

RAPD ANALYSIS ON GENETIC DIVERSITY OF NIGHTSHADE SPECIES IN THE NORTH CENTRAL REGION. Altanbadralt Sharkhuu, Peter B. Goldsbrough, Stephen B. Goodwin and Stephen C. Weller, Departments of Horticulture, and Botany and Plant Pathology, Purdue University, West Lafayette, IN 47907.

Research was conducted to study the genetic diversity of eastern black nightshade species sampled in the North Central (NC) U.S. (Michigan, Indiana, Illinois and Ohio) using Random Amplification of Polymorphic DNA (RAPD) analysis. These species were compared to solanaceous species from the NC and other areas of the U.S. including the annual nightshades horsenettle, American black nightshade and bitter nightshade, and perennials clammy groundcherry and smooth groundcherry. Twenty-five accessions of eastern black nightshade collected from various sites in the NC region were studied. In the initial RAPD analysis, 38 reproducible bands were compared using polymorphisms produced by eight primers. Data were analyzed using the Numerical Taxonomy and Multivariate Analysis System program (NTSYS-pc). This group of eastern black nightshade plants was divided into 11 subgroups by cluster analysis based on the unweighted pair group method with an arithmetic average (UPGMA). A single accession from each subgroup was selected randomly for further RAPD marker analysis with other solanaceous accessions collected from throughout the U.S. In total, 232 RAPD markers were scored for presence or absence of strong reproducible bands for the sample populations and analyzed with NTSYS-pc. A phenetic tree was constructed based on the scored genetic polymorphisms, and subjected to bootstrap analysis. All accessions within a species had a similarity coefficient >0.75 . The genetic relationships developed indicated that eastern black nightshade, black nightshade and American black nightshade species were more genetically similar to each other than to other solanaceous species while bitter nightshade and ground cherry species were distinct. Among the eastern black nightshade accessions studied, all but three were in the same cluster. Accessions of black nightshade, American black nightshade, horsenettle, hairy nightshade and bitter nightshade species were each separated into distinct clusters except for two accessions that were originally considered to be black nightshade and horsenettle species but through RAPD analysis were identified as American black nightshade and eastern black nightshade species. These results confirm that RAPD analysis of genetic polymorphisms is a useful technique to characterize weedy solanaceous species.