

**Title** Genetic relation of putative genes involved in anthocyanin biosynthesis of a hybrid Vanda variety (*V. teres* x *V. hookeriana*) and other orchids

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### Abstract

Flavonoid biosynthesis is one of the most feature attributes, extensively determined in colourful flowers. A hybrid Vanda variety (*V. teres* x *V. hookeriana*), provides an opportunity to examine the expression of genes along the anthocyanin biosynthetic pathway. In this study, we have cloned and sequenced four gene fragments, including phenylalanine ammonia-lyase (PAL), chalcone synthase (CHS), flavanone 3-hydroxylase (F3H) and dihydroflavonol 4-reductase (DFR). The obtained lengths of the nucleotide sequences of PAL, CHS, F3H and DFR fragment were 697 bp, 538 bp, 536 bp and 445 bp, which were encoded to the putative proteins of 231 amino acids (aa), 178 aa, 178 aa and 148 aa, respectively. The nucleotide blast analysis of the four genes had significant homologies with some other orchid species. The putative PAL gene was 93 % and 90 % identical to that of *Phalaenopsis* x *Doritaenopsis* hybrid cultivar orchid and *Bromheadia finlaysoniana* orchid. The putative CHS gene was 91 % identity to that of *Phalaenopsis* hybrid cultivar orchid while the putative DFR gene was 89 % identical to that of *Bromheadia finlaysoniana* orchid and the putative F3H gene was 89 % identical to *Bromheadia finlaysoniana* orchid. Phylogenetic trees of the four predicted proteins from gene data base NCBI revealed that they are most related to a subgroup in the family Orchidaceae except the F3H.