

REVIEW

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Functional diversification and molecular mechanisms of *FLOWERING LOCUS T/TERMINAL FLOWER 1* family genes in horticultural plants

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Abstract

Flowering is an important process in higher plants and is regulated by a variety of factors, including light, temperature, and phytohormones. Flowering restriction has a considerable impact on the commodity value and production cost of many horticultural crops. In *Arabidopsis*, the *FT/TFL1* gene family has been shown to integrate signals from various flowering pathways and to play a key role in the transition from flower production to seed development. Studies in several plant species of the *FT/TFL1* gene family have revealed it harbors functional diversity in the regulation of flowering. Here, we review the functional evolution of the *FT/TFL1* gene family in horticulture plants and its unique regulatory mechanisms; in addition, the *FT/TFL1* family of genes as an important potential breeding target is explored.

Keywords: FLOWERING LOCUS T (FT), TERMINAL FLOWER 1 (TFL1), Flowering, Functional evolution, Horticultural plant

Introduction

Flowering is an important stage in the life history of higher plants that includes the processes of flower bud differentiation, development, and the opening of flowers (Parmar et al. 2017; Xu et al. 2019). An optimal flowering is of great significance for plants to complete their life cycle under suitable environmental conditions (Su et al. 2019). Horticultural plants are critical components of agricultural production; they include fruits, flowers, vegetables, spices, medicinal, and aromatic plants (Karkute et al. 2017). Understanding how environmental factors influence the flowering transition of horticultural plants, as well as the underlying mechanisms involved, can help to improve the commercial value, lower production costs, and augment the annual production and

seasonal supply of horticultural products (Higuchi 2018; Matsoukas et al. 2012).

Flowering time in the model plant *Arabidopsis* is regulated by integrating vernalization, temperature, photoperiod, hormones, age, autonomic pathways, and other floral transition signal transduction pathways (Srikanth and Schmid 2011; Cho et al. 2017). In 1936, M.K. Chailakhyan observed a type of flowering stimulator in *Chrysanthemum* that is produced in its leaves and transported to the shoot apical meristem (SAM) after photoperiod induction; it was designated 'florigen' (Chailakhyan and Krikorian 1975). This flowering element was later identified in *Arabidopsis* as a product of the *FLOWERING LOCUS T* (*FT*) gene (Kardailsky et al. 1999; Tsuji and Taoka 2014; Tsuji 2017). In *Arabidopsis*, *TERMINAL FLOWER 1* (*TFL1*) of the *FT/TFL1* family of proteins has been identified as a local floral inhibitor expressed in the SAM (Shannon and Meeks-Wagner 1991; Bradley et al. 1997). *FT/TFL1* encodes a pair of flowering regulators that are homologous to phosphatidylethanolamine-binding proteins (PEBPs) (Ahn et al. 2006; Karlgren et al. 2011). The

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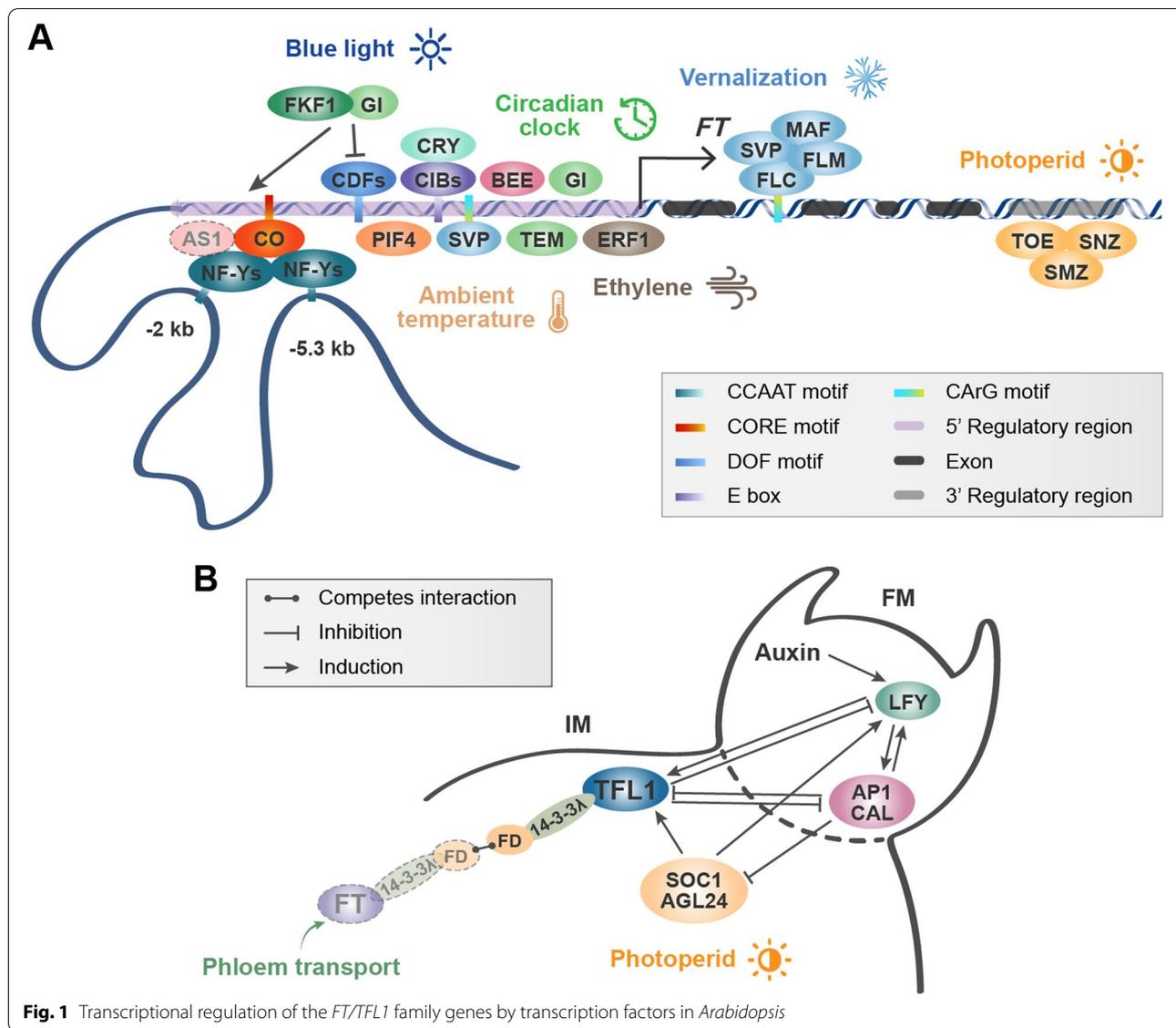


Fig. 1 Transcriptional regulation of the *FT/TFL1* family genes by transcription factors in *Arabidopsis*

PEBP gene family in *Arabidopsis* includes six members: FT (Kim et al. 2013; Xu et al. 2012), TWIN SISTER OF FT (TSF) (Yamaguchi et al. 2005; Michaels et al. 2005; D'Aloia et al. 2011; Song et al. 2015), and MOTHER OF FT AND TFL1 (MFT) (Xi et al. 2010; Yoo et al. 2004) all promote flowering, whereas TFL1 (Kim et al. 2013), *Arabidopsis Thaliana* CENTRORADIALIS HOMOLOG (ATC) (Yoo et al. 2010; Huang et al. 2012) and BROTHER OF FT AND TFL1 (BFT) (Yoo et al. 2010) have function that differ from flowering.

FT protein was induced in *Arabidopsis* leaf vascular tissue phloem companion cells and transferred to the SAM by interacting with FT-INTERACTING PROTEIN 1 (FTIP1), QUIRKY (QKY), and SYNTAXIN OF PLANTS121 (SYP121) (Mathieu et al. 2007; Liu et al.

2012; Putterill and Varkonyi-Gasic 2016; Liu et al. 2019). Long-distance transmission of the FT protein is blocked by its interaction with negatively-charged phosphatidylglycerol (PG) at low temperatures (Liu et al. 2020; Susila et al. 2021). After being transported to the SAM, the FT protein forms a complex with the bZIP transcription factor FD and induces the expression of the floral meristem-identity genes *APETALA1* (*AP1*) and *FRUIT-FULL* (*FUL*) (Abe et al. 2005; Wellmer and Riechmann 2010; Taoka et al. 2013). The interaction of environmental, endogenous, and hormonal signals precisely regulates the spatiotemporal expression of the *FT* gene in leaf phloem companion cells and the flowering in *Arabidopsis* (Fig. 1A). CONSTANS (CO) reflects the correspondence between external light signals and endogenous biological

circadian clock, to activate the expression of *FT* at the right time to induce flowering (Imaizumi and Kay 2006; Song et al. 2015; Goralogia et al. 2017). Moreover, CYCLING DOF FACTORS (CDFs) directly bind to the proximal Block A region of the *FT* promoter to inhibit the transcription of *FT* (Imaizumi et al. 2005; Goralogia et al. 2017). Genes related to the circadian clock, temperature, and blue-light signals, such as GIGANTEA (GI) (Sawa and Kay 2011), BR ENHANCED PRODUCTION 1 (BEE1) (Wang et al. 2019), PHYTOCHROME INTERACTING FACTOR 4 (PIF4) (Kumar et al. 2012), and CIB (cryptochrome-interacting basic-helix-loop-helix) (Liu et al. 2008), bind upstream from the transcription start site (TSS) of the *FT* gene, triggering its expression. TEMPRANILLO (TEM) (Castillejo and Pelaz 2008), TARGET OF EAT 1 (TOE1), TOE2, SCHAFLMÜTZE (SMZ), SCHNARCHZAPFEN (SNZ) (Mathieu et al. 2009), and SHORT VEGETATIVE PHASE (SVP) (Lee et al. 2007) respond to ambient temperature or photoperiod to directly repress *FT* expression. Further, several MADS transcription factors, namely FLOWERING LOCUS C (FLC), SVP, FLOWERING LOCUS M (FLM), and MADS AFFECTING FLOWERING (MAF), can inhibit transcription by binding to the first intron of *FT* at low temperatures or before vernalization (Luo et al. 2021). Other hormone signals also play a role in controlling the initiation of flowering. For example, ERF1, a key member of the ethylene signal transduction pathway, binds directly to the *FT*'s promoter and inhibits its transcription (Chen et al. 2021). Furthermore, polycomb group (Pc-G) proteins reportedly mediate epigenetic gene regulation, which maintains the identity of the inflorescence and floral meristems after floral induction (Müller-Xing et al. 2014). The simultaneous occurrence of H3K27me3 at *FT* has also been demonstrated, using a sequential ChIP analysis (Jiang et al. 2008). The genes of PcG subunits, including EMBRYONIC FLOWER 2 (EMF2), EMF1, CURLY LEAF (CLF), MULTICOPY SUPPRESSOR OF IRA 1 (MSI1) and LIKE HETEROCHROMATIN PROTEIN 1 (LHP1), deposit H3K27me3 in the chromatin of *FT* to repress its expression (Jiang et al. 2008; Schatlowski et al. 2008; Mozgova and Hennig 2015; Merini and Calonje 2015). Unlike other PcG target genes in *Arabidopsis*, modification by H3K27me3 occurs in the promoter, coding region, and downstream region of the *FT* gene (Turck et al. 2007).

In *Arabidopsis*, the antagonism of *TFL1* and floral meristem-specific genes controls flower initiation and the ensuing inflorescence structure. *TFL1*, which is expressed in the central region of the apical meristem but can move to the meristem layer L1, is required for movement into the SAM to regulate floral transition (Conti and Bradley 2007; Goretti et al. 2020). Once in the SAM,

TFL1 interacts with the bZIP transcription factor FD via the 14–3–3 protein, and *FT* and *TFL1* compete for binding FD to regulate the downstream floral meristem identification genes *LEAFY* (*LFY*), *APETALA1* (*API*), and *CAULIFLOWER* (*CAL*), which maintains meristem indeterminacy (Zhu et al. 2020; Goretti et al. 2020) (Fig. 1B). Under long day (LD) conditions, SOC1 and AGL24 bind to *TFL1*'s chromatin regions and directly activate its transcription in the SAM (Azpeitia et al. 2021). *LFY* binds to the *TFL1* promoter and directly activates *TFL1* transcription, a regulatory loop which ensures that flower formation occurs only when *API/CAL* levels are sufficiently high to repress *TFL1* expression and trigger the genetic program required for flower development (Serrano-Mislata et al. 2017). The proteins encoded by the *FT/TFL1* family of genes have small differences in conformation, giving them opposite functions in plants. Hanzawa et al. (2005) showed that changing only a single amino acid in the *Arabidopsis* *TFL1* protein can render *TFL1* to function as a floral activator, and vice versa.

Recent reports in gymnosperms indicate that the ancestor of *FT* functioned in a *TFL1*-like manner (Karlgrén et al. 2011). For example, *PaFTL1* and *PaFTL2* in Norway spruce (*Picea abies*) both repress this conifer tree's growth, and their heterologous expression in *Arabidopsis* also delays the onset of flowering (Karlgrén et al. 2011; Klintonäs et al. 2012). The data to date suggests that the function of *FT* and *TFL1* diverged after the evolutionary separation in different plant species. Moreover, *FT/TFL1* family genes are reportedly involved in other developmental processes and feature functional diversification in regulating flowering time in several species (Karlgrén et al. 2011; Klintonäs et al. 2012). This review summarizes the functional diversification and molecular mechanisms of the *FT/TFL1* family members in horticultural plants, to provide a timely reference for further research on these pivotal genes in horticultural plants.

***FT/TFL1* family genes regulate flowering time in horticultural plants**

In horticultural plants, the number of *FT/TFL1* family genes varies yet they have conserved functions in the process of floral transition (Table 1). For example, in ornamental plants of the Asteraceae—the largest flowering plant family contains the greatest number of species—three *FT-like* genes have been identified in *Chrysanthemum seticuspe*: *CsFTL1*, *CsFTL2*, and *CsFTL3*, which are flowering inducers (Oda et al. 2012; Mao et al. 2016; Sun et al. 2017; Wang et al. 2020a). Mao et al. (2016) found that the archetypal and alternative splicing (AS) forms of *CmFTL1* (*C. morifolium* cultivar 'Jimba') has the function of complementing the late-flowering phenotype of the *Arabidopsis* *ft-10* mutant, and *CmFTL1* can induce

Table 1 Diverse functions of the *FT/TFL1* gene family in horticultural plants

Gene name	Effect on flowering	Other function	Regulatory input	References
Arabidopsis (<i>Arabidopsis thaliana</i>)				
AtFT	Induction	Plant growth; Dormancy	LD	Shannon and Meeks-Wagner, 1991;
AtTSF	Induction		LD	Yoo et al., 2004;
AtTFL1	Inhibition	Inflorescence development	LD	Yamaguchi et al., 2005;
AtBFT	Inhibition	Inflorescence development	LD	Michaels et al., 2005;
AtATC	Inhibition			Xi et al., 2010;
AtMFT	Induction	Seed germination		Yoo et al., 2010;
				D'Aloia et al., 2011;
				Huang et al., 2012;
				Kim et al., 2013;
				Moraes et al., 2019;
				Azpeitia et al., 2021;
				Chen et al., 2021
Chrysanthemum (<i>Chrysanthemum</i> spp.)				
CsFTL1	Induction		LD, NB	Oda et al., 2012;
CsFTL2	Induction		LD, Sucrose	Higuchi et al., 2013;
CsFTL3	Induction		LD, Sucrose	Higuchi and Hisamatsu, 2015;
CsTFL1b	Inhibition			Mao et al., 2016;
CmTFL1a	Inhibition			Sun et al., 2017;
CmTFL1c	Inhibition			Gao et al., 2019;
CsAFT	Inhibition		LD, NB	Wang et al., 2020a, b;
				Haider et al., 2020
Phalaenopsis (<i>Phalaenopsis</i> hybrid)				
PhFT1	Induction			Li et al., 2014;
PhFT3	Induction			Zhou et al., 2018;
PhFT5	Induction			Jiang et al., 2022
PhFT6	Inhibition			
Orchid (<i>Oncidium</i> Gower Ramsey)				
OnFT	Induction			Hou and Yang, 2009
OnTFL1	Inhibition			
Dendrobium (<i>Dendrobium huoshanense</i>)				
DhFT3	Induction		Gibberellin	Song et al., 2021
DhFT1	Induction		Gibberellin	
DhFT2	Induction		Gibberellin	
DhTFL1a	Inhibition			
DhTFL1b	Inhibition			
Tomato (<i>Solanum lycopersicum</i>)				
SP	Inhibition	Indeterminate growth		Molinero-Rosales et al., 2004;
SFT	Induction	Inflorescence development		Lifschitz et al., 2006;
FTL1	Induction		SD	Shalit et al., 2009;
SP5G	Inhibition			Jiang et al., 2013;
SP5G2	Inhibition			Lifschitz et al., 2014;
SP5G3	Inhibition			Cao et al., 2016;
				Song, 2020
Strawberry (<i>Fragaria</i> × <i>ananassa</i>)				
FvFT1	Induction		LD	Koskela et al., 2012;
FvTFL1	Inhibition		LD, Cool temperature	Nakano et al., 2015
Rose (<i>Rosa</i> spp.)				
RoKSN	Inhibition			Iwata et al., 2012;
RoFT	Induction			Randoux et al., 2014, b;
				Otagaki et al., 2015

Table 1 (continued)

Gene name	Effect on flowering	Other function	Regulatory input	References
Poplar (<i>Populus</i> spp.)				
PtFT1	Induction			Mohamed et al., 2010;
PtFT2	Inhibition	Vegetative growth; Shoot dormancy	LD, High temperature	Hsu et al., 2011;
PopCEN1	Inhibition			Gómez-Soto et al., 2022
PopCEN2	Inhibition			
Sugar beet (<i>Beta vulgaris</i>)				
BvFT1	Inhibition		SD, Non-vernalized	Pin et al., 2010
BvFT2	Induction			
Cucumber (<i>Cucumis sativus</i>)				
'short-1' UR CsFT	Induction			Wen et al., 2019;
'short-2' UR CsFT	Induction			Wang et al., 2020b
'long' UR CsFT	Inhibition			
CsTFL1	Inhibition	Determinate growth		
Tulip (<i>Tulipa gesneriana</i>)				
TgFT1	Inhibition			Leeggangers et al., 2018
TgFT2	Induction			
TgFT3	Inhibition			
Potato (<i>Solanum tuberosum</i>)				
StSP5G	Inhibition			Navarro et al., 2011;
StSP5G-like	Inhibition			Lee et al., 2013
StSP6A		Tuber formation		
Onion (<i>Allium cepa</i>)				
AcFT1		Bulb formation	LD	Blackman et al., 2010;
AcFT2	Induction		Vernalization	Lee et al., 2013
AcFT4	Inhibition	Bulb formation		
Kiwifruit (<i>Actinidia</i> spp.)				
Kiwifruit FT	Induction	Dormancy release	Cool temperature	Varkonyi-Gasic et al., 2013
Kiwifruit CEN	Inhibition			
Pineapple (<i>Ananas comosus</i>)				
AcFTL2	Induction		Ethylene	Liu and Fan, 2016;
				Liu et al., 2018

flowering in *C. morifolium* 'Yuuka' (Wang et al. 2020a). Sucrose induces the transcriptional upregulation of *CmFTL2* (*C. morifolium* 'Yuuka') in chrysanthemum leaves and promotes flowering (Sun et al. 2017). However, changing a single amino acid in *CmFTL3* of chrysanthemum results in the loss of its flowering function (Sun et al. 2018). Moreover, there are three *TFL1* homologs in chrysanthemum that act as flowering inhibitors (Higuchi and Hisamatsu 2015; Gao et al. 2019; Haider et al. 2020). The orchid family (Orchidaceae) is the second largest family of flowering plants, for which three *FT-like* genes were identified in *Phalaenopsis*: *PhFT1*, *PhFT3*, and *PhFT5*, heterologous expression of which in *Arabidopsis* cause early flowering phenotype (Zhou et al. 2018; Li et al. 2014). Ectopic expression of *OnFT* could not fully complement the late-flowering phenotype of the *Arabidopsis ft-1* mutant, and it was not regulated by photoperiod but did inhibit flowering in *Oncidium* (Hou and

Yang 2009). Six PEBP family genes (i.e., *DhFT3*, *DhFT1*, *DhMFT*, *DhTFL1b*, *DhFT2*, and *DhTFL1a*) were isolated and characterized from the *Dendrobium huoshanense* genome (Song et al. 2021). Gibberellin (GA) treatment increased the expression of all those *DhFTs* and promoted flowering, while inhibiting the expression of *DhTFL1s* (Song et al. 2021). A year-round tropical orchid, *Arundina graminifolia*, lacks any *TFL1-like* gene, but does have two *FT-like* genes: *AgFT1* and *AgFT2*. The functions of *AgFT1* and *AgFT2* in regulating flowering have not been verified, however (Auberon et al. 2016; Ahmad et al. 2021).

In vegetable crops, the *FT-like* protein StSP3D is essential for flowering in potato (*Solanum tuberosum*) (Navarro et al. 2011). Tomato (*Lycopersicon esculentum*) is the second most globally important vegetable crop (after potato), whose flowering time is jointly controlled by the flowering inducer *SINGLE FLOWER*

TRUSS (*SFT*) and suppressor *SELF PRUNING* (*SP*) (Molinero-Rosales et al. 2004; Jiang et al. 2013). *SFT* is an ortholog of *FT-like* that is expressed in mature leaves and systematically promotes flowering, while *SP* is the ortholog of *TFL1-like* that is instead expressed in young leaves and shoot tips, and inhibits flowering (Shalit et al. 2009). Recently, *FTL1*, which regulates flowering time in tomato, was located and sequenced through map-based cloning. *FTL1* is only specifically expressed under short day (SD) conditions and regulates tomato flowering by promoting the expression of *SFT* (Song 2020). Among fruit crops, in strawberry (*Fragaria × ananassa*) *FvFT1* and *FvTFL1* have antagonistic functions for inducing flowering. Interestingly, owing to a base deletion in *FvTFL1*, strawberry has since become a permanent flowering plant (Koskela et al. 2012; Nakano et al. 2015).

Moreover, perennial woody plants possess flowering-inductive *FT* genes and flowering-inhibitory *TFL1* genes. Poplar (*Populus species*) contains two *FT-like* genes (*PtFT1/PtFT2*) (Hsu et al. 2011) and two *CEN/TFL1-like* genes (*PopCEN1/PopCEN2*) (Mohamed et al. 2010). Overexpression of *PtFT1* in Poplar caused its flowering in the tissue culture stage at 6 weeks; hence, *PtFT1* promotes flowering (Hsu et al. 2006; Hsu et al. 2011; Gómez-Soto et al. 2022). Both *PopCEN1* and *PopCEN2* inhibited flowering, however. Downregulating the expression of *PopCEN1* and *PopCEN2* can accelerate the time of first onset of flowering and the maturity of poplar (Mohamed et al. 2010). In a Chinese continuous-flowering rose plant cultivar, the *TFL1-like* gene *RoKSN* is a flowering suppressor whereas *RoFT* is a floral inducer (Iwata et al. 2012; Otagaki et al. 2015). The insertion of a retrotransposon in *RoKSN* inhibits *RoKSN* expression in roses, thereby facilitating their continuous flowering (Randoux et al., 2014, b). Collectively, these reports suggest the function of *FT/TFL1* family genes is generally conserved in horticultural plants.

Functional diversification of *FT/TFL1-like* in horticultural plants

The functions of proteins encoded by homologous *FT/TFL1-like* genes are not entirely conserved in horticultural plants, in that they show functional diversification in regulating flowering time (Table 1).

Homologous genes of *FT* could contribute to inhibiting flowering. In vegetable crops, the two *FT-like* homologous genes *BvFT1* and *BvFT2* in sugar beet (*Beta vulgaris*) function antagonistically in flowering. Under non-vernalized or SD conditions, the flowering inhibitor *BvFT1* inhibits flowering by limiting the expression of the flowering-inducing factor *BvFT2* (Pin et al., 2010). In

cucumber (*Cucumis sativus*), the structural types in the upstream region (UR) of *CsFT* have differential effects on flowering induction; the ‘short-1’ UR *CsFT* and ‘short-2’ UR *CsFT* accelerate the onset of flowering, whereas the ‘long’ UR *CsFT* delays flowering (Wang et al., 2020b). Four *FT-like* homologous genes have been identified in tomato: *SP3D/SFT* has a florigen function, whereas *SP5G*, *SP5G2*, and *SP5G3* are characterized by flowering inhibitory activity (Cao et al., 2016). *AcFT4* in onion (*Allium cepa*) and both *StSP5G* and *StSP5G-like* in potato are also able to inhibit flowering (Navarro et al., 2011; Lee et al., 2013). In ornamental plants, three PEBP genes were isolated in tulip (*Tulipa gesneriana*): *TgFT1*, *TgFT2*, and *TgFT3*. Overexpression of *TgFT2* in *Arabidopsis* resulted in an early-flowering phenotype, while *TgFT1* and *TgFT3* overexpression resulted in a late-flowering phenotype (Leeggangers et al., 2018). The *PhFT6* in *Phalaenopsis* and *HaFT1* in sunflower (*Helianthus annuus*) can also repress their flowering (Li et al., 2014; Blackman et al., 2010). The two *FT-like* genes *PtFT1/PtFT2* in poplar, a woody perennial species, also have opposing flowering regulatory functions (Hsu et al., 2011; Mohamed et al., 2010). *PtFT1* has a florigen function, whereas *PtFT2*, it induced by LDs and high temperature, reduces the level of GA via the GA 13-hydroxylation pathway and maintains the vegetative growth of poplar to preclude flowering (Gómez-Soto et al., 2022).

In addition to regulating flowering time, members of *FT/TFL1-like* genes are involved in a variety of other processes in horticultural plants. *CsTFL1* inhibits determinate growth and terminal flower formation in cucumbers (Zhao et al., 2018; Wen et al., 2019; Njogu et al., 2020). Navarro et al. (2011) reported that overexpressing the *FT* homologous gene *Hd3a* in potato enabled it to grow more tubers than the wild type, and that the endogenous gene *StSP6A* also had a similar function, thus indicating that *FT* promotes tuber formation. In onion, LDs induced the downregulation of *AcFT4* expression but the upregulation of *AcFT1* expression, which promoted the formation of bulbs and increased the yield (Lee et al., 2013). In tomato *sft* mutants, the inflorescence differentiated into only one flower, the sepals were enlarged, and leaves have excess intercalary leaflets; however, the leaves became smaller blades and lack folioles after the overexpression of *SFT* (Shalit et al., 2009; Lifschitz et al., 2014). In *Dendrobium* Chao Praya Smile, *DoFT*-RNAi transgenic lines also displayed abnormal inflorescence development and delayed pseudobulb formation, suggesting that *DOFT* may have evolved with unknown functions related to the regulation of storage organs and flower development (Wang et al., 2017). *PtFT2* promotes vegetative growth and shoot dormancy in poplar trees (Mohamed et al., 2010); similarly, *FT* and *CEN* are involved in the

regulation of kiwifruit plant growth by integrating developmental and environmental signals (Varkonyi-Gasic et al., 2013). Taken together, these reports show that the functions of members of the *FT/TFL1* gene family have evolved dynamically over the course of horticultural plants' evolution.

Regulation of *FT/TFL1* family genes in horticultural plants

The photoperiodic pathway is the most important and most conserved of the floral induction pathways, and some of the key loci and mechanisms are shared even among distantly related plant species, whereas others are not conserved and give rise to crucial species differences (Matsoukas et al., 2012). The autumn flowering chrysanthemum cultivars are short day plants that require a repeated SD photoperiod for successful flowering, because *CsFTL3* expression increases with such repeated SDs before successful flowering occurs, but their vegetative growth can be strictly maintained under LD or night-break (NB) conditions. When SDs switch to LDs before the involucre-forming stage, those plants do not initiate florets on the apical receptacle, or their capitulum development is strongly suppressed (Higuchi, 2018; Nakano et al., 2019). Recent studies have revealed the transcriptional regulation mechanism of the *FT/TFL1* family genes in chrysanthemum (Fig. 2). *CICRY2* facilitates floral transition in *C. lavandulifolium* by fine-tuning the expression of circadian clock-related genes, such as the downregulation of *LHY* and overexpression of *GI* (Yang et al., 2018). By downregulating *CsFTL3* and *CsAFT*, *CsLHY-SRDX* induced a photoperiod-insensitive floral transition (Oda et al., 2017). The transcription

of another circadian-clock-related gene, *CsGI*, has been shown to increase the necessary night length for blooming, chiefly by maintaining lower levels of *CsAFT* (Oda et al., 2020). In chrysanthemums, *CsPHYB*-mediated light signaling upregulates *CsFTL3* but downregulates *CsAFT* to determine their obligate photoperiodic blooming response (Higuchi et al., 2013). Furthermore, gibberellins function critically in floral induction in response to LDs (Porri et al., 2012). *CmBBX24* inhibits the expression of *CmFTL3*, which regulates flowering primarily through effects on the GA pathway under LDs (Yang et al., 2014). Recently, the role of NF-Y proteins in the aging pathway in chrysanthemum was identified, in that *CmNF-YB8* influences flowering time by directly upregulating the expression of *cmo-MIR156* in the aging pathway (Wei et al., 2017). More recently, the CO homologous protein *CmBBX8* was discovered to target *CmFTL1* for flowering regulation in chrysanthemum (Wang et al., 2020a).

Nevertheless, the functions of *CO1* and *CO2* in poplar do not overlap with those in *Arabidopsis*. The growth of *CO2* RNAi transgenic poplar stopped when LDs transitioned to SDs, and its shoots formed earlier. Overexpression of *CO1* and *CO2* in poplar did not induce the upregulated expression of *FT2* under SD conditions, and its timing of flowering and bud formation did not change (Hsu et al., 2012). Another SD-dependent *FT2* inhibition pathway mediated by *LHY2* was recently discovered in poplar. Under SD conditions, *LHY2* is induced to express and directly bind to the homeopathic element at the 3' end of *FT2* to inhibit its expression, resulting in the arrested growth of poplar (Fig. 3A). But under LD

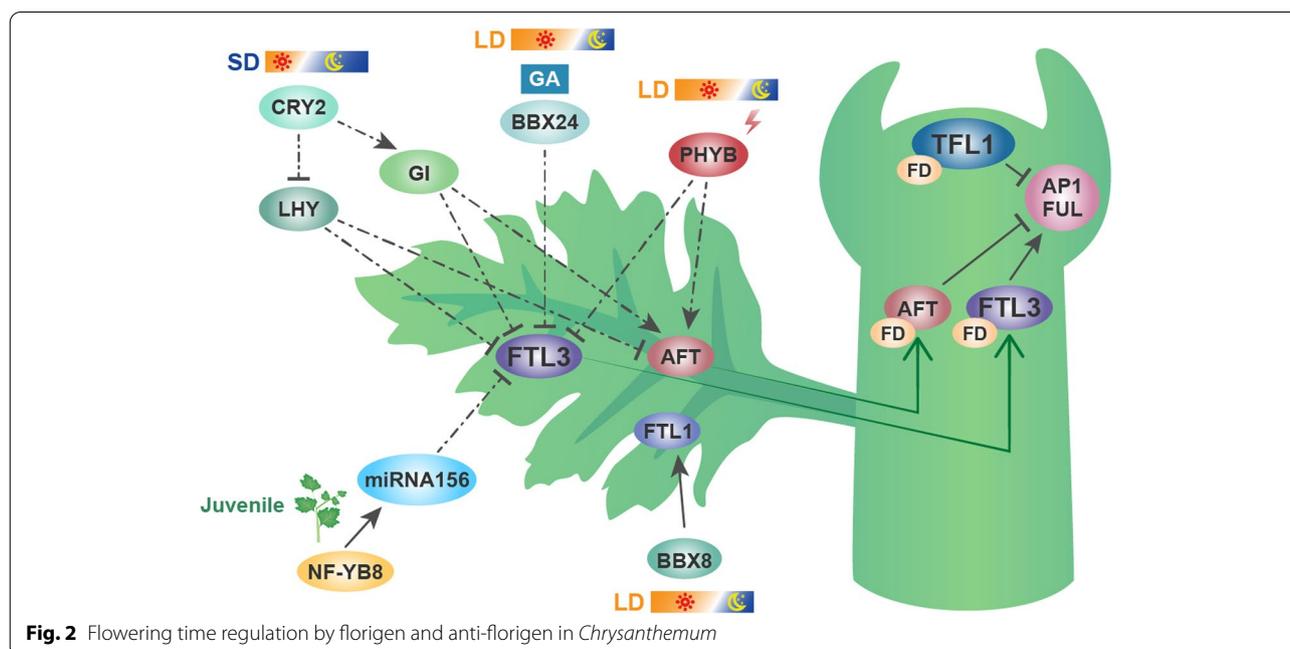
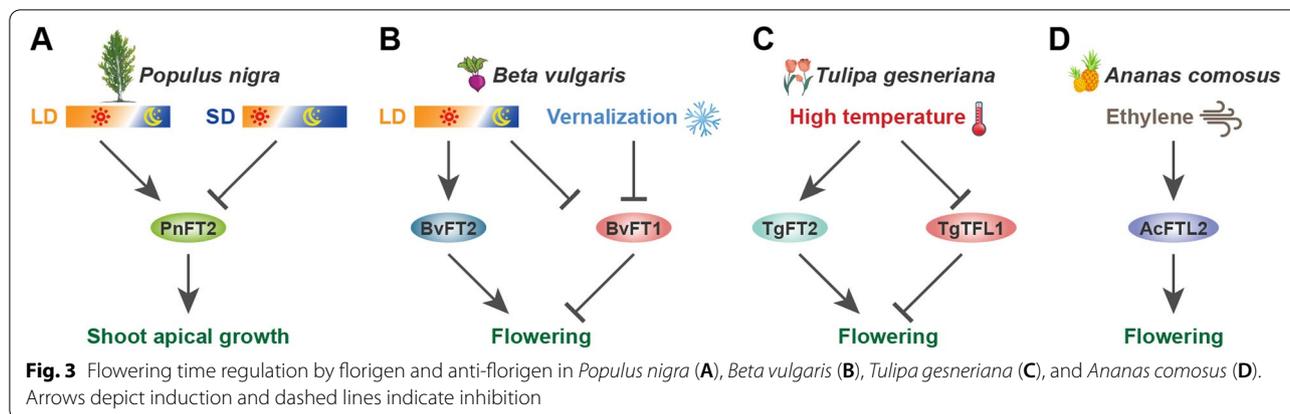


Fig. 2 Flowering time regulation by florigen and anti-florigen in *Chrysanthemum*



conditions, the expression of *LHY2* is low, while *CO* and other activators induce the expression of *FT2*, thereby promoting the flowering of poplar (Ramos-Sánchez et al., 2019; André et al., 2022).

Some *FT* homologs regulate flowering and aspects of development in response to temperature except for photoperiod in horticultural plants. In sugar beet, the expression of the flowering inhibitor *BvFT1* was inhibited by both vernalization and LD conditions and *BvFT2* was induced under LDs (Pin et al., 2010) (Fig. 3B). In strawberry, *FvFT1* was specifically upregulated in mature leaves and this promoted the upregulation of *FvSOC1* in shoot tips, which activated *FvTFL1* expression to inhibit flowering under LDs (Mouhu et al., 2013; Rantanen et al., 2014). Furthermore, *FvTFL1* was regulated by a temperature-dependent pathway independent of photoperiod-dependent regulation (Rantanen et al., 2015). Floral transition of lily (*Lilium longiflorum*) is also induced by low-temperature conditions and is not regulated by photoperiod. In lily, *LIFT*, as a flowering activator, is significantly induced by a period of low-temperature treatment and this promoted flowering; however, without the vernalization treatment, overexpression of *LIFT* also led to a bloom, indicating that *LIFT* is the main regulatory factor controlling flowering in the vernalization pathway (Lazare and Zaccari et al., 2016). After switching from vegetative to reproductive growth, *LIFT* expression was further reduced in floral meristems and small flower buds. Therefore, *LIFT* is thought to be involved in switching the meristem to a flowering state during vernalization, but it does not act as a flowering inducer (Leeggangers et al., 2018). Further, the flowering regulation of *Narcissus tazetta* and tulip is induced by high temperature and does not depend on the photoperiod and vernalization pathways. In narcissus, high temperature induces the transcription of *Narcissus FLOWERING LOCUST1 (NFT1)*, which promotes the expression of the downstream *LFY* homolog gene *NLF*

and induces flowering (Li et al., 2013; Noy-Porat et al., 2013). The floral transition of tulip occurs in the bulb, for which high temperature induces the expression of *TgFT2* and inhibits the expression of *TgTFL1*, which then induces the floral transition (Leeggangers et al., 2018) (Fig. 3C). On the contrary, the chrysanthemum flowering is severely delayed by high temperature during the summer, when the reduction of *CsFTL3* expression at high temperatures are involved in flowering's retardation in *C. seticuspe* (Higuchi, 2018). Interestingly, exogenous ethylene induces the upregulated expression of *FT-like* and *API-like* genes, which promotes transition to flower formation in pineapple (Liu and Fan, 2016; Liu et al., 2018) (Fig. 3D), this starkly differing from their inhibitory effect on *Arabidopsis* flowering (Chen et al., 2021). These findings indicate that not only the functions of members of the *FT/TFL1* family of genes, but also their upstream regulators, have evolved drastically and in cases also divergently in horticultural plants.

The transport of florigens in horticultural plants has also been studied. In *Cucurbita moschata*, LD-induced transport of FT proteins from its leaves to shoot tips promoted the transition into flowering (Lin et al., 2007). Moreover, floral promotion via the graft transmission of FT has been demonstrated in woody plants. For a recent example, when the scion of *JcFT*-RNAi transgenic *Jatropha curcas* was grafted onto *SUC2:JcFT* rootstock, FT protein was transported into the scion which promoted the transition into flowering, whose efficacy depended on the length of the scion (Tang et al., 2022). In trifoliolate orange, its early flowering was induced in the transgenic tomato as well as trifoliolate orange plants transformed with *ToFT*. However, the rootstocks of transgenic trifoliolate orange could not induce flowering of grafted wild-type (WT) juvenile scions because of their low accumulation of total FT protein (Wu et al., 2022). That findings suggests the expression of *FT* must reach a certain threshold to induce flowering. A *TFL1* homolog (*RoKSN*)

in rose was found to be immobile, precluding its transmission via grafting experiments (Randoux et al., 2014, b). Yet when a WT chrysanthemum plant was grafted onto the *CsTFL1*-ox stock, the flowering of the WT scion was delayed vis-à-vis the WT/WT grafting (Higuchi and Hisamatsu, 2015). Spatial expression patterns of *CsTFL1* showed that it was mainly expressed in shoot tips, with low expression levels in leaves (Higuchi and Hisamatsu, 2015; Gao et al., 2019; Haider et al., 2020). These results suggest that *CsTFL1* probably can move long distances through a grafting union as a floral repressor, to systemically regulate an indeterminate apical meristem. Because FT participates in vesicle trafficking (Liu et al., 2020), whether the transport of TFL1 occurs via a similar way awaits investigation.

Outlook

In summary, many studies of diverse horticultural plants have revealed the conserved functioning of members of the *FT/TFL1* gene family, which have evolved dynamically over the course of horticultural plant evolution. Moreover, amino acid substitutions in *FT/TFL1* family genes in *Arabidopsis* and horticultural plants such as sugar beet could cause a conversion in functionality, from having repressor activity to becoming a floral activator and vice versa (Ho and Weigel, 2014; Pin et al., 2010). A single base deletion or the products of a premature stop codon in *TFL1* gene in strawberry facilitates their continuous flowering (Koskela et al., 2012). In cucumber and domesticated tomato, the short upstream region of *CsFT* and mutations in the *cis*-regulatory region of antiflorigen *SP5G* hasten their onset of flowering, respectively (Soyk et al., 2017; Wang et al., 2020b). These results suggest *FT/TFL1* family genes are elite editing targets for manipulating gene structure, to change key flowering characteristics of horticultural plants, using genome editing technology, which is a powerful and precision-breeding approach, although there are legal/ethical concerns (Gao, 2021).

Because *FT/TFL1* family genes integrate multiple regulatory pathways, such as photoperiod, vernalization, and ambient temperature pathway, to govern flowering, not only the functions of their members but also their upstream regulators have drastically evolved in horticultural plants. With ongoing global warming, the rise in ambient temperature is often accompanied by a greater concentration of carbon dioxide (CO₂), which is conducive to the accumulation of photosynthetic products (sugar and starch) in plants. This increase in CO₂ is apt to cause changes in tissues' sugar status or directly drives *FT/TFL1* to regulate flowering (Jagadish et al., 2016). Although studies have found that *FT* can mediate nitrogen's control of flowering, its regulatory mechanism is

still not well understood (Gras et al., 2018; Zhang et al., 2021). Therefore, elucidating in detail how the regulation mechanisms of *FT/TFL1* family genes may respond to various environmental and endogenous stimuli would promote the development of an efficient and energy-saving approach to regulate flowering. Due to the rapid adoption and spread of genomic sequencing technology applied to horticultural plants, genomic resources are becoming increasingly available. This combined with other techniques, namely high-throughput phenotyping, genomic selection, and gene function analysis, will enable us to obtain detailed knowledge of the *FT/TFL1* gene family, so as to modify their action to meet the increasing demand for horticultural products in the future.

Abbreviations

SAM: Shoot apical meristem; *FT*: FLOWERING LOCUS T; *AP1*: APETALA1; *FUL*: FRUITFULL; SD: Short-day; DN: Day-neutral; TSS: Transcription start site; *TFL1*: TERMINAL FLOWER 1; LD: Long-day; PEBPs: Phosphatidylethanolamine-binding proteins; *MFT*: MOTHER OF FT AND TFL1; *TSF*: TWIN SISTER OF FT; *ATC*: *Arabidopsis thaliana* CENTRORADIALIS homolog; *BFT*: BROTHER OF FT AND TFL1; NB: Night-break; GA: Gibberellin; *SFT*: SINGLE FLOWER TRUSS; *SP*: SELF PRUNING; UR: Upstream region; *NFY*: Nuclear Factor Y; *AS1*: ASYMMETRICLEAVES 1; *TEM*: TEMPRANILLO; *TOE1*: TARGET OF EAT 1; *SMZ*: SCHAFLMÜTZE; *SNZ*: SCHNARCHZAPPEN; *BEE1*: BR ENHANCED EXPRESSION 1; *SVP*: SHORT VEGETATIVE PHASE; *PIF4*: PHYTOCHROME INTERACTING FACTOR 4; *FLC*: FLOWERING LOCUS C; *FLM*: FLOWERING LOCUS M; *MAF*: MADS AFFECTING FLOWERING; IM: inflorescence meristem; *LFY*: LEAFY; *CAL*: CAULIFLOWER; FM: floral meristem; *SOC1*: SUPPRESSOR OF OVEREXPRESSION OF CO 1; *AGL24*: AGAMOUS LIKE 24; *NFT1*: FLOWERING LOCUST1; *FTIP1*: FT-INTERACTING PROTEIN 1; *NaKP1*: SODIUM POTASSIUM ROOT DEFECTIVE 1; *PG*: Phosphatidylglycerol; *PcG*: Polycomb group; *LHP1*: LIKE HETEROCHROMATIN PROTEIN 1; *CLF*: CURLY LEAF; *EMF2*: EMBRYONIC FLOWER 2; *MSI1*: MULTICOPY SUPPRESSOR OF IRA 1.

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Authors' contributions

SW and JJ conceptualized the paper, wrote the draft, SW, JJ and FC reviewed and edited the manuscript. YY prepared the figures. All authors read and approved the final manuscript.

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