

Molecular basis of postharvest granulation in orange fruit revealed by metabolite, transcriptome and methylome profiling

Shixiang Yao, Zhengming Wang, Qi Cao, Jiao Xie, Xiaorong Wang, RuiZ hang, Lili Deng, Jian Ming and Kaifang Zeng

Postharvest Biology and Technology, Volume 166, August 2020, 111205

Abstract

Postharvest granulation is a serious physiological disorder during storage in navel orange fruit, while the molecular basis remains largely unknown. Orange fruit exhibited obvious gradient of total soluble solids, which gradually increased from stem to styler region, and granulation occurrence often initiated at the stem and extended towards the rest. Here, we performed systematical analysis of metabolites, coding transcriptome, lncRNAs and single-base resolution methylome in juice sacs during granulation. Through a comparison of RNA-Seq data generated from stem and mid juice sacs of either normal or incipient granulated fruit, 6022 genes were reliably identified to be differentially expressed upon granulation, which uncovers various metabolic pathway underlying the decreasing of sugars and organic acids, and increasing of cell wall components. Further, 486 lncRNAs were differentially expressed in granulated juice sacs, predicted to regulate cell wall metabolism. Genome wide analysis of fruit methylome during granulation indicated that DNA methylation might be unlikely involved in granulation process. A serial of transcription factors, including homolog of *E2Fc* and *UPB1*, potentially play crucial roles in granulation process, mainly *via* regulating the secondary cell wall synthesis. It is the first study to unravel the molecular mechanism underlying postharvest granulation in sweet orange fruit.