

MOLECULAR GENETICS OF AVOCADO

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The primary goal of our research is to construct a genetic map of the avocado genome. To achieve this objective we have created a number of anonymous clones of avocado DNA in the plasmid vector pUC18. These clones are random fragments of the avocado genome and they can be used to detect genetic polymorphisms (called RFLPs) among avocado varieties and cultivars. Examples of the pattern of RFLP variation associated with a panel of cultivars is shown in the attached Figure 1.

Some clones recognize a unique region of the genome (called single-copy probes) and others recognize many sites in the genome. Single-copy probes are most useful for the mapping project. (Figure 1 presents results from a single copy probe.) To date, we have isolated and characterized 28 single-copy probes. We have approximately 100 additional clones that have been constructed, but remain to be characterized.

To test for genetic linkage among the various single-copy probes, we have prepared DNA from 85 Hass seedlings obtained from a single tree within a large Hass orchard. Because it is virtually impossible to control the mating system in avocado, we have assumed that the progeny from an isolated Hass stand are likely to be the products of self-fertilization. If this assumption is valid, we can regard the Hass progeny as F₂ progeny for the purposes of linkage analysis. To date we have screened about 35 of the Hass progeny with 5 probes that are heterozygous in the Hass maternal parent. We will continue this screening program to identify linkage groups for our various probes.

We have prepared DNA from 45 cultivars, hybrids, and closely related *Persea* species and to date we have screened these materials with 14 single-copy probes. Based on these results we can assign a unique genotype to every cultivar in the panel. Put in another way, we can uniquely identify every cultivar. This may have substantial utility in future avocado improvement. We have used a statistical analysis to cluster cultivars based on their genetic similarity as estimated from the RFLP data. The results of the cluster analysis, which are shown in Figure 2, are for the most part consistent with known breeding relationships and with variety assignments.

We have also embarked on an effort to use our probes to assess the role of outcrossing in avocado fruit production. While we do not have final results, we have prepared DNAs from a structured sample of avocado materials. We hope to be able to shed some light on the relationship between outcrossing and fruit set in the near future.

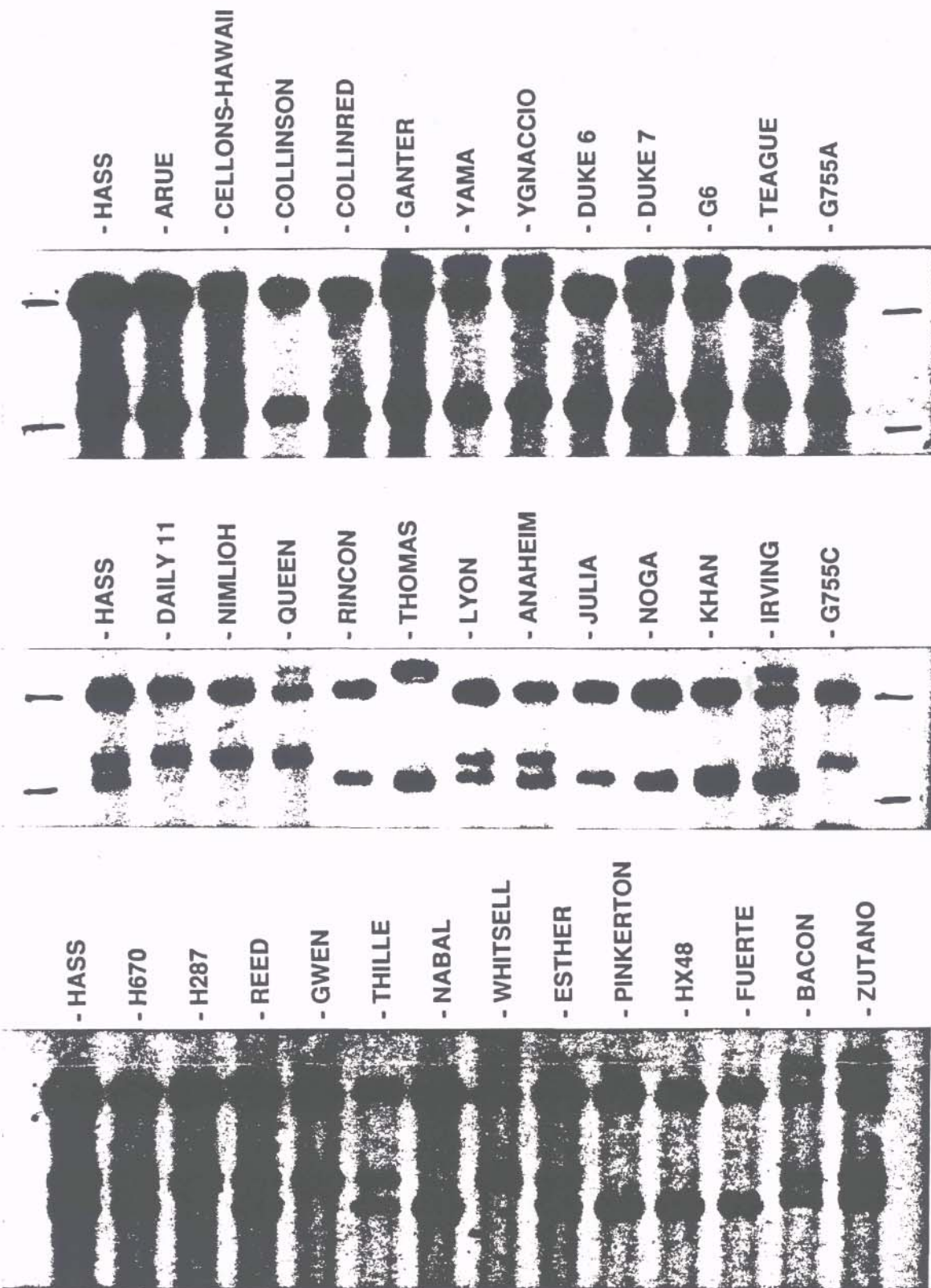


Figure 1 - Southern hybridizations of avocado cultivar DNA's to single-copy probes. Banding patterns correspond to RFLP genotypes.

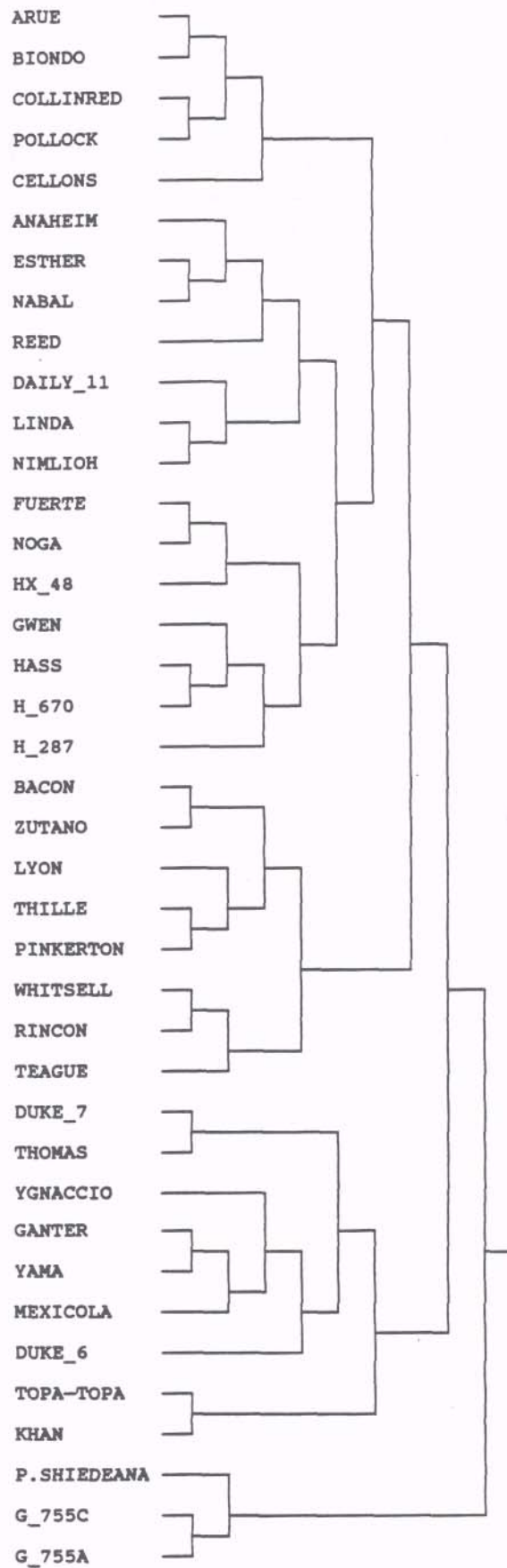


Figure 2 - Tree diagram illustrating general relationships among avocado cultivars based on RFLP analysis.