, we observed a wide variation in disease resistance within our population and were able to identify dosage QTLs influencing resistance of poplar to some of its most important fungal diseases: leaf rust and leaf spot (*Melampsora* sp., *Alternaria* sp.). 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 aim to identify candidate genes for functional analysis by manipulation using CRISPR-Cas9. Such dosage-sensitive candidate genes with significant effects on disease resistance phenotypes could be exploited in breeding programs through the selection of germplasm with naturally-occurring allelic variation or indels/copy number variation covering resistance loci.