

Gene flow in alfalfa under honey bee (*Apis mellifera*) pollination

L. R. Teuber¹, A. Van Deynze², S. Mueller¹, M. McCaslin³, S. Fitzpatrick⁴ and G. Rogan⁵

¹Agronomy and Range Science and ²Seed Biotechnology Center- University of California, Davis, CA; Forage Genetics International, ³Prior Lake, MN and ⁴West Salem, WI; and, ⁵Monsanto Company, St. Louis, MO

Out crossing rate, gene flow and pollinator behavior are very important to proper management of commercial alfalfa (*Medicago sativa* L.) seed production. Recent advances in genetic technology have offered new tools to better understand the dynamics of pollinator-mediated gene flow. Studies by Forage Genetics (2002) and St. Amand *et al.* (2000) have previously used genetically-marked pollen to study alfalfa gene flow with alfalfa leaf cutter bee (*Megachile rotundata* F.), or honey bee (*Apis mellifera* L.) pollination, respectively. The objective of the present study was to measure gene flow using honey bee pollination under commercial seed production conditions in the San Joaquin Valley of California.

This initial study was established in Kings County, California in 2002, and isolated from other alfalfa seed production by at least 6.2 mi (10 km). The Roundup Ready[®] trait conferring Roundup[®] herbicide tolerance was used as a pollen-marking tool as follows. A single, 6 A Roundup Ready alfalfa pollen source plot was

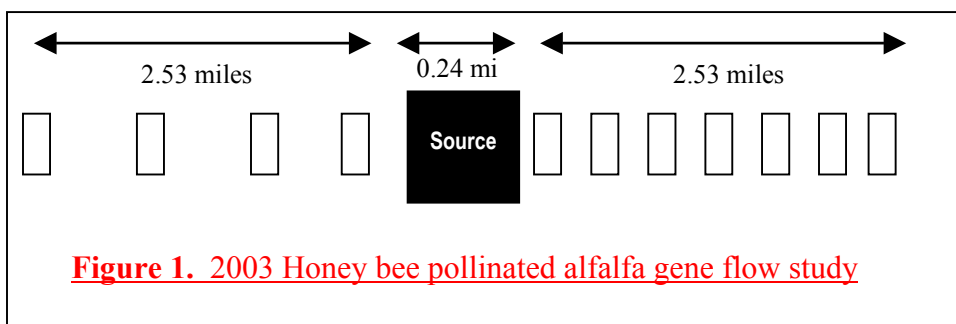


Figure 1. 2003 Honey bee pollinated alfalfa gene flow study

established in the center of the study area (i.e., the genetically-marked pollen source plot) and eleven, conventional (non-marked) alfalfa pollen trap plots (0.54 A/plot) were established at intervals extending West and East of the source (Fig. 1). All isolation distances were bridged by interven-

ing trap plots, except the shortest distance of 900 ft. At seed harvest (2003), a total of 25 samples were taken in a grid pattern from each trap. Seed samples were planted in a Roundup-treated field evaluation wherein the frequency of gene flow was estimated by counting the percentage of Roundup tolerant seedlings; in all, 75,000 to 90,000 seedlings were tested per trap plot. The study was conducted as permitted under USDA-APHIS notification and State regulations.

A significant decrease in gene flow with increasing distance from the source plot was observed (Fig. 2). At 900 ft, honey bee-mediated gene flow was 1.49% and it decreased linearly to 0.20% near 5,000 ft. Gene flow continued to decline out to 2.53 miles where it was detected at a low frequency ($\leq 0.06\%$). Gene flow to the West and the East was not significantly different. These initial, preliminary data will be combined with data from future honey bee pollinated field studies to inform seed production management recommendations so that seed producers may achieve specific seed quality goals.

[®]Roundup Ready and Roundup are trademarks of Monsanto Company

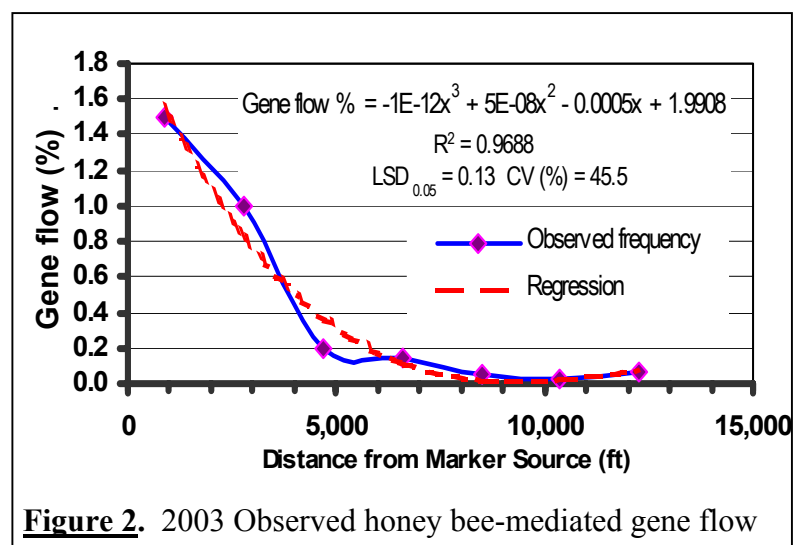


Figure 2. 2003 Observed honey bee-mediated gene flow

References

- Fitzpatrick, S., P. Reisen, and M. McCaslin. 2002. [Alfalfa pollen-mediated gene flow studies, 2000-2001](#). Proc. of the 38th North American Alfalfa Improvement Conference. July 17-21, 2002, Sacramento, California.
- St. Amand *et al.* 2000. Risk of alfalfa transgene dissemination and scale dependent effects. TAG 101: 107-114.