

論文名 : Molecular Studies on *FLOWERING LOCUS T* Gene in *Vanda* Hybrid (要約)

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Vanda is an important ornamental tropical orchid in Thailand and shows great potential in international markets. Since there has been limited research on flowering processes and regulations, flower production programs cannot be properly managed. This study aims to identify ortholog for *FT* gene in *Vanda* and investigate whether expression of *FT* gene of *Vanda* hybrid is regulated by day length. The molecular studies on *FLOWERING LOCUS T* gene in *Vanda* hybrid was carried out in 2 experiments as follows:

Experiment 1: Isolation and functional analysis of *FLOWERING LOCUS T* orthologous gene from *Vanda* hybrid

To understand the genetic mechanisms in the *Vanda* flowering process, the ortholog of the *FLOWERING LOCUS T* (*FT*) gene (*VaFT*) was isolated and characterized by using *Vanda* ‘Ratchaburi-Fusch Katsura’. An open reading frame (ORF) of 531 bp, translating a protein of 176 amino acids (AAs), was obtained. The AA sequence alignment of *VaFT* indicated that it contains a conserved domain, distinctive to the phosphatidylethanolamine-binding proteins (PEBPs) superfamily, and shares high homology with other orchid *FT* proteins: 93% of *PaFT* from *Phalaenopsis aphrodite*, 91% of *CgFT* from *Cymbidium goeringii* and 89% of *OnFT* from *Oncidium Gower Ramsey*. Ectopic expression of *VaFT* in transgenic *Arabidopsis* resulted in activation of floral meristem identity gene *APETALA1* (*API*) and early flowering with fewer rosette leaves than non-transgenic *Arabidopsis*. Our data suggests that *VaFT* is apparently a PEBPs gene in orchids that conducts the transition of flowering.

Experiment 2: Effect of day lengths on *FLOWERING LOCUS T* gene expression in *Vanda* Hybrid by qualitative real time PCR

Photoperiod is an important external environment factor that regulate flower transformation in plant by activation of *FT* gene. To clarify whether expression of *FT* gene of *Vanda* hybrid is regulated by day length, plants were grown under different photoperiod conditions i.e. natural light as control, short-day (8 h of light) for 6 weeks and short-day (8 h of light) for 9 weeks then plants were sampling at week 0, 1, 3, 5, 7, 9 and 10 for qRT-PCR analysis. The results found that percentage of visible bud and flowering were higher when plant received natural light, short-day treatments delayed flowering time. The relative expression of *VaFT* of all treatments showed similar trend of accumulation, with the level higher at week 7th and gradually decreased at week 9th and 10th. These unclear difference among treatments indicate that *Vanda* probably exist of other *FT* genes which may has more relationship with *Vanda* flowering or it is possible that early flowering affected by *FT* gene at the beginning of the experiment because *FT* gene was already expressed at week 0. Further experiments should be performed to determine the relationship between expression of *Vanda API* gene and flowering for *Vanda* plants.

In conclusion, our results indicate that *VaFT* is a putative PEBPs in *Vanda* which regulates flowering transition. Short-day condition delayed flowering of *Vanda* ‘Ratchaburi Fusch - Katsura’ but the relative expression of *VaFT* in plants under different day length conditions was unclear. Further experiments should be performed to determine the relationship between the expression of the *Vanda API* gene and the flowering of *Vanda* plants. Our discovery is the first information on the *Vanda* floral gene which is probably regulating flowering transition in *Vanda*, and further analyses of this gene could provide information to clarify the mechanism of *Vanda* flowering.