

## **Microarrays for Gene Expression and Mapping in Citrus**

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This project is best considered as a supplement to projects 5200-121 (EST Libraries and Bioinformatics) and 5200-125 (Genetic Maps of Sweet Orange and Trifoliolate Orange) which use a new tool, microarrays, to study patterns of gene expression and map genes. Those projects are funded by CRB with matching funds from UC Discovery, but we are not permitted to spend those Discovery funds to purchase the microarrays necessary for the research. This CRB grant supplemented other UC funds and allowed us to purchase the chips needed to conduct the other projects.

The specific objectives of these projects are to use GeneChip® microarrays to: (1) Characterize changes in patterns of gene expression in citrus fruit during postharvest storage, CTV infection of sweet orange on sour orange, and in response to iron chlorosis stress; and (2) Develop detailed genetic maps of sweet orange and trifoliolate orange.

To improve the array content, GeneChip® design and manufacturing were delayed from the original schedule such that we began to receive the chips starting in November. We do not yet have all of the results from the planned experiments, but the initial datasets showed that the microarrays are of excellent quality. We expect results to accumulate rapidly during 2006.



*Figure 1. Image of about 2% of a Citrus GeneChip® used for analysis of iron chlorosis tolerance. Each visible dot is a probe (25-base DNA fragment) from a gene that is expressed in roots during iron chlorosis stress. Dark areas are probes from genes that are not detectably expressed under these conditions. This microarray contains an embedded chip identifier “GeneChip Citrus”.*