Pollen Flow and Productivity in Almond Orchards Using DNA Markers

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This project is aimed at studying pollen flow in almond orchards using DNA markers and paternity analysis. Commercially- important almond cultivars are all self-incompatible which means that intercompatible cultivars with overlapping bloom periods must be planted in the orchard to ensure pollen availability. Besides pollen availability, orchardists depend upon honey bee-vectored pollen transfer among receptive flowers of intercompatible cultivars.

Current knowledge of flight patterns of honey bees suggests that inter-tree flights tend to favor the shortest distance between trees (Robbin Thorp, personal communication). Under unfavorable abiotic conditions (e.g., low temperatures, rain, and wind) bees are likely to forage between near-neighbor flowers resulting in many confining their foraging to small areas of single trees (Robbin Thorp, personal communication). Under these conditions, pollination, fruit set and yields will probably be reduced, and the source of compatible pollen may be the hive rather than nearby trees. We propose to use DNA markers based upon genes that encode specific S-alleles to establish the paternity of nuts obtained from these trees. The use of DNA-based markers, the appropriate selection of cultivars, and the use of standard and dual -cultivar rows will enable us to determine whether the pollen donor (the pollen parent) was adjacent trees (in dual cultivar rows), adjacent pollinizer rows, or pollen from other donors that were likely transported from the hive. The probability that a given cultivar will serve as the pollen donor is likely to vary from year-to-year depending upon the level of bloom period overlap (which varies with both chill and heat unit accumulation) and environmental variables which influence bee flight activity.

The experiment was conducted at the Nickels Estate using four replicated blocks containing "Padre" and "Mission" dual-cultivar rows, and solid "Padre" rows, which are both adjacent to solid rows of "Butte". Eight trees per cultivar were selected from each row generating a total of 32 "Padre" and 32 "Mission" trees in dual-cultivar rows and 32 "Padre" trees in solid rows. Four hundred "Padre" blossoms per dual-cultivar and solid rows were tagged early during the bloom period (corresponding to about 20% of the earliest receptive bloom) and another 400 "Padre" blossoms per row were tagged later during the bloom period (corresponding to the latest-opening 20% of the bloom).

At nut maturity, 200 nuts per row were sampled for paternity analysis from among the tagged fruit corresponding to 'each' of the flower tagging dates. Yields of solid "Padre" rows and "Padre"/"Mission" dual-cultivar rows were taken to determine whether pollen is yield- limiting in the solid "Padre" rows. This was replicated four times in the orchard. Nuts will be processed and "fingerprinted" using DNA markers for S-alleles that correspond to the cross incompatibility group of all of the possible parents to determine the pollen donor (male parent). This will determine the degree to which the successful competitor came from within-row, the adjacent pollinizer row (the presumed conventional source) or from extraneous pollen the bee presumably picked up in the hive. This is possible as the individual S-alleles that determine self-incompatibility have been developed in the Dandekar laboratory. These markers can be used to verify the S-allele of the nut and thus this analysis can be used to determine the pollen parent. Annual variation in bloom overlap, flower density and climatic variables are likely to change the relative "success" of any given pollen source from year to year. This is the first test that we have proposed conducting over a three year period. Currently, nuts have been harvested and are being stratified pending DNA analysis. Stratified nuts will be germinated in batches with the germinated seedlings extracted for DNA that will be used for the paternity analysis.

References

Tamura, M.K., K. Ushijima, H. Sassa, H. Hirano, R. Tao, T.M. Gradziel and A.M. Dandekar. 2000. Identification of self-incompatibility genotypes of almond by allele specific PCR analysis. Theor. Appl.Genet.101: 344-349.