# IDENTIFYING AND VALIDATING NECROTROPHIC EFFECTORS IN THE *POPULUS TRICHOCARPA-SPHAERULINA MUSIVA* PATHOSYSTEM

Kelsey L. Søndreli[1], Robert Brueggeman[2], Jonathan Richards[2],
Timothy Friesen[3], and Jared M. LeBoldus[1,4]

*Sphaerulina musiv*a causes stem cankers on *Populus* species in North America. The literature indicates that the use of resistance genotypes is the best approach to manage *S. musiva*, so it is imperative that we know more about the mechanisms that underlie resistance/susceptibility in the *S. musiva–Populus* pathosystem. RNA-seq was used to identify potential *S. musiva* necrotrophic effectors involved in stem canker formation at two and three weeks post-inoculation. Approximately 20 percent of the total reads were aligned to the *S. musiva* reference genome with the remaining reads aligning to the reference genome of *Populus trichocarpa*. There were 70 genes identified at two weeks post-inoculation and 110 genes identified at three weeks post-inoculation differentially expressed between the inoculated trees and the control. The candidate genes were selected for transformation into *Pichia pastoris*, subsequent protein expression, and infiltration of the proteins into *P. trichocarpa* leaves. This study provides the first evidence that low coverage RNA-seq can be used to identify putative necrotrophic effectors facilitating the study of host-pathogen interactions in the *P. trichocarpa*-*S. musiva* pathosystem.

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[1] Department of Botany and Plant Pathology, Oregon State University, Corvallis, OR 97331, (Kelsey.Sondreli@oregonstate.edu).
[2] Department of Plant Pathology, North Dakota State University, Fargo, ND 58102.
[3] Red River Valley Agricultural Research Center, Cereal Crops Research Unit, U.S. Department of Agriculture–Agricultural Research Service, Fargo, ND 58102.
[4] Forest Engineering Resources and Management Department, Oregon State University, Corvallis, OR 97331.

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