Title	Tropical fruit genomes and postharvest technology
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Abstract

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: actual sequencing, application of bioinformatics to predict genes and confirming the identity of the predicted gene. Full genome sequencing and expressed sequence tags, often coupled to 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 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. 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. The regulatory networks present an opportunity to modify ripening, fruit quality, phytonutrient content and postharvest disease resistance. The data also suggest that direct physiological homology and gene action may not occur between different fruit species.