

PROJECT CONCLUDED: FINAL REPORT

EST Libraries and Bioinformatics for California Citrus

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This project produced fundamental resources and information in the area of “Genomics”, which facilitates other research and practical applications. Using information developed in earlier years of the project or released by others, an Affymetrix citrus GeneChip® was designed by this project and made commercially available.

This GeneChip allows researchers to assess the level of expression (messenger RNA abundance) of most citrus genes in specific tissues or conditions. The chip contains 30,264 probe sets (22 probes each) for measurement of citrus transcripts and 5,023 probe sets (56 probes each) as genetic markers for 3,219 genes. The chip also includes probes covering a region of the trifoliolate orange genome containing a *citrus tristeza virus* resistance locus, as well as probe sets for detection of several viruses, viroids, *Xylella* species, and commonly used transgenes.

Interpretation of data from this chip is supported by gene function annotations and interactive graphical user interfaces in HarvEST: Citrus software. The annotations include information extracted from well developed public databases on the model plant *Arabidopsis* and poplar, as well as a protein database called UniProt. HarvEST: Citrus is available for Windows from harvest.ucr.edu and online through www.harvest-web.org.

At the start of this project citrus lagged far behind most other major agricultural plants in its public genomic resources. This project significantly altered the dynamics in the international citrus research community, such that California became the lead location in citrus genomics.

This CRB project, supported by matching funds from the University of California Industry University Cooperative Research Program and in-kind contributions from Affymetrix, Inc., provided researchers with tools to allow them to capitalize on the genomics revolution in the pursuit of new varieties and management strategies for California citrus.

The main objective in the 2006-2007 fiscal year was to use the citrus chip to address several biological questions that are pertinent to California citrus. The type of information that we gathered relates to genes, proteins and metabolic pathways of citrus.

In 2006-2007 we produced new data related to: (1) development of the easy peeling trait of mandarins, and (2) the response of citrus peels to feeding by thrips. We also studied existing data gathered during the previous year of this project and progressed with the preparation of manuscripts for publication on (1) sweet orange and trifoliolate orange exposed to iron deficient and normal growth conditions, (2) orange fruits held in storage, (3) sweet orange on sour orange rootstock responding to infection with *citrus tristeza virus*, (4) low acid versus high acid lemons and, (5) the basis of easy peeling in mandarins.

Many correlations were drawn from analyses of the data. For example, one result of the easy peeling study is that an ethylene-mediated response is involved. One hypothesis from this observation is that it may be possible to manage the easy peeling trait post-harvest using stimulators and inhibitors of the ethylene response.

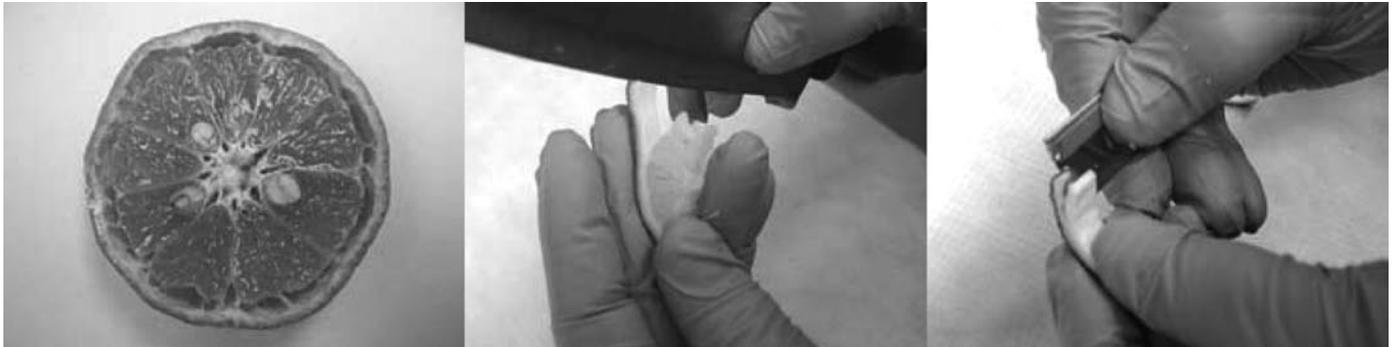


Figure 1. *An image of an easy-peeling mandarin and dissection of the innermost albedo tissue from a young fruit at the onset of rind separation. Studies from this project have provided insights into the basis of this trait, which is of great importance to citrus consumers.*

SUMMARY:

This project vastly changed the landscape of citrus research such that citrus no longer is in a lower tier of experimental systems in relation to genome-wide gene expression studies or genetic marker resources. The best model for citrus genome research now is citrus itself. Continuing use of the new resources, and the applications derived from such use, will facilitate development of improved varieties and cultural practices that benefit California growers and producers.

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