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# Genetic Regulation of Flowering Time in Temperate Grasses: A Survey

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## Abstract

This survey paper provides a comprehensive analysis of the genetic regulation of flowering time in temperate grasses, focusing on wheat and *Brachypodium distachyon*. The study highlights the significance of aligning flowering with optimal environmental conditions to enhance crop yield and resilience, particularly under stress conditions such as drought. The survey is structured to explore the genetic mechanisms, including the roles of photoreceptors, circadian clocks, and key genes like FLOWERING LOCUS T (FT), in regulating flowering time. It examines the photoperiod response, detailing the interaction between photoreceptors and molecular timers, and the implications for stress responses. A comparative analysis between wheat and *Brachypodium distachyon* elucidates similarities and differences in their genetic and physiological mechanisms. The paper further explores the implications of genetic insights for crop improvement, emphasizing the potential applications in breeding strategies and the use of advanced predictive models to enhance breeding efficiency. Key findings underscore the importance of early flowering as a drought escape mechanism and the role of genetic diversity in optimizing phenological responses. The survey concludes by reflecting on the broader implications for future research and agricultural practices, advocating for the continued exploration of genetic diversity and regulatory networks to develop resilient crop varieties in the face of changing climatic conditions.

## 1 Introduction

### 1.1 Significance of Genetic Regulation in Temperate Grasses

The genetic regulation of flowering time in temperate grasses, including wheat and *Brachypodium distachyon*, is crucial for agricultural efficiency, as it synchronizes flowering with favorable environmental conditions, thereby improving crop yield and resilience. This synchronization is particularly important for early flowering as a drought escape mechanism, essential for sustaining wheat productivity under water-limited scenarios [1]. Genetic insights into flowering time manipulation are vital for enhancing grain yield predictions, as exemplified by barley, where such regulatory mechanisms significantly influence agricultural outputs [2].

Furthermore, studying the genetic regulation in *Brachypodium distachyon* serves as a model for investigating specific gene families, such as GRAS genes, which play pivotal roles in plant growth and development. These genetic insights are integral not only for bolstering the resilience of temperate grasses against environmental stresses but also for informing breeding strategies aimed at improving crop performance and sustainability. Consequently, examining genetic regulation in temperate grasses is essential for advancing agricultural practices and ensuring food security amid changing climate conditions.

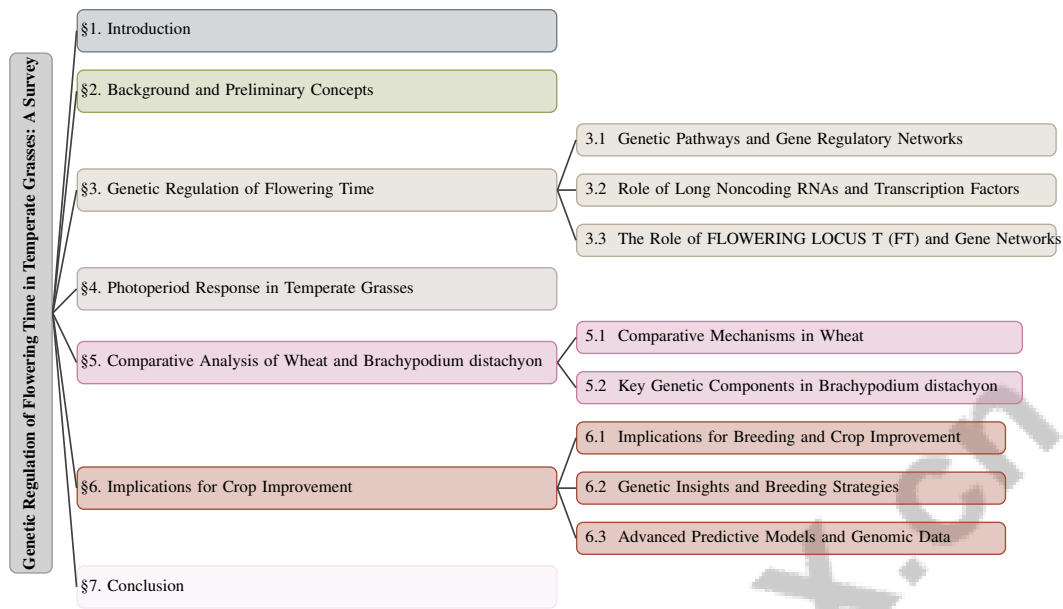


Figure 1: chapter structure

## 1.2 Structure of the Survey

This survey is systematically organized to provide an in-depth analysis of the genetic regulation of flowering time in temperate grasses, focusing on wheat and *Brachypodium distachyon*. It begins with an introduction that highlights the significance of this research area, particularly the role of genetic regulation in optimizing agricultural practices. Following the introduction, the background and preliminary concepts section establishes foundational knowledge on flowering time, genetic regulation, and photoperiod response, underscoring the relevance of wheat and *Brachypodium distachyon* as primary study subjects.

The core of the survey comprises several focused sections. The third section investigates the genetic mechanisms governing flowering time, emphasizing key genes and pathways, including long noncoding RNAs and transcription factors, as well as the specific roles of the FLOWERING LOCUS T (FT) gene and its associated networks. The fourth section addresses the photoperiod response in temperate grasses, detailing the contributions of photoreceptors and circadian clocks to these processes. A comparative analysis of wheat and *Brachypodium distachyon* is provided in the fifth section, elucidating the similarities and differences in their genetic and physiological mechanisms.

The sixth section explores implications for crop improvement, discussing the potential applications of genetic insights in breeding strategies and enhancing crop resilience. This section also considers the role of advanced predictive models and genomic data in improving breeding efficiency. The survey concludes by synthesizing key findings and reflecting on broader implications for future research and agricultural practices. The following sections are organized as shown in Figure 1.

## 2 Background and Preliminary Concepts

### 2.1 Relevance of Wheat and Brachypodium distachyon

Wheat and *Brachypodium distachyon* serve as pivotal models for studying genetic regulation in temperate grasses, each offering distinct insights into flowering time and photoperiod responses. Wheat's genetic complexity, involving genes such as PHOTOPERIOD1 (PPD1), CONSTANS1 (CO1), and CONSTANS2 (CO2), is crucial for understanding photoperiodic flowering responses [3]. Investigating allelic variation in vernalization and photoperiod response genes is essential for optimizing wheat phenology under climate change, thereby enhancing productivity [4]. The integration of genomic, genetic, and phenomic data is vital for developing wheat varieties with improved yield and resilience.

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In contrast, *Brachypodium distachyon* offers a robust framework for functional genomic studies due to its well-characterized genome [5]. It facilitates the exploration of genetic pathways and regulatory mechanisms, including the GRAS gene family [6]. The genetic diversity in *Brachypodium* allows for an in-depth study of regulatory elements like long noncoding RNAs (lncRNAs), which play critical roles in plant development and stress responses. Additionally, research on the auxin response factor (ARF) gene family and the effects of ambient temperature on *Brachypodium* enhances our understanding of plant adaptation to climate change. These attributes underscore the importance of wheat and *Brachypodium distachyon* as models for advancing genetic regulation studies in temperate grasses, with significant implications for improving crop resilience and productivity.

## 2.2 Role of Photoperiod Response

The photoperiod response is a critical adaptive trait in temperate grasses, regulating flowering time through day length perception. This involves complex interactions among photoreceptors like PHYC and circadian clock components, which transmit photoperiod information to key flowering regulators [7]. These molecular pathways and gene networks are essential for the transition from vegetative to reproductive development, highlighting their importance for agricultural applications.

Photoreceptors integrate light signals with circadian rhythms to regulate flowering, ensuring alignment with optimal environmental conditions [8]. In wheat, the interaction among genes such as PHOTOPERIOD1 (PPD1), CONSTANS1 (CO1), and CONSTANS2 (CO2) is crucial for modulating heading time in response to photoperiod changes, illustrating the genetic complexity involved [3]. Moreover, photoperiod influences not only flowering time but also plant responses to abiotic and biotic stresses via intricate signaling pathways [9].

Manipulating photoperiodic cues, such as through Speed Breeding (SB), can optimize growth rates and enhance flowering time regulation, providing valuable insights for crop improvement strategies [10]. Understanding the photoperiod response's role in flowering time regulation is thus vital for advancing genetic research and enhancing the resilience and productivity of temperate grasses amid changing climatic conditions.

In recent years, understanding the genetic regulation of flowering time has become increasingly important for agricultural advancements, particularly in temperate grasses. This review delves into the intricate pathways involved in this process, emphasizing the roles of various genetic components and regulatory mechanisms. Figure 2 illustrates the hierarchical structure of genetic regulation of flowering time, providing a visual representation of the complex interplay between genetic pathways, long noncoding RNAs, transcription factors, and the FLOWERING LOCUS T (FT) gene along with its associated networks. The figure not only highlights key genetic components but also showcases advanced techniques and gene network interactions that are crucial for comprehending and ultimately manipulating flowering time regulation for crop improvement. By integrating these insights, we can better appreciate the multifaceted nature of flowering time regulation and its implications for enhancing agricultural productivity.

## 3 Genetic Regulation of Flowering Time

### 3.1 Genetic Pathways and Gene Regulatory Networks

The regulation of flowering time in temperate grasses, such as wheat and *Brachypodium distachyon*, is governed by intricate genetic pathways and regulatory networks that respond to environmental cues like photoperiod and temperature. The auxin response factor (ARF) gene family in *Brachypodium* has been extensively analyzed, revealing crucial roles in flowering regulation [11]. CRISPR-Cas9 technology has been employed to generate null alleles in genes, including LAXA and cul4laxa double mutants, underscoring specific gene interactions critical for flowering control [12].

As illustrated in Figure 3, which depicts the hierarchical structure of genetic pathways and regulatory networks involved in flowering time regulation, the main concepts are categorized into gene families and mutants, photoperiod and circadian regulation, and predictive models and techniques. This figure highlights the intricate interplay of genetic elements and advanced methodologies in understanding and predicting plant development.

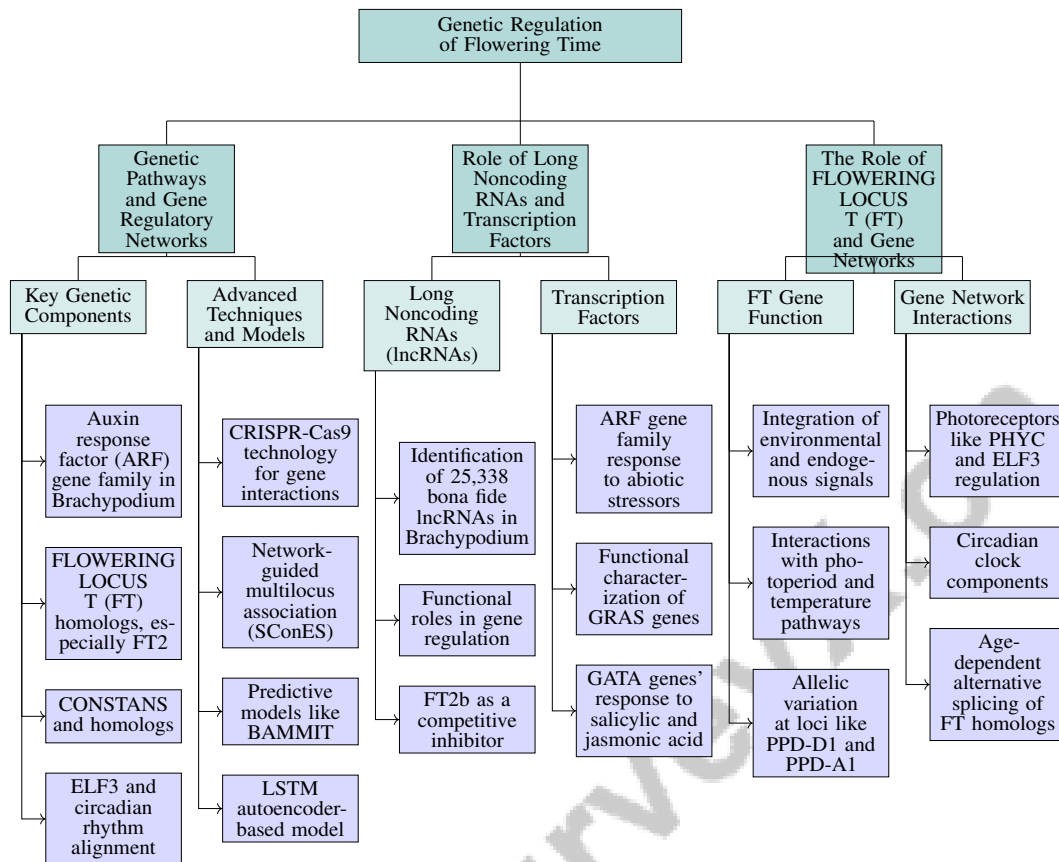


Figure 2: This figure illustrates the hierarchical structure of genetic regulation of flowering time in temperate grasses, focusing on genetic pathways, the role of long noncoding RNAs and transcription factors, and the FLOWERING LOCUS T (FT) gene and associated networks. It highlights key genetic components, advanced techniques, and gene network interactions crucial for understanding and manipulating flowering time regulation for crop improvement.

FLOWERING LOCUS T (FT) homologs, especially FT2, are pivotal in flowering regulation, with mechanisms like age-dependent alternative splicing producing isoforms with distinct roles [13]. CONSTANS and its homologs integrate photoperiodic signals essential for flowering timing [14], while ELF3 aligns photoperiod-induced flowering with circadian rhythms [8].

Advanced techniques such as network-guided multilocus association, exemplified by SConES, have identified SNP sets linked to phenotypes, enhancing our understanding of flowering time's genetic architecture [15]. Comparative studies between model species like *Arabidopsis* and cereals highlight both conserved and divergent regulatory mechanisms, reflecting evolutionary differences in flowering pathways [16].

Recent insights into photoperiod pathway components have enriched our understanding of plant adaptation to seasonal changes [17]. Integrating these genetic insights into predictive models, such as BAMMIT, which considers multiple interacting factors, offers a robust framework for predicting phenotypic outcomes and refining breeding strategies [18]. The Training Population Selection Method (TPSM) optimizes individual selection based on prediction error variance, enhancing genomic selection models [19]. An LSTM autoencoder-based model captures complex genomic data relationships, deepening our understanding of genetic pathways regulating flowering time [2]. These studies highlight the intricate interplay of genetic pathways and regulatory networks governing flowering time, presenting promising avenues for improving crop resilience and productivity.

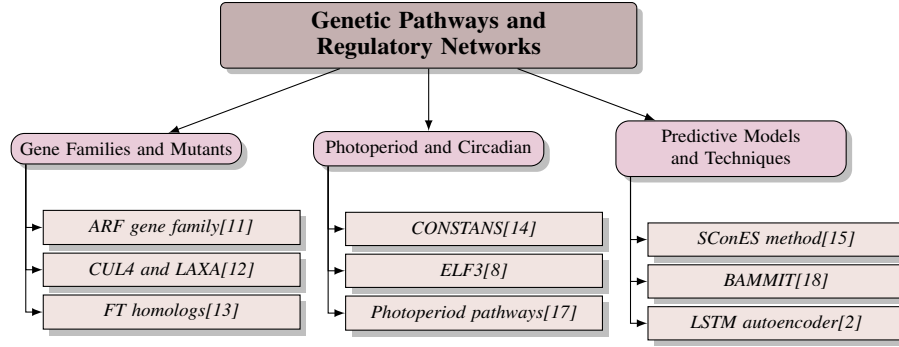


Figure 3: This figure illustrates the hierarchical structure of genetic pathways and regulatory networks involved in flowering time regulation. It categorizes the main concepts into gene families and mutants, photoperiod and circadian regulation, and predictive models and techniques, highlighting the intricate interplay of genetic elements and advanced methodologies in understanding and predicting plant development.

Method Name	Genetic Regulation	Environmental Response	Crop Improvement
GWARF[11]	Arf Gene Family	Abiotic Stressors	Stress Resistance
GRAS-CHAR[6]	GA Signaling	Abiotic Stresses	Improving Crop Resilience
GWE-EXP[5]	-	Stress Responses	Crop Improvement

Table 1: Overview of genetic regulation methods and their applications in environmental response and crop improvement, highlighting the role of ARF and GRAS gene families. The table summarizes key methodologies and their contributions to stress resistance and resilience in crops, illustrating the integration of genetic regulation into breeding strategies.

### 3.2 Role of Long Noncoding RNAs and Transcription Factors

Long noncoding RNAs (lncRNAs) and transcription factors are crucial to the genetic regulation of flowering time in temperate grasses, including wheat and *Brachypodium distachyon*. The identification of 25,338 bona fide lncRNAs in *Brachypodium* provides a valuable resource for understanding their functional roles in gene regulation [20]. These lncRNAs participate in regulatory processes, such as modulating flowering pathways; FT2b, for instance, acts as a competitive inhibitor, blocking the flowering initiation complex [13]. Table 1 provides a comprehensive summary of various genetic regulation methods, detailing their roles in environmental response and implications for crop improvement, thereby emphasizing the significance of transcription factors and lncRNAs in enhancing crop resilience.

The ARF gene family in *Brachypodium* is highly conserved and expressed in response to abiotic stressors, indicating its dual role in plant growth and stress resistance [11]. This underscores the importance of transcription factors in mediating environmental responses and developmental processes. Functional characterization of GRAS genes, including BdSLR1 and BdSLRL1, further clarifies the contributions of transcription factors and lncRNAs to genetic regulation [6].

Transcription factors also contribute to stress response pathways, as demonstrated by the responsiveness of 28 GATA genes in *Brachypodium* to salicylic acid and jasmonic acid, crucial for plant immunity and stress responses [21]. This illustrates the broader regulatory networks linking environmental signals to developmental outcomes.

The interplay between lncRNAs and transcription factors is vital for precise flowering time regulation, enabling plants to adapt to fluctuating environmental conditions. Integrating these genetic components into breeding strategies holds promise for enhancing crop resilience and productivity, as these regulatory elements offer potential targets for genetic manipulation aimed at improving crop traits [5].

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### 3.3 The Role of FLOWERING LOCUS T (FT) and Gene Networks

The FLOWERING LOCUS T (FT) gene is a key component in flowering time regulation, integrating environmental and endogenous signals in temperate grasses like wheat and *Brachypodium distachyon*. FT mediates flowering induction through interactions with genetic pathways responsive to photoperiod and temperature changes [13]. In wheat, allelic variation at loci such as PPD-D1 and PPD-A1 significantly influences phenological responses, impacting flowering timing and environmental adaptation [4].

In *Brachypodium*, FT's role is modulated by photoreceptors like PHYC, which acts as a flowering inducer by regulating ELF3 activity, highlighting functional divergences from Arabidopsis, where PHYC represses flowering [7]. The integration of FT with circadian clock components and photoreceptors forms a complex network that ensures flowering occurs under optimal conditions, aligning reproductive development with favorable environmental cues.

The regulatory network involving FT is essential for the transition from vegetative to reproductive growth, with FT homologs like FT2 playing a significant role. Mechanisms such as age-dependent alternative splicing lead to isoform production with distinct functions, refining flowering time regulation [13]. These interactions within the gene network reveal evolutionary adaptations of temperate grasses to their environments, offering insights into potential genetic targets for crop improvement.

Understanding the role of FLOWERING LOCUS T (FT) and its associated gene networks in regulating flowering time is vital for developing breeding programs aimed at enhancing crop resilience and productivity. This knowledge is particularly critical for synchronizing flowering with varying photoperiods, essential for optimizing environmental conditions. The discovery of mechanisms like FT alternative splicing, which influences flowering timing, highlights the complexity of flowering regulation and its implications for improving crop yields amid climate change [13, 16, 14]. Manipulating these genetic pathways may facilitate the development of varieties better adapted to changing climatic conditions, ensuring sustainable agricultural practices and food security.

## 4 Photoperiod Response in Temperate Grasses

### 4.1 Photoreceptors and Molecular Timers

Photoreceptors and molecular timers are integral to the photoperiod response in temperate grasses, orchestrating flowering time regulation. Phytochromes, such as PHYC in *Brachypodium distachyon*, detect light variations and activate molecular pathways that influence flowering by interacting with the ELF3 gene, which contrasts with its repressive role in *Arabidopsis* [7]. The circadian clock further integrates light signals with internal rhythms, ensuring synchronization of flowering with favorable environmental conditions. ELF3, a component of the evening complex, is pivotal in photoperiodic responses, coordinating with various flowering regulators to adjust timing according to day length [7].

The collaboration between photoreceptors like PHYC and molecular timers such as ELF3 is crucial for aligning flowering with seasonal day length variations, facilitating adaptation to different latitudes. This regulatory network underscores the evolutionary significance of photoperiodic responses in plant development [16, 7].

As illustrated in Figure 4, the figure highlights the roles of photoreceptors and molecular timers in regulating flowering time in temperate grasses, emphasizing the interactions between PHYC and ELF3, and their significance in evolutionary adaptation and crop improvement. Understanding these mechanisms offers valuable insights for breeding programs aimed at enhancing crop resilience and productivity, identifying genetic targets to improve flowering time regulation and adaptation to climate variability.

### 4.2 Photoperiod and Environmental Stress Responses

The interaction between photoperiod and environmental stress responses is vital for the adaptation and survival of temperate grasses. Photoperiod influences not only flowering time but also stress responses, with extended photoperiods enhancing stress resistance, indicating a complex interplay [9].

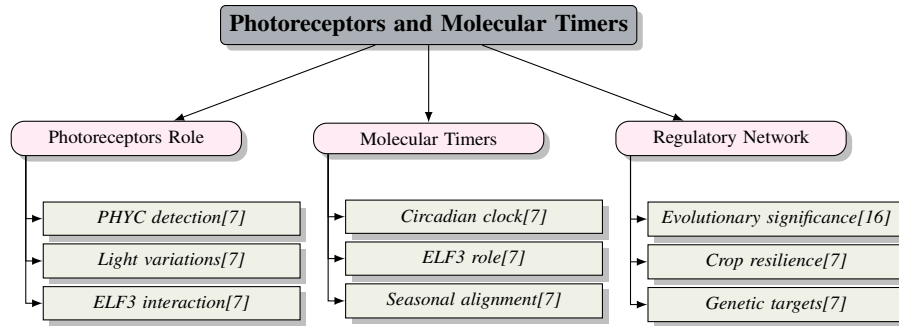


Figure 4: This figure illustrates the roles of photoreceptors and molecular timers in regulating flowering time in temperate grasses, highlighting the interactions between PHYC and ELF3, and their significance in evolutionary adaptation and crop improvement.

This relationship is evident in the expression profiles of auxin response factor (ARF) genes, which are responsive to abiotic stress and modulated by photoperiod changes [11].

Photoperiodic regulation of stress responses involves integrating environmental cues through multiple genetic pathways and regulatory networks, optimizing plant growth and development. Niu et al.'s study elucidates gene functions in stress responses, revealing how photoperiod enhances resilience in temperate grasses [22]. This understanding is critical for developing strategies to improve crop resilience against environmental stresses, a pressing concern amid climate change.

Manipulating photoperiodic cues can enhance stress tolerance in temperate grasses, presenting opportunities for crop improvement. By elucidating the genetic and physiological pathways linking photoperiod and environmental stress responses, breeders can develop varieties more resilient to abiotic stresses such as drought, freezing, and osmotic pressure. This advancement not only enhances crop adaptability to changing climates but also supports sustainable agricultural practices and food security by optimizing crop performance in diverse environments. Key regulatory genes, including *GIGANTEA* and *PHOTOPERIOD1*, are crucial for developing plant varieties that synchronize growth and reproductive cycles with seasonal changes, thereby bolstering resilience to environmental challenges [4, 3, 9, 14].

## 5 Comparative Analysis of Wheat and *Brachypodium distachyon*

### 5.1 Comparative Mechanisms in Wheat

Wheat's adaptation to environmental conditions is driven by genetic regulation and photoperiod response mechanisms involving key genes such as *PHOTOPERIOD1* (PPD1), *CONSTANS1* (CO1), and *CONSTANS2* (CO2), which modulate flowering time according to day length [3]. These genes function within an intricate network that integrates photoreceptor signals and circadian rhythms, optimizing flowering times to maximize yield. Allelic variations at loci like PPD-D1 and PPD-A1 are pivotal for wheat's phenological responses, enabling precise adaptation to diverse climates [4]. Integrating genomic, genetic, and phenomic data is crucial for advancing our understanding of these regulatory mechanisms and enhancing wheat varieties for improved yield and resilience.

Technological advances, including CRISPR-Cas9 gene editing, have facilitated detailed exploration of the genetic pathways governing flowering, allowing for targeted manipulation of key genes and insights into their roles within regulatory networks [12]. Predictive models, such as LSTM autoencoder-based models, further elucidate the complex relationships within genomic data, aiding in phenotypic outcome prediction and the development of superior wheat varieties [2].

Understanding the genetic regulation of photoperiod responses in wheat is vital for adaptation and productivity. By leveraging genetic insights and innovative techniques like speed breeding, researchers can develop wheat varieties tailored to withstand various environmental stresses. This approach accelerates the breeding cycle and optimizes phenological traits by exploiting allelic variations in key genes related to vernalization and photoperiod response, contributing to sustainable agriculture and food security amidst climate change and increasing global food demand [10, 4].



Figure 5 illustrates the key components of comparative mechanisms in wheat, highlighting genetic regulation, technological advances, and phenological adaptation. The first figure, "Plant Growth and Development," presents a dataset through graphs and box plots categorizing key growth metrics like heading time, leaf and branch numbers, seed set timing, and seed characteristics. These visualizations provide insights into mean values and variations. The second figure, "Accelerated plant growth and development under reduced lighting (22-hour photoperiod)," showcases plant responses under different lighting treatments in a controlled environment, facilitating a detailed examination of how extended photoperiods influence growth dynamics. Together, these analyses offer a robust framework for exploring wheat's growth patterns and developmental strategies, enhancing our understanding of plant biology and agricultural applications [23, 10]. This comprehensive visual representation underscores the interplay of genetic regulation, technological advancements such as CRISPR-Cas9 and LSTM models, and the critical role of phenological adaptation in wheat's response to environmental variability.

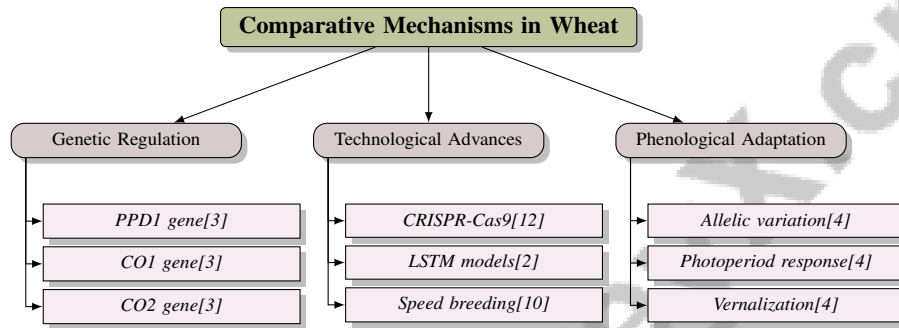


Figure 5: This figure illustrates the key components of comparative mechanisms in wheat, highlighting genetic regulation, technological advances, and phenological adaptation. Genetic regulation involves key genes such as PPD1, CO1, and CO2, which modulate flowering time. Technological advances include CRISPR-Cas9, LSTM models, and speed breeding, facilitating genetic exploration and crop improvement. Phenological adaptation focuses on allelic variations, photoperiod response, and vernalization, crucial for wheat's adaptation to diverse environmental conditions.

## 5.2 Key Genetic Components in *Brachypodium distachyon*

*Brachypodium distachyon* is a valuable model for studying genetic components involved in flowering time regulation and photoperiod response, offering insights relevant to its comparison with wheat. Central to this analysis are specific genes and pathways, such as the photoreceptor PHYC and the circadian clock component ELF3, which are crucial for modulating flowering time in response to photoperiod changes [7]. These components interact within a complex regulatory network to ensure flowering occurs under optimal conditions, reflecting the plant's adaptive strategies.

The genome-wide identification of 19 auxin response factor (ARF) genes in *Brachypodium distachyon* further elucidates the genetic landscape influencing flowering regulation [11]. These ARF genes play integral roles in the plant's response to environmental stimuli and developmental cues, underscoring their relevance in studies aimed at understanding growth and adaptation mechanisms. Comprehensive analysis of ARF gene expression provides a foundation for exploring their functional roles in flowering time regulation and stress responses.

Moreover, the dynamic gene content in *Brachypodium distachyon*, highlighted by Gordon et al., underscores the evolutionary implications of gene variation and adaptation [24]. This variability enhances the plant's ability to adapt to diverse environmental conditions, offering a genetic framework for studying evolutionary biology within temperate grasses.

## 6 Implications for Crop Improvement

### 6.1 Implications for Breeding and Crop Improvement

Research on genetic regulation of flowering time and photoperiod response in temperate grasses significantly impacts breeding strategies for crop resilience and yield enhancement. Liu et al.



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demonstrate the roles of CUL4 and LAXA in trait improvement for cereal crops, providing valuable insights for breeding programs [12]. The adaptability of photoperiodic networks, as discussed by Brambilla et al., facilitates the development of varieties suited to environmental changes, ensuring agricultural sustainability [16]. Furthermore, Roeber et al. identify GIGANTEA as a crucial gene for photoperiod-dependent stress responses, offering a target for increasing crop stress tolerance [9]. Whittal et al. emphasize allelic variations in wheat that enhance adaptability to climate change, supporting breeding efforts [4]. The integration of genomic data, as demonstrated by Alaux et al., enhances breeding strategies by enabling precise decision-making in wheat improvement [25].

Shavrukov et al. highlight early flowering traits as a drought escape mechanism, which can be harnessed in breeding to improve wheat resilience under water scarcity [1]. Advanced predictive models, such as the LSTM autoencoder by Wang et al., improve agricultural dataset predictions, aiding breeders in forecasting phenotypic outcomes and refining breeding strategies [2]. These genetic research advancements and predictive modeling offer promising avenues for enhancing crop resilience and productivity, addressing food security challenges amid global environmental changes.

## **6.2 Genetic Insights and Breeding Strategies**

Incorporating genetic insights into breeding strategies is crucial for improving crop resilience and yield in temperate grasses. Osnato et al. stress the importance of understanding photoperiodic controls for developing climate-resilient crops [17]. By analyzing genetic pathways governing flowering time, breeders can identify key components that enable plant adaptation to environmental shifts. Manipulating photoperiodic and vernalization pathways in wheat and *Brachypodium distachyon* can enhance phenotypic plasticity, creating varieties better suited to variable climates. Research shows that allelic variations at vernalization and photoperiod loci significantly influence phenological traits, optimizing crop performance across diverse environments [4, 23]. Identifying these variations provides targets for genetic selection, enhancing yield and stress tolerance.

Advanced genomic tools and predictive models refine genetic manipulation, improving breeding efficiency. These methodologies facilitate optimal training population selection, yielding reliable genetic breeding value estimates through genetic algorithms. By leveraging high-density genomic data and assessing genetic distances, breeders can enhance predictive accuracy across generations. This dynamic model-building process boosts genomic selection effectiveness and allows informed decisions regarding model recalibration to meet evolving breeding objectives [19, 26]. Incorporating genetic insights into predictive frameworks enables accurate phenotypic outcome forecasts, optimizing selection strategies for desired traits.

Utilizing genetic information in breeding strategies enhances crop resilience and supports sustainable agriculture. Developing climate-resilient crops with improved yield potential addresses challenges posed by global environmental changes, such as rising temperatures and altered photoperiods. This innovative approach aims to mitigate climate change's adverse effects on crop productivity, ultimately contributing to food security for future generations through advanced breeding techniques and genomic resources [2, 4, 16, 10, 23].

## **6.3 Advanced Predictive Models and Genomic Data**

The integration of advanced predictive models and genomic data is transforming breeding efficiency for temperate grasses, such as wheat and *Brachypodium distachyon*. Machine learning algorithms, like the LSTM autoencoder-based model, effectively capture complex genomic dataset relationships, enhancing phenotypic outcome predictions [2]. This model's ability to analyze large-scale genomic data empowers breeders to make informed decisions, optimizing selection strategies for desired traits.

Bayesian additive main effects and multiplicative interaction (BAMMIT) models refine genetic interaction understanding by accounting for multiple interacting factors, providing a robust framework for predicting phenotypic outcomes [18]. These models help identify key genetic components and their interactions, supporting the development of more resilient and productive crop varieties.

Network-guided multilocus association techniques, such as SConES, identify SNP sets linked to specific phenotypes while maintaining connectivity within biological networks [15]. This approach elucidates the genetic architecture underlying complex traits, informing targeted breeding strategies.

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The Training Population Selection Method (TPSM) optimizes training individual selection based on prediction error variance, enhancing genomic selection model reliability [19]. By improving genomic prediction accuracy, TPSM contributes to more efficient breeding programs, reducing time and resources required for developing improved crop varieties.

Collectively, these advanced predictive models and genomic data integration are pivotal in advancing breeding efficiency, offering powerful tools for developing climate-resilient crops with enhanced yield potential. The strategic implementation of advanced agricultural technologies, including speed breeding and machine learning algorithms, is essential for promoting sustainable farming practices. These innovations accelerate breeding cycles, enhance crop genetic improvement, and address challenges posed by global environmental changes. By optimizing resource use and enabling precise genotype-to-phenotype predictions, these technologies play a crucial role in securing food production for future generations while ensuring environmental resilience [10, 2, 25].

## 7 Conclusion

The exploration of genetic regulation in flowering time for temperate grasses, such as wheat and *Brachypodium distachyon*, reveals a nuanced interplay of conserved and unique genetic pathways influenced by environmental factors. This survey underscores the pivotal role of integrating genomic, genetic, and phenotypic data, which has been instrumental in advancing our understanding of these complex interactions and enhancing breeding methodologies. The observed effects of temperature on leaf initiation, seed maturation, and dormancy highlight the adaptive strategies of temperate cereals to climatic variations. Furthermore, the role of GRAS genes in *Brachypodium distachyon* provides valuable insights into genetic regulation, informing future research directions and agricultural practices. Emphasizing traits linked to early flowering and maturity emerges as a key strategy for mitigating the adverse effects of terminal drought, thereby enhancing wheat yield resilience. The enhancement of genetic diversity and investigation of allelic interactions are crucial for optimizing plant responses to diverse environmental conditions, offering promising avenues for future crop improvement initiatives.

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