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Molecular characterization and functional analysis of a *Flowering locus T* homolog gene from a *Phalaenopsis* orchid

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ABSTRACT. Warm day and cool night conditions significantly induce reproductive spike formation in *Phalaenopsis* plants; hence, determining the flowering mechanism regulating the reproductive transition is important. *Flowering locus T* (*FT*) plays important roles in flowering induction in several plants. To explore spike induction by warm days and cool nights in *Phalaenopsis* orchids, we isolated the *FT* (*PhFT*) from *Phalaenopsis* hybrid Fortune Saltzman. The cDNA of *PhFT* was 809-bp long and contained a 531-bp open reading frame encoding a putative protein of 176 amino acids, a 58-bp 5'-untranslated region (UTR), and a 220-bp 3'-UTR. The predicted molecular mass of PhFT was 19.80 kDa, with an isoelectric point of 8.68. The PhFT was predicted to possess the conserved functional regions of the phosphatidylethanolamine-binding protein superfamily. Nucleotide sequence data indicated that *PhFT* contained 3 introns and 4 exons. Sequence alignment and phylogenetic analyses of PhFT revealed high homology to the FT proteins of *Cymbidium goeringii* and *Oncidium* Gower Ramsey. Quantitative real-time polymerase chain reaction analysis indicated that *PhFT* mRNA

was expressed in roots, apical leaves, mature leaves, and flowers. In flowers, *PhFT* was expressed more in developing floral buds than in mature flowers and was predominantly expressed in ovaries and petals. Ectopic expression of *PhFT* in *Arabidopsis ft-1* mutants showed novel early-flowering phenotypes that lost their siliques. Our results indicated that the ectopic expression of *PhFT* could partially complement the late flowering defect in transgenic *Arabidopsis ft-1* mutants. Our findings suggest that *PhFT* is a putative *FT* homolog in *Phalaenopsis* plants that regulates flowering transition.

Key words: *Flowering locus T*; Flowering transition; Gene expression; *Phalaenopsis* orchids; Warm day and cool night conditions

