

山葡萄不同着色时期果皮转录组测序分析

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摘 要:【目的】探究山葡萄果皮转色过程中相关基因的表达。【方法】以不同成熟期的山葡萄果皮为材料,采用高通量测序技术进行转录组分析,探讨其转色过程中花色苷含量及其相关基因的变化。【结果】经过测序得到3个时期的 clean reads 分别为:转色前 20 157 930 条,50%着色期 16 197 432 条,完熟期 16 410 824 条;GC 含量分别为 48.41%、48.04%和 49.54%;各时期的 Q30 大于等于 94.73%。通过与参考基因组进行序列比对,各样品 Read 与参考基因组的比对效率为 60.57%~67.77%,并且唯一比对位置的数量均超过 58.99%,比对到基因组上的序列绝大部分分布在外显子区,均为 96.3%以上。本试验将3个样品中转色前分别与50%成熟期和完熟期进行了基因差异表达统计分析,结果显示 COG 功能注释分别为 1 305、1 602 个。【结论】明确了山葡萄果皮转色过程中相关基因的变化,为进一步大量挖掘山葡萄果皮成熟过程中重要表达基因奠定一定的基础。

关键词: 山葡萄;转录组;测序;功能注释

中图分类号:S663.1

文献标志码:A

文章编号:1009-9980(2017)07-0781-09

Sequencing analysis of transcriptome of *Vitis amurens* during different periods of coloration

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Abstract: 【Objective】*Vitis amurens* is one of the most cold-resistant *Vitis* plants, therefore, it is a valuable resource for cold-resistant breeding in *Vitis* plants. The fruits of *V. amurens* are rich in proteins, carbohydrates, minerals and many kinds of vitamins. The fruit color is an important character influencing fruit quality. The fruit color is mainly decided by content and composition of anthocyanins. The biosynthesis process of anthocyanin is very complicated is influenced by many genes. Therefore the study of the expression of related genes during color transformation of the fruits is of great value. 【Methods】The fruit skins of *V. amurens* were collected during different ripening stages, before color-changed, 50% color-changed and full ripe stage as experimental materials and high-throughput sequencing technology IlluminaHiSeq was used to conduct sequencing. After data filtering, we got Clean Data and run sequence comparison with designated reference genome to obtain Mapped Data and then we did transcriptome analysis. 【Results】Through transcriptome sequencing and analysis of the related genes in the skins toward three different ripening stages, clean reads were obtained and they were 20 157 930 for before color-changed, 16 197 432 for 50% color-changed and 16 410 824 for full ripe stage, the GC contents were 48.41%、48.04% and 49.54% respectively. The Q30 contents of three different maturation periods were or were over 94.73%, indicating the high quality of transcriptome sequencing and the high accuracy of the data. TopHat2 was adopted to do sequence alignment between Clean Reads and reference genome to obtain the position information of maturation related genes on reference genome or genes. The sequence alignment efficiency between reads of three different maturation periods and reference genome was from 60.57% to

收稿日期: 2016-12-28 接受日期: 2017-03-16

基金项目: 国家自然科学基金(31260067);吉教科合字[2016]第255号

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