8.11 Gene Expression in *Citrus sinensis* Fruit Tissues Harvested from Huanglongbing-Infected Trees

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Global gene expression in HLB-infected fruit tissues was evaluated using an Affymetrix array containing 30,279 *Citrus* spp. ESTs. Flavedo (FF), vascular tissue (VT), and juice vesicle (JV) tissue of symptomatic (SY), asymptomatic (AS), and healthy (H) fruit harvested from sweet orange Hamlin and Valencia cultivars was investigated. Transcriptional profiles indicated the number of genes impacted by HLB was highest in FF and VT and least in JV. In Hamlin, over 860 genes were changed in SYVT and SYFF compared with H tissues. In Valencia, fewer genes were changed in SYVT and SYFF, but approximately 50% additional genes (397 genes) were changed in SYJV compared with Hamlin. As in SY tissues, ASVT and ASFF were strongly impacted and had similar gene changes in Valencia. However, only 28 genes were altered in ASJV compared with HJV. The top five gene groups with high numbers of changes included transporters, carbohydrate metabolism, genetic information processes, phytohormone metabolism, and defense responses. Highest titer of the HLB bacterium was found specifically located in SYVT. Gene changes in SYVT were associated with host-pathogen interaction and seed abortion, and those in SYJV with fruit size, juice sac maturity and morphology, and juice quality. Similar to SY fruit, girdled fruit were small and could abscise prematurely. A comparison of gene expression between HLB-infected and girdled treatments will be presented to differentiate HLB-mediated gene changes from those related to girdling-related carbohydrate loss.