

Comparative transcriptomic analysis of storage roots in cassava during postharvest physiological deterioration

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Abstract

Cassava is an important starchy and food crop; however, the commercial value of cassava is seriously constrained by postharvest physiological deterioration (PPD). In this study, the molecular mechanism underlying PPD was studied by comparative physiological and transcriptomic analyses. Physiological analyses indicated that the contents of H₂O₂ and malondialdehyde (MDA), and the activities of superoxide dismutase (SOD) and catalase (CAT) all increased along with PPD development. Further transcriptomic analysis investigated the distribution of the differential expression profiling and identified a total of 10,347 differentially expressed genes (DEGs) during PPD. Notably, most of the genes encoding antioxidant enzymes and protein kinases showed significant upregulation at transcriptional levels, indicating the activation of antioxidant system and kinase-mediated signaling pathway during the PPD process. In addition, the genes involved in the starch synthesis pathway were repressed, whereas the genes associated with the starch degradation pathway were induced, thus leading to a decrease in starch content during the PPD process. Together, this study yields new insight into the transcriptional regulation network during the PPD process and provides potential gene resources for the delay of PPD in cassava.