

GERMPLASM EVALUATION AND FUNCTIONAL ANALYSES OF KEY GENES INVOLVED IN BETALAIN BIOSYNTHESIS IN PITAYA

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ABSTRACT

In this study, genetic diversity, whole genome sequencing and key genes involved in betalain biosynthesis of pitaya were studied. The genetic diversity of 121 pitaya germplasms were analyzed using SCoT molecular markers. Specific markers related to red and white pulp colors were obtained. We sequenced, and assembled the high-quality, chromosome-level genome of the *Hylocereus undatus* cultivar using PacBio along with Illumina sequencing platforms and Hi-C technology. The assembly had a 1.41 Gb overall size, and the scaffold N50 reached 127.15 Mb. Totally 27,753 protein-coding genes were predicted, and 26,371 genes (95.1%) have been annotated. A total of 53 genes involved in betalain biosynthesis were identified from the *H. undatus* genome. Results from VIGS, transient expression, yeast recombinant expression, and genetic transformation showed that *HmoCYP76AD1*, *HmoDODA α 1*, and *HmocDOPA5GT* play key roles in pitaya betalain biosynthesis. These studies present valuable information for the genetic diversity of pitaya germplasm and provide a guide for breeder to develop new pitaya cultivars efficiently.

Keywords: pitaya, germplasms, SCoT, genome sequencing, betalain biosynthesis