

From Genomes to Ecosystem health: using computational biology and functional genomics to battle exotic pathogens



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Background

- *Populus* is a keystone species within many ecosystems occurring across most of North America in native populations that are hundreds- to thousands-of-years old.
- *Populus* is ecologically and commercially important as a bioenergy feedstock but can be susceptible to pathogens such as *Septoria*.
- *Septoria* causes stem canker and leaf spot diseases that limit the survival and production of poplar as a biofuels feedstock.

Science

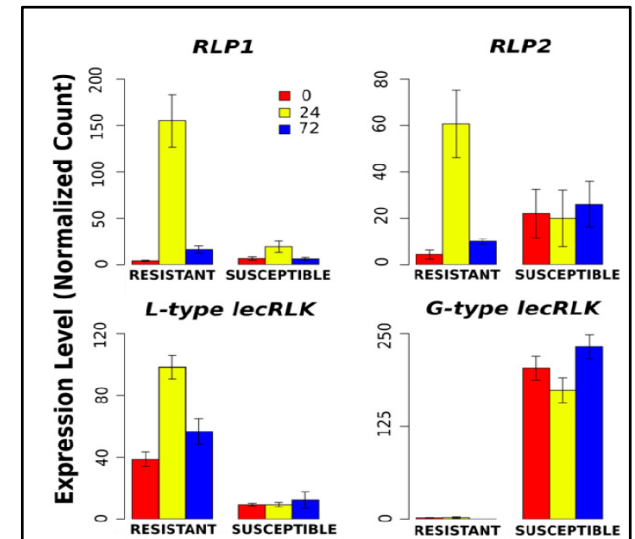
- *Populus* genes that render resistance to *Septoria* were discovered in less than 3 years using an approach that combined:
 1. Robust high-throughput phenotyping of >3,000 plants (OSU)
 2. Deep genome resequencing (>1,000) coupled with transcriptomics (JGI)
 3. Data-driven CompBio (28M SNPs) and rapid molecular validation (ORNL)
 4. Protein expression of receptor kinases and ligand binding assays (UGA)

Significance

- The described approach demonstrates the power of population-wide re-sequencing of an undomesticated plant species to identify genes that can mitigate emerging diseases in native ecosystems. This work leads to the breeding and engineering of poplar genotypes that are resistant to *Septoria*.



Septoria stem cankers under field conditions and greenhouse-based phenotyping showing resistant and susceptible genotypes.



Transcriptional response of four candidate receptor kinases in response to *Septoria* inoculation in resistant and susceptible genotypes.