Gene Flow from Glyphosate-Resistant Common Waterhemp under Field Condition

Debalin Sarangi* and Amit J. Jhala
Department of Agronomy & Horticulture; University of Nebraska- Lincoln, NE
*debalin.sarangi@huskers.unl.edu

Introduction

- Most of the herbicide resistance traits in weed species are nuclear inherited and can be transferred through pollen migration (Jasieniuk et al. 1996).
- The dioecious and anemophily natures of common waterhemp are believed to aid in rapid spreading of herbicide resistance alleles (Liu et al. 2012).
- Recently, glyphosate-resistant common waterhemp biotypes are confirmed from seven eastern Nebraska counties (Sarangi et al. 2015).
- Limited information is available on common waterhemp pollen biology and dispersal; however there is a lack of scientific literature about pollen mediated gene flow in field.

Objective

To quantify pollen-mediated gene flow from glyphosate-resistant to glyphosate-susceptible common waterhemp biotypes under field condition

Materials and Methods

Field experiments: Clay County, NE in 2013 and 2014

- A donor (10-m diam; 80 sq m)- receptor (80 × 80 m) design (Figure 1) was used for this study by modifying the study conducted by Jhala et al. (2011).
- Approximately 550 plants of glyphosate-resistant common waterhemp were grown in the greenhouse and transplanted to the pollen-donor block.
- Receptor area was divided into eight directional blocks (cardinal: N, S, E, and W; ordinal: NE, SW, SE, and SW) and known glyphosate-susceptible biotypes were planted at specific distances up to 50 m from the donor block.
- The male waterhemp plants in the receptor area were detected visually prior to the pollination and were removed to check the pollen competition and cross-pollination in the receptor blocks.
- Flowering synchrony between donor and receptor, and hourly meteorological data were recorded throughout this study.
- Seeds from each of the glyphosate-susceptible common waterhemp mother-plant were harvested separately.

Greenhouse screening: The seedlings were grown in the greenhouse and sprayed with 2× rate of Glyphosate (Touchdown HiTech®, Syngenta Crop Prot.), where 1× = 1,050 g ae ha^{-1}. Gene flow frequency was determined by using glyphosate-resistant trait as a selective marker.

Statistical analysis:

- The mean frequencies of gene flow at each distance were subjected to nonlinear regression using software R (R Foundation for Statistical Computing, Austria)

Exponential decay model:

$$p = ae^{-d/b}$$

Where, *p* is predicted frequency of gene flow; *a* is the intercept; *d* is the mean distance; *b>0* is curve parameter determining steepness of the curve

- Data were tested for the assumptions of normality and homogeneity of variances with the Shapiro-Wilk test and the Levene's test in SAS (SAS Institute Inc, Cary, NC), respectively.
- The effect of distance and direction on the frequency of gene flow were evaluated separately in randomized complete block design in SAS.

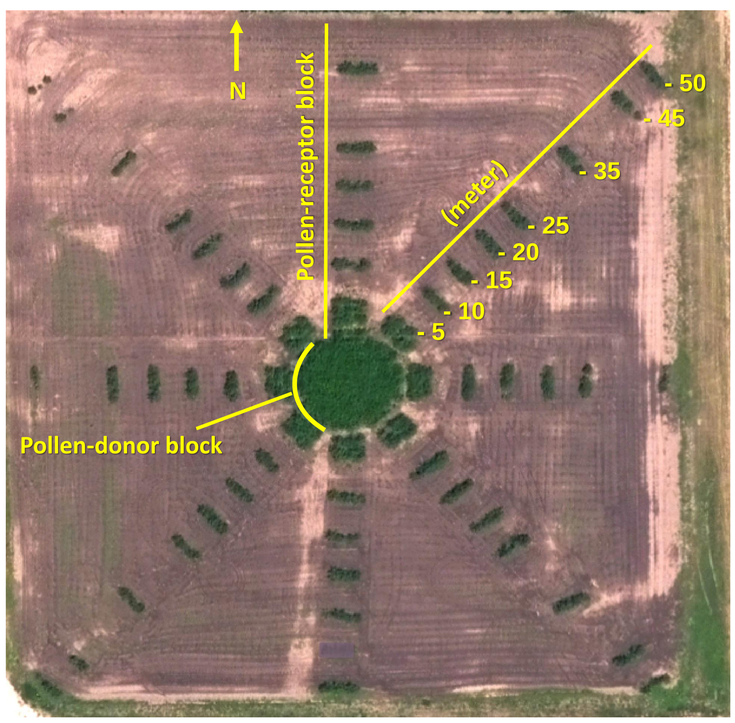

Figure 1. Aerial view of the experimental site

Results and Discussion

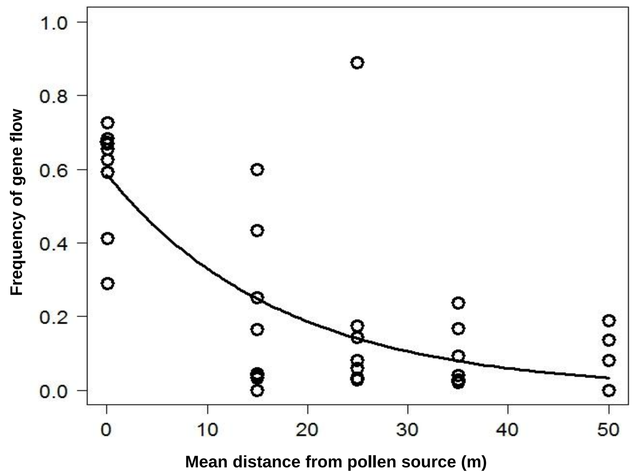

Figure 2. Pollen-mediated gene flow frequency over distances

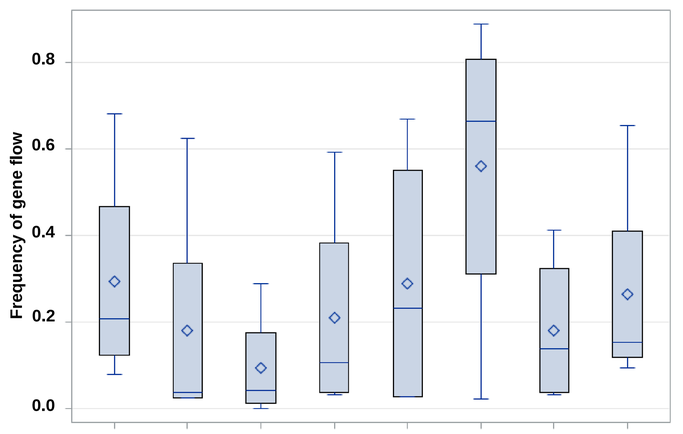

Figure 3. Pollen-mediated gene flow frequency over directions

Table 1. Parameter estimates and the distances where 50% (O_{50}), and 90% (O_{90}) reduction in gene flow frequency occurred

Parameters	Estimate	Standard error
a	0.58	0.06
b	17.49	3.98
O_{50}	12.12	2.76
O_{90}	40.27	9.16

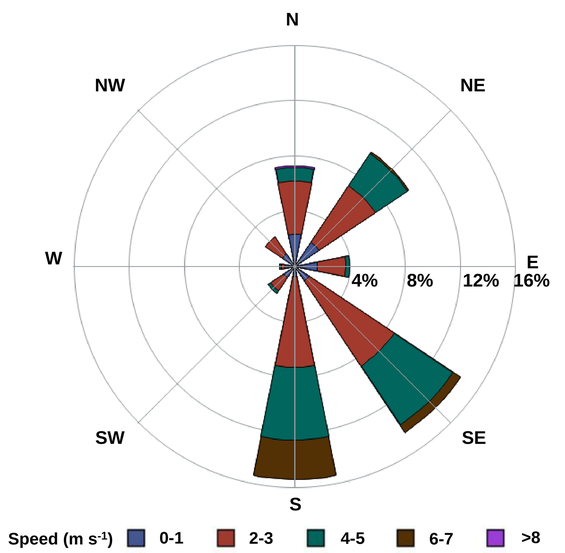

Figure 4. Distribution and frequency of wind speed and direction (blowing from) during anthesis

- Floral synchrony data suggested that maximum pollen was shedded between early July to mid of August.
- Mean distances from the pollen-source had a significant effect (P= 0.0002) on the frequency of gene flow; whereas directions had no effect (P= 0.43) (Figure 2 and 3).
- Frequency of gene flow was highest near the source; averaging 0.5813 at 0.1 m from the source, whereas it was 0.1015 at 50 m (Figure 2). Similar trend was observed by Jhala et al. (2011) and Yerka et al. (2012) in flax and common lambsquarters, respectively.
- Gene flow frequency was reduced by 50% (O_{50}) and 90% (O_{90}) at the distance of 12.12 m and 40.27 m from the pollen source, respectively (Table 1). The similar results were reported by Liu et al. (2012), where most pollen deposition occurred within 25 m and it reduced by 90% at 50 m.

Conclusions

- Frequency of gene flow from glyphosate-resistant common waterhemp was reduced exponentially with the increasing distance from the pollen source.
- As high genetic variability is always present in common waterhemp biotypes, the data from ongoing *in vivo* shikimate accumulation assay and glyphosate resistance screening for more number of common waterhemp seedlings is warranted.
- Molecular works with the use of suitable genetic markers are essential.
- Gene flow study in landscape is required as several factors influence the pollen-mediated gene flow including: wind velocity, presence of vectors, population size, biology of plants, geographical barriers, vegetative canopy type, and environmental factors.

Literature Cited

- Jasieniuk M, Brûlé-Babel AL, and Morrison IN (1996) *Weed Sci* 44:176-193
- Jhala AJ, Bhatt H, Topinka K, and Hall LM (2011) *Heredity* 106:557-566
- Liu J, Davis AS, and Tranel PJ (2012) *Weed Sci* 60:416-422
- Sarangi D, Sandell LD, Knezevic SZ, Aulakh JS, Lindquist JL, Irmak S, and Jhala AJ (2015) *Weed Tech (In press)*
- Yerka MK, Leon N, and Stoltenberg DE (2012) *Weed Sci* 60:600-606