

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

Jared M. LeBoldus (your email: jared.leboldus@science.oregonstate.edu), Susanna Keriö¹,

Wellington Muchero², Jin-Gui Chen³, and Steven Strauss⁴.

¹ Department of Botany and Plant Pathology, , Oregon State University, Corvallis, OR, USA.

² Forest Engineering, Resources and Management Department, Oregon State University, Corvallis, OR, USA.

³ Biosciences Division, Oak Ridge National Laboratory, Oak Ridge, TN, USA.

⁴ Department of Ecosystems and Society, Oregon State University, Corvallis, OR, USA.

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 has enabled 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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