PANELLA, LEE[1]* and Mary K. Hjort[2], USDA, Agricultural Research Service, 1701 Center Ave., Fort Collins, CO 80526 and Colorado State University, Department of Physiology, Fort Collins, CO 80523. -
Genetic diversity among isolates of Rhizoctonia root rot pathogenic to sugarbeet.

Currently, it is possible to assay the pathogenicity to sugarbeet of an isolate of *Rhizoctonia solani* through a greenhouse bioassay only, which may take 12 to 16 weeks. Recent work done on the phylogenetics of this pathogen has not been well correlated with the host specificity of the fungus. Whether the pathogenicity to sugarbeet has evolved once or more than once in this fungus could substantially influence its interaction(s) with the sugarbeet plant. *R. solani* is divided into anastomosis groups (AGs) based on the ability of the hyphae to fuse and exchange genetic material, or, more recently, into intraspecific groups (ISGs) based on molecular markers. The polymerase Chain Reaction (PCR) was used with the ITS1 and ITS4 primers to amplify the DNA of *R. solani* coding for the 5.8S ribosomal RNA gene (rDNA) as well as the two flanking ITS regions. Five restriction enzymes, Alu I, Hae III, Hha I, Hinf I, Hpa II, and Rsa I, were used to create restriction fragment length polymorphisms (RFLPs) from the amplified DNA fragments. Data from 92 isolates of *R. solani* were analyzed using the SIMQUAL program (NTSYS-pc from Exter Software) based on Jaccard's coefficient. The resulting similarity matrix was used to create a phenogram. There was good discrimination between AG-2-2 (causal agent of sugarbeet crown and root rot) and the other AGs, but not adequate discrimination within this AG or among the other AGs. More genetic markers are needed to discriminate adequately. Isozyme markers from four enzyme systems (α- Acid phosphatase (α-ACP), Phosphoglucomutase (PGM), Glucose-6-Phosphate-dehydrogenase (G6PDH), and Malate dehydrogenase (MDH)) are being screened to further distinguish among isolates. Greenhouse tests will be used to determine the pathogenicity of the isolates of *R. solani* to sugarbeet. These data will be correlated with the phylogenetic information to genetically "fingerprint" those isolates pathogenic to sugarbeet.