

# RNA-Seq analysis and transcriptome assembly of raspberry fruit (*Rubus idaeus* "Heritage") revealed several candidate genes involved in fruit development and ripening

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Using Illumina HiSeq 2000 sequencing platform (100 bp double-end reads), we performed transcriptome analysis of flower (F), green (G) and pink (P) fruit stages of red raspberry.

Transcriptome was obtained by the de-novo assembly of 298 Million high-quality reads through Trinity assembler, out of the 41,650 high quality transcripts, 18,171 coding sequences were successfully characterized using databases such as UniProtKB, NCBI Non-Redundant, KEGG, Gene Ontology, and InterPro-Scan. A total of 2409 transcripts were further identified as differentially expressed genes (DEGs) between the three libraries generated, and 253 DEGs were found between different fruit stages. Singular enrichment analysis of gene ontology (GO) detected an important group of DEGs over-expressed during fruit development; and associated with ethylene, auxin conjugation, abscisic acid response, brassinosteroids biosynthesis and signaling, and cell-wall disassembly processes. Our transcriptome data provides valuable insights on genes involved in the ripening process of *Rubus* fruit, as a representative of non-model fruit species, and may help in

developing these cultivars with improved fruit quality characteristics in the years to come.