

BOLTON, MELVIN D.^{1,2*}, SPANNER, REBECCA² AND SECOR, GARY A.², ¹USDA-ARS, Red River Valley Agricultural Research Center, Fargo, ND, USA; ²Department of Plant Pathology, North Dakota State University, Fargo, ND, USA. **Use of genome-wide association to identify mutations involved with DMI-resistance in *Cercospora beticola*.**

Management of *Cercospora* leaf spot relies on the application of fungicides. A widely-used class of fungicides is the sterol demethylation-inhibiting (DMI) fungicides that inhibit the cytochrome P450 14 α -demethylase CYP51. CYP51 is an enzyme that catalyzes a key step in fungal ergosterol biosynthesis, which is required for fungal survival. Quantitative resistance to DMIs has emerged in *C. beticola* populations due to their widespread use. To identify mutations responsible for DMI resistance, a genome-wide association study was undertaken using 200 isolates harvested from sugarbeet fields in the Red River Valley of ND and MN. Approximately half of the isolates were DMI-sensitive (EC_{50} value <1) while the other half were DMI-resistant (EC_{50} value \geq 1). After Illumina whole genome resequencing, genome wide association identified three loci highly correlated with DMI-resistance. The results of this study will be reported.