Transcriptome profiling and identification of the functional genes involved in berry development and ripening in Vitis vinifera

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Transcriptome profiling and identification of the functional genes involved in berry development and ripening in *Vitis vinifera*

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Abstract

The length of berry lag phase determines the overall time needed for grape berries to get mature, but the functional gene networks in this phase have not been well documented. In order to reveal the origin of the somatic variation and regulation mechanism of grape berry development and ripening, an early ripening mutant of *Vitis vinifera* with a shorter lag phase was used for transcriptome profiling. The RNA-seq results revealed that 2021 and 2470 genes were up- and down-regulated, respectively, in the early ripening mutant compared to the wild type. The GO and KEGG enrichment analysis indicated that the up-regulated genes belonged to several pathways and metabolisms, among which the most significant constituents were for biosynthesis of secondary metabolites and flavonoid biosynthesis. The down-regulated genes were involved in biosynthesis of secondary metabolites, plant hormone signal transduction, and photosynthesis. Many transcription factors including WRKYs, AP2-EREBPs, and MYBs were also differentially expressed, suggesting their regulatory roles in berry development and ripening. The transcriptomic comparisons suggested that the prominent up-regulation of an *Arabidopsis SnRK3.23, CIPK23* or *PKS17* homolog could have driven the early ripening phenotype in the mutant by activating the downstream VvABF2 transcription factor in the ABA signaling. At the same time, ethylene and auxin were also involved in this process. As a result, the major ripening related genes, e.g., *MYBA1*, *MYBA2*, *VvUFGT*, *GRIP22*, and *STS* were activated in the mutant. The results are of importance for future studies on manipulation of grape berry ripening time.

Keywords: early ripening; transcriptome; mutant; sequencing; *Vitis vinifera*

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