



Floral-promoting *GmFT* homologs trigger photoperiodic after-effects: An important mechanism for early-maturing soybean varieties to regulate reproductive development and adapt to high latitudes

Junya Wang^{1,2} | Xin Xu²  | Peiguo Wang² | Lixin Zhang² | Lifeng Liu² | Luping Liu² | Tingting Wu² | Wenwen Song² | Shan Yuan² | Bingjun Jiang²  | Wensheng Hou²  | Cunxiang Wu² | Shi Sun² | Lijie Yu¹ | Tianfu Han^{1,2}

¹Key Laboratory of Plant Biology, College of Life Science and Technology, Harbin Normal University, Harbin, China

²Ministry of Agriculture and Rural Affairs Key Laboratory of Soybean Biology (Beijing), Institute of Crop Sciences, Chinese Academy of Agricultural Sciences, Beijing, China

Correspondence

Tianfu Han
Email: hantianfu@caas.cn

Funding information

National Natural Science Foundation of China, Grant/Award Number: 32201869; China Agriculture Research System, Grant/Award Number: CARS-04; CAAS Agricultural Science and Technology Innovation Project

Abstract

Soybean (*Glycine max*) is a typical short-day plant, but has been widely cultivated in high-latitude long-day (LD) regions because of the development of early-maturing genotypes which are photoperiod-insensitive. However, some early-maturing varieties exhibit significant responses to maturity under different daylengths but not for flowering, depicting an evident photoperiodic after-effect, a poorly understood mechanism. In this study, we investigated the postflowering responses of 11 early-maturing soybean varieties to various preflowering photoperiodic treatments. We confirmed that preflowering SD conditions greatly promoted maturity and other postflowering developmental stages. Soybean homologs of *FLOWERING LOCUS T* (*FT*), including *GmFT2a*, *GmFT3a*, *GmFT3b* and *GmFT5a*, were highly accumulated in leaves under preflowering SD treatment. More importantly, they maintained a high expression level after flowering even under LD conditions. *E1* RNAi and *GmFT2a* overexpression lines showed extremely early maturity regardless of preflowering SD and LD treatments due to constitutively high levels of floral-promoting *GmFT* homolog expression throughout their life cycle. Collectively, our data indicate that high and stable expression of floral-promoting *GmFT* homologs play key roles in the maintenance of photoperiodic induction to promote postflowering reproductive development, which confers early-maturing varieties with appropriate vegetative growth and shortened reproductive growth periods for adaptation to high latitudes.

KEYWORDS

flowering time, maintenance, maturity, photoperiod sensitivity

1 | INTRODUCTION

Soybean (*Glycine max* (L.) Merr.) has evolved to adapt to a broad range of climates in regions from 53°N to 35°S latitude across the world (Hyten et al., 2006; Zhang et al., 2020), although it is a typical short-day plant (SDP). Since photoperiod is determined by latitude, soybean varieties with divergent photoperiod sensitivity are utilised in different regions (Zhang et al., 2020). A total of 14 Maturity Groups (MG) from MG 0000 to MG X are characterised to describe photoperiod sensitivity (Alliprandini et al., 2009; Jia et al., 2014; Song et al., 2019; Lu et al., 2013; Zhang et al., 2007). Nowadays, high-latitude regions with long-day (LD) environments are some of the major soybean production areas (Sinegovskii et al., 2018; Wilcox, 2004; Xu et al., 2021). In the northern part of northeast China, the early-maturing varieties belong to MG 0000–MG 0 (Jia et al., 2014; Liu, Song, et al., 2020). Indeed, these early-maturing soybean varieties present a similar flowering time when grown under SD and LD photoperiods, while displaying a diverse maturation (Han et al., 1995, 2006).

The molecular basis of high-latitude adaptation in early-maturing varieties has been systematically investigated. Mutations in multiple *E* genes, mostly recessive at the *E1*, *E2*, *E3* and *E4* loci, were first discovered to contribute to the adaptation of early-maturing varieties in northern regions (Liu et al., 2009; Watanabe et al., 2009, 2011; Xia et al., 2012). Additionally, the floral-promoting genes *GmFT2a* (Kong et al., 2010; Li et al., 2021; Sun et al., 2011), *GmFT5a* (Cai et al., 2020; Li et al., 2021; Yue et al., 2021), *GmFT5b* (Su et al., 2024), *GmFT2b* (Chen et al., 2020), *GmFUL2a* (Jong, Cheng, et al., 2022) and *GmSOC1a* (Kou et al., 2022) and the floral-inhibiting genes *GmPRR3b* (Li et al., 2020; Lu et al., 2020; Wang et al., 2020) and *E1La* (Dong, Li, et al., 2022) were found to regulate the maturation of soybean. According to the 'Teer-board' model, breeders can create early-maturing soybean varieties by modifying the expression levels of floral inhibitors and floral promoters bilaterally (Liu et al., 2018).

Florigen is a graft-transmissible signal produced in the leaves that induces floral initiation at the shoot apex (Andrés & Coupland, 2012). FT (FLOWERING LOCUS T) protein is likely at least a part of the florigen signalling pathway that promotes floral development (Corbesier et al., 2007). *GmFT2a* and *GmFT5a*, the floral-promoting FT homologs in soybean, have been demonstrated as the mobile factors that move from leaves to roots (Wang et al., 2021). In soybean, FT homologs serve various roles in flowering: *GmFT2a*, *GmFT2b*, *GmFT3a*, *GmFT3b* and *GmFT5a* promote flowering and maturity, while *GmFT1a* and *GmFT4* repress these processes (Cai et al., 2020; Kong et al., 2010; Lee et al., 2021; Liu et al., 2018; Nan et al., 2014; Su et al., 2022; Sun et al., 2011; Yuan et al., 2022).

In 1920, Garner and Allard performed preflowering (from emergence to flowering) SD treatments to early-maturing soybean plants and found that this treatment produced a weak promotion of flowering, but a more significant promotion of postflowering (from flowering to maturity) development (Garner & Allard, 1920). This phenomenon is referred to as a photoperiodic after-effect

(PAE) (Garner, 1937). Subsequently, the PAE was observed in wild and cultivated soybean (Han & Gai, 1999; Han & Wang, 1995a; Han et al., 1995, 2006; Liu et al., 1983; Xu & Lu, 1988; Xu et al., 1990), and also in several other plants such as *Tithonia speciosa* (Stoughton & Hole, 1937) and chrysanthemum (Greulach, 1942). However, the molecular mechanism of the PAE remains poorly understood.

In the present study, we investigated the after-effect of preflowering photoperiodic treatments on the postflowering development and agronomic traits of soybean. We revealed the important function of floral-promoting *GmFT* homologs in the photoperiod after-effect through gene expression analysis and functional analysis of *E1* RNAi plants and *GmFT* overexpression lines. Collectively, we conclude that the PAE is caused by the maintenance of high expression levels of floral-promoting *GmFT* homologs. This phenomenon also indicates that maturity exhibits a stronger photoperiod sensitivity than flowering, which ensures appropriate vegetative growth and shortened reproductive period of the early-maturing soybean varieties to adapt to high latitudes with changing photoperiods from LD to SD in the growing season.

2 | MATERIALS AND METHODS

2.1 | Plant materials

Eleven representative varieties from MG 00 and MG 0 (Supporting Information S1: Table S1), the photoperiod-insensitive and early-maturing variety Heihe27 (HH27) (MG 0) and Dongnong36 (DN36) (MG 000), the photoperiod-sensitive and late-maturing variety Zigongdongdou (ZGDD) (MG XIII), *E1* RNAi transgenic lines at generation T_5 (in the ZGDD background) (Liu, Gao, et al., 2020), and the *35S:GmFT2a* overexpression (OE) line at generation T_{11} (*35S:GmFT2a* OE; in the ZGDD background) (Sun et al., 2011) were used in this study.

2.2 | Photoperiodic treatments and growth conditions

Two groups of photoperiodic treatments were conducted in this study, this includes SD → LD and LD → LD. For the SD → LD group, a preflowering (from emergence to flowering) SD photoperiod (12 h light/12 h dark) was applied, and then a postflowering (from flowering to maturity) LD photoperiod (18 h light/6 h dark) was applied. For the LD → LD group, preflowering and postflowering LD photoperiods (18 h light/6 h dark) were applied.

To analyse the after-effect of the preflowering photoperiodic treatments on the postflowering development of early-maturing varieties, the five MG 00 and six MG 0 varieties (Supporting Information S1: Table S1) were grown outdoors in Beijing, China (39°58'N, 116°19'E) from May to September in 2020 and 2021. Varieties planted in 2020 were used to investigate the phenotypes

and agronomic traits, and varieties planted in 2021 were used for crude protein and oil quantification. Soybean plants were exposed to preflowering SD or LD and then postflowering LD treatments. The SD treatments consisted of 12 h light/12 h dark where sunshine was applied from 7:00 to 19:00 and dark treatment was conducted from 19:00 to 7:00 the following day. LD treatments consisted of 18 h light/6 h dark where sunshine was applied from 7:00 to 19:00 and 100 $\mu\text{mol}\cdot\text{m}^{-2}\cdot\text{s}^{-1}$ fluorescent light was extended from 19:00 to 1:00 the following day; dark treatment was conducted from 1:00 to 7:00 the following day.

For gene expression and function analysis, HH27, DN36, ZGDD, *E1* RNAi plants and 35S:*GmFT2a* OE plants were grown in growth chambers at 26°C under photoperiod conditions which preflowering SD or LD and postflowering LD treatments were conducted.

2.3 | Transcriptome analysis and gene function annotation

The unifoliolate leaves of HH27 treated with preflowering SD or LD and postflowering LD were sampled at 4 h after day light at R1 (beginning bloom) and R3 (beginning pod) stages. Each sample was collected from three individual plants. Three biological replicates were analysed. Total mRNA from leaves was extracted using RNA Easy Fast Plant Tissue kits (Tiangen) and used for cDNA library building and sequencing. cDNA was sequenced with the HiSeq. A total of 4000 platform (Illumina) following the manufacturer's protocols. Clean reads were obtained by removing reads with adapters, reads containing ploy-N ($N > 10\%$) and low-quality reads (reads with $Q < 5$ bases for $>50\%$ in the raw data). The clean data were mapped to the soybean genome Wm82.a4.v1. Gene expression levels were determined using the fragments per kilobase of transcript per million reads (FPKM) to compare among the different samples.

2.4 | Gene expression analysis

The unifoliolate leaves of HH27 plants treated with preflowering SD or LD and postflowering LD were sampled at 4 h after dawn at the V1 (unifoliolate fully developed), V2 (first trifoliolate fully developed), V3 (second trifoliolate fully developed), R1, R3 and R5 (beginning seed). The unifoliolate leaves of *E1* RNAi plants and 35S:*GmFT2a* OE plants treated with preflowering SD or LD and postflowering LD were sampled at 4 h after dawn at R5. Each sample was collected from three individual plants. Total mRNA from leaves was isolated using RNA Easy Fast Plant Tissue kits (Tiangen) and cDNA was synthesised using FastKing RT kits (Tiangen). The transcript levels of the floral-promoting genes (*GmFT2a*, *GmFT3a*, *GmFT3b*, *GmFT5a* and *GmFT6*), and floral-inhibiting genes (*GmFT1a*, *GmFT4* and *E1*) were detected using KAPA SYBR DNA Polymerase (KAPA Biosystems) on a QuantStudio 7 Flex system (Applied Biosystems). The qPCR data were

analysed using the 2^{-C_t} method with *GmActin* as an internal reference gene (Jian et al., 2008). Primers used for qPCR are listed in Supporting Information S2: Table S2.

2.5 | Phenotyping and statistical analysis

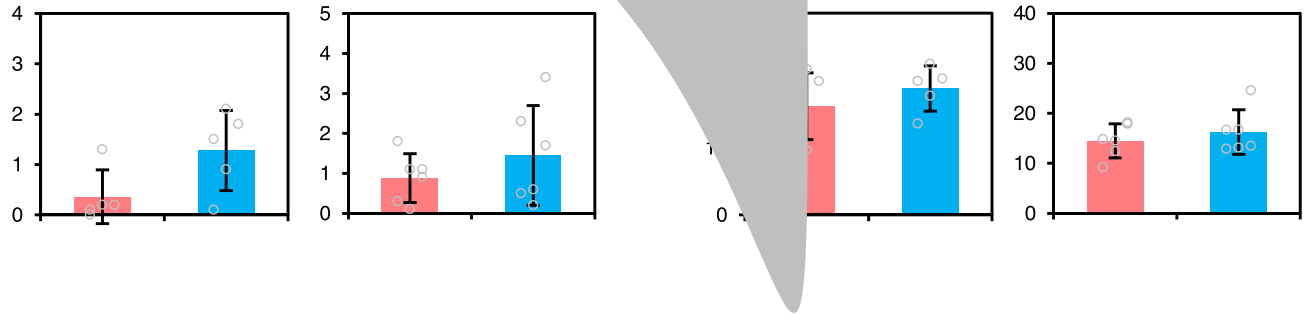
Soybean developmental stages of emergence (VE), V1, V2, V3, R1 (one open flower at any node on the main stem), R3 (a 0.5-cm long pod on one of the four uppermost nodes on the main stem), R5 (a 3-mm long seed in pod in one of the four uppermost nodes on the main stem), beginning maturity (R7, one pod on the main stem has reached mature pod colour) and full maturity (R8, 95% of pods have reached mature pod colour) were recorded according to the description of Fehr and Caviness (1977). We recorded the VE, V1, V2, V3, R1, R3, R5 and R7 of eleven early-maturing soybean varieties treated with preflowering SD or LD and postflowering LD photoperiods (Supporting Information Table S3). A total of seven ~ twenty plants were recorded for each variety. Once these plants reached the R8, we documented their plant height, node number, branch number and seed number per plant (Supporting Information Table S4).

The photoperiod response sensitivity (PRS) was calculated using Equation (1) indicated below, and the PAE was calculated according to Equation (2) (Fei et al., 2009). The data were analysed using Excel and R packages, and are presented as the mean \pm

3 | RESULTS

3.1 | The postflowering responses of early-maturing soybean varieties to preflowering photoperiodic treatments

Five and six early-maturing varieties in the MG 00 and MG 0 groups, respectively, were selected to identify the PAE (Supporting Information S1: Table S1). These plants were treated with preflowering SD or LD and postflowering LD. The results showed that the flowering time (VE



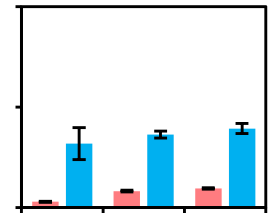
3.3 | Transcriptome profiling and expression analysis of flowering-time genes in soybean plants responsive to preflowering photoperiodic treatments

To identify the flowering-time related genes influenced by preflowering SD treatments, we identified differentially expressed genes (DEGs) by performing transcriptomic sequencing of the early-maturing variety Heihe27 (MG 0) at R1 and R3 under preflowering SD or LD and postflowering LD conditions. A total of 8608 and 7650 DEGs were found to be up-regulated and down-regulated, respectively, in plants treated with SD compared to LD at R1 (Figure S1), and 10 615 and 10 282 DEGs showed differential expression at R3 (Figure S2). A majority of DEGs were classified under the molecular function category at R1 (Figure S3), whereas most DEGs belonged to the cell component category at R3 (Figure S4). There were 10 308 DEGs that exhibited differential expression patterns in both R1 and R3 (Figure S5). Further analysis revealed that among these common DEGs, 25 DEGs show

homology to flowering-time related genes through screening their functional annotations (Figure 3).

The first set of DEGs included *FT* (*GmFT2a*, *GmFT3a*, *GmFT3b*, *GmFT5a* and *GmFT6*), *CONSTANS-LIKE* (*Glyma.16G067000*), *RELATIVE OF EARLY FLOWERING* (*Glyma.04G191900*, *Glyma.06G174000*, *Glyma.04G192000* and *Glyma.06G173800*), *EARLY FLOWERING MYB* (*Glyma.17G178500* and *Glyma.06G213400*), *EARLY FLOWERING IN SDS* (*Glyma.06G117700* and *Glyma.04G245400*), *EARLY FLOWERING 8* (*Glyma.15G176400*) and *FLOWERING TIME CONTROL PROTEIN FPA* (*Glyma.13G075300*) homologs that were significantly up-regulated ($p < 0.05$) at R1 and R3 in Heihe27 plants treated with preflowering SD compared to those treated with preflowering LD (Figure 3). In contrast, another set of genes like *CRYPTOCHROME* (*GmCRY1a* and *GmCRY1b*), *GIGANTEA* (*E2* and *GmGI3*), *PHYTOCHROME-INTERACTING FACTOR 3* (*Glyma.19G222000*), *FLOWERING LOCUS K* (*Glyma.03G160000*), *EARLY FLOWERING* (*Glyma.08G361700* and *Glyma.17G231600*), *CONSTANS-LIKE* (*Glyma.02G152900*) homologs were significantly down-regulated ($p < 0.05$) at R1 compared to R3 (Figure 3).

FT is regarded as the integrator of signals in the flowering pathway of plants (Andrés & Coupland, [2012](#)). In soybean, *FT* homologs are divided into two types including floral promoters (e.g., *GmFT2a*, *GmFT2b*, *GmFT3a*, *GmFT3b*, *GmFT5a* and *GmFT5b*)



3.4 | The PAE of early-maturing soybean lines overexpressing floral-promoting *GmFT* homologs

E1 has a high expression level in LD and a low expression level in SD and regulates the flowering and maturity of soybean by inhibiting the expression of floral-promoting *GmFT* (Chen et al., 2020; Nan et al., 2014; Su et al., 2022; Xia et al., 2012). We grew *E1* RNAi (in ZGDD background) and wild-type ZGDD plants under preflowering SD or LD and postflowering LD conditions. The results indicated that the flowering time and maturity of *E1* RNAi plants displayed no significant difference ($p > 0.05$) between preflowering SD and LD (Figure 5a,b). In *E1* RNAi plants, *E1* was dramatically down-regulated ($p < 0.01$) and the floral-promoting *GmFT2a*, *GmFT3a*, *GmFT3b* and *GmFT5a* were all highly up-regulated ($p < 0.01$) compared to

wild-type ZGDD plants (Figure 5c-g). Importantly, *GmFT2a*, *GmFT3a*, *GmFT3b* and *GmFT5a* exhibited a higher expression level both in preflowering SD and LD when *E1* was suppressed (Figure 5d-g).

To test whether the floral-promoting *GmFT* homologs are required for the PAE in soybean, *35S:GmFT2a* overexpression plants (*35S:GmFT2a* OE, in ZGDD background) and wild-type ZGDD plants were treated with preflowering SD or LD and postflowering LD. The flowering time of *35S:GmFT2a* OE plants was 12.1 ± 1.5 and 11.7 ± 0.6 d after emergence under SD and LD conditions, which were significantly earlier than the MG 00 and MG 0 varieties (Figures 1a,d and 6a). Moreover, the flowering time and maturity of *35S:GmFT2a* OE plants displayed no significant difference ($p > 0.05$) between preflowering SD and LD treatments (Figure 6a,b). Next, we analysed the expression level of *GmFT2a* in *35S:GmFT2a* OE and wild-type ZGDD plants and found

that 35 S:*GmFT2a* OE plants showed a high expression level of *GmFT2a* even under LD → LD conditions (Figure 6c). Additionally, *GmFT2a* displayed constitutively high expression levels no matter the preflowering SD and LD treatment (no significant difference; $p > 0.05$) (Figure 6c). Thus, the high expression of the floral-promoting *GmFT2a* regulates the PAE of early-maturing varieties.

4 | DISCUSSION

4.1 | The characteristics of photoperiodic after-effect (PAE) in early-maturing soybean varieties

Soybean is an SDP in which flowering is promoted by SD conditions and suppressed by LD conditions (Garner & Allard, 1920; Wu et al., 2006). The PAE was discovered in parallel with the photoperiodic response in soybean (Garner & Allard, 1920). Indeed, the PAE is a continuation of the photoperiodic response in soybean plants after flowering. Thus, preflowering SD-induced factors are also required for postflowering developments. This phenomenon is consistent with the previous notion that the photoperiodic response exists in the whole life cycle from emergence to maturity in soybean (Han et al., 1995, 2006; Wu et al., 2006; Xu et al., 2021). Early-maturing varieties display no difference in the flowering time under SD and LD conditions but greatly accelerated the postflowering maturation process after SD preflowering exposure compared to LD. Hence, the maturation of early-maturing soybean varieties is sensitive to photoperiods and is impacted during reproductive growth, but not during vegetative growth. In other words, the maturity of early-maturing varieties is more sensitive to photoperiod than flowering time. According to this, we propose that early-

maturing varieties adapt to high latitudes mainly by adjusting the length of their reproductive maturation period.

Besides the developmental status, the PAE also influences the formation of important agronomic traits including plant height, node number, pod number, seed number, biomass and so on (Han et al., 1995; Liu et al., 1983; Xu et al., 1990). Additionally, quality-related traits, like protein and oil content, oleic acid and linoleic acid proportions in oil, are also influenced by preflowering photoperiodic treatments (Han et al., 1995). Protein content is negatively correlated with the PAE, revealing that the preflowering SD treatment is unbeneficial to seed protein accumulation for early-maturing varieties with low levels of protein content that are prevalently found in high latitudes (Han et al., 1995, 1997; Song et al., 2016).

4.2 | Floral-promoting *GmFT* homologs play key roles in the PAE

The photoperiodic response of soybean is controlled by multiple genes, including the photoreceptor phytochrome A (*E3* and *E4*) (Liu et al., 2008; Watanabe et al., 2009), circadian evening complex components (*J* and *LUX*) (Bu et al., 2021; Lu et al., 2017; Yue et al., 2017), central flowering repressor (*E1*) (Xia et al., 2012) and downstream integrators (floral-promoting *GmFT2a* and *GmFT5a*, and floral-inhibiting *GmFT1a*) (Liu et al., 2018; Nan et al., 2014; Sun et al., 2011). In the present study, we demonstrated that these integrators, mainly the floral-promoting *GmFT* homologs of *GmFT2a*, *GmFT3a*, *GmFT3b* and *GmFT5a*, are greatly up-regulated in the early-maturing varieties treated with preflowering SD and continuously maintain a high expression level postflowering even under LD conditions. It was proposed that *E1-FT* module may play a central role in the PAE and two factors may contribute to maintain high expression levels of the floral-promoting *GmFT* homologs after photoperiod conversion. First, *E1*, the upstream inhibiting gene of floral-promoting *GmFT* homologs, showed low expression level under preflowering SD treatment compared to preflowering LD treatment. Second, the total or partial dysfunction of *E1* resulting from mutations in early-maturing soybean varieties decrease the inhibition to the expression of flowering-promoting *GmFTs*. These observations revealed that PAE on postflowering development are caused by the same mechanism as the photoperiodic response before flowering, and further indicate that the PAE is another presentation of the complete photoperiodic response in the whole life cycle of soybean (Han & Wang, 1995b).

FT is a part of the florigen signal that promotes floral development (Corbesier et al., 2007; Tamaki et al., 2007). In soybean, the floral-promoting *GmFT* homologs *GmFT2a* and *GmFT5a* have been demonstrated as the mobile factors that move from leaves to roots (Wang et al., 2021). In our study, we characterised the effect of floral-promoting *GmFT* homologs on both vegetative and reproductive development, especially how *GmFT* responds to preflowering SD on the postflowering development in early-maturing soybean

improving the grammar and word usage in the writing of the manuscript.

CONFLICT OF INTEREST STATEMENT

The authors declare no conflict of interest.

DATA AVAILABILITY STATEMENT

All raw data for RNA sequencing have been submitted to NCBI as BioProject PRJNA1027571.

ORCID

Xin Xu  <http://orcid.org/0000-0002-8571-5034>

Bingjun Jiang  <http://orcid.org/0000-0002-8172-4646>

Wensheng Hou  <http://orcid.org/0000-0002-6342-4308>

REFERENCES

- Alliprandini, L.F., Abatti, C., Bertagnolli, P.F., Cavassim, J.E., Gabe, H.L., Kurek, A. et al. (2009) Understanding soybean maturity groups in Brazil: environment, cultivar classification, and stability. *Crop Science*, 49, 801–808. Available from: <https://doi.org/10.2135/cropsci2008.07.0390>
- Andrés, F. & Coupland, G. (2012) The genetic basis of flowering responses to seasonal cues. *Nature Reviews Genetics*, 13, 627–639. Available from: <https://doi.org/10.1038/nrg3291>
- Bu, T., Lu, S., Wang, K., Dong, L., Li, S., Xie, Q. et al. (2021) A critical role of the soybean evening complex in the control of photoperiod sensitivity and adaptation. *Proceedings of the National Academy of Sciences of the United States of America*, 118(8). e2010241118. Available from: <https://doi.org/10.1073/pnas.2010241118>
- Cai, Y., Wang, L., Chen, L., Wu, T., Liu, L., Sun, S. et al. (2020) Mutagenesis of *GmFT2a* and *GmFT5a* mediated by CRISPR/Cas9 contributes for expanding the regional adaptability of soybean. *Plant Biotechnology Journal*, 18(1), 298–309. Available from: <https://doi.org/10.1111/pbi.13199>
- Chen, L., Cai, Y., Qu, M., Wang, L., Sun, H., Jiang, B. et al. (2020) Soybean adaption to high-latitude regions is associated with natural variations of *GmFT2b*, an ortholog of *FLOWERING LOCUS T*. *Plant, Cell & Environment*, 43(4), 934–944. Available from: <https://doi.org/10.1111/pce.13695>
- Corbesier, L., Vincent, C., Jang, S., Fornara, F., Fan, Q., Searle, I. et al. (2007) FT protein movement contributes to long-distance signaling in floral induction of *Arabidopsis*. *Science*, 316(5827), 1030–1033. Available from: <https://doi.org/10.1126/science.1141752>
- Dong, L., Cheng, C., Fang, C., Kong, L., Yang, H., Hou, Z. et al. (2022) Parallel selection of distinct *Tof5* alleles drove the adaptation of cultivated and wild soybean to high latitude. *Molecular Plant*, 15, 308–321. Available from: <https://doi.org/10.1016/j.molp.2021.10.004>
- Dong, L., Li, S., Wang, L., Su, T., Zhang, C., Bi, Y. et al. (2022) The genetic basis of high-latitude adaptation in wild soybean. *Current Biology*, 33(2), 252–262. Available from: <https://doi.org/10.1016/j.cub.2022.11.061>
- Fehr, W.R. & Caviness, C.E. (1977) Stages of soybean development. Special Report 80. Iowa Agricultural and Home Economics Experimental Station, Ames, Iowa. <https://dr.lib.iastate.edu/handle/20.500.12876/90239>
- Fei, Z.H., Wu, C.X., Sun, H.B., Hou, W.S., Zhang, B.S. & Han, T.F. (2009) Identification of photothermal responses in soybean by integrating photoperiod treatments with planting-date experiments. *Acta Agronomica Sinica*, 35(8), 1525–1531. Available from: <https://doi.org/10.3724/SP.J.1006.2009.01525>
- Garner, W.W. (1937) Recent work on photoperiodism. *The Botanical Review*, 3(5), 259–275. Available from: <https://doi.org/10.1007/bf02872312>
- Garner, W.W. & Allard, H.A. (1920) Effect of the relative length of day and night and other factors of the environment on growth and reproduction in plants. *Journal of Agricultural Research*, 18(2), 553–606.
- Greulach, V.A. (1942) Photoperiodic after-effects in six composites. *Botanical Gazette*, 103(4), 698–709.
- Han, T. & Gai, J. (1999) Phytohormonal analysis of some photoperiod effects night4/F1D[(,)-alenonmica f7nica

- with duplication of the *phytochrome A* gene. *Genetics*, 180(2), 995–1007. Available from: <https://doi.org/10.1534/genetics.108.092742>
- Liu, H., Liang, H. & Zhang, J. (1983) The after-effect of light duration on the development of soybeans. *Acta Agriculturae Universitatis Pekinensis*, 9(3), 67–72.
- Liu, L., Gao, L., Zhang, L., Cai, Y., Song, W., Chen, L. et al. (2020) Co-silencing *E1* and its homologs in an extremely late-maturing soybean cultivar confers super-early maturity and adaptation to high-latitude short-season regions. *Journal of Integrative Agriculture*, 21(2), 326–335. Available from: [https://doi.org/10.1016/S2095-3119\(20\)63391-3](https://doi.org/10.1016/S2095-3119(20)63391-3)
- Liu, L., Song, W., Wang, L., Sun, X., Qi, Y., Wu, T. et al. (2020) Allele combinations of maturity genes *E1–E4* affect adaptation of soybean to diverse geographic regions and farming systems in China. *PLoS One*, 15. e0235397. Available from: <https://doi.org/10.1371/journal.pone.0235397>
- Liu, W., Jiang, B., Ma, L., Zhang, S., Zhai, H., Xu, X. et al. (2018) Functional diversification of *Flowering Locus T* homologs in soybean: *GmFT1a* and *GmFT2a/5a* have opposite roles in controlling flowering and maturation. *New Phytologist*, 217(3), 1335–1345. Available from: <https://doi.org/10.1111/nph.14884>
- Lu, S., Dong, L., Fang, C., Liu, S., Kong, L., Cheng, Q. et al. (2020) Stepwise selection on homeologous PRR genes controlling flowering and maturity during soybean domestication. *Nature Genetics*, 52, 428–436. Available from: <https://doi.org/10.1038/s41588-020-0604-7>
- Lu, S., Zhao, X., Hu, Y., Liu, S., Nan, H., Li, X. et al. (2017) Natural variation at the soybean *J* locus improves adaptation to the tropics and enhances yield. *Nature Genetics*, 49(5), 773–779. Available from: <https://doi.org/10.1038/ng.3819>
- Nan, H., Cao, D., Zhang, D., Li, Y., Lu, S., Tang, L. et al. (2014) *GmFT2a* and *GmFT5a* redundantly and differentially regulate flowering through interaction with and upregulation of the bZIP transcription factor *GmFDL19* in soybean. *PLoS One*, 9(5). e97669. Available from: <https://doi.org/10.1371/journal.pone.0097669>
- Pu, M. & Pan, T. (1982) A study on the regionalization of soybean producing area in China. *Soybean Science*, 1(2), 105–121.
- Sinegovskii, M., Yuan, S., Sinegovskaya, V. & Han, T. (2018) Current status of the soybean industry and research in the Russia Federation. *Soybean Science*, 37(1), 1–7. Available from: <https://doi.org/10.11861/j.issn.1000-9841.2018.01.0001>
- Song, W., Sun, S., Ibrahim, S.E., Xu, Z., Wu, H., Hu, X. et al. (2019) Standard cultivar selection and digital quantification for precise classification of maturity groups in soybean. *Crop Science*, 59, 1997–2006. Available from: <https://doi.org/10.2135/cropsci2019.02.0095>
- Song, W., Yang, R., Wu, T., Wu, C., Sun, S., Zhang, S. et al. (2016) Analyzing the effects of climate factors on soybean protein, oil contents, and composition by extensive and high-density sampling in China. *Journal of Agricultural and Food Chemistry*, 64(20), 4121–4130. Available from: <https://doi.org/10.1021/acs.jafc.6b00008>
- Stoughton, R.H. & Hole, D.R. (1937) Photoperiodic after-effect. *Nature*, 140, 808. Available from: <https://doi.org/10.1038/140808a0>
- Su, Q., Chen, L., Cai, Y., Chen, Y., Yuan, S. & Li, M. et al. (2022) Functional redundancy of *FLOWERING LOCUS T 3b* in soybean flowering time regulation. *International Journal of Molecular Sciences*, 23, 2497. Available from: <https://doi.org/10.3390/ijms23052497>
- Su, Q., Chen, L., Cai, Y., Wang, L., Chen, Y., Zhang, J. et al. (2024) The *FLOWERING LOCUS T 5b* positively regulates photoperiodic flowering and improves the geographical adaptation of soybean. *Plant, Cell and Environment*, 47, 246–258. Available from: <https://doi.org/10.1111/pce.14739>
- Sun, H., Jia, Z., Cao, D., Jiang, B., Wu, C., Hou, W. et al. (2011) *GmFT2a*, a soybean homolog of *FLOWERING LOCUS T*, is involved in flowering transition and maintenance. *PLoS One*, 6(12). e29238. Available from: <https://doi.org/10.1371/journal.pone.0029238>
- Tamaki, S., Matsuo, S., Wong, H.L., Yokoi, S. & Shimamoto, K. (2007) Hd3a protein is a mobile flowering signal in rice. *Science*, 316(5827), 1033–1036. Available from: <https://doi.org/10.1126/science.1141753>
- Wang, L., Sun, S., Wu, T., Liu, L., Sun, X., Cai, Y. et al. (2020) Natural variation and CRISPR/Cas9-mediated mutation in *GmPRR37* affect photoperiodic flowering and contribute to regional adaptation of soybean. *Plant Biotechnology Journal*, 18(9), 1869–1881. Available from: <https://doi.org/10.1111/pbi.13346>
- Wang, T., Guo, J., Peng, Y., Lyu, X., Liu, B., Sun, S. et al. (2021) Light-induced mobile factors from shoots regulate rhizobium-triggered soybean root nodulation. *Science*, 374(6563), 65–71. Available from: <https://doi.org/10.1126/science.abh2890>
- Watanabe, S., Hideshima, R., Xia, Z., Tsubokura, Y., Sato, S., Nakamoto, Y. et al. (2009) Map-based cloning of the gene associated with the soybean maturity locus *E3*. *Genetics*, 182(4), 1251–1262. Available from: <https://doi.org/10.1534/genetics.108.098772>
- Watanabe, S., Xia, Z., Hideshima, R., Tsubokura, Y., Sato, S., Yamanaka, N. et al. (2011) A map-based cloning strategy employing a residual heterozygous line reveals that the *GIGANTEA* gene is involved in soybean maturity and flowering. *Genetics*, 188(2), 395–407. Available from: <https://doi.org/10.1534/genetics.110.125062>
- Wilcox, J.R. (2004) World distribution and trade of soybean. In: *SOYBEANS: improvement, production, and uses*. In: Boerma, H.R. & Specht, J.E. (Eds.) *American Society of Agronomy, Crop Science Society of America*, 3rd edition. Madison: and Soil Science Society of America Press, pp. 1–14. <https://doi.org/10.2134/agronmonogr16.3ed.c1>
- Wu, C., Ma, Q., Yam, K.M., Cheung, M.Y., Xu, Y., Han, T. et al. (2006) In situ expression of the *GmNMH7* gene is photoperiod-dependent in a unique soybean (*Glycine max* [L.] Merr.) flowering reversion system. *Planta*, 223(4), 725–735. Available from: <https://doi.org/10.1007/s00425-005-0130-y>
- Wu, C.X., Li, J.C., Sha, A.H., Zeng, H.Y., Sun, S. & Yang, G.M. et al. (2013) Maturity group classification of check varieties in national soybean uniform trials of China. *Acta Agronomica Sinica*, 38, 1977–1987. Available from: <https://doi.org/10.3724/SP.J.1006.2012.01977>
- Xia, Z., Watanabe, S., Yamada, T., Tsubokura, Y., Nakashima, H., Zhai, H. et al. (2012) Positional cloning and characterization reveal the molecular basis for soybean maturity locus *E1* that regulates photoperiodic flowering. *Proceedings of the National Academy of Sciences of the United States of America*, 109(32), 2155–2164. Available from: <https://doi.org/10.1073/pnas.1117982109>
- Xu, B. & Lu, Q. (1988) Soybean ecology. III comparative study on photoperiod induction of wild (*G. soja*) and cultivated (*G. max*) soybeans. *Soybean Science*, 7(4), 269–275.
- Xu, L., Zhong, J. & Liu, H. (1990) The after-effect of photoperiod on the development and phenological traits of soybean. *Chinese Journal of Agriculture Meteorology*, 11(1), 22–28.
- Xu, X., Zhang, L., Cao, X., Liu, L., Jiang, B., Zhang, C. et al. (2021) Cytiledons facilitate the adaptation of early-maturing soybean varieties to high-latitude long-day environments. *Plant, Cell & Environment*, 44(8), 2551–2564. Available from: <https://doi.org/10.1111/pce.14120>
- Yuan, S., Wang, Y., Wang, J., Zhang, C., Zhang, L. & Jiang, B. et al. (2022) *GmFT3a* fine-tunes flowering time and improves adaptation of soybean to higher latitudes. *Frontiers in Plant Science*, 13, 929747. Available from: <https://doi.org/10.3389/fpls.2022.929747>
- Yue, L., Li, X., Fang, C., Chen, L., Yang, H., Yang, J. et al. (2021) *FT5a* interferes with the *Dt1-AP1* feedback loop to control flowering time and shoot determinacy in soybean. *Journal of Integrative Plant Biology*, 63(6), 1004–1020. Available from: <https://doi.org/10.1111/jipb.13070>

- Yue, Y., Liu, N., Jiang, B., Li, M., Wang, H., Jiang, Z. et al. (2017) A single nucleotide deletion in *J* encoding *GmELF3* confers long juvenility and is associated with adaption of tropic soybean. *Molecular Plant*, 10(4), 656–658. Available from: <https://doi.org/10.1016/j.molp.2016.12.004>
- Zhang, L., Liu, W., Tsegaw, M., Xu, X., Qi, Y., Sapey, E. et al. (2020) Principles and practices of the photo-thermal adaptability improvement in soybean. *Journal of Integrative Agriculture*, 19(2), 295–310. Available from: [https://doi.org/10.1016/S2095-3119\(19\)62850-9](https://doi.org/10.1016/S2095-3119(19)62850-9)
- Zhang, L.X., Kyei-Boahen, S., Zhang, J., Zhang, M.H., Freeland, T.B., Watson, C.E. et al. (2007) Modifications of optimum adaptation zones for soybean maturity groups in the USA. *Crop Management*, 6(1), 1–11. Available from: <https://doi.org/10.1094/CM-2007-0927-01-RS>

SUPPORTING INFORMATION

Additional supporting information can be found online in the Supporting Information section at the end of this article.

How to cite this article: Wang, J., Xu, X., Wang, P., Zhang, L., Liu, L., Liu, L. et al. (2024) Floral-promoting *GmFT* homologs trigger photoperiodic after-effects: an important mechanism for early-maturing soybean varieties to regulate reproductive development and adapt to high latitudes. *Plant, Cell & Environment*, 1–12. <https://doi.org/10.1111/pce.14833>