



IDENTIFICATION OF DIFFERENTIALLY EXPRESSED GENES DURING THE RIPENING OF AVOCADO FRUIT

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Introduction. Avocado (*Persea americana* Mill.) is a climacteric fruit well recognized by its benefits on human health, mainly because of the high content of vitamins, fatty acids and other lipids that accumulate over its ripening. Ripening of climacteric fruits involves a series of coordinated metabolic events that alter the biochemistry, physiology and gene expression (1). To date, little is known about the molecular regulation of the synthesis of those metabolites in avocado fruit. The goal of this study was to identify differentially expressed genes during ripening of avocado.

Methods. Total RNA was isolated from immature and mature belonging 10 ecotypes of avocados. Sequencing was performed in a SOLiD v3 system generating ~5 to 20 million reads per sample. Transcript abundance was analyzed using CLC Genomic 5.5 software. Trimmed reads (quality >20, length >25 bp) were mapped against a cDNA reference using default parameters. After quantile normalization using RPKM, differentially expressed (DE) genes were identified using Kal's Z-test with a FDR <0.05 and a fold change ± 2 . Functional classification was performed using BLAST2GO (2).

Results. The results of trimmed and mapping against the cDNA reference, are summarized in table 1. A total of 1,223 genes were DE between immature and mature fruits. From those, 440 were preferentially expressed in mature and 783 were preferentially expressed in immature tissues. To gain more information about the molecular function of the identified genes, they were classified according to their Gene Ontology into biological processes terms. In mature fruits, genes related to metabolic processes were up-regulated, meanwhile in immature fruits, genes related to signaling were down-regulated and those related to reproduction and fruit growth were up-regulated (Fig.1). Among the most DE genes, a gene, that codes for a delta-12 fatty acid desaturase presented a fold change of 992. This means that is highly expressed in the mature stage. This is a key gene in the

biosynthesis of linoleic acid, which is an essential fatty acid in humans.

Table 1. Summary statistics for SOLiD reads.

	Immature	Mature
Total reads	65,155,846	64,743,988
Reads after trim	27,302,216	31,530,501
Mapped reads	19,244,244	23,669,635
Non specifically	7,873,413	9,288,067
Uniquely	11,370,831	14,381,568

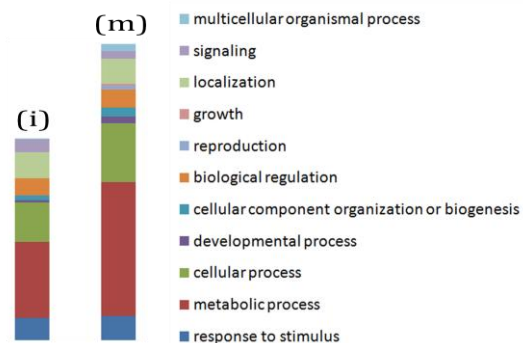


Fig. 1 Gene Ontology classification (level 2) of differentially expressed transcripts. (i) immature and (m) mature avocado fruits.

Conclusions. This analysis provides a strong tool for compression of the avocado ripening at the genetic level and identified a set of genes that putatively are regulating avocado fruit maturation. This study also provides a framework for the identification of genes for the development of new varieties with improved nutritional and commercial traits.

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