

Improving Peel Quality of California Citrus Fruit

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An essential component of high quality citrus fruit is an external finish free of blemishes, defects, and disease. The peel or rind of citrus fruit, composed of flavedo and albedo layers, is a highly physiologically active tissue prone to injury and environmental influence.

Our study is establishing relationships between internal fruit quality, specific disorders, and expression of specific genes. This information will increase our mechanistic understanding of the underlying causes of peel disorders and facilitate development of diagnostic and therapeutic strategies to overcome them. This in turn will greatly enable conventional (chemical), biological (biochemical), and genetic (breeding or transformation) control strategies.

Our study has two specific objectives: 1). Identify transcripts expressed in peel tissues of citrus fruit by their spatial and temporal expression during normal fruit development, and 2). Identify genes associated with normal citrus peel development and with manifestation of peel disorders.

We have completed the research to identify genes associated with citrus peel development and manifestation of peel-related disorders. Two large experiments that were in progress have been completed.

The first concerned fruit development and quality. We have analyzed flavedo, albedo, and juice sac tissues from lemon, mandarin orange, grapefruit, Valencia and Navel orange to compare and contrast differences in gene expression and to discover citrus fruit-specific genes. Three individual fruits of each type were examined separately as biological replicates for this experiment, which contained 1.4 million probe sets of data (1,357,695 data sets) obtained from 15 million data features (14,934,645 data features).

The second experiment analyzed puff tissues in fruit at immature, intermediate, and mature stages. These were collected from trees at the Rutz ranch (in San Diego County) that previously showed puff development and normal fruit from the same location. This experiment has also been completed and contained 1.3 million probe sets of data (1,267,182 data sets) obtained from 14 million data features (13,939,002 data features).

The GeneChips that we used (Affymetrix) allows us to analyze over 30,000 genes from citrus trees. Based on one-way ANOVA of the microarray results, we have identified 8,433 genes associated with the puff disorder ($p < 0.05$), and 5,324 genes differentially expressed between at least two of the five types of fruit ($p < 0.0001$), with 2,112 genes common to both groups. The 5,324 genes associated with fruit types are also grouped according to the three tissues where they were differentially expressed, and all possible combination of the three.

These results, and further analysis of the microarray data at different levels of statistical significance, lay the groundwork for identifying important networks of interacting genes. Newly developed computational tools for network analysis can be applied to microarray results to further define specific genes and their interactions that give rise to the diversity of fruit traits and disorders that occur during fruit development.



One objective of this project is to identify genes associated with manifestations of peel disorders like puff.

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