

RNA-SEQ AND METABOLITE PROFILING OF TWO PEACH VARIETIES

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In order to generate a detailed description of the transcriptome, an Illumina RNA-Seq experiment was conducted on two fruit developmental stages of peach varieties Bolero and OroA, that exhibit contrasting quality traits including flesh texture, fruit weight and aroma. In addition, GC/MS analysis was conducted on 26 metabolites belonging to primary and secondary metabolism. Mapping of Illumina reads to the publicly available peach genome sequence allowed estimation of expression levels from RNA-Seq data. Considering the two maturation stages, a total of 1274 differentially expressed transcripts, within and between the two varieties, were identified. When considering currently available peach gene annotations, the data allowed the identification of 277 intronic transcripts, 5807 novel isoforms, and 992 unknown intergenic transcripts. RNA-seq data were also a source for the identification of SNPs. Comparing Bolero and OroA transcriptomes, a total of 16804 SNPs were found. These will be used for enrichment of the SSR-based genetic map previously obtained from an F1 population from the cross of the two cultivars (Eduardo et al., 2011, *Tree Genetics & Genomes* 7:323–335) and QTL analysis of fruit quality traits. Benefits of using an RNA-seq approach for transcriptome analysis are discussed taking into account previous microarray experiments conducted on the same cultivars.