

WEED-TO-WEED GENE FLOW – WHAT IS THE POTENTIAL FOR GLYPHOSATE RESISTANCE MOVEMENT VIA INTERSPECIFIC HYBRIDIZATION? Micheal D.K. Owen and Ian A. Zelaya, Professor, Agronomy Department, Iowa State University, Ames, IA 50011-1011 and Project Team Leader, Syngenta Ltd., Weed Control Research, Jealott's Hill International Research Centre, Bracknell, Berkshire RG42 6EY, United Kingdom

When evaluating herbicide resistance and the potential for herbicide resistance dissemination within agroecosystems, most studies focus on weed seed production, viability and dispersal, the species mating system, and the genetics associated with the resistance trait. However, far less attention has been centered on the potential for herbicide resistance spread through interspecific hybridization (introgression). For that matter, the ability of weeds to hybridize with near relatives has not been well-studied or documented in agro-ecosystems, however some data exists for Amaranthaceae. While some studies describe gene flow and successful transmission of herbicide resistance alleles from cultivated crop species to their weedy relatives, little data exists regarding the between weed species gene flow. Part of the problem describing weed hybridization is recognition of the hybrids in the field; this is particularly challenging since hybrids in most cases resemble (phenotypically) the parents.

Herbicide resistance potentially represents an effective marker to document hybridization between weed species. This study assessed the introgression of herbicide resistant alleles in the important genii *Ambrosia*, *Conyza* and *Helianthus*, considering the importance of Asteraceae weeds in current agroecosystems. The study used the cross resistant triazolopyrimidine, sulfonanilide and sulfonyleurea (SU) giant ragweed (*A. trifida* L.; $2n = 24$) and imidazolinone and SU common sunflower (*H. annuus* L.; $2n = 34$) populations from Iowa, in addition to a glyphosate resistant horseweed (*C. canadensis* L. Cronq.; $2n = 18$) population from Delaware. The herbicide susceptible common ragweed (*A. artemisiifolia* L.; $2n = 36$), Jerusalem artichoke (*H. tuberosus* L.; $2n = 102$), and dwarf fleabane (*C. ramosissima* Cronq.; $2n = 18$) populations originated from Iowa. In all three genii evaluated, herbicide resistance was expressed as a nuclear allele, partially dominant (*Ambrosia* and *Helianthus*) or over dominant (*Conyza*) trait in first filial interspecific hybrid generation (F_1^H). Herbicide resistance transfer frequency in the F_1^H ranged from 40 to 60%, 0 to 9%, and 30 to 50% in *Ambrosia*, *Conyza*, and *Helianthus*, respectively.

Inheritance of herbicide resistance in the selfed F_1^H generation (F_2^H) followed the mono-factorial model in all evaluated genii; F_1^H backcrosses confirmed successful introgression of the herbicide resistance allele to parents. Thus, interspecific hybridization is possible and may be a potentially important avenue for the dissemination of herbicide resistance, specifically glyphosate resistance, and the promotion of genetic diversity within compatible weed species.

The occurrence of glyphosate resistant hybrid weeds may complicate the containment of glyphosate resistance in current crop production systems. However, it has yet to be determined if interspecific hybridization of weed species is frequent and pervasive within the agro-ecosystems. If the occurrence of weed hybridization is relatively frequent, important ecological studies should be conducted to determine if the weedy hybrids are well-adapted to current crop production systems and thus may evolve into economically important weed problems. The movement of glyphosate resistance via gene flow as a companion to the hybridization process could improve the adaptation of weedy hybrid progeny to the agro-ecosystem. Despite the likely negative implications of evolved glyphosate resistance and weed hybridization, the occurrence of glyphosate resistance could be a useful marker to assess weed hybridization.