Title Development and utilization of genomic tools to identify candidate genes for melon (*Cucumis melo*) fruit quality

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Abstract

Melon species include a wide variety of cultivars producing fruits differing in many fruit traits. Great efforts have been made trying to understand the genetic mechanisms underlying these traits, but, without genomic sequences, research in this area is limited. In this experiment, a total of 3269 unigenes have been developed, adding in about 30-fold gene sequence to the current melon ESTs collection. In addition, a melon validated cDNA microarray has also been generated and was used to a transcriptome comparison of fruit maturation in a climacteric (Dulce) and non-climacteric (Rochet) melon, which display diversity in multiple traits of interest including flesh color, aroma volatile production, sugar content and softening process. Our goal was, first, to introduce to the melon research community new genomic tools and resources including ESTs and microarrays, to provide public genomics infrastructure to assist research at the molecular level for species of the Cucurbitaceae family. Second, to shed light on molecular mechanisms that underlie ripening while simultaneously increasing the reservoir of ripening related genes for melon species. By focusing our analysis on the expression patterns of genes that may participate in biological pathways related to the fruit quality traits, we were able to identify specific differences that were consistent with the variable fruit traits between these two varieties and including fruit softening, aroma, flavor and carotenoids biosynthesis. Our results suggest that the quick softening phenotype of Dulce during ripening was mainly caused by the concomitant up regulation of isoforms of genes involved in cell wall degradation including PGs, GALs, XTHs, EXPs and PME. Multiple regulatory mechanisms may contribute to the orange color (beta-carotene) of Dulce flesh but their gene targets are clear in that transcriptional regulation of DXR and PDS appears to be highly consistent with the carotenoid accumulation profiles of Dulce versus Rochet. Aroma variation between Dulce and Rochet is likely due to reduced transcription and enzyme activity of AAT.