Molecular Characterization and Structural Analysis of Flavonoid Biosynthetic Genes and a Putative *CaF3'5'H* in *Curcuma alismatifolia* 'Blue-Tung'

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Abstract

Curcuma alismatifolia (Siam Tulip) is a commercially significant floriculture crop native to Thailand. Diversifying bract coloration is a primary objective for enhancing its global market competitiveness. In this study, we investigated the molecular basis of bract pigmentation by characterizing six core structural genes in the flavonoid biosynthetic pathway: *CHS, CHI, F3H, F3'5'H, DFR,* and *ANS*. Through a comparative analysis of genomic DNA and cDNA from the purple-bracted cultivar 'Blue-Tung', we successfully elucidated the exon-intron architecture and obtained the complete Coding Sequences (CDS) for *CHS, F3'5'H,* and *DFR*. Notably, we report for the first time a novel sequence of putative *CaF3'5'H*. Structural analysis via homology modeling further identified conserved motifs essential for Cytochrome P450 enzyme functionality, providing insights into its catalytic role. These genomic resources and identified sequences serve as a foundational framework for functional genomics and the development of molecular markers to facilitate precision breeding for color traits in *C. alismatifolia*.

Keywords: *Curcuma alismatifolia*, Siam Tulip, Flavonoid biosynthesis pathway, Exon-intron architecture, DNA sequences, the purple-bracted cultivar ‘Blue-Tung’.