

NATWICK, MARI B.\*<sup>1,2</sup>, NATHAN A. WYATT<sup>1</sup>, GARY A. SECOR<sup>2</sup>, and MELVIN D. BOLTON<sup>1</sup>, <sup>1</sup>United States Department of Agriculture, Northern Crop Science Laboratory, Fargo, North Dakota, USA, <sup>2</sup>North Dakota State University, Department of Plant Pathology, Fargo, North Dakota, USA.

**Identification and characterization of *Cercospora beticola* effector candidates associated with adaptation to the sugarbeet resistance gene BvCr4.**

*Cercospora* leaf spot (CLS), caused by the fungal pathogen *Cercospora beticola*, is the most economically important disease of sugarbeet. If left unmanaged, CLS can significantly reduce crop yields and sugar content. Recently, growers have adopted the use of commercial varieties utilizing the resistance gene *BvCr4* (CR+) to help manage CLS. Unfortunately, populations of *C. beticola* that are capable of overcoming *BvCr4* have been identified worldwide. Although a genome wide association study (GWAS) conducted on European populations of *C. beticola* identified a single gene (*AvrCr4*) associated with resistance mediated by *BvCR4*, there was no subsequent functional validation of this gene. Moreover, it is not clear if American *C. beticola* populations also utilize this gene to overcome the *BvCr4* resistance mechanism. To gain an understanding of how American *C. beticola* strains have adapted to *BvCr4*, we conducted a population genomic analysis with populations collected from sugarbeet plants throughout American growing regions with and without *BvCr4*. Through this analysis, we identified 14 fungal genes putatively associated with the ability to overcome *BvCr4*. We have developed *C. beticola* mutants lacking these candidate genes to functionally validate them. Characterization of these mutants will be presented. This research aims to elucidate the interaction between *C. beticola* and the CLS-resistance gene, *BvCR4*, in order to broaden understanding of the *BvCr4* resistance phenotype and predict durability of similar resistance genes. In addition, this knowledge will allow for the design of molecular-based assays to identify *BvCr4*-resistant strains.