STRAUSBAUGH, CARL A.[1*], IMAD A. EUJAYL[1], LEE W. PANELLA[2] and LINDA E. HANSON[3], [1]USDA-ARS, NWISRL, 3793 North 3600 East, Kimberly, ID 83341, [2]USDA-ARS, 1701 Center Avenue, Ft. Collins, CO 80526 and [3]USDA-ARS, 494 PSSB, Michigan State University, East Lansing, MI 48824. **Genetic diversity and pathogenicity of *Rhizoctonia* on sugarbeet**.

ABSTRACT

Rhizoctonia root rot causes serious losses on sugarbeet worldwide. In order to help explain why Rhizoctonia root rot resistant/tolerant sugarbeet cultivars have not performed well in some areas of the Intermountain West (IMW), a survey was conducted. In the IMW from 2004 to 2006, 94 *Rhizoctonia solani* field isolates were collected from sugarbeet roots. These field isolates were compared with 19 tester strains for genetic diversity based on sequencing of the ITS-5.8*s* rDNA region. Greenhouse pathogenicity tests on sugarbeet and silage corn were conducted and plant damage was assessed using a randomized complete block design with at least four replications. The majority (91%) of the isolates had identity with the AG-2-2 IIIB or AG-4 subgroups. Based on the phylogenetic analysis, 23 clades were evident of which 9 had isolates that could cause root rot in sugarbeet. Seven (6 AG-2-2 IIIB and 1 AG-4 HG-II) of 18 isolates tested could attack both sugarbeet and corn, with two of the six AG-2-2 IIIB isolates causing less corn root rot than the others. To reduce Rhizoctonia root rot on sugarbeet and corn, close crop rotations and the isolates utilized for selecting host resistance need further consideration.

Objectives:

To aid breeding efforts and the development of management options for Rhizoctonia root rot, a survey of *Rhizoctonia solani* isolates from sugarbeet in the western U.S. were compared for pathogenicity on sugarbeet and corn and genetic diversity.

Procedures:

Sugarbeet roots symptomatic for Rhizoctonia root rot were collected from commercial fields and piling grounds in the Intermountain West region of the U.S. from 2004 to 2006. Using standard microbiological techniques, 94 isolates were obtained and identified using a light microscope. The 94 field isolates were compared with 19 tester strains and a noninoculated check in the greenhouse on the root rot susceptible cultivar, Monohikari. The experimental design was a randomized complete block design with four replications. The experiment was repeated once. The plants were inoculated at the eight-leaf growth stage by placing an infested kernel next to the root. Four weeks after inoculation, percent foliar discoloration was determined. The top fresh weight was recorded and the roots were measured at the crown and then bisected through the infected area to visually estimate the percentage of root tissue rotted. A disease index based on these four variables was established. Isolations from the rotted tissue were conducted to confirm Koch's postulates. A similar study was conducted on corn with 18 *R. solani* isolates and a noninoculated check in the greenhouse on the Pioneer silage corn hybrid, PHI 1. The plants were inoculated by placing an infested barley kernel next to the seed at the one- to two-leaf growth stage. Three weeks after inoculation at the five- to six-leaf growth stage,

the top fresh weight was determined and the roots were visually evaluated for root lesion number and area. Isolations from the rotted tissue were conducted to confirm Koch's postulates. DNA was isolated from all 113 isolates/strains using DNeasy Plant Mini Kit. Polymerase chain reactions were performed with the ITS1 and ITS4 primers. Amplicons were sequenced and compared to GenBank accessions to confirm species identity and anastomosis grouping using BLASTn 2.2.17. Phylogenetic anaylsis was performed using PAUP 4. Maximum parsimony analysis was performed with the heuristic search with simple taxon addition sequences, tree bisection-reconnection branch swapping, and MaxTrees = 100. Confidence intervals in tree topologies were estimated by bootstrap analysis with 1,000 replicates. Distance matrix analysis was conducted with the neighbor-joining algorithm and the Jukes-Cantor genetic distance model.

Conclusions:

Phylogenetic analysis of 113 isolates/strains of *R. solani* based on sequencing of the ITS-5.8*s* rDNA region revealed 23 clades. The majority of the isolates had identity with AG-2-2 IIIB or AG-4 subgroups. The disease severity index indicated that isolates/strains within nine clades could cause root rot on sugarbeet. Of the 18 isolates tested on corn, seven (6 AG-2-2 IIIB and 1 AG-4 HG-II) isolates could cause more root lesion area than the noninoculated check. Five of the seven isolates generated more lesion area than the other two isolates. The two weaker isolates and two nonpathogenic isolates on corn all fell on the same branch in the phylogram and may represent a subgroup within AG-2-2 IIIB that may need to be considered separate from the other more pathogenic AG-2-2 IIIB isolates. When selecting germplasm for resistance to *R. solani* the traditional disease class scoring system (0-7 or 1-9) would be preferable. However, when comparing isolates for virulence as in this study, the variables and disease severity index utilized would be preferable for this purpose. These data and observations should prove useful in guiding future research and management options for controlling Rhizoctonia root rot.