

EST Libraries and Bioinformatics for California Citrus

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This project provides foundational information in the area of “Genomics”. The information is about the genes, proteins and metabolic pathways of citrus. This information facilitates other research and practical applications. Research applications include identification of genes that underlay pathogen resistance and development of transgenic strategies to investigate gene-trait relationships and develop new varieties. Practical applications include genetic markers for breeding and variety identification, and new methods to measure fruit quality.

At the start of this project, citrus lagged far behind most other major agricultural plants in its public genomic resource base. In addition, investigators in Florida and internationally had accumulated considerable information that was not being shared publicly. This project has significantly altered the dynamics in the international citrus research community, such that California is now the leading location in citrus genomics. This shift in national and worldwide leadership will ensure that the California citrus industry will not miss opportunities to capitalize on the genomics revolution.

One 2004-2005 objective was to finish the collection of expressed gene sequences pertinent to citrus genomics in general and California citrus specifically that would precede the design and production of a citrus genome array. This was accomplished. Our project reached a final mark of about 124,000 EST sequencing reactions, among which were nearly 100,000 sequences of sufficiently high quality to include them in microarray design. This was coupled with about 66,000 other high quality EST sequences collectively from all other sources worldwide to provide the information base for the citrus genome array.



Figure 1. Affymetrix citrus Gene Chip.

Another objective was to produce an Affymetrix citrus GeneChip®. This was accomplished (Figure 1). We worked intensively with the Affymetrix Chip Design team from January through October 2005 to define the content of the citrus Gene Chip. It contains 30,264 probe sets (22 probes each) for measurement of citrus transcripts, and 5,023 probe sets (56 probes each) to serve as genetic markers for 3,219 genes. The citrus Gene Chip also includes tiling of one region of the *Poncirus trifoliata* 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 Gene Chip is supported by gene function annotations and interactive graphical user interfaces in the HarvEST:Citrus software (harvest.ucr.edu).

Another objective was to begin to use the citrus Gene Chip to address issues pertinent to California citrus. We received the first batch of Gene Chips in November and immediately used them to analyze samples of *C. sinensis* and *P. trifoliata* exposed to iron deficient and normal growth conditions. Publication of the results of this study should occur in 2006.

Overall perspective: This project has 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.

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