

GENE FLOW IN ALFALFA (*MEDICAGO SATIVA* L.) WHEN HONEY BEES (*APIS MELLIFERA* L.) ARE USED AS POLLINATORS. Larry R. Teuber¹, Allen Van Deynze¹, Shannon Mueller², Ken L. Taggard¹, Larry K. Gibbs¹, Mark McCaslin³, Sharie Fitzpatrick³, and Glenn Rogan⁴. ¹Department of Plant Sciences University of California, Davis, CA 95616; ²University of California Cooperative Extension, Fresno, CA; ³Forage Genetics International, West Salem, Wisconsin; and ⁴Monsanto, St Louis, MO.

Honey bees (*Apis mellifera* L.) are essential to alfalfa (*Medicago sativa* L.) seed production in California. It is well known that honey bees will forage up to several miles from their hive. A range finding study was conducted to determine the extent of potential gene flow between alfalfa cultivars within the foraging range of honey bees. The study was conducted as a federally regulated study using the roundup resistance (RR) trait as a marker source. This source was located 6.2 miles from any commercial alfalfa seed production. Trap plots were located at regular intervals to both the East and West of the source plot starting 900 feet to a distance of 2.5 miles. A very low frequency of gene flow could be detected at 2.5 miles. In this study, gene flow was less than 0.5 % at a distance of one mile. The RR trait has now been completely deregulated and a larger study has been funded and will be conducted in the San Joaquin Valley of California starting in 2006. This study will look at both bridged and unbridged gene flow out to distances of 5 miles. A second study will examine the potential for gene flow from forage producing fields into adjacent seed production fields. From each of these studies we expect to be able to examine honey bee pollinator behavior and devised potential strategies for monitoring and minimizing gene flow during seed production.