

IDENTIFICATION OF POLYMORPHIC PLASTIDIC DNA SEQUENCES FOR WATERHEMP POPULATION GENETICS. Jianyang Liu, Kate Thinglum, Patrick J. Tranel, and Adam S. Davis, Post Doctoral Researcher, Graduate Research Assistant, Associate Professor, University of Illinois, Urbana, IL 61801 and Ecologist, USDA-ARS Invasive Weed Management Unit, Urbana, IL 61801.

Waterhemp (*Amaranthus tuberculatus*) is a major problem weed in the North Central states, and it has developed resistances to a number of commonly used herbicides. As a dioecious species, waterhemp may spread herbicide-resistance traits among populations by the dispersal of both seeds and pollen. To model the patterns of herbicide resistance spread, it is necessary to estimate the relative contributions of seed and pollen movement to total gene flow, as they are of different dispersal modes. Chloroplast DNA (cpDNA) is maternally inherited, and disperses in seeds but not in pollen. In light of that, comparing the spatial distribution of cpDNA polymorphisms with that of biparentally inherited nuclear DNA would help to evaluate the relative influences of seed and pollen dispersal on total gene flow and their effectiveness in spreading resistance. In this study, we investigated cpDNA polymorphisms by amplifying non-coding regions which are reported to be highly polymorphic in other species, and a set of cpSSR primers developed with SSR Finder were also tested. Due to the relative rarity of variation in the conserved cpDNA genome, low polymorphisms in waterhemp cpDNA have been found thus far. A single nucleotide polymorphism was found in the *rpoB-trnC^{GCA}* region, and this polymorphism was not directly related to the geographic distance between samples. In addition, the *rpl32-ndhF* and *trnL^{UAG}-rpl32* regions were also found to be potentially polymorphic and, therefore, useful for population-level studies.