

JASWAL, RAJDEEP*^{1,2}, LEONARD BARNABAS EBINEZER^{1,2}, GARY SECOR², MELVIN D. BOLTON^{1,2} and NATHAN WYATT^{1,2}, ¹United States Department of Agriculture – Agricultural Research Service, Sugarbeet and Potato Research Unit, Edward T. Schaffer Agricultural Research Center, 1307 18th Street North, Fargo, ND 58102, ²North Dakota State University, Department of Plant Pathology, Walster Hall 306, Fargo, ND 58102.

Decoding the biotrophic phase of *Cercospora beticola* through functional characterization of effectors.

Cercospora beticola, causal agent of Cercospora leaf spot (CLS), is the most prominent foliar disease of sugarbeet. The infection caused by *C. beticola* can significantly deteriorate sugarbeet foliar tissue leading to severe yield losses. Despite being a pathogen of high economic importance, very limited information is available regarding the molecular mechanisms deployed by *C. beticola* to manipulate the sugarbeet host. Recently, we sequenced a large globally diverse population of *C. beticola* to identify effector genes that are conserved among the species and leveraged RNAseq data to select potential effectors that were transcriptionally active during the biotrophic phase of *C. beticola* infection. Candidate effectors were transiently expressed in *Nicotiana benthamiana* using to screen for cell death inducing activity. Majority of the selected candidate did not induce any cell death inducing phenotype in *N. benthamiana* leaves however four effectors demonstrated cell death suppression activity. Effectors suppressing cell death were also able to suppress the production of reactive oxygen species (ROS) induced due to host defense pathways activation. Further, *In planta* localization studies of fluorescently tagged candidates highlighted chloroplast to their potential target site. The current study provides a framework for understanding the function of *C. beticola* biotrophic effectors and their role in plant defense manipulation.