

USING MOLECULAR MARKERS TO EXAMINE RELATIONSHIP AMONG WEEDY SOLANUM SPECIES. Altanbadralt Sharkhuu, Peter B. Goldsbrough, and Stephen C. Weller, Graduate Research Assistant and Professors, Purdue University, Department of Horticulture and Landscape Architecture, West Lafayette, IN 47907.

Molecular marker research is being conducted to relate biological, ecological and genetic factors to growth pattern of a variety of Solanaceous species common in the Midwestern United States. Seeds of more than two hundred samples belonging to six nightshade (*Solanum americanum*, *S. nigrum*, *S. ptycanthum*, *S. carolinense*, *S. sarrachoides* and *S. dulcamara*) and three groundcherry (*Physalis angulata*, *P. heterophyl* and *P. subglabrata*) weed species were collected throughout Ohio, Indiana, Illinois and Michigan. The experiment used RAPD molecular marker analysis to evaluate the degree of genetic variation occurring within and between of these species. Multiple independent DNA samples were obtained from individual greenhouse grown plants. Eight primers were used in the RAPD analysis based on consistency of results in preliminary experiments. A total of 412 RAPD markers for 114 individuals belonging to the sampled species were run. Seventy of these individuals were scored (presence or absence of strong reproducible bands) by the Numerical Taxonomy and Multivariate Analysis System program. Based on the scored genetic polymorphisms, a genetic tree was formed. Bootstrap analysis was used to assess the significance of the genetic relationships observed in the tree. The genetic relationships indicate: black nightshade and American nightshade species are more genetically similar to each other than to other nightshade species; eastern black nightshade separated into 2 closely related groups as did hairy nightshade; horsenettle separated into 3 distinct groups; and bitter nightshade and groundcherry groupings were distinct from each other and from all nightshade species. The results show that RAPD analysis is useful for distinguishing genetic relationships within a particular nightshade species and allows a determination of genetic variation between nightshade species.