HANSON, LINDA E.*[1], GARY D. FRANC[2], and LEE PANELLA[1], [1]USDA-ARS, SBRU, 1701 Centre Avenue, Fort Collins, CO 80526 and [2]University of Wyoming, Laramie, WY. **Characterization of genes associated with potential for fungicide resistance in *Cercospora beticola*.**

ABSTRACT

The recent development and widespread use of fungicides with highly specific modes of action has greatly increased the potential for development of fungicide insensitivity in the pathogen population. Disease control failures have been reported with pathogens such as *Cercospora beticola* in sugar beet, and powdery mildews and leaf spots in other crops due to reduced fungicide sensitivity. Determining the modes of action of fungicides has enabled elucidating specific genetic mechanisms for resistance to several classes of fungicides, including classes used for Cercospora leaf spot control such as benzimiazoles, strobilurins, and sterol demethylase inhibitors. There have been ongoing efforts to determine the baseline sensitivity of sugar beet pathogens such as *C. beticola* to important fungicides. As the genetics of resistance to many of these fungicide classes is determined, there is the potential to determine the characteristics of important target genes in the population to obtain a better idea of some of the inherent risks for fungicide resistance development. Information on these gene sequences also can be used to develop improved and rapid screening methods. Information on important target genes for several classes of fungicides that are used or have been used for Cercospora leaf spot control is being collected. Sequence data for the *C. beticola* β-tubulin gene indicated a single resistance mutation in all isolates examined to date, from different locations and different years. This mutation has been demonstrated in other fungi to confer a high level of resistance to benzimidazole fungicides and to show little evidence of fitness costs to the fungus. In addition, this mutation is predicted to add a new restriction site for a specific restriction enzyme. Because this enzyme was found to function in the PCR buffer system used, thus PCR-RFLP is a potential mechanism for rapid resistance detection. In addition, allele specific PCR primers are being developed to test for the potential to use these in resistance detection

As well the β-tubulin gene, PCR amplification is being done for other genes that code for known fungicide targets. A portion of the cytochrome *b* gene, which encodes a target for strobilurins, has been amplified from *C. beticola* and analysis will be initiated. In addition, degenerate primers are being designed for other important target genes. Analysis of these genes can provide information about variability in the population and can allow rapid screening for changes in the population associated with changes in fungicide sensitivity. This information can be used to determine the efficacy of fungicide resistance management for this major sugar beet pathogen.