

Transcriptomic analysis reveals key genes associated with the biosynthesis regulation of phenolics in fresh-cut pitaya fruit (*Hylocereus undatus*)

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Abstract

Wounding stress induces phenolic accumulation in pitaya fruit (*Hylocereus undatus*). This study aimed to elucidate the possible molecular mechanism underlying the wound-induced phenolic biosynthesis in fresh-cut pitaya fruit based on transcriptomic and bioinformatic analysis. Wounding stress induced the activation of metabolic pathways associated with phenolic biosynthesis, including secondary metabolism such as phenylpropanoid pathway and flavonoid pathway, signaling molecules metabolism such as ethylene, reactive oxygen species and jasmonic acid, and primary metabolism such as glycolysis, pentose phosphate pathway and shikimate pathway. Moreover, weighted gene coexpression network analysis and evolutionary relationship analysis revealed that 1 HuMYB, 3 HubHLHs, 7 HuAP2-EREBPs could be identified as putative transcription factors participating in the regulation of wound-induced phenolic biosynthesis in pitaya fruit. These findings validated previous study that wounding stress induces the conversion of hexose pool to supply essential carbon skeletons for the phenolic accumulation in fresh-cut pitaya fruit in transcriptional level and provide important and useful genetic information for further studies on the functions of transcription factors in wounding response in pitaya fruit.