

VIRULENCE OF *SPHAERULINA MUSIVA* ISOLATES DETERMINED BY GENOME-WIDE ASSOCIATION MAPPING, HOST INFECTION, AND COLONIZATION

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The ascomycete *Sphaerulina musiva* causes Septoria leaf spot and stem canker of *Populus*, and is considered to be the most serious pathogen affecting poplar cultivation in North America. Knowledge of *S. musiva* virulence factors can promote the development of efficient control strategies against the disease, and improve the accuracy of risk analysis. In this project, we characterized the virulence of 120 *S. musiva* isolates from geographically distinct populations in a non-wounding spray inoculation experiment. The isolates were sequenced (Illumina 150bp Paired End HiSeq 3000) and used for genome-wide association mapping. In a second set of experiments, we selected a subset of six *S. musiva* isolates with either high or low virulence, which were used to inoculate two genotypes (GW9823 and GW11026) of black cottonwood (*Populus trichocarpa*). The degree of host colonization was estimated by qPCR, and qualitative differences in host colonization were analyzed by microscopic inspection. We will report the genes associated with the observed virulence differences, and discuss the significance of the results from the second set of experiments in the context of disease resistance breeding.

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Citation for proceedings: Nelson, C. Dana; Koch, Jennifer L.; Snieszko, Richard A., eds. 2020. Proceedings of the Sixth International Workshop on the Genetics of Host-Parasite Interactions in Forestry—Tree Resistance to Insects and Diseases: Putting Promise into Practice. e-Gen. Tech. Rep. SRS-252. Asheville, NC: U.S. Department of Agriculture Forest Service, Southern Research Station. 170 p.