

Dissecting Genetic Resistance to Willow Leaf Rust (*Melampsora* spp.) in Shrub Willow (*Salix* spp.)

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<http://willow.cals.cornell.edu>

Project Goals: The goals of this project are to characterize the genetic diversity of the willow rust pathogen, *Melampsora* spp., and utilize the diversity of *Salix* to identify genes for rust resistance that can be exploited in breeding improved cultivars for bioenergy.

Willow leaf rust (*Melampsora* spp.) is a devastating plant pathogen that can cause considerable premature defoliation in shrub willow (*Salix* spp.) grown as a biomass energy crop, significantly reducing yield. In order to map resistance to willow leaf rust and other traits of interest including yield components, insect resistance, and physiological traits, we have developed three mapping resources, a small association panel planted on three sites, an F₂ mapping population of *Salix purpurea* with 485 progeny planted in Geneva, NY, and eight species hybrid F₁ mapping populations with a common parent of *S. purpurea*. Each of these F₁ hybrid families has either *S. purpurea* 94006 as the female parent (the reference genome) or *S. purpurea* 94001 as the male parent crossed to individuals of *S. suchowensis*, *S. viminalis*, *S. udensis*, *S. integra*, *S. koriyanagi*, or *S. alberti*. These mapping populations were planted in adjacent field trials in Geneva, NY with 88 to 150 individuals in each family in four randomized complete blocks. Each individual was genotyped by genotyping-by-sequencing and genetic maps developed from segregating SNP markers. During the summers of 2015 and 2017, ratings were collected for damage from imported willow leaf beetle (*Plagioderia versicolora*), potato leafhopper (*Empoasca fabae*), and willow leaf rust severity, as well as stem diameters, height, and specific leaf area measurements. Characterization of QTL controlling these traits will be presented. We have also collected *Melampsora* isolates from across the Northeast and have used GBS to characterize the diversity of the rust population. PacBio genome sequencing of one *Melampsora americana* isolate is underway at JGI.

Funding statement.

This material is based upon work that is supported by the National Institute of Food and Agriculture, U.S. Department of Agriculture, under award number 2015-67009-23957.