

MORPHOLOGY OF WATERHEMP X SMOOTH PIGWEED HYBRIDS. Federico Trucco, Patrick J. Tranel, A. Lane Rayburn, and Kenneth R. Robertson, Graduate Research Assistant, Associate Professor, Associate Professor, and Professor, Department of Crop Sciences and State Natural History Survey, University of Illinois, Urbana, IL 61801.

Many populations of *Amaranthus* species have been reported resistant to one or multiple herbicides. Hybridization among these species is thought to contribute to their evolutionary adaptability and may be a route for resistance transfer. Previous work suggests high potential for hybridization between waterhemp (*A. rudis* and *A. tuberculatus*) and smooth pigweed. However, the apparent morphological similarity between waterhemp and its hybrid progeny makes field surveys for hybrids difficult to conduct. The objective of this study was to identify reliable morphological characters that could be used to distinguish waterhemp from waterhemp x smooth pigweed hybrids. To do this, hybrids were obtained from field crosses and their identities corroborated with molecular and cytogenetic tools. Hybrids and individuals of the parental species were grown in the greenhouse and evaluated for more than 25 morphological characters. Significant differences ( $\alpha = 0.05$ ) between hybrids and either or both of the two parents were obtained for nine characters or algebraic relations. In summary, hybrid leaf length-to-width ratio was intermediate to that of parents. Hybrids had longer pistillate bracts and tepals and a greater tepal-length-to-uricle-length ratio than waterhemp. Staminate bracts were longest in hybrids, and staminate bract-length-to-tepal-length ratio in hybrids was greater than in waterhemp. In general, hybrid female inflorescences exhibited globular patterns at branching points and an overall feathery appearance. However, the qualitative characters evaluated were not as reliable. Although many quantitative characters show statistical significance when individuals of known identity are used, it might be difficult to use any one of these characters to positively identify hybrids. Rather, a combination of these characters could be used to identify putative hybrids in field surveys and molecular or cytogenetic tools used to confirm/contradict expected identities.