

## OUTCROSSING IN AVOCADO: IS THERE A RELATIONSHIP WITH YIELD?

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The primary objective of this project is to investigate the potential relationship between yield and outcrossing rate in avocado. There has been considerable debate about the need to provide cross pollination in large plantings of HASS avocados. We are attempting to use genetic markers to obtain data on pollination success as a function of cultivar source, distance, and climatic region, and at the same time correlate outcrossing with yield. Using two methods, restriction fragment length polymorphisms (RFLP's) and random amplified polymorphic DNA markers (RAPD's), we have established a set of genetic markers which successfully detect outcrosses among HASS fruits and seedlings.

Our previous work with RFLP's have enabled us identify pollination events from specific sources (BACON, FUERTE, and ZUTANO cultivars). In a recent study we sampled fruit from three HASS orchards in the Temecula area and used our RFLP probes to assay for outcrossing (Figure 1). This method involved collecting the fruit, growing seedlings, and then preparing DNA samples which were tested with our probes. While this procedure is adequate for small samples, it is too costly and time consuming for studies requiring larger sample sizes.

The RAPD method will enable us to overcome this disadvantage. An assay using this technique requires very little DNA in comparison to the RFLP method. We have developed a method to extract DNA from the embryo contained in the avocado seed to perform these assays, eliminating the need to grow seedlings and allowing us to process larger samples. Using the outcrossed material from the RFLP study, we have tested approximately 100 RAPD primers and found several that detect outcrossing from the BACON, FUERTE, and ZUTANO sources.

The research plan involves selecting HASS orchards from two major climatic regions where outcrossing requirements may differ. From each of these regions two areas will be chosen (Ventura/Santa Barbara and Temecula/Escondido). Trees will be sampled from three distance classes (1,5, and 15 rows) from each of three potential pollen sources (BACON, FUERTE, and ZUTANO). At least 20 fruits will be assayed from each tree, and replicated twice for each distance class. In addition, from each of these four areas we will collect HASS fruit from an orchard that is isolated from other pollen sources as a control. This plan will require that we assay approximately 2000 progeny. For yield data we are estimating the number of fruit per tree for all of the trees sampled. From this we hope to determine if there is a positive correlation between yield and outcrossing rates.

We have located suitable sites in Temecula and Santa Barbara and are continuing to look for sites in San Diego County and the Ventura area. We have collected material from Temecula and are beginning to prepare DNA from seed material for our assays.

<u>SAMPLE</u>	<u># ASSAYED</u>	<u># OUTCROSSED (%)</u>	<u>SOURCE(S)</u>
A 1	7	5 (71)	4 FUERTE, 1 ZUTANO
A 2	6	5 (83)	4 FUERTE, 1 BACON
A 5	5	3 (60)	3 FUERTE
A 10	8	4 (50)	2 FUERTE, 2 BACON
A 15	4	2 (50)	2 FUERTE
B 2	8	8 (100)	8 BACON
B 5	8	8 (100)	8 BACON
B 10	5	5 (100)	3 BACON, 1 ZUTANO, 1 FUERTE
C 1	6	6 (100)	4 ZUTANO, 2 FUERTE
C 2	5	3 (60)	1 ZUTANO, 1 FUERTE, 1 BACON
C 5	8	6 (75)	1 ZUTANO, 4 FUERTE, 1 BACON

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A - Stucker Ranch, Temecula (FUERTE)  
B - Kanning Ranch, Temecula (BACON)  
C - Dent Ranch, Temecula (ZUTANO, FUERTE)

**Figure 1 - HASS seedlings assayed for outcrossing using RFLP probes. Sample numbers refer to distance in rows from targeted pollen source (A1 = 1 row, A2 = 2 rows, etc.).**