Received: 20 May 2024 | Accepted: 24 February 2025

DOI: 10.1002/tpg2.70017

The Plant Genome

REVIEW

Special Section: Tribute to Ron Phillips: Crop Genetics, Genomics and Biotechnology

Exploring the multifaceted dynamics of flowering time regulation in field crops: Insight and intervention approaches

Yogesh Dashrath Naik[1] | **Rajeev N. Bahuguna**[2] | **Pedro Garcia-Caparros**[3] | **Rebecca S. Zwart**[4] | **M. S. Sai Reddy**[5] | **Reyazul Rouf Mir**[6] | **Uday Chand Jha**[7] | **B. Fakrudin**[8] | **Manish K. Pandey**[9] | **Dinakar Challabathula**[10] | **Vinay Kumar Sharma**[1] | **Umesh K. Reddy**[11] | **Chanda Venkata Sameer Kumar**[12] | **Venugopal Mendu**[13] | **P. V. Vara Prasad**[14] | **Somashekhar M. Punnuri**[15] | **Rajeev K. Varshney**[16] | **Mahendar Thudi**[4,15]

[1]Department of Agricultural Biotechnology and Molecular Biology, Dr. Rajendra Prasad Central Agricultural University, Pusa, Bihar, India

[2]National Agri-Food Biotechnology Institute, Mohali, Punjab, India

[3]Agronomy Department of Superior School Engineering, University of Almería, Almería, Spain

[4]Centre for Crop Health and School of Agriculture and Environmental Science, University of Southern Queensland, Toowoomba, Australia

[5]Department of Entomology, Dr. Rajendra Prasad Central Agricultural University, Pusa, Bihar, India

[6]Faculty of Agriculture, Sher-e-Kashmir University of Agricultural Sciences and Technology, Sopore, Kashmir, India

[7]Indian Council of Agricultural Research, Indian Institute of Pulses Research, Kanpur, Uttar Pradesh, India

[8]Department of Biotechnology and Crop Improvement, University of Horticultural Sciences, Bagalkot, Karnataka, India

[9]International Crops Research Institute for the Semi-Arid Tropics, Hyderabad, Telangana, India

[10]Department of Biotechnology, Central University of Tamil Nadu, Thiruvarur, Tamil Nadu, India

[11]Department of Biology, West Virginia State University, Morgantown, West Virginia, USA

[12]Department of Genetics and Plant Breeding, Professor Jayashankar Telangana State Agricultural University, Hyderabad, Telangana, India

[13]Department of Agronomy, Agribusiness & Environmental Sciences, Texas A&M University, Kingsville, Texas, USA

[14]Department of Agronomy, Kansas State University, Manhattan, Kansas, USA

[15]College of Agriculture, Family Sciences and Technology, Fort Valley State University, Fort Valley, Georgia, USA

[16]WA State Agricultural Biotechnology Centre, Centre for Crop and Food Innovation, Murdoch University, Murdoch, Western Australia, Australia

Correspondence
Mahendar Thudi and Somashekhar M. Punnuri, College of Agriculture, Family Sciences and Technology, 1005 State University Dr, Fort Valley State University,

Abstract

The flowering time (FTi) plays a critical role in the reproductive success and yield of various crop species by directly impacting both the quality and quantity of grain yield. Achieving optimal FTi is crucial for maximizing reproductive success and ensuring

---

Abbreviations: AP1, apetala1; *CO*, *CONSTANS*; Ehd2, early heading date-2; *FLC*, *FLOWERING LOCUS C*; *FT*, *FLOWERING LOCUS T*; FTi, flowering time; FUL, fruitful; G1, gigantea; GWAS, genome-wide association studies; Hd, heading date; LFY, leafy; NGS, next-generation sequencing; OsG1, OsGigantea; PVE, phenotypic variance explained; QTL, quantitative trait loci; QTL-seq, QTL-sequencing; SEP3, sepallata-3; *SOC1*, *SUPPRESSOR OF OVEREXPRESSION OF CONSTANS-1*; SPL15, squamosa promoter binding protein-like-15; TAR2, tryptophan aminotransferase related 2; TILLING, targeting induced local lesions in genomes; TOE1, target of eat 1; Vgt1, vegetative to generative transition 1; VRN, vernalization.

Fort Valley, GA, USA.
Email: mahendar.thudi@usq.edu.au and punnuris@fvsu.edu

Rajeev K. Varshney, WA State Agricultural Biotechnology Centre, Centre for Crop and Food Innovation, Murdoch University, Murdoch, WA 6150, Australia.
Email: rajeev.varshney@murdoch.edu.au

Assigned to Associate Editor Roberto Tuberosa.

overall agricultural productivity. While genetic factors undoubtedly influence FTi, photoperiodism and vernalization are recognized as key contributors to the complex physiological processes governing flowering in plants. Identifying candidate genes and pathways associated with FTi is essential for developing genomic interventions and plant breeding to enhance adaptability to diverse environmental conditions. This review highlights the intricate nature of the regulatory mechanisms of flowering and emphasizes the vital importance of precisely regulating FTi to ensure plant adaptability and reproductive success. Special attention is given to essential genes, pathways, and genomic interventions geared toward promoting early flowering, particularly under challenging environmental conditions such as drought, heat, and cold stress as well as other abiotic stresses that occur during the critical flowering stage of major field crops. Moreover, this review explores the significant progress achieved in omics technologies, offering valuable insights and tools for deciphering and regulating FTi. In summary, this review aims to provide a comprehensive understanding of the mechanisms governing FTi, with a particular focus on their crucial role in bolstering yields under adverse environmental conditions to safeguard food security.

Plain Language Summary

Flowering is crucial in agricultural crops because it produces seeds that grow into new plants or are used for human consumption. The timing of flowering is also important, particularly in the context of climate change. Extreme weather conditions can adversely affect flowering and reduce crop productivity. Early-flowering varieties complete their life cycle prior to the onset of extreme environmental conditions, allowing them to escape the detrimental effects of heat and drought stress. Recent advances in DNA sequencing have led to the identification of key genes directly involved in flowering, such as *FT* (*FLOWERING LOCUS T*), *FLC* (*FLOWERING LOCUS C*), and *VRN* (Vernalization). Additionally, various genomic approaches such as QTL-seq, genome editing, trait mapping, and speed breeding have been used to better understand the complexity of flowering time. This integrated approach provides a promising solution for regulating flowering time and improving crop adaptability to adverse conditions.

1 | INTRODUCTION

Crop production and climate change are intricately linked, with climate change serving as a prominent instigator of both biotic and abiotic stresses that adversely impact crop yields (Abbass et al., 2022). Climate change manifests through elevated carbon dioxide (CO_2) levels, temperature fluctuations, intensified rainfall, and an increased frequency of extreme weather events (Parmesan & Hanley, 2015). The anticipation of more frequent and widespread occurrences of extreme heat, prolonged droughts, and heavy rainfall underscores the urgency to address these challenges. Projections indicate a potential doubling of maize (*Zea mays* L.) yield reduction due to heat stress during anthesis by 2080, emphasizing the gravity of the situation (Deryng et al., 2014). Severe moisture stress has similarly led to significant yield reductions in maize and soybean (*Glycine max*; H. Nguyen et al., 2023). Grain legume crops like chickpea (*Cicer arietinum*), lentil (*Lens culinaris*), faba bean (*Vicia faba*), and pea (*Pisum sativum*) face heightened vulnerability to terminal heat and drought stresses, necessitating the development of crop varieties resilient to diverse stresses for global food security (V. V. Kumari et al., 2021).

To address these challenges, plant breeders are leveraging the genetic diversity within crops to develop improved varieties with desirable traits. These traits, including canopy temperature, stay green, leaf chlorophyll, leaf area, stomatal conductance, relative water content, root length and flowering time (FTi), have been identified as crucial features for improving stress tolerance (Fahad et al., 2017). FTi is the duration for a plant to produce fully developed flowers, which emerges as a key trait in mitigating the impacts of terminal heat and drought stresses on crop yield (Shavrukov et al., 2017). The initiation of flowering marks a fundamental transition in the life cycle of annual plants, playing a vital role in their fitness and reproductive success (Rubin et al., 2019). The regulation of FTi is a complex process that integrates multiple internal genetic components and external signals (day length, temperature and adverse environmental conditions) to ensure optimal reproductive success (Amasino, 2010). Epigenetic factors such as histone modifications, DNA methylation, and microRNAs further contribute to this regulatory complexity (Yaish et al., 2011). *Arabidopsis* serves as a model plant for understanding flowering regulation, with vernalization triggering flowering by controlling key genes such as *FLOWERING LOCUS C* (*FLC*) and *FLOWERING LOCUS T* (*FT*) (Chavez-Hernández et al., 2022). Legumes, responding to cold for flowering, use their versions of the FTi gene (*FTa*, *FTb*, and *FTc*) (Surkova & Samsonova, 2022), while cereals predominantly rely on vernalization genes (*VRN1*, *VRN2*, and *VRN3*) such as *Vrn-1* and *Ppd-1* in wheat (*Triticum aestivum*; Kennedy & Geuten, 2020; Mizuno et al., 2023).

While the physiological and molecular basis of flowering is not entirely understood, recent advances in next-generation sequencing (NGS) and functional genomics have provided valuable insights into the molecular pathways involved (Chavez-Hernández et al., 2022; D. Ma et al., 2021; Osnato et al., 2022). Whole-genome sequencing aids in identifying single nucleotide polymorphisms, facilitating the identification of genomic regions or candidate genes associated with important traits. Numerous studies have explored the FTi trait in various plant species, including model plants and major crops such as maize, rice (*Oryza sativa* L.), soybean, and chickpea. In the face of climate change, the timing of flowering becomes crucial for many field crops. Initiating flowering early in the growing season can help mitigate the adverse effects of climate change, but careful consideration is needed to avoid limiting seed production (Kehrberger & Holzschuh, 2019). Early maturing legume and oilseed crops offer potential solutions for cultivation in specific areas, utilizing fallow land through short-duration cultivation. Conversely, delaying flowering is essential for crops harvested for plant parts such as tubers or roots, emphasizing the need for precise control over FTi to achieve successful breeding outcomes and expedite genetic enhancement.

This review explores recent advancements in understanding the molecular and physiological basis of flowering in crop plants, focusing on the use of the FTi trait as a tool for adaptation to abiotic and biotic stresses at terminal growth stages. Key genes, pathways, and genomic interventions promoting early-flowering strategies for enhanced crop productivity are discussed. Additionally, the importance of early maturing varieties and the potential of genomic interventions in improving crop productivity and stress tolerance are highlighted.

Core Ideas

- Flowering time (FTi) is regulated by intricate molecular processes involving gene expression, hormones, and other internal/external signals.
- FTi is crucial for crops adapting to extreme conditions, affecting seed production and survival.
- Identifying genes and pathways for FTi is vital for genomic interventions and breeding, enhancing adaptability to diverse environments.
- Modern genetic and genomic tools offer sustainable solutions for expediting breeding programs to regulate FTi.

2 | IMPACT OF CLIMATE CHANGE ON FLOWERING TIME

In response to dynamic environmental shifts, plants have developed adaptive mechanisms over time. Two crucial elements of climate change, specifically rising temperatures and elevated carbon dioxide (CO_2) levels, can impact plant fitness and various processes related to flowering (Jagadish et al., 2016; Tun et al., 2021) and yield formation (Prasad et al., 2002). Temperature plays a pivotal role in the regulation of FTi, directly influencing both development and vernalization processes. Regions experiencing faster increases in winter temperatures (ranging from 0.4 to 2.4°C) observe a notable reduction in flower numbers and seed production (Jagadish et al., 2016). Intriguingly, plant species with multiple inflorescences are more affected by elevated winter temperatures than those with single inflorescences (Y. Liu et al., 2012). In different species of rice, exposure to higher temperatures (+5°C above ambient) decreased duration from sowing to 50% flowering and decreased pollen production, pollen viability, spikelet fertility, number of filled grains, grain weights, and harvest index (Prasad et al., 2006). Enhanced CO_2 levels are known to stimulate increased accumulation of photosynthate, such as trehalose-6-phosphate (T6P) in plants (Jagadish et al., 2016; Springer & Ward, 2007). Disrupting T6P production also disturbs the activation of the *FT* gene (Wahl et al., 2013). For example, soybean experiments conducted in controlled chambers with elevated temperature and CO_2 levels demonstrate the induction of early flowering, accompanied by molecular-level changes involving the upregulation of flowering activators and the downregulation of repressors in response to high temperatures (No et al., 2021).

In *Arabidopsis*, drought stress induces early flowering under long daylight but delays flowering under shorter daylight. The photoperiodic gene *GI*, encoding the GIGANTEA protein, plays a crucial role in this process (Riboni et al., 2013). *GI* is present in many plant species, contributing to critical functions such as regulating circadian rhythm, responding to light signals, tolerating cold, signaling hormones, and controlling flowering in a day length-dependent manner (Brandoli et al., 2020). However, it is important to note that while early flowering is a critical adaptation for surviving severe terminal stress, it may adversely impact plant yield under milder chronic stress conditions (Franks, 2011). Another study involving barley (*Hordeum vulgare*) genotypes exposed to nitrogen deficiency, drought, and salinity demonstrated that increased yield is accompanied by pleiotropic effects arising from FTi-associated genes, resulting in a shorter life cycle, an extended grain-filling period, and an increase in grain size in barley (Wiegmann et al., 2019). Salinity significantly delays flowering in *Arabidopsis*, involving several regulatory factors. The flowering delay under salt stress is influenced by DELLA proteins, which act as negative regulators of GA signaling, and by ethylene (Kazan & Lyons, 2015). Additionally, salt stress reduces the expression of *CO* (*CONSTANS*) and *FT*, further contributing to the delayed flowering response (Kazan & Lyons, 2015). Interestingly, high salt stress has been reported to reduce plant biomass while inducing an early-flowering phenotype and smaller flowers in tomato (F. Sun et al., 2024).

3 | PHYSIOLOGICAL BASIS OF FLOWERING TIME

3.1 | Photoperiodic flowering in plants

Field crops can have either a facultative or obligate response to photoperiod, and depending on the crop species, these responses could be accelerated either by short days or long days. A long photoperiod is defined as having at least 16 h of light and not more than 8 h of darkness in a 24-h cycle. On the other hand, a short photoperiod is defined as having no more than 10 h of light and at least 14 h of darkness in a 24-h cycle (Hamner, 1944). Short-day plants will flower earlier, exclusively during short days (long nights), while long-day plants will flower earlier during long days (short nights) (Allard & Garner, 1940) (Figure 1). Plants detect light through specialized structures called photoreceptors, which enable them to sense a broad range of wavelengths. Phytochromes serve as the primary photoreceptors in plants, detecting red and far-red light and transmitting light signals (Qiu et al., 2023). These photoreceptors in plants are crucial for triggering genome-wide changes in the expression of nuclear and organelle genes, facilitating photomorphogenesis (Griffin & Toledo-Ortiz, 2022). In *Arabidopsis*, the *CO* gene is a central hub for integrating various internal and external signals to induce photoperiodic flowering. In contrast, the *CO* ortholog in rice, *Heading date 1* (*Hd1*), plays a dual role by promoting flowering under short-day conditions and inhibiting it under long-day conditions (C. Sun et al., 2022).

3.2 | Vernalization and flowering time

Temperature plays a crucial role in controlling flowering in many plants, often depending on the plant's developmental stage. Some plants require a prolonged cold period (vernalization) to trigger flowering. They perceive these temperature changes through alterations in cellular processes. For instance, plant cell membranes change their fluidity in response to temperature variations, which can influence various signaling pathways and affect the activity of proteins in the flowering process (Ding & Yang, 2022). Vernalization leads to molecular changes, including epigenetic modifications of the floral repressor gene *FLC* in *Arabidopsis* (P. K. Huang et al., 2024). Before vernalization occurs in *Arabidopsis*, elevated levels of *FLC* prevent the transition to flowering. Notably, this repression is accompanied by increased trimethylation of lysine 27 (*K27me3*) on histone H3, which serves as an epigenetic mark associated with gene silencing. In monocots, such as cereal crops like wheat and barley, *VRN2* serves as a repressor of flowering, and its expression is suppressed by vernalization to induce flowering (Trevaskis et al., 2007; L. Yan et al., 2006). Consequently, the activation of *VRN1* plays an important role in triggering flowering in wheat and barley (Deng et al., 2015; L. Yan et al., 2006). Wild emmer wheat, which served as the progenitor of modern bread wheat, displays substantial variation in the *VRN1* gene (Samineni et al., 2015). Interestingly, utilizing an expedited vernalization technique through an extended photoperiod of 22 h of daylight and 2 h of night time exposure at a temperature of 10°C substantially reduces the generation time for winter wheat and barley, enabling up to five generations per year compared to the standard two generations (Cha et al., 2022). The vernalization process and its epigenetic regulation provide valuable insights for manipulating FTi in crop plants and enhancing agricultural productivity. However, further research in this field is essential to unravel the complexities of vernalization and its molecular mechanisms.

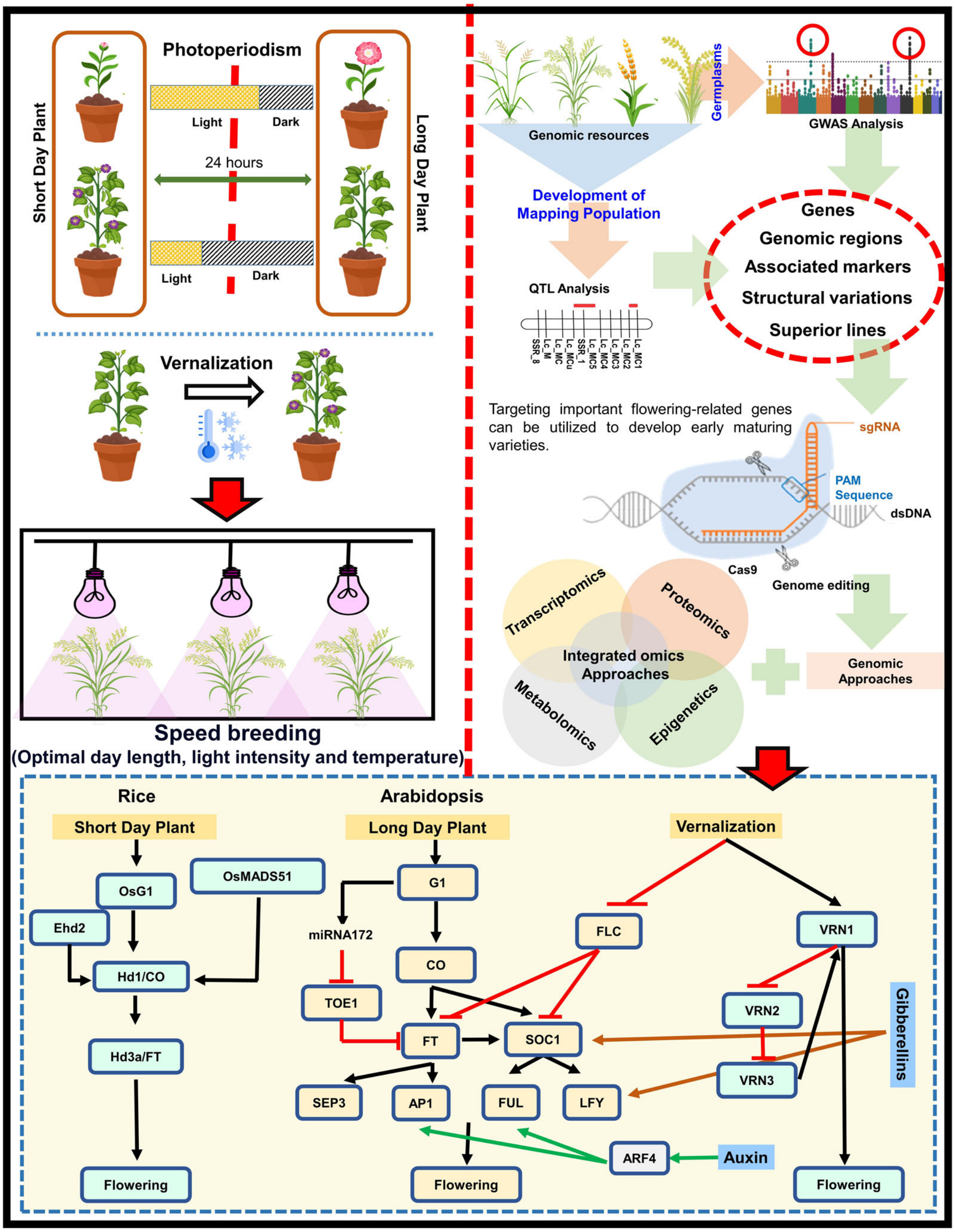

FIGURE 1 Molecular and physiological aspects of flowering. Summary of different environmental cues for flowering response, including photoperiod and vernalization. Understanding these aspects of flowering has led to the development of the speed breeding approach, which minimizes the period required to reach maturity. The figure also illustrates genomic approaches such as QTL mapping, association mapping, and genome editing. It emphasizes the integration of multi-omics approaches for a comprehensive understanding of the molecular basis of flowering. The yellow box below highlights the molecular or genetic control of flowering in short-day plants (rice), long-day plants (*Arabidopsis*), and vernalization. The pathways illustrating how auxin and gibberellin regulate or activate other genes, such as *FUL*, *LFY*, *SOC1*, and *AP1*, are also presented. *AP1, APETALA1; ARF4, AUXIN RESPONSE FACTOR4; CO, CONSTANS; Ehd2, Early heading date2; FLC, FLOWERING LOCUS C; FT, FLOWERING LOCUS T, FUL, FRUITFULL; G1, GIGANTEA; Hd, Heading date; LFY, LEAFY; OsG1, OsGIGANTEA; SEP3, SEPALLATA 3; SOC1, SUPPRESSOR OF OVEREXPRESSION OF CONSTANS 1; TOE1, TARGET OF EAT 1; VRN, VERNALIZATION*.

3.3 | Plant hormones and flowering time

Plant hormones act as messengers that help plants respond to environmental cues (Campos-Rivero et al., 2017). However, when it comes to the complex process of flower bud formation, a single plant hormone alone is not enough to exert a strong influence (Domagalska et al., 2010). Interactions among various plant hormones, including auxin, gibberellin, ethylene, indole-3-acetic acid, cytokinins, and abscisic acid, have been demonstrated to play key roles in triggering flower induction across plant species (Matsoukas, 2014; B. Yan et al., 2019). During plant reproduction, auxin plays a vital role in several aspects. It helps to identify where flowers will form and continues to control the growth and arrangement of flower parts. Additionally, auxin influences later stages of reproduction, determining reproductive success (Krizek, 2011). In rice, increasing the expression of the *OsFPFL4* (FPF1-like protein 4 of rice) gene raises auxin levels while reducing its activity, which lowers auxin levels and influences the FTi (Guo et al., 2020). In wheat (*T. aestivum* L.), the gene *TaIAA15-1A* (Indole-3-Acetic Acid 15-1A) regulates FTi by interacting with the auxin response factor (P. Su et al., 2023). In cultivated strawberry plants, auxin response factor 4 (*FaARF4*) gene is documented to be more active during flowering, and the introgression of this gene in *Arabidopsis* and woodland strawberries (*Fragaria ananassa*) led to early-flowering phenotypes (Dong et al., 2021).

Trehalose 6-phosphate (*T6P*) has been found to stimulate the expression of an auxin biosynthesis gene, tryptophan aminotransferase related 2 (*TAR2*), affecting auxin levels and activating storage processes (Meitzel et al., 2020). During the transition to the flowering stage, increased tissue sucrose levels lead to higher T6P levels, which influence FTi. Indeed, lower T6P levels have been linked to delayed flowering, while higher T6P promotes earlier flowering in plants (Wahl et al., 2013). It has also been reported that GA suppresses the expression of the flowering induction gene *LFY*, while IAA (indole-3-acetic acid) treatment enhances its expression (D. Singh et al., 2023). Hormonal signaling pathways are also involved in the regulation of key flowering genes, such as *FLC*, *CO*, and *FT* (Conti, 2017). For example, GA promotes flowering by activating specific genes such as *SUPPRESSOR OF OVEREXPRESSION OF CONSTANS* 1 (*SOC1*), *LEAFY* (*LFY*), and *FT* (Bao et al., 2020; Mutasa-Göttgens & Hedden, 2009). In another study on barley, GA inhibitors, particularly trinexapac-ethyl applied via exogenous spray, showed the greatest potential for delaying flowering (Kupke et al., 2022). Additionally, DELLA proteins and GA homeostasis are essential regulatory elements within the GA pathway (Bao et al., 2020). DELLA proteins are key regulators in the GA signaling pathway, while they control the expression of genes such as *SOC1* and *FT*, which are keys for plant growth and flowering (M. Li, An, et al., 2016). It is also reported that the gibberellin-insensitive mutant causes dwarfing and earlier flowering in *Arabidopsis*, while it delays flowering in maize (Lawit et al., 2010). In *Arabidopsis*, *BRAHMA* (*BRM*) is involved in GA-signaling-mediated flowering through the assembly of the DELLA-BRM-NF-YC module (C. Zhang, Jian, et al., 2023). Florigen is a protein hormone encoded by the *FT* gene, produced in the leaves, and subsequently transported to the shoot apical meristem (Corbesier et al., 2007). It has a dual role in flowering plants: (i) triggering flowering by promoting the transition to floral development and (ii) growth attenuation in other vegetative meristems (Shalit-Kaneh et al., 2019). All the studies highlight the role of phytohormones in flower development and emphasize their overlapping roles in various developmental processes.

4 | MOLECULAR BASIS OF FLOWERING TIME

4.1 | Genes involved in flowering time were identified in crop plants

The availability of genomic resources and synteny in crops has further advanced the identification of flowering-associated genes. Extensive research in field crops has revealed key insights into the genetic regulation of flowering and identifying various candidate genes (Table 1). Different crop species have unique genetic regulators that control flowering and respond to environmental signals. Many flowering-related genes found in *Arabidopsis* and rice are conserved in legumes (Weller & Ortega, 2015). The *FT* gene belongs to a family found in all angiosperms. *FT* gene is crucial in regulating FTi by integrating environmental signals. They transmit this information from the photoperiod detection site in the leaves to the flower formation site at the shoot apex (N. Lee, Ozaki, et al., 2023). In addition to their role in flowering, *FT* homologs influence various seasonal developmental changes, such as germination, tuber/nodule formation, dormancy onset, and side branching control. This gene family includes *FT* orthologs and paralogs, some of which inhibit flowering (N. Lee, Ozaki, et al., 2023). Another key protein in flowering is the *CO* protein, consisting of an N-terminal B-box domain, a C-terminal *CCT* domain, and a central region rich in glutamine sequences. It is recognized as *AtCO* in *Arabidopsis*, which facilitates flowering in long days and involves stress response (B. Zhang, Feng, et al., 2023). Researchers later identified its rice counterpart, *HD1*, which shares significant amino acid sequence similarities with *AtCO*. Studies have shown that *HD1* functions similarly to *CO* in the flowering pathway, confirming *HD1* as a ortholog of *AtCO* in rice (Nemoto et al., 2016).

4.2 | Transcription factors and their role in flowering time

Transcription factors are essential in regulating early or late flowering in plants. These proteins interact with specific DNA sequences to control gene regulation. The MADS-box transcription factor is a well-known and crucial regulator that plays a central role in floral development. *FLC* gene encodes

TABLE 1 Summary of the important essential genes in major field crops involved in flowering time.

Crop	Gene	Key role	Reference
Maize (*Zea mays*)	ZEA CENTRORADIALIS 8 (*ZCN8*)	Functions as a floral activator and is involved in photoperiod sensitivity	Meng et al. (2011)
	ZmCCT	Regulates photoperiod-dependent flowering and also response to abiotic stresses	Hung et al. (2012); Su et al. (2021)
	ZmMADS69	Functions as a flowering activator through the *ZmRap2.7-ZCN8* regulatory module	Y. Liang, Liu, et al. (2018)
	ZmCCT9	Enhances maize adaptation to higher latitudes	C. Huang et al. (2017)
Rice (*Oryza sativa*)	Heading-date 1 (*Hd1*) and Early heading date 1 (*Ehd1*)	Involved in regulation of flowering and reduces the number of primary branches in a panicle	Endo-Higashi and Izawa (2011)
	RICE FLOWERING LOCUS T1 (*RFT1*)	Contributes to flowering time divergence	Ogiso-Tanaka et al. (2013)
	Heading date 3a (*Hd3a*), Heading date 1 (*Hd1*), and Early heading date 1 (*Ehd1*)	Expression of these genes is highly correlated with flowering time	Takahashi et al. (2009)
	Flowering-Related RING Protein 1 (*FRRP1*)	*FRRP1* probably regulates flowering time by affecting histone *H2B* monoubiquitination	Du et al. (2016)
Wheat (*Triticum aestivum*)	*TaFT3*	Mutant alleles confer delayed flowering	Halliwell et al. (2016)
	MiR172-APETALA2-like genes	*miR172* promotes flowering	Debernardi et al. (2022)
	O-linked N-acetylglucosamine transferase (*OGT*)	Involved in fine regulation of flowering time	Fan et al. (2021)
	EARLY FLOWERING 3	Contributes to the regulation of heading date	Wittern et al. (2023)
Sorghum (*Sorghum bicolor*)	Pseudoresponse regulator protein 37 (*PRR37*)	Controls photoperiodic flowering	Murphy et al. (2011)
	Maturity2 (*Ma2*)	Delayed flowering in long days by selectively enhancing the expression of *SbPRR37* (*Ma1*) and *SbCO*	Casto et al. (2019)
	Ghd7 (*Ma6*)	Increases photoperiod sensitivity and delays flowering by inhibiting expression of the floral activator *SbEhd1* and genes encoding FT	Murphy et al. (2014)
Barley (*Hordeum vulgare*)	*FLOWERING LOCUS T4*	Specifically delayed spikelet initiation and reduced the number of spikelet primordia and grains per spike	Pieper et al. (2021)
	FLOWERING TIME LOCUS T 1 (*FT1*) and *CONSTANS-LIKE PROTEIN 1* (*CO1*)	Involved in regulating flowering time	Qian et al. (2020)
	VERNALIZATION-H2 (*VRN-H2*)	Strong repressor of flowering under long days before vernalization	Mulki and von Korff (2016)
	HvCEN, *HvELF3*, and *HvFT1*	Responsible for early flowering	Casas et al. (2021)
	Ppd-H1	The major determinant of photoperiod response	Cosenza et al. (2024); Maurer et al. (2015)

(Continues)

TABLE 1 (Continued)

Crop	Gene	Key role	Reference
Soybean (*Glycine max*)	*GmMDEs*	Regulated flowering time and stem growth habit by affecting the expression levels of other genes	Zhai et al. (2022)
	GmEID1	Modulates light signaling through the evening complex to control flowering time and yield	Qin et al. (2023)
	GmFT3a	Promotes flowering by regulating the expression of downstream flowering-related genes and also affects the expression of other *GmFT*s	S. Yuan et al. (2022)
Chickpea (*Cicer arietinum*)	Chickpea Early Flowering 1 (*Efl1*)	Ortholog of *Arabidopsis* EARLY FLOWERING 3 (*ELF3*) that confers early flowering in chickpea	Ridge et al. (2017)
Lentil (*Lens culinaris*)	*LcFTa1, LcFTb1*, and *LcFTb2*	Involved in flowering time in response to light quality.	H. Y. Yuan et al. (2021)
	Early flowering 3 (elf3)	Associated with photoperiod insensitive flowering and fast absolute growth rate	Roy et al. (2023)
	DTF6a and *DTF6b (FTa1 gene)*	Confer early flowering under extremely short photoperiods alone	Rajandran et al. (2022)
Brassica rapa	*FLOWERING LOCUS C* (*BrFLC*)	Key gene for vernalization	Takada et al. (2019)
	FT and *FLC*	Key role in the timing of the initiation of flowering	Scheben et al. (2020)
	PSEUDO RESPONSE REGULATOR 7 (PRR7) and *FY*	Key roles in the circadian clock pathway and upregulated in both leaf and shoot tissues	Jian et al. (2019)
	BnaFT.A2	Key role in flowering time regulation	Cai et al. (2021)
Cotton (*Gossypium herbaceum*)	Early flowering 4 (*ELF4*)	Participate in the plant biological clock's regulation process, photoperiod, hypocotyl elongation, and flowering time	Tian et al. (2021)
	GhAAI66	Triggers a phase transition to induce early flowering	Qanmber et al. (2019)
	FRUITFULL-like (*FUL-like*)	Promotes the vegetative-to-reproductive transition and represses inflorescence branching by inducing floral meristem maturation	Jiang et al. (2022)

a MADS-box protein that acts as a repressor of flowering and is essential for the process of vernalization (Sheldon et al., 2000). *FLC* inhibits the expression of two flowering-promoting genes, *FT* and *SOC1* (Deng et al., 2011). Further, it is also reported that *FLC* binds to many other genes and is involved in vegetative development by interacting with the gene *SQUAMOSA PROMOTER BINDING PROTEIN-LIKE 15* (*SPL15*), which delays the transition from juvenile to adult phase (Deng et al., 2011). *HD-ZIP I*-class transcription factor (*GhHB12*) exhibits specific expression in axillary buds in cotton (*Gossypium herbaceum*). Furthermore, in cotton, RNA sequencing analysis revealed that *GhSPL4*, a member of the *SBP* transcription factor family targeted by *GhmiR156*, was significantly upregulated in early-flowering cultivars (Y. Zhou et al., 2022). Regulatory interaction leads to bushy plant architecture and delayed flowering, specifically under long-day conditions (X. He et al., 2018). In rice, *Hd1 Binding Protein 1* (*HBP1*), two basic helix-loop-helix (*bHLH*) transcription factors, and *POH1* were identified as transcriptional regulators of *Hd1* (Yin et al., 2023). Additionally, B-box transcription factors are pivotal regulators in flowering, photomorphogenesis, shade-avoidance, stress responses, and hormonal pathways (Y. Liu et al., 2020). Recent research has also identified their significance in the flowering of crops such as tomato (*Solanum lycopersicum*) (Wu et al., 2023; D. Xu et al., 2023). These findings highlight the diverse roles of transcription factors in controlling FTi and their significance in plant adaptation to biotic and abiotic stresses. Additionally, a recent study suggests that the transcription factor *AtERF19* plays a dual role in regulating the number and size of flower organs (P. F. Lee, Zhan, et al., 2023). It achieves this by modulating genes associated with CLV–WUS signaling for flower production and influencing auxin signaling for flower organ size.

Flowering regulation involves *FLD* and *FLC* genes controlled by epigenetic mechanisms such as ubiquitination, acetylation, methylation, and hormone signaling (P. Kumari et al., 2022). In *Arabidopsis* and rice, proteins such as *TRITHORAX* (*TRX*) and *SET DOMAIN GROUP* (*SDG*) control histone methylations. For instance, *SDG2* mainly handles H3K4me3, with a small role played by *ARABIDOPSIS HOMOLOG OF TRITHORAX1* (*AXT1*) and *ATX2*. *SDG8* and *SDG4/26* are responsible for H3K36me3, and ATXR5/6 focuses on H3K27me1 (see S. Liu et al., 2023). *SDG725*, the initial H3K36-methyltransferase identified in rice, is crucial for depositing H3K36me2/3 on *Hd3a* chromatin, thereby hastening the flowering process (Sui et al., 2013).

4.3 | The regulatory elements associated with flowering time

Gene promoters play a critical role in expressing FTi-related genes by controlling when and where these genes are activated. They serve as regulatory regions upstream of the target genes, providing binding sites for transcription factors and other regulatory molecules. In *Brassica napus*, the discovery of two flower-specific promoters, *FSP046* and *FSP061*, highlights the potential of these promoters for agricultural use due to their tissue specificity and consistent expression in petals (Y. Li, Dong, et al., 2019). Similarly, *AGL24*, a gene in *Arabidopsis*, functions as a positive flowering promoter. Vernalization enhances its expression and activity (Michaels et al., 2003). Differences in DNA methylation within the *ZmCCT10* promoter in maize influenced *ZmCCT10* gene expression, subsequently affecting FTi (Z. Zhou et al., 2023). Salvi et al. (2007) narrowed down the major FTi QTL (vegetative to generative transition 1; *Vgt1*) in maize and identified an ∼2-kb noncoding region located 70 kb upstream of an AP2-like transcription factor. Castelletti et al. (2014) identified a miniature transposon (MITE) insertion within this conserved noncoding sequence at *Vgt1*, strongly associated with early flowering across independent analyses. Additionally, it was reported that this region at *Vgt1* was minimally methylated; however, the region near the MITE insertion in the early-flowering maize allele was heavily methylated (Castelletti et al., 2014). A precise understanding of the structural composition of these noncoding regions and their functional influence on gene expression patterns contributes to our knowledge of FTi control and offers potential targets for crop improvement.

5 | FLOWERING TIME IS A KEY TRAIT IN ADDRESSING ABIOTIC STRESSES

Crops face various challenges and have evolved with different strategies to counteract such constraints on productivity. These strategies involve allocating additional resources to enhance their immune responses and adjusting their reproductive processes to ensure successful reproduction (Lyons et al., 2015). Early-flowering/maturing varieties of crop plants have emerged as a promising strategy to adapt to the impact of abiotic stresses. These varieties exhibit accelerated plant development, allowing the life cycle of the plant to be completed before the onset of adverse environmental conditions, such as terminal drought or terminal heat stress (Mondal et al., 2015; Shavrukov et al., 2017). This adaptive mechanism (stress escape) is widely observed in native plant populations and can be applied to major crops. Additionally, cultivating early maturing legumes into fallow land, particularly in fallow rice land, could provide numerous benefits, such as restoring soil fertility, nitrogen fixation, suppressing weed growth, and utilizing fallow land (Kebede, 2021). Using the concept of early maturation and adopting stress escape mechanisms, plant breeders can enhance resilience and improve agricultural productivity in the face of abiotic stresses, thereby contributing to sustainable farming systems. Early flowering in wheat serves as a survival strategy, even though it can reduce grain yield under long photoperiod conditions, primarily by impacting floral growth and development (Y. Zhang, Guo, et al., 2023). Early flowering may be vital in wheat production under terminal drought, as it reduces the risk of dehydration during the critical flowering and post-anthesis grain filling stages.

In numerous botanical investigations, the intricate interplay between FTi and environmental variables, including complex ecological conditions and abiotic stressors, has been subject to scholarly scrutiny across a spectrum of species. Under conditions of water scarcity, the temporal regulation of FTi undergoes discernible alterations at the molecular level. For instance, K. Song et al. (2017) observed significant alterations in the expression profiles of key genes associated with FTi in response to drought stress in maize. Notably, genes such as *PRR37*, the transcription factor *HY5*, and *CO* were identified as being particularly susceptible to modulation, leading to a hastened onset of anthesis. Similarly, investigations in the model plant *Arabidopsis thaliana* unveiled perturbations in the expression patterns of pivotal flowering-related genes, including *FT*, *SCO1*, and *LEAFY*, consequent to drought imposition. Such genetic disregulation was associated with observable floral anomalies, including aberrant anther development and diminished pollen viability (Z. Su et al., 2013). Further elucidating these molecular intricacies, RNA sequencing analyses uncovered noteworthy alterations in the expression levels of flowering-time regulators such as *Hd3a*, *CONZ1*, and *ZCN8* in maize, genes conventionally associated with the promotion of flowering under short-day conditions. Notably, under the influence of drought stress, these genes exhibited downregulation, implicating their role in mitigating the floral response under adverse environmental conditions (Kim et al., 2021).

Elevated temperatures exert a pronounced effect on the modulation of FTi under both short-day and long-day conditions in *A. thaliana* (Balasubramanian et al., 2006). This regulatory mechanism involves the upregulation of key MADS-box transcription factors, including *SHORT VEGETATIVE PHASE* (*SVP*), *FLOWERING LOCUS M* (*FLM*), and *FT*. These genes play pivotal roles in the promotion of floral transition, thereby facilitating the acceleration of flowering onset in response to thermal stimuli (Pose et al., 2013). Similarly, in rice, high temperatures elicit an early-flowering response, characterized by the enhanced expression of genes such as *Ghd7*. The transcriptional activation of *Ghd7* serves as a critical molecular determinant in the regulation of FTi under temperature-induced conditions (Luan et al., 2009; V. Song et al., 2012). Furthermore, extending this paradigm, X. Chen et al. (2019) have contributed novel insights into the molecular mechanisms underlying the temperature-mediated regulation of floral development. Specifically, their research highlights the downregulation of HSP70-16, a heat shock protein, at higher temperatures (27°C), which correlates with the manifestation of floral abnormalities characterized by the overlapping tips of two lateral sepals and eventual failure of flower opening. Conversely, empirical evidence from diverse studies consistently underscores the phenomenon of delayed flowering in response to lower temperatures. Noteworthy among these investigations are those delineating the downregulation of key flowering-time regulators such as *FCA* and *FVE* in *A. thaliana* under cooler climatic conditions (Ausin et al., 2004; Y. He et al., 2003). Similarly, investigations by Luan et al. (2009) and V. Song et al. (2012) corroborate these findings, revealing a concomitant decrease in transcript levels of *Ehd1*, *Hd3a*, and *RFT1* in rice plants exposed to reduced temperatures. Moreover, insights from the literature shed light on the intricate regulatory dynamics governing FTi in response to temperature cues. Yoo et al. (2007) illuminate the regulatory influence of *LOV1* on *CO* expression, a pivotal floral promoter, suggesting a mechanism wherein *LOV1* exerts negative modulation over *CO* transcript levels, thereby impacting FTi regulation. Furthermore, the intricate interplay between photoperiod and cold temperature signals in seasonal flowering regulation is elucidated by J. H. Lee and Park (2015), who delineate an elaborate feedforward-feedback loop involving key regulatory nodes such as *INDUCER OF CBF EXPRESSION 1* (*ICE1*), *FLC*, and *SOC1* in *Arabidopsis*. Collectively, these scholarly endeavors underscore the intricate molecular networks orchestrating the temporal dynamics of flowering in response to temperature fluctuations, thereby enriching our understanding of the adaptive strategies employed by plants to navigate environmental variability.

6 | BIOTIC STRESSES AND THEIR RELATIONSHIP WITH FLOWERING TIME

Biotic factors can exert control over the transition to flowering, with potentially harmful effects on plants. Additionally, different crops exhibit varying photoperiod sensitivities due to adaptation to different growth environments or breeding targets (Gómez-Ariza et al., 2015). Herbivory and pathogen infections can profoundly affect plant development. These effects include early flowering (Elzinga et al., 2007; Lyons et al., 2015) and delayed flowering (Schiestl et al., 2014). Plants use altered flowering timing to escape herbivores (Parachnowitsch & Caruso, 2008). Some plants adjust by increasing flower production during early flowering in response to herbivory, possibly due to the production of defense compounds like glucosinolates (Schiestl et al., 2014).

Mechanical damage or wounding also accelerates flowering (Hanley & Fegan, 2007), suggesting that herbivory-induced effects on flowering may be attributed, at least in part, to wounding. Genetic mechanisms that underlie the crosstalk between stress responses and FTi are crucial. MicroRNAs play a significant role in regulating gene expression in response to both biotic and abiotic stress conditions (Ruiz-Ferrer & Voinnet, 2009), often leading to the reorganization of gene expression associated with flower initiation and development (see Table 2). The interrelationship between biotic stresses and FTi in plants is complex and influenced by various factors, including genetic mechanisms, microRNAs, tolerance levels, and the strategies employed by both plants and stressors to adapt to their environments.

In green gram (*Vigna radiata*) cultivation, insect pests remain a persistent challenge, resulting in yield losses. Notably, it has been observed that early-maturing varieties of green gram experienced decreased pest infestations (Mulwa et al., 2023). In the case of pigeonpea (*Cajanus cajan*), early-flowering genotypes exhibit characteristics such as reduced canopy size, fewer branches, and fewer pods per plant (Saxena et al., 2019). Conversely, late flowering enhances insect pollination in oil crops such as turnip rape (*Brassica campestris*; Toivonen et al., 2019). The intricate relationship between FTi regulation and biotic stressors has received comparatively scant attention in botanical research, with the majority of investigations concentrated within the *Arabidopsis* genus.

TABLE 2 Interrelation of flowering time and biotic stresses.

Sl. No.	Characters	Host	Causal factor/organism	Effects	Reference
A	Resistance and susceptibility of disease/insect pest	*Arabidopsis*	Early flowering	Increased susceptibility to *Verticillium* spp.	Veronese et al. (2003)
		Arabidopsis	Late flowering	Resistance to *F. oxysporum*	Lyons et al. (2015)
		Triticum	Direct impact of Frost on the flowering phase	Increased susceptibility to aphids	Lacoste et al. (2015)
B	Early and delay of flowering	*Arabidopsis*	*Fusarium oxysporum*	Alters flowering	Lyons et al. (2015)
		Arabidopsis	*Pseudomonas syringae*	Alters flowering	Korves and Bergelson (2003)
		Arabidopsis	*Myzus persicae*	Delays flowering	Züst et al. (2011)
		Brassica rapa	*Spodoptera littoralis*	Delays flowering	Schiestl et al. (2014)
		Brassica rapa	*Pieris brassicae*	Increased flower production during the early flowering	Schiestl et al. (2014)
		Arabidopsis	*Meloidogyne incognita*	Accelerates flowering	Xue et al. (2013)
C	Escape of insect attack	*Oenothera biennis*	Delaying flowering	Avoid predation by the moth *Mompha brevivittella*	Agrawal et al. (2013)
		Lobelia siphilitica	Late flowering	Decreased herbivory by the weevil, *Cleopmiarus hispidulus*	Parachnowitsch and Caruso (2008)
D	Photoperiod effects	*Zea mays Hm1*A	*Cochliobolus carbonum* race 1 (CCR1)	Lower susceptibility to infection	Marla et al. (2018)
		Brassica juncea	*Alternaria brassicicola*	Lower susceptibility to infection	Macioszek et al. (2021)
		A. thaliana Col-0	*Pyricularia oryzae syn. Magnaporthe oryzae*	Lower susceptibility to infection	Shimizu et al. (2021)

Of note, studies examining the impact of *Fusarium oxysporum* infection have revealed accelerated FTi alongside the modulation of key floral integrator genes, notably including *FLC*, *FT*, and *GI*. These findings underscore the multifaceted nature of plant–pathogen interactions, wherein the pathogenic infection elicits systemic responses influencing not only defense mechanisms but also developmental pathways, such as FTi regulation (Lyons et al., 2015). Similarly, investigations into the nematode *Meloidogyne incognita* infection have unveiled intriguing insights into the modulation of FTi in response to biotic stress. Specifically, the infection triggers enhanced expression of the 8D05 effector protein, thereby promoting a hastened flowering response (Xue et al., 2013). Moreover, a novel allele of the flowering regulatory gene *FLK*, which encodes a triple KH-repeat protein, has also been discovered. Mutants lacking *FLK* exhibited late flowering and reduced resistance to *Pseudomonas syringae* but enhanced resistance to *Botrytis cinerea* (Fabian et al., 2023). These findings suggest that regulatory genes such as *FLK* could play a key role in regulating plant flowering and immune response.

7 | CONVENTIONAL METHODS TO INDUCE EARLY FLOWERING

Conventional breeding techniques, such as intra-/interspecific hybridization, have been the primary methods to enhance agronomical traits like early flowering and high yield. Another commonly used method for inducing early flowering is the manipulation of photoperiod, where the duration of light exposure is controlled to mimic shorter days, triggering the flowering response (Paradiso & Proietti, 2022). This can be achieved by using light-blocking covers or adjusting the duration of artificial light in controlled environments. The quantity and quality of light plants receive directly impact processes such as photosynthesis, photomorphogenesis, flowering, and fruiting (Ouzounis et al., 2015). Additionally, different wavelengths of light have specific effects on plant development and physiology. Red and blue light is highly efficient for photosynthesis, and blue light impacts stomatal opening and chlorophyll biosynthesis (Paradiso et al., 2011). Another approach is the application of plant hormones, such as GA, which can stimulate flowering and promote early maturity (Coelho et al., 2018). Additionally, temperature manipulation, such as cold or heat stress exposure, can accelerate flowering in some plant species (Khodorova & Boitel-Conti, 2013). These methods are often employed in breeding programs and agricultural practices to induce early flowering, allowing for shorter growth cycles and adaptation to specific environmental conditions. It is important to note that the effectiveness of these methods may vary depending on the plant species and specific environmental factors. These traditional methods of flowering induction in plants have certain limitations that make them less desirable as long-term solutions. These methods often rely on labor-intensive practices, requiring manual intervention such as pruning, light manipulation, or treatments such as vernalization. Such induction requires time and adds to the cost due to the need for a significant workforce and resources. To overcome these limitations, there is a growing need to explore alternative approaches, such as genomics or multi-omics approaches, that offer more efficient and cost-effective means of controlling flowering in plants.

8 | MULTI-OMICS INTERVENTIONS FOR REGULATING FLOWERING TIME

Multi-omics interventions have emerged as powerful approaches for unravelling and manipulating the complex regulatory networks involved in flowering control in plants (N. Liang, Cheng, et al., 2018; Tian et al., 2021; L. Wang, Fang, et al., 2020). By integrating multiple high-throughput omics techniques, such as genomics, transcriptomics, proteomics, and metabolomics, researchers can gain comprehensive insights into the molecular mechanisms underlying flowering and identify potential targets for intervention (Figure 1). Genomics studies have enabled the identification and characterizing of genes and genetic variants associated with FTi regulation. Quantitative trait loci (QTL) mapping, genome-wide association studies (GWAS), and genome editing have been extensively utilized for the manipulation and modification of various traits associated with yield, insect pests, and disease resistance in plants (Gangurde et al., 2022; Jha et al., 2023; Thudi et al., 2023). Similarly, for early-flowering traits, researchers have discovered numerous flowering-related genes and genetic markers in various crop species. This genomic information provides a foundation for understanding the genetic basis of FTi and facilitates targeted genetic modifications for manipulating this trait.

Transcriptomics studies have revealed dynamic changes in gene expression profiles during different flowering stages (V. K. Singh et al., 2013). Using RNA sequencing (RNA-seq) techniques, researchers could identify key regulatory genes and unravel the intricate transcriptional networks involved in flowering control (Z. Li, Zhang, et al., 2016). Comparative transcriptomics studies between early and late flowering genotypes or under different environmental conditions have shed light on the regulatory mechanisms underlying this trait (Kaashyap et al., 2022). Gene ontology analysis in a rice transcriptomics study revealed that drought-responsive genes impacted FTi by affecting flower development, reproduction, and pollen–pistil interaction. Furthermore, drought conditions significantly affected the expression levels of crucial FTi genes, such as *PRR37*, *CO*, and transcription factor *HY5* (K. Song et al., 2017). The study by K. Song et al. (2017)

emphasizes the complex interplay between drought stress and the regulation of FTi in rice. Another survey of gene expression analysis revealed higher expression of *Hd1*, *FT-1*, *OsFKF1, OsELF3-2*, and *OsGI* in the Yongyou-538 variety. *Os02g0771100* showed lower expression than the Ninggeng 4 variety in response to variations in temperature and light resources (M. Yin et al., 2021). These differences in gene expression may contribute to the distinct flowering responses observed between the two varieties.

Proteomics and metabolomics approaches complement genomics and transcriptomics studies by providing insights into the functional consequences of gene expression-related changes. The proteomic analysis allows for identifying and quantifying proteins involved in flowering regulation, providing an understanding of protein function and interaction networks. Similarly, metabolomic profiling enables identifying and quantifying small biomolecules, such as hormones and signaling compounds, which play critical roles in FTi (Arkhimandritova et al., 2020; Chakraborty et al., 2022).

9 | GENOMIC INTERVENTIONS FOR REGULATING FLOWERING TIME

Genomic interventions for regulating flowering involve applying genetic and molecular techniques to manipulate the genes and pathways responsible for the FTi in plants. These interventions optimize flowering and enhance crop productivity for specific agricultural needs. Genomic interventions regulating FTi have great potential in optimizing crop yields, adapting plants to changing environments, and ensuring sustainable agriculture (Varshney et al., 2018). However, carefully considering ecological and genetic impacts is necessary for their successful implementation.

9.1 | Targeting induced local lesions in genomes by sequencing

The targeting induced local lesions in genomes (TILLING) approach involves chemical-induced random mutagenesis and high-throughput screening to detect point mutations in specific genomic regions. It is a versatile and practical reverse genetic approach applicable to various types of genomes (L. Chen et al., 2014). In the context of mutation discovery in amplicons, NGS has become the preferred tool for mutation detection due to its ability to quickly analyze many amplicons (Fanelli et al., 2021). Ethyl methane sulfonate (EMS) as a chemical mutagen offers distinct advantages over alternative mutagens. EMS treatment generates diverse mutations, including missense and truncation mutations. This diversity provides greater flexibility compared to insertional mutagenesis (McCallum et al., 2000). Moreover, EMS exhibits high efficiency in inducing random point mutations, even in polyploid plants, allowing for the acquisition of multiple alleles of a specific gene within a small population (Greene et al., 2003). Most TILLING populations have been established in predominantly autogamous (self-pollinated) species, including rice (Till et al., 2007), barley (Talame et al., 2008), and peanut (*Arachis hypogaea*; Guo et al., 2015). This characteristic simplifies the process of self-fertilization in M_1 plants to generate the M_2 population (Fanelli et al., 2021). Interestingly, the TILLING approach can identify mutants with early-flowering characteristics. In sunflower (*Helianthus annuus*), the TILLING by sequencing strategy was employed to identify multiple mutations in selected flowering-associated genes (Fanelli et al., 2021). This application of TILLING provides a powerful tool for uncovering genes involved in flowering control, facilitating the development of crop varieties with improved flowering traits and ultimately increasing agricultural productivity.

9.2 | QTL mapping

Genetic markers are integral components of modern plant breeding strategies. These markers are specific DNA sequences or variations in the genome that provide as genetic signposts, enabling researchers and breeders to identify and track desirable traits (Hasan et al., 2021). QTL mapping is primarily based on identifying associations between genetic markers and phenotypic traits in a population with genetic segregation. Advancements in high-throughput genotyping technologies, such as NGS and genotyping arrays, have significantly accelerated the molecular mapping process (Naik et al., 2024). These technologies enable the simultaneous genotyping of millions of SNP markers across a population, facilitating more precise and efficient identification of genetic loci associated with traits of interest. However, QTL mapping has emerged as a widely utilized method for studying various traits related to yield and other vital characteristics (Jha et al., 2021; S. B. Lee et al., 2018). In terms of FTi, numerous studies have been conducted across various crop species to investigate the genetic control, environmental factors, and molecular mechanisms underlying FTi regulation (see Table 3).

In soybean, various genomic regions were identified using different mapping populations. A mapping population was developed in soybean using well-known genotypes for early flowering, including ZK193, Suinong 14 and Dongnong 50 (Kong et al., 2018; F. Sun et al., 2019). Using bi-parental population, Kong et al. (2018) identified several QTLs specifically controlling either FTi or the reproductive period. For instance, the QTL *qRP-B1* on chromosome 11 influences reproductive period traits but does not affect FTi. Meanwhile, *qR1-J* on chromosome 16 and *qR1-L* on chromosome

TABLE 3 Summary genomic regions or genes responsible for flowering traits in major crops identified using quantitative trait loci (QTL) mapping.

Crop	Mapping population	QTL/genes	PVE (%)	References
Maize (*Zea mays*)	Huangzaosi × Mo17 (*n* = 121)	71 QTLs	7.9–21.3	Leng et al. (2022)
	Ye 478 × Qi 319	25 QTLs	3.97–23.68	L. Wang et al. (2021)
	Mutant F7p × Gaspe flint	*vgt1* and *vgt2*	–	Chardon et al. (2005)
Rice (*Oryza sativa*)	G23 × NG9108 (*n* = 251)	*qFOT6*	–	Hu et al. (2023)
	Milyang23 × H143	*OsPRR37/PRR37*	–	Koo et al. (2013)
	CO39 × Moroberekan	15 QTLs	7–40	Maheswaran et al. (2000)
	Nipponbare × Kasalath	*Hd1*	–	Yano et al. (2000)
Wheat (*Triticum aestivum*)	CDC Go × Attila, Cutler × AC Barrie and Peace × CDC Stanley (*n* = 698)	*Vrn-A1*, *Vrn-B1*, *Rht-A1* and *Rht-B1*	2.5–19.2	Semagn et al. (2021)
	Weimai 8 × Luohan 2, Weimai 8 × Yannong 19 and Weimai 8 × Jimai 20 (*n* = 526)	25 QTLs	6.6–32	Zhao et al. (2019)
	Japanese common wheat × synthetic hexaploids	2 QTLs	16 and 73	A. T. Nguyen et al. (2015)
Sorghum (*Sorghum bicolor*)	TX. 100 M × 80 M	*Ma2 QTL*	–	Casto et al. (2019)
	SC lines and exotic progenitor lines	*Ma1*	–	Higgins et al. (2014)
	Kikuchi Zairai × SC112	7 QTLs	3.4–9.4	El Mannai et al. (2012)
Barley (*Hordeum vulgare*)	Double round-robin population	*Ppd-H1* and 3 QTLs	–	Cosenza et al. (2024)
	Beka × Logan	5 QTLs	–	Casas et al. (2021)
	winter-type × spring-type	*qDHE.ak-1HS*, *Ppd-H1*, and *Ppd-H2*	6–39	Sameri et al. (2011)
	Apex × Prisma (*n* = 94)	21 QTLs	33–71	X. Yin et al. (2005)
Soybean (*Glycine max*)	Noir × Archer and Noir × M336-1	4 QTLs	5.6–40.4	L. Wang, Fang, et al. (2020)
	AGS292 × K3 (*n* = 75)	*qDTF-10*, *qDTF-16-1*, and *qDTF-16-2*	23.9–56.1	F. Sun et al. (2019)
	Dongnong 50 × Williams 82 and Suinong 14 × Enrei (*n* = 126, 140)	17 QTLs	14.2–78.9	Kong et al. (2018)
	Toyomusume × Suinong 10	5 QTLs	5.6–46	Yang et al. (2017)
	AGS292 × K3 (*n* = 91)	*qFT-B2-1*, *qFT-C1-1*, *qFT-K*, *qFT-D2*, and *qFT-F*	18.1–50.5	S. Lu et al. (2015)
Pearl Millet (*Pennisetum glaucum*)	ICMS 8511-S1-17-2-1-1-B-P03 × AIMP 92901-S1-183-2-2-B-08	Single QTL	9.4	Kumar et al. (2021)
	ICMB 841-P3 × 863B-P2	6 QTLs	23–48	Kumar et al. (2017)
Chickpea (*Cicer arietinum*)	NAM populations (Gokce, *C. reticulatum* and *C. echinospermum*)	3 QTLs	–	Lakmes et al. (2022)
	(ICCV 96029 × CDC Frontier, ICC 5810 × CDC Frontier, BGD 132 × CDC Frontier and ICC 16641 × CDC Frontier)	*efl-1*, *efl-3*, and *efl-4*	5.66–88.14	Mallikarjuna et al. (2017)
	ICCV 96029 × CDC Frontier	7 QTLs	9–44	Daba et al. (2016)
	ICC 3996 × ILWC 184 (*n* = 306)	2 QTLs	90.2	Aryamanesh et al. (2009)
Lentil (*Lens culinaris*)	ILL 2601 × ILL 5588 (*n* = 173)	9 QTLs	–	Rajandran et al. (2022)

(Continues)

TABLE 3 (Continued)

Crop	Mapping population	QTL/genes	PVE (%)	References
	Lens culinaris cv. Lupa × *L. orientalis* accession BGE 016880	13 QTLs	1.7–62.9	H. Y. Yuan et al. (2021)
	Precoz × WA8649041	Single QTL	57	Kahriman et al. (2015)
	Lupa × BG16880 (*n* = 113)	3 QTLs	–	Fratini et al. (2007)
Pigeonpea (*Cajanus cajan*)	UAS Dwarf × HDM04-1	13 QTLs	3.18–51.4	Kumawat et al. (2012)
	Pusa Dwarf × H2001-4.	*qFL5.1* and *qMT5.1*	15.3 and 11.6	Geddam et al. (2014)
Faba bean (*Vicia faba*)	Vf6 × Vf27 (*n* = 124)	12 QTLs	5.3–17.9	Aguilar-Benitez et al. (2021)
	Icarus × Ascot	16 QTLs	7–38	Catt et al. (2017)
Peanut (*Arachis hypogaea*)	Silihong × Jinonghei 3	19 QTLs	1.15–21.82	W. Liang et al. (2020)
	Silihong × Jinonghei 3	15 QTLs	4.6–12.4	L. Wang, Yang, et al. (2020)
Rapeseed (*Brassica napus*)	SGDH284 × 158A	*cqDTF-C02* and *cqDTF-C06*	32.04 and 16	L. Chen et al. (2022)
	NO.2127 × ZY821	*qFTA2.1a* and *qFTA2.1b*	25.4 and 49.1	Cai et al. (2021)
	Spring type × Winter type	Single QTL	9	Scheben et al. (2020)
	GW × DZ	*qFTYL16-16*, *qFTYL16-2*, *qFTYL16-5*, *qFTYL17-6*, and *qFTSY17-7*	3.74–12.28	Y. Xu et al. (2020)
	F1 (Regent × Lagoda) and F1 (Lagoda × Regent)	*DTF1* and *DTF2*	21.7 and 15	ArifUzZaman et al. (2016)

Abbreviation: PVE, phenotypic variance explained.

19 are associated with FTi but not with reproductive period (Kong et al., 2018). In an F_2 mapping population in soybean, the major QTL *qFT12-1* for FTi was mapped to chromosome 12, with a phenotypic variance explained (PVE) of 20.5%. This QTL, initially located within a 567-kb region, was refined to 56.4 kb through recombinant plant analysis, identifying genes such as *Glyma.12G073900* (Y. Li, Dong, et al., 2019). These findings may indicate that FTi and reproductive period operate through relatively independent genetic mechanisms. In lentil, QTLs such as *DTF6a* and *DTF6b* were identified, and DTF6a alone conferring early flowering under short photoperiods (Rajandran et al., 2022). These QTL findings guide breeding strategies, enhancing legume resilience to environmental stress.

Many QTL studies have explored the genetic control of FTi in maize. Salvi et al. (2009) conducted a meta-QTL analysis from 29 independent across all chromosomes associated with FTi. QTL analysis has revealed loci influencing FTi in maize, with PVE from 7.9% to 21.3% across 71 QTLs in an RIL population (Leng et al., 2022). Because of the limited effect of individual QTLs, only a few QTLs for maize FTi have been fine-mapped and cloned despite the large number identified. Vegetative to generative transition 1 (*Vgt1*) is the first FTi QTL cloned in maize. It has been narrowed down to an ∼2 kb noncoding region, which functions as a cis-regulatory element for *ZmRap2.7*, an *AP2* transcription factor located about 70 kb downstream (Salvi et al., 2007). Fine mapping of *qDTA3-2* QTL in maize led to the identification of MADS-box transcription factor and *ZmMADS69*. Functional studies revealed that mutants of *ZmMADS69* with reduced expression exhibited delayed flowering, while the overexpression of *ZmMADS69* resulted in accelerated flowering (Liang et al., 2018).

In rice, QTLs for early maturity and photoperiod insensitivity mitigate heat stress during anthesis. For instance, *qFOT6* on chromosome 6, identified via QTLseq and GradedPool-seq, has shown consistent results across multiple environments (Hu et al., 2023). Additionally, the *EH7-2* gene, also on chromosome 6, significantly affects heading date with a PVE up to 23.68% (Koo et al., 2013). Wheat's adaptability relies on flowering-related loci like *Vrn-A1*, *Rht-B1*, and QTLs on chromosomes 2DS and 5AL, contributing up to 73% in PVE (A. T. Nguyen et al., 2015). In barley, new QTLs for FTi have been identified, along with a novel functional allelic variant of the primary regulatory gene *Ppd-H1* (Cosenza et al., 2024). These findings support breeding strategies to develop climate-resilient cereal varieties.

9.3 | QTL-seq approach

The QTL-seq approach has emerged as a highly effective strategy for rapidly identifying major QTLs that governs economically important traits in crop plants. QTL-seq involves whole-genome re-sequencing of two DNA bulks derived from progeny displaying extreme phenotypes. This method offers several advantages over traditional QTL mapping approaches. First, it allows for more efficient and precise localization of candidate genomic regions. Second, it avoids the necessity of the entire population's DNA marker development and genotyping, resulting in a more efficient and cost-effective procedure. This method has proven to be effective in unraveling the genetic basis of FTi in various crop plants, including pigeonpea (V. Singh et al., 2022), chickpea (Srivastava et al., 2017), lentil (Shivaprasad et al., 2024), rapeseed (*B. napus*) (Tang et al., 2023), cucumber (*Cucumis sativus*) (H. Lu et al., 2014) and cabbage (*Brassica oleracea*) (Shu et al., 2018). Using QTL-seq and gene expression profiling, a candidate QTL (*BnaC08cqDTF*) associated with early flowering in rapeseed was characterized. This analysis identified Cryptochrome 2 (*CRY2*), encoded by *BnaC08G0010400ZS*, within an 86-kb genomic region on chromosome 08 (Tang et al., 2023). This approach was also used to identify the candidate gene (*Ef1.1*) from a major QTL on chromosome 1, associated with early flowering in cucumber (H. Lu et al., 2014). In lentil, this approach identified three important QTLs (*LcqDTF3.1*, *LcqDTF3.2* and *LcqDTF3.3*) for flowering time, along with 13 genes associated with the flowering pathway (Shivaprasad et al., 2024). Overall, the utilization of QTL-seq has brought about a revolution in exploring the genetic foundations of intricate traits such as FTi in crop plants.

9.4 | Genome-wide association studies

GWAS relies on linkage disequilibrium and has been widely applied to investigate the genetic basis of crucial traits in diverse plant species. This method explores the association between genetic variations across the entire genome and phenotypic variations in traits within a natural population. By analyzing numerous genetic markers distributed throughout the genome, GWAS facilitates the identification of candidate genes or genomic regions linked to quantitative traits (Gangurde et al., 2022; Thudi et al., 2023). Several studies have employed GWAS to investigate FTi. For instance, in soybean, GWAS identified the association of the *Dt1* gene with both maturity and plant height, while candidate genes homologous to *Arabidopsis* flowering genes were linked to days to flowering (J. Zhang et al., 2015). Another study with 278 soybean accessions identified 37 significant marker-trait associations (MTAs) with FTi and pod development traits across 14 chromosomes (M. Li, Liu, et al., 2019). In lentil, two loci, *DTF6a* and *DTF6b*, were identified, where dominant alleles led to early flowering (Rajandran et al., 2022). In wheat, a study identified 32 significant MTAs for days to heading, revealing important genes (*Ppd-A* and *Ppd-B*) for photoperiod and vernalization-associated genes (*Vrn-A1* and *VrnA7*) (Gupta et al., 2020). Additionally, in canola, significant MTAs were found with FT paralogs, indicating the regulatory role of FTi paralogs in influencing productivity traits (Raman et al., 2019). In *B. napus*, 10 main-effect associations were found with flowering-time-related climatic indices using association mapping. Five candidate genes, including *BnaFLCs*, *BnaFTs*, *BnaA02.VIN3* and *BnaC09.PRR7*, were validated through haplotype, selective sweep and co-expression analyses (X. Han et al., 2022). Additionally, GWAS identified 21 haplotypes with candidate genes linked to FTi in rapeseed, with structural variation in *BnVIN3-C03* on chromosome C03 showing a strong association with this trait (L. Huang et al., 2021). This report suggests that GWAS analysis can enhance our understanding of the genetic architecture of FTi, including the number of genes involved and their interactions.

9.5 | Gene editing

Gene editing technologies, such as CRISPR/Cas9, enable precise alterations in the plant genome, including the targeted alteration of specific FTi genes. By harnessing the knowledge gained from identifying key genes, researchers can utilize gene editing approaches to engineer plants with desired traits, such as FTi. For instance, researchers employed CRISPR/Cas9 in soybean to target the night light-inducible and clock-regulated 2 (*LNK2*) gene and revealed that mutations in *LNK2* led to a shortened FTi (Z. Li et al., 2021), which has important implications for soybean breeding, particularly in high-latitude regions. CRISPR/Cas9 was also used to modify the *E1* gene in soybean, resulting in two types of mutations that induced early flowering under extended daylight conditions (J. Han et al., 2019). On the other hand, scientists studied the *BnaSVP* (short vegetative phase) gene in rapeseed, which shares homology with the *Arabidopsis SVP* gene known to influence flowering. Mutation in four copies of *BnaSVP* with CRISPR/Cas9 resulted in mutant lines exhibiting early-flowering traits under both summer and winter conditions (Ahmar et al., 2022). This demonstrates potential benefits for fine-tuning FTi in oilseed crops to maximize productivity and adaptability.

In sorghum, *FT* gene was targeted, and a frame-shift mutation in the gene led to a significant delay of 10 days in

FTi, confirming the involvement of this gene in regulating the flowering process (Char et al., 2020). Similarly, it has been documented that *OsFLZ2* gene is a negative regulator of FTi in rice (Y. Ma et al., 2022). Y. Ma et al. (2022) showed that *OsFLZ2* destabilizes *OsMADS51*, reducing its activation of the downstream gene *Ehd1* and shedding light on rice flowering mechanisms. G. Wang, Wang, et al. (2020) identified a late-flowering gene in rice (*OsGhd7*), which delayed flowering when overexpressed. In contrast, CRISPR/Cas9 knockouts of *OsGhd7* accelerated flowering, with timing influenced by the field location. In another study, researchers edited rice's *uORFs* of the *Hd2* gene. These edited lines exhibited delayed flowering, ranging from 4 to 11 days compared to the wild type. Similarly, overexpression of *TFL1* in *Arabidopsis* caused late flowering, as it prevented the expression of *LFY* and *AP1* genes (Ratcliffe et al., 1999), while knockout of *TFL1* expression through CRISPR/Cas9 caused changes such as reduced growth and continuous flowering (Charrier et al., 2019). The delayed flowering was supported by decreased expression of pivotal flowering-related genes, specifically *Ehd1*, *Hd3a* and *RFT1*, compared to the wild type (Y. Liu et al., 2021). These studies together emphasize the versatility of CRISPR/Cas9 as a potent tool for modifying the genetic elements that influence FTi in different crop varieties. Such advancements hold immense promise for agricultural practices, enabling the development of crops with optimized flowering traits, improving adaptability to diverse environments, and ultimately contributing to global food security and sustainability.

10 | CURRENT CHALLENGES AND FUTURE PROSPECTS

In the context of climate change, unravelling the intricate interplay between the photoperiod pathway and environmental variables, notably temperature, has assumed paramount importance. Although plants demonstrate adaptability to changing temperatures in their developmental processes, there exists a notable gap in our understanding of how the photoperiod pathway precisely interacts with temperature cues (Jagadish et al., 2016). Equally crucial is the necessity for a diverse array of crop varieties with favorable agronomic traits to bolster the plasticity and resilience of crops amid these challenges. This diversity not only provides options for adaptation but also serves to mitigate potential losses in agricultural productivity. For instance, the identification of early morning flowering in rice as a potential trait to withstand heat stress highlights the significance of integrating traits like early morning flowering QTL (*qEMF3*) through introgression, thereby enhancing heat resilience and augmenting grain yield under heat stress conditions (Ishimaru et al., 2022). Moreover, deepening our comprehension of the intricate connections between the photoperiod pathway and environmental conditions is critical to developing crop varieties that thrive under evolving climatic scenarios.

The landscape of plant research has been revolutionized by advancements in NGS and in vitro functional studies. The accessibility of technologies for efficiently generating large-scale population and functional genomic data facilitates the application of research findings across diverse systems. The utilization of gene-editing tools, notably CRISPR/Cas9, represents a potent avenue for advancing our insight into the pivotal roles played by photoreceptors and vernalization-related genes in plant development and the regulation of FTi. Through precise modifications using these tools, researchers can delineate the specific functions and interactions of these genes across various plant species. Furthermore, genome editing tools hold substantial promise for confirming gene functions across a broader taxonomic spectrum. Nevertheless, deciphering the genes and their regulatory mechanisms that determine FTi in conjunction with environmental factors such as temperature, photoperiod, CO_2, and various abiotic stresses and their interactions continues to be a focal point of research. Conversely, comparative studies on flowering pathways are indispensable for understanding the evolution of unique life histories, such as gregarious flowering or masting. Additionally, delving into the role of epigenetic modifications in FTi and their potential adaptive significance presents a promising avenue in evolutionary epigenetics, where the exploration of the occurrence and adaptive significance of natural epigenetic variations in FTi is still unfolding.

11 | CONCLUSION

The exploration of FTi in plants is an intricate and multifaceted domain, encompassing diverse environmental signals, genetic elements and regulatory pathways. While significant strides have been taken in identifying pivotal candidate genes, unraveling the precise functions and regulations governing genes associated with photoperiod and vernalization is crucial for a nuanced comprehension of FTi regulation. Notably, the advent of gene editing technologies, particularly CRISPR/Cas9, has ushered in novel avenues for elucidating gene functions and manipulating genes related to flowering. These technologies offer the potential to gain insights into the specific roles and interactions within the flowering modulation pathway. Furthermore, the progress in NGS technologies, functional studies, and omics technologies has broadened our molecular-level understanding of FTi. Nevertheless, there remains much to explore and comprehend, particularly concerning the intricate interplay between FTi and various environmental factors. Future research endeavors should employ diverse approaches, including comparative analyses and evolutionary studies, to comprehensively understand FTi diversity and its adaptive significance.

AUTHOR CONTRIBUTIONS

Yogesh Dashrath Naik: Writing—original draft; writing—review and editing. **Rajeev N. Bahuguna**: Writing—original draft; writing—review and editing. **Pedro Garcia-Caparros**: Writing—original draft; writing—review and editing. **Rebecca S. Zwart**: Writing—original draft; writing—review and editing. **M. S. Sai Reddy**: Writing—original draft; writing—review and editing. **Reyazul Rouf Mir**: Writing—original draft; writing—review and editing. **Uday Chand Jha**: Writing—original draft; writing—review and editing. **B. Fakrudin**: Writing—original draft; writing—review and editing. **Manish K. Pandey**: Writing—original draft; writing—review and editing. **Dinakar Challabathula**: Writing—original draft; writing—review and editing. **Vinay Kumar Sharma**: Writing—review and editing. **Umesh K. Reddy**: Writing—review and editing. **Chanda Venkata Sameer Kumar**: Writing—review and editing. **Venugopal Mendu**: Writing—review and editing. **P. V. Vara Prasad**: Writing—review and editing. **Somashekhar M. Punnuri**: Conceptualization; writing—original draft; writing—review and editing. **Rajeev K. Varshney**: Conceptualization; writing—original draft; writing—review and editing. **Mahendar Thudi**: Conceptualization; visualization; writing—original draft; writing—review and editing.

ACKNOWLEDGMENTS

YDN acknowledges the Department of Biotechnology, Government of India, for the DBT-JRF fellowship for his Ph.D. program.

Open access publishing facilitated by University of Southern Queensland, as part of the Wiley - University of Southern Queensland agreement via the Council of Australian University Librarians.

CONFLICT OF INTEREST STATEMENT

The authors declare no conflicts of interest.

DATA AVAILABILITY STATEMENT

There are no original data associated with this article.

ORCID

Yogesh Dashrath Naik https://orcid.org/0000-0002-4336-9364
M. S. Sai Reddy https://orcid.org/0000-0002-7616-5210
Manish K. Pandey https://orcid.org/0000-0002-4101-6530
Rajeev K. Varshney https://orcid.org/0000-0002-4562-9131
Mahendar Thudi https://orcid.org/0000-0003-2851-6837

REFERENCES

Abbass, K., Qasim, M. Z., Song, H., Murshed, M., Mahmood, H., & Younis, I. (2022). A review of the global climate change impacts, adaptation and sustainable mitigation measures. *Environmental Science and Pollution Research International*, *29*(28), 42539–42559. https://doi.org/10.1007/s11356-022-19718-6

Agrawal, A. A., Johnson, M. T., Hastings, A. P., & Maron, J. L. (2013). A field experiment demonstrating plant life-history evolution and its eco-evolutionary feedback to seed predator populations. *American Naturalist*, *181*(S1), S35–S45. https://doi.org/10.1086/666727

Aguilar-Benitez, D., Casimiro-Soriguer, I., Maalouf, F., & Torres, A. M. (2021). Linkage mapping and QTL analysis of flowering time in faba bean. *Scientific Reports*, *11*(1), 13716. https://doi.org/10.1038/s41598-021-92680-4

Ahmar, S., Zhai, Y., Huang, H., Yu, K., Hafeez Ullah Khan, M., Shahid, M., Abdul Samad, R., Ullah Khan, S., Amoo, O., Fan, C., & Zhou, Y. (2022). Development of mutants with varying flowering times by targeted editing of multiple SVP gene copies in *Brassica napus* L. *The Crop Journal*, *10*(1), 67–74. https://doi.org/10.1016/j.cj.2021.03.023

Allard, H. A., & Garner, W. W. (1940). *Further observations of the response of various species of plants to length of day* (Technical bulletin No. 727). United States Department of Agriculture.

Amasino, R. (2010). Seasonal and developmental timing of flowering. *Plant Journal*, *61*(6), 1001–1013. https://doi.org/10.1111/j.1365-313X.2010.04148.x

ArifUzZaman, M., Mamidi, S., McClean, P., & Rahman, M. (2016). QTL mapping for root vigor and days to flowering in *Brassica napus* L. *Canadian Journal of Plant Science*, *97*(1), 99–109. https://doi.org/10.1139/CJPS-2016-0048

Arkhimandritova, S., Shavarda, A., & Potokina, E. (2020). Key metabolites associated with the onset of flowering of guar genotypes (*Cyamopsis tetragonoloba* (L.) Taub). *BMC Plant Biology*, *20*(1), 291. https://doi.org/10.1186/s12870-020-02498-x

Aryamanesh, N., Nelson, M. N., Yan, G., Clarke, H. J., & Siddique, K. H. M. (2009). Mapping a major gene for growth habit and QTLs for Ascochyta blight resistance and flowering time in a population between chickpea and *Cicer reticulatum*. *Euphytica*, *173*(3), 307–319. https://doi.org/10.1007/s10681-009-0086-2

Ausin, I., Alonso-Blanco, C., Jarillo, J. A., Ruiz-Garcia, L., & Martinez-Zapater, J. M. (2004). Regulation of flowering time by FVE, a retinoblastoma-associated protein. *Nature Genetics*, *36*, 162–166. https://doi.org/10.1038/ng1295

Balasubramanian, S., Sureshkumar, S., Lempe, J., & Weigel, D. (2006). Potent induction of *Arabidopsis thaliana* flowering by elevated growth temperature. *PLoS Genetics*, *2*, e106. https://doi.org/10.1371/journal.pgen.0020106

Bao, S., Hua, C., Shen, L., & Yu, H. (2020). New insights into gibberellin signaling in regulating flowering in *Arabidopsis*. *Journal of Integrative Plant Biology*, *62*(1), 118–131. https://doi.org/10.1111/jipb.12892

Brandoli, C., Petri, C., Egea-Cortines, M., & Weiss, J. (2020). Gigantea: Uncovering new functions in flower development. *Genes*, *11*(10), 1142. https://doi.org/10.3390/genes11101142

Cai, D., Zhang, S., Wang, J., He, J., Yi, L., & Zhu, J. (2021). Fine mapping of a minor QTL on chromosome 2 controlling flowering time in *Brassica napus* L. *Genetic Resources and Crop Evolution*, *69*, 1137–1146. https://doi.org/10.1007/s10722-021-01290-6

Campos-Rivero, G., Osorio-Montalvo, P., Sánchez-Borges, R., Us-Camas, R., Duarte-Aké, F., & De-la-Peña, C. (2017). Plant hormone signaling in flowering: An epigenetic point of view. *Journal of Plant Physiology*, *214*, 16–27. https://doi.org/10.1016/j.jplph.2017.03.018

Casas, A. M., Gazulla, C. R., Monteagudo, A., Cantalapiedra, C. P., Moralejo, M., Pilar Gracia, M. P., Ciudad, F. J., Thomas, W. T. B., Molina-Cano, J. L., Boden, S., Contreras-Moreira, B., & Igartua, E. (2021). Candidate genes underlying QTL for flowering time and their interactions in a wide spring barley (*Hordeum vulgare* L.) cross. *The Crop Journal*, *9*(4), 862–872. https://doi.org/10.1016/j.cj.2020.07.008

Castelletti, S., Tuberosa, R., Pindo, M., & Salvi, S. (2014). A MITE transposon insertion is associated with differential methylation at the maize flowering time QTL Vgt1. *G3*, *4*(5), 805–812. https://doi.org/10.1534/g3.114.010686

Casto, A. L., Mattison, A. J., Olson, S. N., Thakran, M., Rooney, W. L., & Mullet, J. E. (2019). Maturity 2, a novel regulator of flowering time in *Sorghum bicolor*, increases expression of *SbPRR37* and *SbCO* in long days delaying flowering. *PLoS ONE*, *14*(4), e0212154. https://doi.org/10.1371/journal.pone.0212154

Catt, S. C., Braich, S., Kaur, S., & Paull, J. G. (2017). QTL detection for flowering time in faba bean and the responses to ambient temperature and photoperiod. *Euphytica*, *213*(6), 1–13. https://doi.org/10.1007/s10681-017-1910-8

Cha, J. K., O'Connor, K., Alahmad, S., Lee, J. H., Dinglasan, E., Park, H., Lee, S.-M., Hirsz, D., Kwon, S.-W., Kwon, Y., Kim, K.-M., Ko, J.-M., Hickey, L. T., Shin, D., & Dixon, L. E. (2022). Speed vernalization to accelerate generation advance in winter cereal crops. *Molecular Plant*, *15*(8), 1300–1309. https://doi.org/10.1016/j.molp.2022.06.012

Chakraborty, A., Chaudhury, R., Dutta, S., Basak, M., Dey, S., Schäffner, A. R., & Das, M. (2022). Role of metabolites in flower development and discovery of compounds controlling flowering time. *Plant Physiology and Biochemistry*, *190*, 109–118. https://doi.org/10.1016/j.plaphy.2022.09.002

Char, S. N., Wei, J., Mu, Q., Li, X., Zhang, Z. J., Yu, J., & Yang, B. (2020). An Agrobacterium-delivered CRISPR/Cas9 system for targeted mutagenesis in sorghum. *Plant Biotechnology Journal*, *18*(2), 319–321. https://doi.org/10.1111/pbi.13229

Chardon, F., Hourcade, D., Combes, V., & Charcosset, A. (2005). Mapping of a spontaneous mutation for early flowering time in maize highlights contrasting allelic series at two-linked QTL on chromosome 8. *Theoretical and Applied Genetics*, *112*(1), 1–11. https://doi.org/10.1007/s00122-005-0050-z

Charrier, A., Vergne, E., Dousset, N., Richer, A., Petiteau, A., & Chevreau, E. (2019). Efficient targeted mutagenesis in apple and first time edition of pear using the CRISPR-Cas9 system. *Frontiers in Plant Science*, *10*, 40. https://doi.org/10.3389/fpls.2019.00040

Chavez-Hernández, E. C., Quiroz, S., García-Ponce, B., & Álvarez-Buylla, E. R. (2022). The flowering transition pathways converge into a complex gene regulatory network that underlies the phase changes of the shoot apical meristem in *Arabidopsis thaliana*. *Frontiers in Plant Science*, *13*, 852047. https://doi.org/10.3389/fpls.2022.852047

Chen, L., Hao, L., Parry, M. A., Phillips, A. L., & Hu, Y. G. (2014). Progress in TILLING as a tool for functional genomics and improvement of crops. *Journal of Integrative Plant Biology*, *56*(5), 425–443. https://doi.org/10.1111/jipb.12192

Chen, L., Lei, W., He, W., Wang, Y., Tian, J., Gong, J., Hao, B., Cheng, X., Shu, Y., & Fan, Z. (2022). Mapping of two major QTLs controlling flowering time in *Brassica napus* using a high-density genetic map. *Plants*, *11*(19), 2635. https://doi.org/10.3390/plants11192635

Chen, X., Shi, L., Chen, Y., Zhu, L., Zhang, D., Xiao, S., Aharoni, A., Shi, J., & Xu, J. (2019). Arabidopsis *HSP70-16* is required for flower opening under normal or mild heat stress temperatures. *Plant, Cell and Environment*, *42*(4), 1190–1204. https://doi.org/10.1111/pce.13480

Coelho, L. L., Fkiara, A., Mackenzie, K. K., Müller, R., & Lütken, H. (2018). Exogenous application of gibberellic acid improves flowering in Kalanchoë. *HortScience*, *53*(3), 342–346. https://doi.org/10.21273/HORTSCI12720-17

Conti, L. (2017). Hormonal control of the floral transition: Can one catch them all? *Developmental Biology*, *430*(2), 288–301. https://doi.org/10.1016/j.ydbio.2017.03.024

Corbesier, L., Vincent, C., Jang, S., Fornara, F., Fan, Q., Searle, I., Giakountis, A., Farrona, S., Gissot, L., Turnbull, C., & Coupland, G. (2007). FT protein movement contributes to long-distance signaling in floral induction of Arabidopsis. *Science*, *316*(5827), 1030–1033. https://doi.org/10.1126/science.1141752

Cosenza, F., Shrestha, A., Van Inghelandt, D., Casale, F. A., Wu, P. Y., Weisweiler, M., Li, J., Wespel, F., & Stich, B. (2024). Genetic mapping reveals new loci and alleles for flowering time and plant height using the double round-robin population of barley. *Journal of Experimental Botany*, *75*(8), 2385–2402. https://doi.org/10.1093/jxb/erae010

Daba, K., Deokar, A., Banniza, S., Warkentin, T. D., & Tar'an, B. (2016). QTL mapping of early flowering and resistance to Ascochyta blight in chickpea. *Genome*, *59*(6), 413–425. https://doi.org/10.1139/gen-2016-0036

Debernardi, J. M., Woods, D. P., Li, K., Li, C., & Dubcovsky, J. (2022). *MiR172-APETALA2-like* genes integrate vernalization and plant age to control flowering time in wheat. *PLoS Genetics*, *18*(4), e1010157. https://doi.org/10.1371/journal.pgen.1010157

Deng, W., Casao, M. C., Wang, P., Sato, K., Hayes, P. M., Finnegan, E. J., & Trevaskis, B. (2015). Direct links between the vernalization response and other key traits of cereal crops. *Nature Communications*, *6*, 5882. https://doi.org/10.1038/ncomms6882

Deng, W., Ying, H., Helliwell, C. A., Taylor, J. M., Peacock, W. J., & Dennis, E. S. (2011). *FLOWERING LOCUS C* (*FLC*) regulates development pathways throughout the life cycle of Arabidopsis. *Proceedings of the National Academy of Sciences of the United States of America*, *108*(16), 6680–6685. https://doi.org/10.1073/pnas.1103175108

Deryng, D., Conway, D., Ramankutty, N., Price, J., & Warren, R. (2014). Global crop yield response to extreme heat stress under multiple climate change futures. *Environmental Research Letters*, *9*(3), 034011. https://doi.org/10.1088/1748-9326/9/3/034011

Ding, Y., & Yang, S. (2022). Surviving and thriving: How plants perceive and respond to temperature stress. *Developmental Cell*, *57*(8), 947–958. https://doi.org/10.1016/j.devcel.2022.03.010

Domagalska, M. A., Sarnowska, E., Nagy, F., & Davis, S. J. (2010). Genetic analyses of interactions among gibberellin, abscisic acid and brassinosteroids in the control of flowering time in *Arabidopsis thaliana*. *PLoS ONE*, *5*(11), e14012. https://doi.org/10.1371/journal.pone.0014012

Dong, X., Li, Y., Guan, Y., Wang, S., Luo, H., Li, X., Li, H., & Zhang, Z. (2021). Auxin-induced *AUXIN RESPONSE FACTOR4* activates *APETALA1* and *FRUITFULL* to promote flowering in woodland strawberry. *Horticulture Research*, *8*(1), 115. https://doi.org/10.1038/s41438-021-00550-x

Du, Y., He, W., Deng, C., Chen, X., Gou, L., Zhu, F., Guo, W., Zhang, J., & Wang, T. (2016). Flowering-related RING protein 1 (*FRRP1*) regulates flowering time and yield potential by affecting histone H2B monoubiquitination in rice (*Oryza sativa*). *PLoS ONE*, *11*(3), e0150458. https://doi.org/10.1371/journal.pone.0150458

El Mannai, Y., Shehzad, T., & Okuno, K. (2012). Mapping of QTLs underlying flowering time in sorghum [*Sorghum bicolor* (L.) Moench]. *Breeding Science*, *62*(2), 151–159. https://doi.org/10.1270/jsbbs.62.151

Elzinga, J. A., Atlan, A., Biere, A., Gigord, L., Weis, A. E., & Bernasconi, G. (2007). Time after time: Flowering phenology and biotic interactions. *Trends in Ecology & Evolution*, *22*(8), 432–439. https://doi.org/10.1016/j.tree.2007.05.006

Endo-Higashi, N., & Izawa, T. (2011). Flowering time genes *Heading date 1* and *Early heading date 1* together control panicle development in rice. *Plant & Cell Physiology*, *52*(6), 1083–1094. https://doi.org/10.1093/pcp/pcr059

Fabian, M., Gao, M., Zhang, X. N., Shi, J., Vrydagh, L., Kim, S. H., Patel, P., Hu, A. R., & Lu, H. (2023). The flowering time regulator *FLK* controls pathogen defense in *Arabidopsis thaliana*. *Plant Physiology*, *191*(4), 2461–2474. https://doi.org/10.1093/plphys/kiad021

Fahad, S., Bajwa, A. A., Nazir, U., Anjum, S. A., Farooq, A., Zohaib, A., Sadia, S., Nasim, W., Adkins, S., Saud, S., Ihsan, M. Z., Alharby, H., Wu, C., Wang, D., & Huang, J. (2017). Crop production under drought and heat stress: Plant responses and management options. *Frontiers in Plant Science*, *8*, 1147. https://doi.org/10.3389/fpls.2017.01147

Fan, M., Miao, F., Jia, H., Li, G., Powers, C., Nagarajan, R., Alderman, P. D., Carver, B. F., Ma, Z., & Yan, L. (2021). O-linked N-acetylglucosamine transferase is involved in the fine regulation of flowering time in winter wheat. *Nature Communications*, *12*(1), 2303. https://doi.org/10.1038/s41467-021-22564-8

Fanelli, V., Ngo, K. J., Thompson, V. L., Silva, B. R., Tsai, H., Sabetta, W., Montemurro, C., Comai, L., & Harmer, S. L. (2021). A TILLING by sequencing approach to identify induced mutations in sunflower genes. *Scientific Reports*, *11*(1), 9885. https://doi.org/10.1038/s41598-021-89237-w

Franks, S. J. (2011). Plasticity and evolution in drought avoidance and escape in the annual plant *Brassica rapa*. *New Phytologist*, *190*(1), 249–257. https://doi.org/10.1111/j.1469-8137.2010.03603.x

Fratini, R., Durán, Y., García, P., & Pérez de la Vega, M. P. (2007). Identification of quantitative trait loci (QTL) for plant structure, growth habit and yield in lentil. *Spanish Journal of Agricultural Research*, *5*(3), 348–356. https://doi.org/10.5424/sjar/2007053-255

Gangurde, S. S., Xavier, A., Naik, Y. D., Jha, U. C., Rangari, S. K., Kumar, R., Reddy, M. S. S., Channale, S., Elango, D., Mir, R. R., Zwart, R., Laxuman, C., Sudini, H. K., Pandey, M. K., Punnuri, S., Mendu, V., Reddy, U. K., Guo, B., Gangarao, N. V. P. R., … Thudi, M. (2022). Two decades of association mapping: Insights on disease resistance in major crops. *Frontiers in Plant Science*, *13*, 1064059. https://doi.org/10.3389/fpls.2022.1064059

Geddam, S. B., Raje, R. S., Prabhu, K. V., Singh, N. K., Chauhan, D. A., Jain, P., Khare, A., Yadav, R., & Tyagi, A. (2014). Validation of QTLs for earliness and plant type traits in pigeonpea (*Cajanus cajan* (L.) Millsp.). *Indian Journal of Genetics and Plant Breeding*, *74*(4), 471–477. https://doi.org/10.5958/0975-6906.2014.00872.4

Gómez-Ariza, J., Galbiati, F., Goretti, D., Brambilla, V., Shrestha, R., Pappolla, A., Courtois, B., & Fornara, F. (2015). Loss of floral repressor function adapts rice to higher latitudes in Europe. *Journal of Experimental Botany*, *66*(7), 2027–2039. https://doi.org/10.1093/jxb/erv004

Greene, E. A., Codomo, C. A., Taylor, N. E., Henikoff, J. G., Till, B. J., Reynolds, S., Enns, L. C., Burtner, C., Johnson, J. E., Odden, A. R., Comai, L., & Henikoff, S. (2003). Spectrum of chemically induced mutations from a large-scale reverse-genetic screen in *Arabidopsis*. *Genetics*, *164*(2), 731–740. https://doi.org/10.1093/genetics/164.2.731

Griffin, J. H., & Toledo-Ortiz, G. (2022). Plant photoreceptors and their signalling components in chloroplastic anterograde and retrograde communication. *Journal of Experimental Botany*, *73*(21), 7126–7138. https://doi.org/10.1093/jxb/erac220

Guo, Y., Abernathy, B., Zeng, Y., & Ozias-Akins, P. (2015). TILLING by sequencing to identify induced mutations in stress resistance genes of peanut (*Arachis hypogaea*). *BMC Genomics*, *16*, 1–13. https://doi.org/10.1186/s12864-015-1348-0

Guo, Y., Wu, Q., Xie, Z., Yu, B., Zeng, R., Min, Q., & Huang, J. (2020). *OsFPFL4* is involved in the root and flower development by affecting auxin levels and ROS accumulation in rice (*Oryza sativa*). *Rice*, *13*, 2. https://doi.org/10.1186/s12284-019-0364-0

Gupta, P., Kabbaj, H., El Hassouni, K., Maccaferri, M., Sanchez-Garcia, M., Tuberosa, R., & Bassi, F. M. (2020). Genomic regions associated with the control of flowering time in durum wheat. *Plants*, *9*(12), 1628. https://doi.org/10.3390/plants9121628

Halliwell, J., Borrill, P., Gordon, A., Kowalczyk, R., Pagano, M. L., Saccomanno, B., Bentley, A. R., Uauy, C., & Cockram, J. (2016). Systematic investigation of *FLOWERING LOCUS T*-like Poaceae gene families identifies the short-day expressed flowering pathway gene, *TaFT3* in wheat (*Triticum aestivum* L.). *Frontiers in Plant Science*, *7*, 857. https://doi.org/10.3389/fpls.2016.00857

Hamner, K. C. (1944). Photoperiodism in plants. *Annual Review of Biochemistry*, *13*(1), 575–590. https://doi.org/10.1146/annurev.bi.13.070144.003043

Han, J., Guo, B., Guo, Y., Zhang, B., Wang, X., & Qiu, L. J. (2019). Creation of early flowering germplasm of soybean by CRISPR/Cas9 technology. *Frontiers in Plant Science*, *10*, 1446. https://doi.org/10.3389/fpls.2019.01446

Han, X., Tang, Q., Xu, L., Guan, Z., Tu, J., Yi, B., Liu, K., Yao, X., Lu, S., & Guo, L. (2022). Genome-wide detection of genotype environment interactions for flowering time in *Brassica napus*. *Frontiers in Plant Science*, *13*, 1065766. https://doi.org/10.3389/fpls.2022.1065766

Hanley, M. E., & Fegan, E. L. (2007). Timing of cotyledon damage affects growth and flowering in mature plants. *Plant, Cell & Environment*, *30*(7), 812–819. https://doi.org/10.1111/j.1365-3040.2007.01671.x

Hasan, N., Choudhary, S., Naaz, N., Sharma, N., & Laskar, R. A. (2021). Recent advancements in molecular marker-assisted selection and applications in plant breeding programmes. *Journal of Genetic Engineering and Biotechnology*, *19*(1), 128. https://doi.org/10.1186/s43141-021-00231-1

He, Y., Michaels, S. D., & Amasino, R. M. (2003). Regulation of flowering time by histone acetylation in Arabidopsis. *Science*, *302*, 1751–1754. https://doi.org/10.1126/science.1091109

He, X., Wang, T., Xu, Z., Liu, N., Wang, L., Hu, Q., Luo, X., Zhang, X., & Zhu, L. (2018). The cotton *HD-Zip* transcription factor *GhHB12* regulates flowering time and plant architecture via the *GhmiR157-GhSPL* pathway. *Communications Biology*, *1*, 229. https://doi.org/10.1038/s42003-018-0234-0

Higgins, R. H., Thurber, C. S., Assaranurak, I., & Brown, P. J. (2014). Multiparental mapping of plant height and flowering time QTL in partially isogenic sorghum families. *G3*, *4*(9), 1593–1602. https://doi.org/10.1534/g3.114.013318

Hu, X., Chen, G., Zhang, R., Xu, M., Zhao, L., Tang, H., Ni, J., & Zhou, M. (2023). Multi-year QTL mapping and RNA-seq reveal candidate genes for early floret-opening time in japonica rice. *Agriculture*, *13*(4), 859. https://doi.org/10.3390/agriculture13040859

Huang, L., Min, Y., Schiessl, S., Xiong, X., Jan, H. U., He, X., Qian, W., Guan, C., Snowdon, R. J., Hua, W., Guan, M., & Qian, L. (2021). Integrative analysis of GWAS and transcriptome to reveal novel loci regulation flowering time in semi-winter rapeseed. *Plant Science*, *310*, 110980. https://doi.org/10.1016/j.plantsci.2021.110980

Huang, P. K., Schmitt, J., & Runcie, D. E. (2024). Exploring the molecular regulation of vernalization-induced flowering synchrony in *Arabidopsis*. *New Phytologist*, *242*(3), 947–959. https://doi.org/10.1111/nph.19680

Huang, C., Sun, H., Xu, D., Chen, Q., Liang, Y., Wang, X., Xu, G., Tian, J., Wang, C., Li, D., Wu, L., Yang, X., Jin, W., Doebley, J. F., & Tian, F. (2017). *ZmCCT9* enhances maize adaptation to higher latitudes. *Proceedings of the National Academy of Sciences of the United States of America*, *115*(2), E334–E341. https://doi.org/10.1073/pnas.1718058115

Hung, H. Y., Shannon, L. M., Tian, F., Bradbury, P. J., Chen, C., Flint-Garcia, S. A., McMullen, M. D., Ware, D., Buckler, E. S., Doebley, J. F., & Holland, J. B. (2012). *ZmCCT* and the genetic basis of day-length adaptation underlying the post domestication spread of maize. *Proceedings of the National Academy of Sciences of the United States of America*, *109*(28), 1913–1921. https://doi.org/10.1073/pnas.1203189109

Ishimaru, T., Hlaing, K. T., Oo, Y. M., Lwin, T. M., Sasaki, K., Lumanglas, P. D., Simon, E.-V. M., Myint, T. T., Hairmansis, A., Susanto, U., Ayyenar, B., Muthurajan, R., Hirabayashi, H., Fukuta, Y., Kobayasi, K., Matsui, T., Yoshimoto, M., & Htun, T. M. (2022). An early-morning flowering trait in rice can enhance grain yield under heat stress field conditions at flowering stage. *Field Crops Research*, *277*, 108400. https://doi.org/10.1016/j.fcr.2021.108400

Jagadish, S. V. K., Bahuguna, R. N., Djanaguiraman, M., Gamuyao, R., Prasad, P. V. V., & Craufurd, P. Q. (2016). Implications of high temperature and elevated CO_2 on flowering time in plants. *Frontiers in Plant Science*, *7*, 913. https://doi.org/10.3389/fpls.2016.00913

Jha, U. C., Nayyar, H., Chattopadhyay, A., Beena, R., Lone, A. A., Naik, Y. D., Thudi, M., Prasad, P. V. V., Gupta, S., Dixit, G. P., & Siddique, K. H. M. (2023). Major viral diseases in grain legumes: Designing disease resistant legumes from plant breeding and OMICS integration. *Frontiers in Plant Science*, *14*, 1183505. https://doi.org/10.3389/fpls.2023.1183505

Jha, U. C., Nayyar, H., Palakurthi, R., Jha, R., Valluri, V., Bajaj, P., Chitikineni, A., Singh, N. P., Varshney, R. K., & Thudi, M. (2021). Major QTLs and potential candidate genes for heat stress tolerance identified in chickpea (*Cicer arietinum* L.). *Frontiers in Plant Science*, *12*, 655103. https://doi.org/10.3389/fpls.2021.655103

Jian, H., Zhang, A., Ma, J., Wang, T., Yang, B., Shuang, L. S., Liu, M., Li, J., Xu, X., Paterson, A. H., & Liu, L. (2019). Joint QTL mapping and transcriptome sequencing analysis reveal candidate flowering time genes in *Brassica napus* L. *BMC Genomics*, *20*(1), 21. https://doi.org/10.1186/s12864-018-5356-8

Jiang, X., Lubini, G., Hernandes-Lopes, J., Rijnsburger, K., Veltkamp, V., de Maagd, R. A., Angenent, G. C., & Bemer, M. (2022). *FRUITFULL*-like genes regulate flowering time and inflorescence architecture in tomato. *Plant Cell*, *34*(3), 1002–1019. https://doi.org/10.1093/plcell/koab298

Kaashyap, M., Ford, R., Mann, A., Varshney, R. K., Siddique, K. H. M., & Mantri, N. (2022). Comparative flower transcriptome network analysis reveals DEGs involved in chickpea reproductive success during salinity. *Plants*, *11*(3), 434. https://doi.org/10.3390/plants11030434

Kahriman, A., Temel, H. Y., Aydoğan, A., & Tanyolac, M. B. (2015). Major quantitative trait loci for flowering time in lentil. *Turkish Journal of Agriculture and Forestry*, *39*(4), 588–595. https://doi.org/10.3906/tar-1408-16

Kazan, K., & Lyons, R. (2015). The link between flowering time and stress tolerance. *Journal of Experimental Botany*, *67*(1), 47–60. https://doi.org/10.1093/jxb/erv441

Kebede, E. (2021). Contribution, utilization and improvement of legumes-driven biological nitrogen fixation in agricultural systems. *Frontiers in Sustainable Food Systems*, *5*, 767998. https://doi.org/10.3389/fsufs.2021.767998

Kehrberger, S., & Holzschuh, A. (2019). How does timing of flowering affect competition for pollinators, flower visitation and seed set in an early spring grassland plant? *Scientific Reports*, *9*(1), 15593. https://doi.org/10.1038/s41598-019-51916-0

Kennedy, A., & Geuten, K. (2020). The role of *FLOWERING LOCUS C* relatives in cereals. *Frontiers in Plant Science*, *11*, 617340. https://doi.org/10.3389/fpls.2020.617340

Khodorova, N. V., & Boitel-Conti, M. (2013). The role of temperature in the growth and flowering of geophytes. *Plants*, *2*(4), 699–711. https://doi.org/10.3390/plants2040699

Kim, K. H., Song, K., Park, J. M., Kim, J. Y., & Lee, B. M. (2021). RNA-Seq analysis of gene expression changes related to delay of flowering time under drought stress in tropical maize. *Applied Sciences*, *11*(9), 4273. https://doi.org/10.3390/app11094273

Kong, L., Lu, S., Wang, Y., Fang, C., Wang, F., Nan, H., Su, T., Li, S., Zhang, F., Li, X., Zhao, X., Yuan, X., Liu, B., & Kong, F. (2018). Quantitative trait locus mapping of flowering time and maturity in soybean using next-generation sequencing-based analysis. *Frontiers in Plant Science*, *9*, 995. https://doi.org/10.3389/fpls.2018.00995

Koo, B. H., Yoo, S. C. Y., Park, J. W., Kwon, C. T., Lee, B. D., An, G., Zhang, Z., Li, J., Li, Z., & Paek, N.-C. (2013). Natural variation in *OsPRR37* regulates heading date and contributes to rice cultivation at a wide range of latitudes. *Molecular Plant*, *6*(6), 1877–1888. https://doi.org/10.1093/mp/sst088

Korves, T. M., & Bergelson, J. (2003). A developmental response to pathogen infection in Arabidopsis. *Plant Physiology*, *133*(1), 339–347. https://doi.org/10.1104/pp.103.027094

Krizek, B. A. (2011). Auxin regulation of Arabidopsis flower development involves members of the *AINTEGUMENTA-LIKE/PLETHORA* (*AIL/PLT*) family. *Journal of Experimental Botany*, *62*(10), 3311–3319. https://doi.org/10.1093/jxb/err127

Kumar, S., Hash, C. T., Nepolean, T., Satyavathi, C. T., Singh, G., Mahendrakar, M. D., Yadav, R. S., & Srivastava, R. K. (2017). Mapping QTLs controlling flowering time and important agronomic traits in pearl millet. *Frontiers in Plant Science*, *8*, 1731. https://doi.org/10.3389/fpls.2017.01731

Kumar, S., Hash, C. T., Singh, G., Nepolean, T., & Srivastava, R. K. (2021). Mapping QTLs for important agronomic traits in an Iniadi-derived immortal population of pearl millet. *Biotechnology Notes*, *2*, 26–32. https://doi.org/10.1016/j.biotno.2021.06.001

Kumari, P., Khan, S., Wani, I. A., Gupta, R., Verma, S., Alam, P., & Alaklabi, A. (2022). Unravelling the role of epigenetic modifications in development and reproduction of angiosperms: A critical appraisal. *Frontiers in Genetics*, *13*, 819941. https://doi.org/10.3389/fgene.2022.819941

Kumari, V. V., Roy, A., Vijayan, R., Banerjee, P., Verma, V. C., Nalia, A., Pramanik, M., Mukherjee, B., Ghosh, A., Reja, M. H., Chandran, M. A. S., Nath, R., Skalicky, M., Brestic, M., & Hossain, A. (2021). Drought and heat stress in cool-season food legumes in sub-tropical regions: Consequences, adaptation, and mitigation strategies. *Plants*, *10*(6), 1038. https://doi.org/10.3390/plants10061038

Kumawat, G., Raje, R. S., Bhutani, S., Pal, J. K., Mithra, A. S., Gaikwad, K., Sharma, T. R., & Singh, N. K. (2012). Molecular mapping of QTLs for plant type and earliness traits in pigeonpea (*Cajanus cajan* L. Millsp.). *BMC Genetics*, *13*, 84. https://doi.org/10.1186/1471-2156-13-84

Kupke, B. M., Tucker, M. R., Able, J. A., & Porker, K. D. (2022). Manipulation of barley development and flowering time by exogenous application of plant growth regulators. *Frontiers in Plant Science*, *12*, 694424. https://doi.org/10.3389/fpls.2021.694424

Lacoste, C., Nansen, C., Thompson, S., Moir-Barnetson, L., Mian, A., McNee, M., & Flower, K. C. (2015). Increased susceptibility to aphids of flowering wheat plants exposed to low temperatures. *Environmental Entomology*, *44*(3), 610–618. https://doi.org/10.1093/ee/nvv024

Lakmes, A., Jhar, A., Penmetsa, R. V., Wei, W., Brennan, A. C., & Kahriman, A. (2022). Inheritance of seed weight and growth habit in 10 intercross chickpea (*Cicer arietinum*) nested association mapping populations. *Plant Breeding*, *142*(1), 86–96. https://doi.org/10.1111/pbr.13065

Lawit, S. J., Wych, H. M., Xu, D., Kundu, S., & Tomes, D. T. (2010). Maize DELLA proteins dwarf plant8 and dwarf plant9 as modulators of plant development. *Plant and Cell Physiology*, *51*(11), 1854–1868. https://doi.org/10.1093/pcp/pcq153

Lee, S. B., Hur, Y. J., Cho, J. H., Lee, J. H., Kim, T. H., Cho, S. M., Song, Y.-C., Seo, Y.-S., Lee, J., Kim, T., Park, Y.-J., Oh, M.-K., & Park, D.-S. (2018). Molecular mapping of *qBK1WD*, a major QTL for bakanae disease resistance in rice. *Rice*, *11*(1), 3. https://doi.org/10.1186/s12284-017-0197-7

Lee, N., Ozaki, Y., Hempton, A. K., Takagi, H., Purusuwashi, S., Song, Y. H., Endo, M., Kubota, A., & Imaizumi, T. (2023). The *FLOWERING LOCUS T* gene expression is controlled by high-irradiance response and external coincidence mechanism in long days in Arabidopsis. *New Phytologist*, *239*(1), 208–221. https://doi.org/10.1111/nph.18932

Lee, J. H., & Park, C. M. (2015). Integration of photoperiod and cold temperature signals into flowering genetic pathways in Arabidopsis. *Plant Signaling & Behavior*, *10*(11), e1089373. https://doi.org/10.1080/15592324.2015.1089373

Lee, P. F., Zhan, Y. X., Wang, J. C., Cheng, Y. H., Hsu, W. H., Hsu, H. F., Chen, W., & Yang, C. (2023). The *AtERF19* gene regulates meristem activity and flower organ size in plants. *Plant Journal*, *114*(6), 1338–1352. https://doi.org/10.1111/tpj.16196

Leng, P., Khan, S. U., Zhang, D., Zhou, G., Zhang, X., Zheng, Y., Wang, T., & Zhao, J. (2022). Linkage mapping reveals QTL for flowering time-related traits under multiple abiotic stress conditions in maize. *International Journal of Molecular Sciences*, *23*(15), 8410. https://doi.org/10.3390/ijms23158410

Li, M., An, F., Li, W., Ma, M., Feng, Y., Zhang, X., & Guo, H. (2016). DELLA proteins interact with FLC to repress flowering transition. *Journal of Integrative Plant Biology*, *58*(7), 642–655. https://doi.org/10.1111/jipb.12451

Li, Z., Cheng, Q., Gan, Z., Hou, Z., Zhang, Y., Li, Y., Li, H., Nan, H., Yang, C., Chen, L., Lu, S., Shi, W., Chen, L., Wang, Y., Fang, C., Kong, L., Su, T., Li, S., Kou, K., … Dong, L. (2021). Multiplex CRISPR/Cas9-mediated knockout of soybean *LNK2* advances flowering time. *The Crop Journal*, *9*(4), 767–776. https://doi.org/10.1016/j.cj.2020.09.005

Li, Y., Dong, C., Hu, M., Bai, Z., Tong, C., Zuo, R., Liu, Y., Cheng, X., Cheng, M., Huang, J., & Liu, S. (2019). Identification of flower-specific promoters through comparative transcriptome analysis in *Brassica napus*. *International Journal of Molecular Sciences*, *20*(23), 5949. https://doi.org/10.3390/ijms20235949

Li, Y., Dong, Y., Wu, H., Hu, B., Zhai, H., Yang, J., & Xia, Z. (2019). Positional cloning of the flowering time QTL *qFT12-1* reveals the link between the clock related PRR homolog with photoperiodic response in soybeans. *Frontiers in Plant Science*, *10*, 1303. https://doi.org/10.3389/fpls.2019.01303

Li, M., Liu, Y., Tao, Y., Xu, C., Li, X., Zhang, X., Han, Y., Yang, X., Sun, J., Li, W., Li, D., Zhao, X., & Zhao, L. (2019). Identification of genetic loci and candidate genes related to soybean flowering through genome wide association study. *BMC Genomics*, *20*(1), 987. https://doi.org/10.1186/s12864-019-6324-7

Li, Z., Zhang, P., Lv, J., Cheng, Y., Cui, J., Zhao, H., & Hu, S. (2016). Global dynamic transcriptome programming of rapeseed (*Brassica napus* L.) anther at different development stages. *PLoS ONE*, *11*(5), e0154039. https://doi.org/10.1371/journal.pone.0154039

Liang, N., Cheng, D., Liu, Q., Cui, J., & Luo, C. (2018). Difference of proteomics vernalization-induced in bolting and flowering transitions of Beta vulgaris. *Plant Physiology and Biochemistry*, *123*, 222–232. https://doi.org/10.1016/j.plaphy.2017.12.017

Liang, Y., Liu, Q., Wang, X., Huang, C., Xu, G., Hey, S., Lin, H., Li, C., Xu, D., Wu, L., Wang, C., Wu, W., Xia, J., Han, X., Lu, S., Lai, J., Song, W., Schnable, P. S., & Tian, F. (2018). ZmMADS69 functions as a flowering activator through the ZmRap2.7-ZCN8 regulatory module and contributes to maize flowering time adaptation. *New Phytologist*, *221*(4), 2335–2347. https://doi.org/10.1111/nph.15512

Liang, Y., Liu, Q., Wang, X., Huang, C., Xu, G., Hey, S., & Tian, F. (2018). Zm MADS 69 functions as a flowering activator through the ZmRap2. 7-ZCN 8 regulatory module and contributes to maize flowering time adaptation. *New Phytologist*, *221*(4), 2335–2347. https://doi.org/10.1111/nph.15512

Liang, W., Yang, X., Cui, S., Wang, J., Hou, M., Mu, G., Li, Z., & Liu, L. (2020). Identification of main effect and epistatic QTLs controlling initial flowering date in cultivated peanut (*Arachis hypogaea* L.). *Journal of Integrative Agriculture*, *19*(10), 2383–2393. https://doi.org/10.1016/S2095-3119(20)63211-7

Liu, S., He, M., Lin, X., & Kong, F. (2023). Epigenetic regulation of photoperiodic flowering in plants. *The Plant Genome*, *16*(4), e20320. https://doi.org/10.1002/tpg2.20320

Liu, Y., Lin, G., Yin, C., & Fang, Y. (2020). B-box transcription factor 28 regulates flowering by interacting with constans. *Scientific Reports*, *10*(1), 17789. https://doi.org/10.1038/s41598-020-74445-7

Liu, X., Liu, H., Zhang, Y., He, M., Li, R., Meng, W., Wang, Z., Li, X., & Bu, Q. (2021). Fine-tuning flowering time via genome editing of upstream open reading frames of *heading date 2* in rice. *Rice*, *14*(1), 59. https://doi.org/10.1186/s12284-021-00504-w

Liu, Y., Mu, J., Niklas, K. J., Li, G., & Sun, S. (2012). Global warming reduces plant reproductive output for temperate multi-inflorescence species on the Tibetan Plateau. *New Phytologist*, *195*(2), 427–436. https://doi.org/10.1111/j.1469-8137.2012.04178.x

Lu, S., Li, Y., Wang, J., Srinivas, P., Nan, H., Cao, D., Wang, Y., Li, J., Li, X., Fang, C., Shi, X., Yuan, X., Watanabe, S., Feng, X., Liu, B., Abe, J., & Kong, F. (2015). QTL mapping for flowering time in different latitude in soybean. *Euphytica*, *206*(3), 725–736. https://doi.org/10.1007/s10681-015-1501-5

Lu, H., Lin, T., Klein, J., Wang, S., Qi, J., Zhou, Q., Sun, J., Zhang, Z., Weng, Y., & Huang, S. (2014). QTL-seq identifies an early flowering

QTL located near *Flowering Locus T* in cucumber. *Tag. Theoretical and Applied Genetics Theoretische Und Angewandte Genetik*, *127*(7), 1491–1499. https://doi.org/10.1007/s00122-014-2313-z

Luan, W., Chen, H., Fu, Y., Si, H., Peng, W., Song, S., Liu, W., Hu, G., Sun, Z., Xie, D., & Sun, C. (2009). The effect of the crosstalk between photoperiod and temperature on the heading-date in rice. *PLoS ONE*, *4*, e5891. https://doi.org/10.1371/journal.pone.0005891

Lyons, R., Rusu, A., Stiller, J., Powell, J., Manners, J. M., & Kazan, K. (2015). Investigating the association between flowering time and defense in the *Arabidopsis thaliana–Fusarium oxysporum* interaction. *PLoS ONE*, *10*(6), e0127699. https://doi.org/10.1371/journal.pone.0127699

Ma, Y., Dong, J., Yang, W., Chen, L., Wu, W., Li, W., Zhou, L., Wang, J., Chen, J., Yang, T., Zhang, S., Zhao, J., & Liu, B. (2022). OsFLZ2 interacts with OsMADS51 to fine-tune rice flowering time. *Development*, *149*(24), 200862. https://doi.org/10.1242/dev.200862

Ma, D., Liu, B., Ge, L., Weng, Y., Cao, X., Liu, F., Mao, P., & Ma, X. (2021). Identification and characterization of regulatory pathways involved in early flowering in the new leaves of alfalfa (*Medicago sativa* L.) by transcriptome analysis. *BMC Plant Biology*, *21*(1), 8. https://doi.org/10.1186/s12870-020-02775-9

Macioszek, V. K., Sobczak, M., Skoczowski, A., Oliwa, J., Michlewska, S., Gapínska, M., Ciereszko, I., & Kononowicz, A. K. (2021). The effect of photoperiod on necrosis development, photosynthetic efficiency and “Green Islands” formation in *Brassica juncea* infected with *Alternaria brassicicola*. *International Journal of Molecular Sciences*, *22*(16), 8435. https://doi.org/10.3390/ijms22168435

Maheswaran, M., Huang, N., Sreerangasamy, S. R., & McCouch, S. R. (2000). Mapping quantitative trait loci associated with days to flowering and photoperiod sensitivity in rice (*Oryza sativa* L.). *Molecular breeding*, *6*(2), 145–155. https://doi.org/10.1023/A:1009618621720

Mallikarjuna, B. P., Samineni, S., Thudi, M., Sajja, S. B., Khan, A. W., Patil, A., Viswanatha, K. P., Varshney, R. K., & Gaur, P. M. (2017). Molecular mapping of flowering time major genes and QTLs in chickpea (*Cicer arietinum* L.). *Frontiers in Plant Science*, *8*, 1140. https://doi.org/10.3389/fpls.2017.01140

Marla, S. R., Chu, K., Chintamanani, S., Multani, D. S., Klempien, A., DeLeon, A., Bong-suk, K., Dunkle, L. D., Dilkes, B. P., & Johal, G. S. (2018). Adult plant resistance in maize to northern leaf spot is a feature of partial loss-of-function alleles of Hm1. *PLoS Pathogens*, *14*(10), e1007356. https://doi.org/10.1371/journal.ppat.1007356

Matsoukas, I. G. (2014). Interplay between sugar and hormone signaling pathways modulate floral signal transduction. *Frontiers in Genetics*, *5*, 218. https://doi.org/10.3389/fgene.2014.00218

Maurer, A., Draba, V., Jiang, Y., Schnaithmann, F., Sharma, R., Schumann, E., Kilian, B., Reif, J. C., & Pillen, K. (2015). Modelling the genetic architecture of flowering time control in barley through nested association mapping. *BMC Genomics*, *16*(1), 290. https://doi.org/10.1186/s12864-015-1459-7

McCallum, C. M., Comai, L., Greene, E. A., & Henikoff, S. (2000). Targeting Induced Local Lesions IN Genomes (TILLING) for plant functional genomics. *Plant Physiology*, *123*(2), 439–442. https://doi.org/10.1104/pp.123.2.439

Meitzel, T., Radchuk, R., McAdam, E. L., Thormählen, I., Feil, R., Munz, E., Hilo, A., Geigenberger, P., Ross, J. J., Lunn, J. E., & Borisjuk, L. (2020). Trehalose 6-phosphate promotes seed filling by activating auxin biosynthesis. *New Phytologist*, *229*(3), 1553–1565. https://doi.org/10.1111/nph.16956

Meng, X., Muszynski, M. G., & Danilevskaya, O. N. (2011). The *FT*-like *ZCN8* gene functions as a floral activator and is involved in photoperiod sensitivity in maize. *Plant Cell*, *23*(3), 942–960. https://doi.org/10.1105/tpc.110.081406

Michaels, S. D., Ditta, G., Gustafson-Brown, C., Pelaz, S., Yanofsky, M., & Amasino, R. M. (2003). *AGL24* acts as a promoter of flowering in Arabidopsis and is positively regulated by vernalization. *Plant Journal*, *33*(5), 867–874. https://doi.org/10.1046/j.1365-313x.2003.01671.x

Mizuno, N., Matsunaka, H., Yanaka, M., Ishikawa, G., Kobayashi, F., & Nakamura, K. (2023). Natural variations of wheat *EARLY FLOWERING 3* highlight their contributions to local adaptation through fine-tuning of heading time. *Theoretical and Applied Genetics*, *136*(6), 139. https://doi.org/10.1007/s00122-023-04386-y

Mondal, S., Joshi, A. K., Huerta-Espino, J., & Singh, R. P. (2015). Early maturity in wheat for adaptation to high temperature stress. In advances in wheat genetics: From genome to field. *Proceedings of the 12th international wheat genetics symposium* (pp. 239–245). Springer. https://doi.org/10.1007/978-4-431-55675-6_26

Mulki, M. A., & von Korff, M. (2016). CONSTANS controls floral repression by up-regulating *VERNALIZATION2* (*VRN-H2*) in barley. *Plant Physiology*, *170*(1), 325–37. https://doi.org/10.1104/pp.15.01350

Mulwa, G. K., Kitonyo, O. M., & Nderitu, J. H. (2023). Earliness and crop morphological traits modulate field pest infestation in green gram. *Journal of Economic Entomology*, *116*(2), 462–471. https://doi.org/10.1093/jee/toac205

Murphy, R. L., Klein, R. R., Morishige, D. T., Brady, J. A., Rooney, W. L., Miller, F. R., Dugas, D. V., Klein, P. E., & Mullet, J. E. (2011). Coincident light and clock regulation of pseudoresponse regulator protein 37 (PRR37) controls photoperiodic flowering in sorghum. *Proceedings of the National Academy of Sciences of the United States of America*, *108*(39), 16469–16474. https://doi.org/10.1073/pnas.1106212108

Murphy, R. L., Morishige, D. T., Brady, J. A., Rooney, W. L., Yang, S., Klein, P. E., & Mullet, J. E. (2014). *Ghd7* (Ma6) represses sorghum flowering in long days: *Ghd7* alleles enhance biomass accumulation and grain production. *The Plant Genome*, *7*(2), plantgenome2013.11.0040. https://doi.org/10.3835/plantgenome2013.11.0040

Mutasa-Göttgens, E., & Hedden, P. (2009). Gibberellin as a factor in floral regulatory networks. *Journal of Experimental Botany*, *60*(7), 1979–1989. https://doi.org/10.1093/jxb/erp040

Naik, Y. D., Zhao, C., Channale, S., Nayak, S. N., Bhutia, K. L., Gautam, A., Kumar, R., Niranjan, V., Shah, T. M., Mott, R., Punnuri, S., Pandey, M. K., Wang, X., Varshney, R. K., & Thudi, M. (2024). Bioinformatics for plant genetics and breeding research. *Frontier technologies for crop improvement* (pp. 35–64). Singapore: Springer Nature Singapore. https://doi.org/10.1007/978-981-99-4673-0_3

Nemoto, Y., Nonoue, Y., Yano, M., & Izawa, T. (2016). Hd1, a CONSTANS ortholog in rice, functions as an Ehd1 repressor through interaction with monocot-specific CCT-domain protein Ghd7. *Plant Journal*, *86*(3), 221–233. https://doi.org/10.1111/tpj.13168

Nguyen, A. T., Nishijima, R., Kajimura, T., Murai, K., & Takumi, S. (2015). Quantitative trait locus analysis for flowering-related traits using two F_2 populations derived from crosses between Japanese common wheat cultivars and synthetic hexaploids. *Genes & Genetic Systems*, *90*(2), 89–98. https://doi.org/10.1266/ggs.90.89

Nguyen, H., Thompson, A., & Costello, C. (2023). Impacts of historical droughts on maize and soybean production in the southeastern United States. *Agricultural Water Management*, *281*, 108237. https://doi.org/10.1016/j.agwat.2023.108237

No, D. H., Baek, D., Lee, S. H., Cheong, M. S., Chun, H. J., Park, M. S., Cho, H. M., Jin, B. J., Lim, L. H., Lee, Y. B., Shim, S. I., Chung, J.-I., & Kim, M. C. (2021). High-temperature conditions promote soybean flowering through the transcriptional reprograming of flowering genes in the photoperiod pathway. *International Journal of Molecular Sciences*, *22*(3), 1314. https://doi.org/10.3390/ijms22031314

Ogiso-Tanaka, E., Matsubara, K., Yamamoto, S. I., Nonoue, Y., Wu, J., Fujisawa, H., Ishikubo, H., Tanaka, T., Ando, T., Matsumoto, T., & Yano, M. (2013). Natural variation of the *RICE FLOWERING LOCUS T 1* contributes to flowering time divergence in rice. *PLoS ONE*, *8*(10), e75959. https://doi.org/10.1371/journal.pone.0075959

Osnato, M., Cota, I., Nebhnani, P., Cereijo, U., & Pelaz, S. (2022). Photoperiod control of plant growth: Flowering time genes beyond flowering. *Frontiers in Plant Science*, *12*, 805635. https://doi.org/10.3389/fpls.2021.805635

Ouzounis, T., Razi Parjikolaei, B., Fretté, X., Rosenqvist, E., & Ottosen, C. O. (2015). Predawn and high intensity application of supplemental blue light decreases the quantum yield of PSII and enhances the amount of phenolic acids, flavonoids and pigments in *Lactuca sativa*. *Frontiers in Plant Science*, *6*, 19. https://doi.org/10.3389/fpls.2015.00019

Parachnowitsch, A. L., & Caruso, C. M. (2008). Predispersal seed herbivores, not pollinators, exert selection on floral traits via female fitness. *Ecology*, *89*(7), 1802–1810. https://doi.org/10.1890/07-0555.1

Paradiso, R., Meinen, E., Snel, J. F. H., De Visser, P., Van Ieperen, W., Hogewoning, S. W., & Marcelis, L. F. M. (2011). Spectral dependence of photosynthesis and light absorptance in single leaves and canopy in rose. *Scientia Horticulturae*, *127*(4), 548–554. https://doi.org/10.1016/j.scienta.2010.11.017

Paradiso, R., & Proietti, S. (2022). Light-quality manipulation to control plant growth and photomorphogenesis in greenhouse horticulture: The state of the art and the opportunities of modern LED systems. *Journal of Plant Growth Regulation*, *41*(2), 742–780. https://doi.org/10.1007/s00344-021-10337-y

Parmesan, C., & Hanley, M. E. (2015). Plants and climate change: Complexities and surprises. *Annals of Botany*, *116*(6), 849–864. https://doi.org/10.1093/aob/mcv169

Pieper, R., Tomé, F., Pankin, A., & von Korff, M. (2021). *FLOWERING LOCUS T4* delays flowering and decreases floret fertility in barley. *Journal of Experimental Botany*, *72*(1), 107–121. https://doi.org/10.1093/jxb/eraa466<./bib>

Pose, D., Verhage, L., Ott, F., Yant, L., Mathieu, J., Angenent, G. C., Immink, R. G. H., & Schmid, M. (2013). Temperature-dependent regulation of flowering by antagonistic FLM variants. *Nature*, *503*, 414–417. https://doi.org/10.1038/nature12633

Prasad, P. V. V., Boote, K. J., & Allen, L. H. (2006). Adverse high temperature effects pollen viability, seed-set, seed yield and harvest index of grain-sorghum [*Sorghum bicolor* (L.) Moench) are more severe at elevated carbon dioxide due to higher tissue temperatures. *Agricultural and Forest Meteorology*, *139*, 237–251. https://doi.org/10.1016/j.agrformet.2006.07.003

Prasad, P. V. V., Boote, K. J., Allen, L. H., Jr., & Thomas, J. M. G. (2002). Effects of elevated temperatures and carbon dioxide on seed-set and yield of kidney bean (*Phaseolus vulgaris* L.). *Global Change Biology*, *8*, 710–721. https://doi.org/10.1046/j.1365-2486.2002.00508.x

Qanmber, G., Lu, L., Liu, Z., Yu, D., Zhou, K., Huo, P., Li, F., & Yang, Z. (2019). Genome-wide identification of *GhAAI* genes reveals that *GhAAI66* triggers a phase transition to induce early flowering. *Journal of Experimental Botany*, *70*(18), 4721–4736. https://doi.org/10.1093/jxb/erz239

Qian, C., Yan, X., Shi, Y., Yin, H., Chang, Y., Chen, J., Ingvarsson, P. K., Nevo, E., & Ma, X.-F. (2020). Adaptive signals of flowering time pathways in wild barley from Israel over 28 generations. *Heredity*, *124*(1), 62–76. https://doi.org/10.1038/s41437-019-0264-5

Qin, C., Li, H., Zhang, S., Lin, X., Jia, Z., Zhao, F., Wei, X., Jiao, Y., Li, Z., Niu, Z., Zhou, Y., Li, X., Li, H., Zhao, T., Liu, J., Li, H., Lu, Y., Kong, F., & Liu, B. (2023). *GmEID1* modulates light signaling through the evening complex to control flowering time and yield in soybean. *Proceedings of the National Academy of Sciences of the United States of America*, *120*(15), e2212468120. https://doi.org/10.1073/pnas.2212468120

Qiu, L., Zhou, P., Wang, H., Zhang, C., Du, C., Tian, S., Wu, Q., Wei, L., Wang, X., Zhou, Y., Huang, R., Huang, X., & Ouyang, X. (2023). Photoperiod genes contribute to daylength-sensing and breeding in rice. *Plants*, *12*(4), 899. https://doi.org/10.3390/plants12040899

Rajandran, V., Ortega, R., Vander Schoor, J. K., Butler, J. B., Freeman, J. S., Hecht, V. F. G., Erskine, W., Murfet, I. C., Bett, K. E., & Weller, J. L. (2022). Genetic analysis of early phenology in lentil identifies distinct loci controlling component traits. *Journal of Experimental Botany*, *73*(12), 3963–3977. https://doi.org/10.1093/jxb/erac107

Raman, H., Raman, R., Qiu, Y., Yadav, A. S., Sureshkumar, S., Borg, L., Rohan, M., Wheeler, D., Owen, O., Menz, I., & Balasubramanian, S. (2019). GWAS hints at pleiotropic roles for *FLOWERING LOCUS T* in flowering time and yield-related traits in canola. *BMC Genomics*, *20*(1), 636. https://doi.org/10.1186/s12864-019-5964-y

Ratcliffe, O. J., Bradley, D. J., & Coen, E. S. (1999). Separation of shoot and floral identity in Arabidopsis. *Development*, *126*(6), 1109–1120. https://doi.org/10.1242/dev.126.6.1109

Riboni, M., Galbiati, M., Tonelli, C., & Conti, L. (2013). *GIGANTEA* enables drought escape response via abscisic acid-dependent activation of the florigens and *SUPPRESSOR OF OVEREXPRESSION OF CONSTANS1*. *Plant Physiology*, *162*(3), 1706–1719. https://doi.org/10.1104/pp.113.217729

Ridge, S., Deokar, A., Lee, R., Daba, K., Macknight, R. C., Weller, J. L., & Tar'an, B. (2017). The chickpea early flowering 1 (*Efl1*) locus is an ortholog of Arabidopsis *ELF3*. *Plant Physiology*, *175*(2), 802–815. https://doi.org/10.1104/pp.17.00082

Roy, A., Reddy, M. H., Sarkar, M., Sagolsem, D., Murmu, S. K., Das, C., Roy, D., Ganguly, S., Nath, R., Bhattacharyya, P. K., Sarker, A., & Bhattacharyya, S. (2023). A mis-splicing *early flowering 3* (*elf3*) allele of lentil is associated with yield enhancement under terminal heat stress. *Journal of Applied Genetics*, *64*(2), 265–273. https://doi.org/10.1007/s13353-023-00753-z

Rubin, M. J., Schmid, K. M., & Friedman, J. (2019). Assortative mating by flowering time and its effect on correlated traits in variable environments. *Ecology and evolution*, *9*(1), 471–481. https://doi.org/10.1002/ece3.4765

Ruiz-Ferrer, V., & Voinnet, O. (2009). Roles of plant small RNAs in biotic stress responses. *Annual Review of Plant Biology*, *60*, 485–510. https://doi.org/10.1146/annurev.arplant.043008.092111

Salvi, S., Castelletti, S., & Tuberosa, R. (2009). An updated consensus map for flowering time QTLs in maize. *Maydica*, *54*(4), 501.

Salvi, S., Sponza, G., Morgante, M., Tomes, D., Niu, X., Fengler, K. A., Meeley, R., Ananiev, E. V., Svitashev, S., Bruggemann, E., &

Li, B. (2007). Conserved noncoding genomic sequences associated with a flowering-time quantitative trait locus in maize. *Proceedings of the National Academy of Sciences of the United States of America*, *104*(27), 11376–11381. https://doi.org/10.1073/pnas.0704145104

Sameri, M., Pourkheirandish, M., Chen, G., Tonooka, T., & Komatsuda, T. (2011). Detection of photoperiod responsive and non-responsive flowering time QTL in barley. *Breeding Science*, *61*(2), 183–188. https://doi.org/10.1270/jsbbs.61.183

Samineni, S., Kamatam, S., Thudi, M., Varshney, R. K., & Gaur, P. M. (2015). Vernalization response in chickpea is controlled by a major QTL. *Euphytica*, *207*(2), 453–461. https://doi.org/10.1007/s10681-015-1571-4

Saxena, K., Choudhary, A. K., Srivastava, R. K., Bohra, A., Saxena, R. K., & Varshney, R. K. (2019). Origin of early maturing pigeonpea germplasm and its impact on adaptation and cropping systems. *Plant Breeding*, *138*(3), 243–251. https://doi.org/10.1111/pbr.12696

Scheben, A., Severn-Ellis, A. A., Patel, D., Pradhan, A., Rae, S. J., Batley, J., & Edwards, D. (2020). Linkage mapping and QTL analysis of flowering time using ddRAD sequencing with genotype error correction in *Brassica napus*. *BMC Plant Biology*, *20*(1), 546. https://doi.org/10.1186/s12870-020-02756-y

Schiestl, F. P., Kirk, H., Bigler, L., Cozzolino, S., & Desurmont, G. A. (2014). Herbivory and floral signaling: Phenotypic plasticity and tradeoffs between reproduction and indirect defense. *New Phytologist*, *203*(1), 257–266. https://doi.org/10.1111/nph.12783

Semagn, K., Iqbal, M., Chen, H., Perez-Lara, E., Bemister, D. H., Xiang, R., Zou, J., Asif, M., Kamran, A., N'Diaye, A., Randhawa, H., Pozniak, C., & Spaner, D. (2021). Physical mapping of QTL in four spring wheat populations under conventional and organic management systems. I. Earliness. *Plants*, *10*(5), 853. https://doi.org/10.3390/plants10050853

Shalit-Kaneh, A., Eviatar-Ribak, T., Horev, G., Suss, N., Aloni, R., Eshed, Y., & Lifschitz, E. (2019). The flowering hormone florigen accelerates secondary cell wall biogenesis to harmonize vascular maturation with reproductive development. *Proceedings of the National Academy of Sciences of the United States of America*, *116*(32), 16127–16136. https://doi.org/10.1073/pnas.1906405116

Shavrukov, Y., Kurishbayev, A., Jatayev, S., Shvidchenko, V., Zotova, L., Koekemoer, F., de Groot, S., Soole, K., & Langridge, P. (2017). Early flowering as a drought escape mechanism in plants: How can it aid wheat production? *Frontiers in Plant Science*, *8*, 1950. https://doi.org/10.3389/fpls.2017.01950

Sheldon, C. C., Rouse, D. T., Finnegan, E. J., Peacock, W. J., & Dennis, E. S. (2000). The molecular basis of vernalization: The central role of *FLOWERING LOCUS C* (*FLC*). *Proceedings of the National Academy of Sciences*, *97*(7), 3753–3758. https://doi.org/10.1073/pnas.97.7.3753

Shimizu, S., Yamauchi, Y., & Ishikawa, A. (2021). Photoperiod following inoculation of Arabidopsis with *Pyricularia oryzae* (syn. *Magnaporthe oryzae*) influences on the plant-pathogen interaction. *International Journal of Molecular Sciences*, *22*(9), 5004. https://doi.org/10.3390/ijms22095004

Shivaprasad, K. M., Dikshit, H. K., Mishra, G. P., Sinha, S. K., Aski, M., Kohli, M., Mishra, D. C., Singh, A. K., Gupta, S., Singh, A., Tripathi, K., Kumar, R. R., Kumar, A., Jha, G. K., Kumar, S., & Varshney, R. K. (2024). Delineation of loci governing an extra-earliness trait in lentil (*Lens culinaris* Medik.) using the QTL-Seq approach. *Plant Biotechnology Journal*, *22*(10), 2932–2949. https://doi.org/10.1111/pbi.14415

Shu, J., Liu, Y., Zhang, L., Li, Z., Fang, Z., Yang, L., Zhuang, M., Zhang, Y., & Lv, H. (2018). QTL-seq for rapid identification of candidate genes for flowering time in broccoli × cabbage. *Theoretical and Applied Genetics*, *131*(4), 917–928. https://doi.org/10.1007/s00122-017-3047-5

Singh, V. K., Garg, R., & Jain, M. (2013). A global view of transcriptome dynamics during flower development in chickpea by deep sequencing. *Plant Biotechnology Journal*, *11*(6), 691–701. https://doi.org/10.1111/pbi.12059

Singh, D., Sharma, S., Jose-Santhi, J., Kalia, D., & Singh, R. K. (2023). Hormones regulate the flowering process in saffron differently depending on the developmental stage. *Frontiers in Plant Science*, *14*, 1107172. https://doi.org/10.3389/fpls.2023.1107172

Singh, V., Sinha, P., Obala, J., Khan, A. W., Chitikineni, A., Saxena, R. K., & Varshney, R. K. (2022). QTL-seq for the identification of candidate genes for days to flowering and leaf shape in pigeonpea. *Hereditary*, *128*(6), 411–419. https://doi.org/10.1038/s41437-021-00486-x

Song, K., Kim, H. C., Shin, S., Kim, K. H., Moon, J. C., Kim, J. Y., & Lee, B. M. (2017). Transcriptome analysis of flowering time genes under drought stress in maize leaves. *Frontiers in Plant Science*, *8*, 267. https://doi.org/10.3389/fpls.2017.00267

Song, Y., Gao, Z., & Luan, W. (2012). Interaction between temperature and photoperiod in regulation of flowering time in rice. *Science China. Life Sciences*, *55*, 241–249. https://doi.org/10.1007/s11427-012-4300-4

Springer, C. J., & Ward, J. K. (2007). Flowering time and elevated atmospheric CO_2. *New Phytologist*, *176*(2), 243–255. https://doi.org/10.1111/j.1469-8137.2007.02196.x

Srivastava, R., Upadhyaya, H. D., Kumar, R., Daware, A., Basu, U., Shimray, P. W., Tripathi, S., Bharadwaj, C., Tyagi, A. K., & Parida, S. K. (2017). A multiple QTL seq strategy delineates potential genomic loci governing flowering time in chickpea. *Frontiers in Plant Science*, *8*, 1105. https://doi.org/10.3389/fpls.2017.01105

Su, Z., Ma, X., Guo, H., Sukiran, N. L., Guo, B., Assmann, S. M., & Ma, H. (2013). Flower development under drought stress: Morphological and transcriptomic analyses reveal acute responses and long-term acclimation in Arabidopsis. *The Plant Cell*, *25*(10), 3785–3807. https://doi.org/10.1105/tpc.113.115428

Su, P., Sui, C., Wang, S., Liu, X., Zhang, G., Sun, H., Wan, K., Yan, J., & Guo, S. (2023). Genome-wide evolutionary analysis of AUX/IAA gene family in wheat identifies a novel gene *TaIAA15-1A* regulating flowering time by interacting with ARF. *International Journal of Biological Macromolecules*, *227*, 285–296. https://doi.org/10.1016/j.ijbiomac.2022.12.175

Sui, P., Shi, J., Gao, X., Shen, W. H., & Dong, A. (2013). *H3K36* methylation is involved in promoting rice flowering. *Molecular Plant*, *6*(3), 975–977. https://doi.org/10.1093/mp/sss152

Sun, C., He, C., Zhong, C., Liu, S., Liu, H., Luo, X., Li, J., Zhang, Y., Guo, Y., Yang, B., Wang, P., & Deng, X. (2022). Bifunctional regulators of photoperiodic flowering in short day plant rice. *Frontiers in Plant Science*, *13*, 1044790. https://doi.org/10.3389/fpls.2022.1044790

Sun, F., Wang, Y., Liu, G., Fang, D., Sun, M., Bao, Z., & Ma, F. (2024). Salt stress induces SFT expression to promote early flowering and inhibits floral organ development by disturbing cell cycle in tomato. *Vegetable Recipes*, *17*, 1–11. https://doi.org/10.48130/vegres-0024-0017

Sun, F., Xu, M., Park, C., Dwiyanti, M. S., Nagano, A. J., Zhu, J., Watanabe, S., Kong, F., Liu, B., Yamada, T., & Abe, J. (2019). Characterization and quantitative trait locus mapping of late-flowering from a Thai soybean cultivar introduced into a photoperiod-insensitive genetic background. *PLoS ONE*, *14*(12), e0226116. https://doi.org/10.1371/journal.pone.0226116

Surkova, S. Y., & Samsonova, M. G. (2022). Mechanisms of vernalization-induced flowering in legumes. *International Journal of Molecular Sciences*, *23*(17), 9889. https://doi.org/10.3390/ijms23179889

Takada, S., Akter, A., Itabashi, E., Nishida, N., Shea, D. J., Miyaji, N., Mehraj, H., Osabe, K., Shimizu, M., Takasaki-Yasuda, T., Kakizaki, T., Okazaki, K., Dennis, E. S., & Fujimoto, R. (2019). The role of *FRIGIDA* and *FLOWERING LOCUS C* genes in flowering time of *Brassica rapa* leafy vegetables. *Scientific Reports*, *9*(1), 13843. https://doi.org/10.1038/s41598-019-50122-2

Takahashi, Y., Teshima, K. M., Yokoi, S., Innan, H., & Shimamoto, K. (2009). Variations in Hd1 proteins, Hd3a promoters and Ehd1 expression levels contribute to diversity of flowering time in cultivated rice. *Proceedings of the National Academy of Sciences*, *106*(11), 4555–4560. https://doi.org/10.1073/pnas.0812092106

Talame, V., Bovina, R., Sanguineti, M. C., Tuberosa, R., Lundqvist, U., & Salvi, S. (2008). TILLMore, a resource for the discovery of chemically induced mutants in barley. *Plant Biotechnology Journal*, *6*(5), 477–485. https://doi.org/10.1111/j.1467-7652.2008.00341.x

Tang, J., Liu, H., Quan, Y., Yao, Y., Li, K., Tang, G., & Du, D. (2023). Fine mapping and causal gene identification of a novel QTL for early flowering by QTL-seq, Target-seq and RNA-seq in spring oilseed rape. *Theoretical and Applied Genetics*, *136*(4), 80. https://doi.org/10.1007/s00122-023-04310-4

Thudi, M., Samineni, S., Li, W., Boer, M. P., Roorkiwal, M., Yang, Z., Ladejobi, F., Zheng, C., Chitikineni, A., Nayak, S., He, Z., Valluri, V., Bajaj, P., Khan, A. W., Gaur, P. M., van Eeuwijk, F., Mott, R., Xin, L., & Varshney, R. K. (2023). Whole genome resequencing and phenotyping of MAGIC population for high resolution mapping of drought tolerance in chickpea. *The Plant Genome*, *17*(1), e20333. https://doi.org/10.1002/tpg2.20333

Tian, M., Wu, A., Zhang, M., Zhang, J., Wei, H., Yang, X., Ma, L., Lu, J., Fu, X., Wang, H., & Yu, S. (2021). Genome-wide identification of the early flowering 4 (ELF4) gene family in cotton and silent GhELF4-1 and GhEFL3-6 decreased cotton stress resistance. *Frontiers in Genetics*, *12*, 686852. https://doi.org/10.3389/fgene.2021.686852

Till, B. J., Cooper, J., Tai, T. H., Colowit, P., Greene, E. A., Henikoff, S., & Comai, L. (2007). Discovery of chemically induced mutations in rice by TILLING. *BMC Plant Biology*, *7*, 1–12. https://doi.org/10.1186/1471-2229-7-19

Toivonen, M., Herzon, I., Rajanen, H., Toikkanen, J., & Kuussaari, M. (2019). Late flowering time enhances insect pollination of turnip rape. *Journal of Applied Ecology*, *56*(5), 1164–1175. https://doi.org/10.1111/1365-2664.13349

Trevaskis, B., Hemming, M. N., Dennis, E. S., & Peacock, W. J. (2007). The molecular basis of vernalization-induced flowering in cereals. *Trends in Plant Science*, *12*(8), 352–357. https://doi.org/10.1016/j.tplants.2007.06.010

Tun, W., Yoon, J., Jeon, J. S., & An, G. (2021). Influence of climate change on flowering time. *Journal of Plant Biology*, *64*(3), 193–203. https://doi.org/10.1007/s12374-021-09300-x

Varshney, R. K., Singh, V. K., Kumar, A., Powell, W., & Sorrells, M. E. (2018). Can genomics deliver climate-change ready crops? *Current Opinion in Plant Biology*, *45*(3), 205–211. https://doi.org/10.1016/j.pbi.2018.03.007

Veronese, P., Narasimhan, M. L., Stevenson, R. A., Zhu, J. K., Weller, S. C., Subbarao, K. V., & Bressan, R. A. (2003). Identification of a locus controlling Verticillium disease symptom response in *Arabidopsis thaliana*. *Plant Journal*, *35*(5), 574–587. https://doi.org/10.1046/j.1365-313x.2003.01830.x

Wahl, V., Ponnu, J., Schlereth, A., Arrivault, S., Langenecker, T., Franke, A., Feil, R., Lunn, J. E., Stitt, M., & Schmid, M. (2013). Regulation of flowering by trehalose-6-phosphate signaling in *Arabidopsis thaliana*. *Science*, *339*(6120), 704–707. https://doi.org/10.1126/science.1230406

Wang, L., Fang, C., Liu, J., Zhang, T., Kou, K., Su, T., Li, S., Chen, L., Cheng, Q., Dong, L., Kong, F., Liu, B., & Lu, S. (2020). Identification of major QTLs for flowering and maturity in soybean by genotyping-by-sequencing analysis. *Molecular breeding*, *40*, 1–12. https://doi.org/10.1007/s11032-020-01178-w

Wang, G., Wang, C., Lu, G., Wang, W., Mao, G., Habben, J. E., Song, C., Wang, J., Chen, J., Gao, Y., Liu, J., & Greene, T. W. (2020). Knockouts of a late flowering gene via CRISPR–Cas9 confer early maturity in rice at multiple field locations. *Plant Molecular Biology*, *104*(1–2), 137–150. https://doi.org/10.1007/s11103-020-01031-w

Wang, L., Yang, X., Cui, S., Zhao, N., Li, L., Hou, M., Mu, G., Liu, L., & Li, Z. (2020). High-density genetic map development and QTL mapping for concentration degree of floret flowering date in cultivated peanut (*Arachis hypogaea* L.). *Molecular Breeding*, *40*(2), 1–14. https://doi.org/10.1007/s11032-019-1083-3

Wang, L., Zhou, Z., Li, R., Weng, J., Zhang, Q., Li, X., Wang, B., Zhang, W., Song, W., & Li, X. (2021). Mapping QTL for flowering time-related traits under three plant densities in maize. *The Crop Journal*, *9*(2), 372–379. https://doi.org/10.1016/j.cj.2020.07.009

Weller, J. L., & Ortega, R. (2015). Genetic control of flowering time in legumes. *Frontiers in Plant Science*, *6*, 207. https://doi.org/10.3389/fpls.2015.00207

Wiegmann, M., Maurer, A., Pham, A., March, T. J., Al-Abdallat, A., Thomas, W. T. B., Bull, H. J., Shahid, M., Eglinton, J., Baum, M., Flavell, A. J., Tester, M., & Pillen, K. (2019). Barley yield formation under abiotic stress depends on the interplay between flowering time genes and environmental cues. *Scientific Reports*, *9*(1), 6397. https://doi.org/10.1038/s41598-019-42673-1

Wittern, L., Steed, G., Taylor, L. J., Ramirez, D. C., Pingarron-Cardenas, G., Gardner, K., Greenland, A., Hannah, M. A., & Webb, A. A. R. (2023). Wheat *EARLY FLOWERING* 3 affects heading date without disrupting circadian oscillations. *Plant Physiology*, *191*(2), 1383–1403. https://doi.org/10.1093/plphys/kiac544

Wu, Z., Fu, D., Gao, X., Zeng, Q., Chen, X., Wu, J., & Zhang, N. (2023). Characterization and expression profiles of the *B-box* gene family during plant growth and under low-nitrogen stress in Saccharum. *BMC Genomics*, *24*(1), 79. https://doi.org/10.1186/s12864-023-09185-9

Xu, D., Liu, X., Guo, C., Lin, L., & Yin, R. (2023). The B-box transcription factor 4 regulates seedling photomorphogenesis and flowering in tomato. *Scientia Horticulturae*, *309*, 111692. https://doi.org/10.1016/j.scienta.2022.111692

Xu, Y., Zhang, B., Ma, N., Liu, X., Qin, M., Zhang, Y., Wang, K., Guo, N., Zuo, K., Liu, X., Zhang, M., Huang, Z., & Xu, A. (2020). Quantitative trait locus mapping and identification of candidate genes controlling flowering time in *Brassica napus* L. *Frontiers in Plant Science*, *11*, 626205. https://doi.org/10.3389/fpls.2020.626205

Xue, B., Hamamouch, N., Li, C., Huang, G., Hussey, R. S., Baum, T. J., & Davis, E. L. (2013). The *8D05* parasitism gene of meloidogyne incognita is required for successful infection of host roots. *Phytopathology*, *103*(2), 175–181. https://doi.org/10.1094/PHYTO-07-12-0173-R

Yaish, M. W., Colasanti, J., & Rothstein, S. J. (2011). The role of epigenetic processes in controlling flowering time in plants exposed to stress. *Journal of Experimental Botany*, *62*(11), 3727–3735. https://doi.org/10.1093/jxb/err177

Yan, L., Fu, D., Li, C., Blechl, A., Tranquilli, G., Bonafede, M., Sanchez, A., Valarik, M., Yasuda, S., & Dubcovsky, J. (2006). The wheat and barley vernalization gene VRN3 is an orthologue of FT. *Proceedings of the National Academy of Sciences of the United States of America*, *103*(51), 19581–19586. https://doi.org/10.1073/pnas.0607142103

Yan, B., Hou, J., Cui, J., He, C., Li, W., Chen, X., Li, M., & Wang, W. (2019). The effects of endogenous hormones on the flowering and fruiting of *Glycyrrhiza uralensis*. *Plants*, *8*(11), 519. https://doi.org/10.3390/plants8110519

Yang, G., Zhai, H., Wu, H., Zhang, X., Lu, S., Wang, Y., Li, Y., Hu, B., Wang, L., Wen, Z., Wang, D., Wang, S., Kyuya, H., Xia, Z., & Xie, F. (2017). QTL effects and epistatic interaction for flowering time and branch number in a soybean mapping population of Japanese × Chinese cultivars. *Journal of Integrative Agriculture*, *16*(9), 1900–1912. https://doi.org/10.1016/S2095-3119(16)61539-3

Yano, M., Katayose, Y., Ashikari, M., Yamanouchi, U., Monna, L., Fuse, T., Baba, T., Yamamoto, K., Umehara, Y., Nagamura, Y., & Sasaki, T. (2000). Hd1, a major photoperiod sensitivity quantitative trait locus in rice, is closely related to the Arabidopsis flowering time gene CONSTANS. *Plant Cell*, *12*(12), 2473–2484. https://doi.org/10.1105/tpc.12.12.2473

Yin, M., Ma, H., Wang, M., Chu, G., Liu, Y., Xu, C., Zhang, X., Wang, D., & Chen, S. (2021). Transcriptome analysis of flowering regulation by sowing date in Japonica Rice (*Oryza sativa* L.). *Scientific Reports*, *11*(1), 15026. https://doi.org/10.1038/s41598-021-94552-3

Yin, X., Struik, P. C., van Eeuwijk, F. A., Stam, P., & Tang, J. (2005). QTL analysis and QTL-based prediction of flowering phenology in recombinant inbred lines of barley. *Journal of Experimental Botany*, *56*(413), 967–976. https://doi.org/10.1093/jxb/eri090

Yin, Y., Yan, Z., Guan, J., Huo, Y., Wang, T., Li, T., Cui, Z., Ma, W., Wang, X., & Chen, W. (2023). Two interacting basic helix-loop-helix transcription factors control flowering time in rice. *Plant Physiology*, *192*(1), 205–221. https://doi.org/10.1093/plphys/kiad077

Yoo, S. Y., Kim, Y., Kim, S. Y., Lee, J. S., & Ahn, J. H. (2007). Control of flowering time and cold response by a NAC-domain protein in Arabidopsis. *PLoS ONE*, *2*(7), e642. https://doi.org/10.1371/journal.pone.0000642

Yuan, H. Y., Caron, C. T., Ramsay, L., Fratini, R., de la Vega, M. P., Vandenberg, A., Weller, J. L., & Bett, K. E. (2021). Genetic and gene expression analysis of flowering time regulation by light quality in lentil. *Annals of Botany*, *128*(4), 481–496. https://doi.org/10.1093/aob/mcab083

Yuan, S., Wang, Y., Wang, J., Zhang, C., Zhang, L., Jiang, B., Wu, T., Chen, L., Xu, X., Cai, Y., Sun, S., Chen, F., Song, W., Wu, C., Hou, W., Yu, L., & Han, T. (2022). *GmFT3a* fine-tunes flowering time and improves adaptation of soybean to higher latitudes. *Frontiers in Plant Science*, *13*, 929747. https://doi.org/10.3389/fpls.2022.929747

Zhai, H., Wan, Z., Jiao, S., Zhou, J., Xu, K., Nan, H., Liu, Y., Xiong, S., Fan, R., Zhu, J., Jiang, W., Pang, T., Luo, X., Wu, H., Yang, G., Bai, X., Kong, F., & Xia, Z. (2022). *GmMDE* genes bridge the maturity gene E1 and florigens in photoperiodic regulation of flowering in soybean. *Plant Physiology*, *189*(2), 1021–1036. https://doi.org/10.1093/plphys/kiac092

Zhang, B., Feng, M., Zhang, J., & Song, Z. (2023). Involvement of *CONSTANS*-like proteins in plant flowering and abiotic stress response. *International Journal of Molecular Sciences*, *24*(23), 16585. https://doi.org/10.3390/ijms242316585

Zhang, Y., Guo, X., Zhang, Z., Li, J., Zhang, S., Sun, W., Xiao, X., Sun, Z., Xue, X., & Wang, Z. (2023). *Overcoming the trade-off between early flowering and high yield in wheat: Light regimens, developmental dynamics and transcriptome landscapes*. https://doi.org/10.22541/au.168416330.08894049/v1

Zhang, C., Jian, M., Li, W., Yao, X., Tan, C., Qian, Q., Hu, Y., Liu, X., & Hou, X. (2023). Gibberellin signaling modulates flowering via the DELLA–BRAHMA–NF-YC module in Arabidopsis. *Plant Cell*, *35*(9), 3470–3484. https://doi.org/10.1093/plcell/koad166

Zhang, J., Song, Q., Cregan, P. B., Nelson, R. L., Wang, X., Wu, J., & Jiang, G. L. (2015). Genome-wide association study for flowering time, maturity dates and plant height in early maturing soybean (*Glycine max*) germplasm. *BMC Genomics*, *16*(1), 217. https://doi.org/10.1186/s12864-015-1441-4

Zhao, C. H., Sun, H., Liu, C., Yang, G. M., Liu, X. J., Wang, Y. P., Lv, F. X., Wu, C. Y., Xu, J. W., Wu, Y. Z., & Cui, F. (2019). Detection of quantitative trait loci for wheat (*Triticum aestivum* L.) heading and flowering date. *The Journal of Agricultural Science*, *157*(1), 20–30. https://doi.org/10.1017/S0021859619000200

Zhou, Y., Myat, A. A., Liang, C., Meng, Z., Guo, S., Wei, Y., Sun, G., Wang, Y., & Zhang, R. (2022). Insights into MicroRNA-mediated regulation of flowering time in cotton through small RNA sequencing. *Frontiers in Plant Science*, *13*, 761244. https://doi.org/10.3389/fpls.2022.761244

Zhou, Z., Lu, X., Zhang, C., Li, M., Hao, Z., Zhang, D., Yong, H., Han, J., Li, X., & Weng, J. (2023). A differentially methylated region of the *ZmCCT10* promoter affects flowering time in hybrid maize. *The Crop Journal*, *11*(5), 1380–1389. https://doi.org/10.1016/j.cj.2023.05.006

Züst, T., Joseph, B., Shimizu, K. K., Kliebenstein, D. J., & Turnbull, L. A. (2011). Using knockout mutants to reveal the growth costs of defensive traits. *Proceedings of the Royal Society B: Biological Sciences*, *278*(1718), 2598–2603. https://doi.org/10.1098/rspb.2010.2475

How to cite this article: Naik, Y. D., Bahuguna, R. N., Garcia-Caparros, P., Zwart, R. S., Reddy, M. S. S., Mir, R. R., Jha, U. C., Fakrudin, B., Pandey, M. K., Challabathula, D., Sharma, V. K., Reddy, U. K., Kumar, C. V. S., Mendu, V., Prasad, P. V. V., Punnuri, S. M., Varshney, R. K., & Thudi, M. (2025). Exploring the multifaceted dynamics of flowering time regulation in field crops: Insight and intervention approaches. *The Plant Genome*, *18*, e70017. https://doi.org/10.1002/tpg2.70017