

Towards durable resistance to *Septoria* stem canker and leaf spot: a molecular understanding of resistance.

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Fuels developed from lignocellulosic biomass offer a potential renewable and clean alternative to conventional fossil-based energy sources. *Populus* is one of DOE's "flagship" plant species that is of special interest as a biofuel feedstock. *Septoria* canker is the major limiting factor in the use of *Populus* as a biomass feedstock in the central and eastern United States. An effective disease resistance-breeding program has not been developed due to an absence of information on the genetic basis of resistance. To identify resistance alleles, we combine the re-sequenced *P. trichocarpa* genome-wide association population with our robust disease resistance phenotyping platform. This enables us to: (1) identify and analyze alleles conferring resistance to *Septoria* stem canker and/or leaf-spot disease; (2) use a combination of stable and transient expression systems in *Populus* and *Nicotiana* to validate the function of the encoded proteins of the identified genes; and (3) field test resistant genotypes in order to validate their performance under changing environmental conditions.

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