TRADEOFF BETWEEN FERTILITY AND GENE INTROGRESSION IN THE BC_1 GENERATION OF WATERHEMP X SMOOTH PIGWEED HYBRIDS. Federico Trucco, Tatiana Tatum, A. Lane Rayburn, and Patrick J. Tranel, Graduate Research Assistant, Graduate Research Assistant, Associate Professor, and Associate Professor, Department of Crop Sciences, University of Illinois, Urbana, IL 61801.

Numerous recent studies have resurfaced the importance of interspecies hybridization as an evolutionary force. In the realm of weed science, such studies have addressed the likelihood of monogenic herbicide resistance transfer. In particular, field studies have established high potential for hybridization between two important and often coexisting weedy amaranths, waterhemp and smooth pigweed. In essence, pre-mating reproductive barriers between these species are believed to be limited to pollen competition and availability. Moreover, a greenhouse study showed that a herbicide resistance gene (*ALS*) from smooth pigweed could be introgressed into an advanced waterhemp background (BC_2). However, evidence is lacking in support of such transfer in nature. Post-zygotic reproductive barriers may minimize, if not preclude, natural introgression. Indeed, waterhemp x smooth pigweed hybrids are characterized by reduced fertility and even floral neuterism. The purpose of this study was to assess hybrid sterility by profiling BC_1 populations, with specific emphasis on *ALS* introgression. In essence, progeny obtained from backcrossing F_1 females with pollen from waterhemp or smooth pigweed were profiled for genomic constitution, fertility and *ALS* identity. Genomic constitution was inferred from nuclear DNA content and ploidy analyses. Fertility was assessed by measuring seed output and by pollen evaluation. Finally, introgression of *ALS* was determined via a molecular marker system. The obtained data showed that most progeny were homoploid ($2\underline{n} = 32$) and, thus, observed nuclear DNA content (2C) variation could not be explained by aneuploidy. In fact, given the reported difference in the average size of smooth pigweed and waterhemp chromosomes, 2C variation could be explained in the context of random chromosomal assortment into haploid gametes ($\underline{n}=16$). With regard to the genetics of hybrid sterility, fertility indicators (seed production and percent abnormal-size pollen, i.e. micropollen) showed segregation inconsistent with that expected of a single-locus model. Also, lack of correlation between genome reconstitution (as indicated by 2C values) and fertility measurements did not support Fisher's infinitesimal model for post-mating reproductive isolation. The data obtained can be explained best by a system where rather few (but not just one) loci are responsible for fertility penalties. Approximately 3% of the progeny obtained reconstituted parental fecundity. Introgression at *ALS* was negatively correlated with fertility as indicated by seed output ($P = 0.05$) or percent micropollen ($P = 0.03$). Briefly, heterozygotes produced 39% of the seed output and 52% more micropollen than their homozygote siblings. Furthermore, the waterhemp *ALS* allele was not identified in any of the 29 monoecious progeny evaluated. Finally, lack of correlation between dry mass accumulation and *ALS* identity suggests that fecundity penalty in *ALS* introgression is not due to heterozygosity at *ALS* itself. Rather, linkage of *ALS* to a locus associated (directly or via epistasis) with hybrid sterility may explain the fertility penalty related with *ALS* introgression. Moreover, this linkage might explain why sequenced herbicide-resistance *ALS* alleles from smooth pigweed and nearby waterhemp populations show independent evolution.