

## USING A POPLAR HYBRID TO EXPLORE HOST PLANT GENETIC CONTROL OF ASSOCIATING INSECT AND FUNGAL SPECIES

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Community genetics is the study of the influence of host genotype on associating arthropods, fungi, pathogens, and predators, such that related individuals support similar, heritable communities. Understanding how shifts in the genes of a population contribute to ecosystem function effectively links ecology and evolutionary biology. Observing these interactions allows genes associated with pest resistance and susceptibility to be identified within a host plant. This in turn could aid in the cross design of commercially valuable biofuel crops such as those in the Salicaceae family, which include poplar and willow species. To test the extent to which genes of *Populus* have extended phenotypes on arthropod communities, surveys were conducted in a *P. trichocarpa* × *P. deltoides* pseudo-backcross plantation. Trees were observed for the arthropods *Pemphigus populitransversus*, *Mordwilkoja vagabunda*, *Phyllocolpa bozemani*, and *Phyllocnistis populiella*. Individuals were also scored for *Melampsora* leaf rust, *Septoria musiva* leaf spot, and *Septoria musiva* stem canker fungal infections. Broad-sense heritability ( $H^2_c$ ) revealed a significant genetic factor controlling both insect and fungal pests. Several quantitative trait loci (QTL) intervals were discovered to be associated with these biotic stressors that contain numerous candidate genes which mediate their interactions. There was also an elevated number of tandem duplications and chromosome rearrangements in the intervals for several biotic phenotypes. Future work will be aimed at understanding the contribution of structural variation in mediating biotic interactions.

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