

PANELLA , L.¹, S. MITCHELL ², C. JESTER ², R. DEAN ², E. G. RUPPEL ¹ and S. KRESOVICH², USDA Agricultural Research Service ¹ Sugarbeet Research Unit, 1701 Center Ave., Fort Collins, CO 80526, ²Plant Genetic Resources Conservation Unit, University of Georgia, Griffin, GA 20223. Determination of genetic relationships among isolates of *Rhizoctonia solani* Kühn based on DNA sequence.

Understanding the genetic relationships among different isolates of a plant pathogen is a necessary prerequisite to understanding the interaction between that pathogen and the host plant. Sequence data from 75 isolates of *Rhizoctonia solani* were used to develop a phylogeny, with emphasis on anastomosis group (AG) 2-2, which contains isolates pathogenic to sugarbeet. The internal transcribed spacers and 5.8S rDNA gene were sequenced with an Perkin-Elmer/Applied Biosystems model 377[®] automated sequencer. The sequencing reaction was PCR-based and used primers flanking the large and small nuclear rDNA genes, as well as internal primers on the 5.8S rDNA gene. The neighbor joining method was used to construct a phylogenetic tree. There was agreement between the phylogenetic grouping and anastomosis grouping. The four isolates that were originally grouped by sequence data outside their anastomosis group were found to have been assigned to the wrong anastomosis group when retested. Distinct subgroups within anastomosis group also were delineated. There were two groups within AG1, one containing isolates from the U.S. and one containing isolates from Japan. Subgroups AG-2-2IIIB and AG-2-2IV also were distinctly grouped within AG-2-2. It is also hoped that unique sequences can be found that are diagnostic of anastomosis group and specifically of the sugarbeet pathogenic isolates within AG-2-2. This research increased our understanding of the genetic relationships among the anastomosis groups of this important plant pathogen.