Title Tropical fruit genomes sequencing and postharvest product quality

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Abstract

The sequencing of tropical fruit genomes is entering a new phase, as sequencing technology undergoes dramatic changes in speed and cost. The three major steps in genome sequencing are the actual sequencing, the application of bioinformatics to predict gene and confirming the identity of the microarray technology provide the possibility to determine the genes expressed and their regulation at specific stages of fruit development. The most difficult is the third step of connecting the predicted genes to physiological function and directly confirming that connection.

Papaya (*Carica papaya* L.) is the first fleshy fruit with a climacteric ripening pattern to be sequenced. As a member of the Rosids superorder in the order Brassicales, papaya apparently lacks the genome duplication that occurred twice in Arabidopsis. The predicted papaya genes that are homologous to those potentially involved in fruit growth, development, and ripening were investigated. Compared to Arabidopsis and tomato, fewer genes were predicted in papaya that may impact sugar accumulation, ethylene synthesis and response, respiration, chlorophyll degradation and carotenoid synthesis were predicted. Similar or fewer genes were found in papaya for the enzymes leading to volatile production than so far determined for tomato.

The presence of fewer papaya genes in most fruit development and ripening categories suggests less subfunctionalization of gene action. The lack of whole genome duplication and reductions in most gene families and biosynthetic pathways make papaya a valuable and unique tool to study fruit evolution and the complex regulatory networks active in fruit ripening and quality development.

Using a papaya microarray preliminary data has shown that as ripening begins the genes associated with cellulose synthase are highly expressed in green fruit and decreased 8-fold at 30% ripe stage. In the 30% ripe fruit cell-wall genes that increased include a 4-fold increase in polygalacturonases, 3-fold for pectinesterases and pectate lyase, 2-fold glucanases, endoxylanase, xyloglucan-endotransglycosylase, ß-1,4-xylosidase, glucosidase, ß-glucuronidase, and chitinase. A ß- and œ-galactosidase both decline at this stage. Four expansions increased and two declined. In addition, two of the three predicted ethylene receptors are up-regulated and the third is not expressed in either stages, auxin-related genes mostly declined, as do most GA-related genes. Cytokinin genes involved in degradation are up-regulated with ABA genes showing little change

between the two stages. This data suggests that the regulatory networks present an opportunity to modify ripening, fruit quality, phytonutrients content and postharvest disease resistance in targeted way. The data also suggests that direct physiological homology and gene action may not occur between different fleshy fruit species.