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MOLECULAR-GENETIC CONTROL OF FLOWERING TIME IN SUNFLOWER AND THE SELECTION SIGNIFICANCE OF EARLY MATURITY

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Abstract. *This article provides a comprehensive review of the molecular mechanisms underlying the trait of early maturity in sunflower (Helianthus annuus L.) breeding, with a specific focus on the functional role of the FLO (FLORICAULA/LEAFY) gene family based on an analysis of contemporary literature. The study synthesizes global research findings to analyze nucleotide sequence variations within FLO genes (SNP polymorphism) and their direct impact on the acceleration of plant ontogeny. Furthermore, the genetic diversity of functional genotypes identified through sequencing technologies and their adaptability to diverse climatic conditions are comparatively evaluated. The review discusses the prospects of marker-assisted selection (MAS) strategies for enhancing the sunflower gene pool and the potential for the effective utilization of FLO genes in the breeding process. By interpreting global research results from the past decade, the functional significance of SNP (Single Nucleotide Polymorphism) markers arising from nucleotide substitutions within the FLO gene structure is scientifically substantiated.*

The study further elucidates the correlational links between the genetic diversity of sunflower lines from various phylogenetic groups and the adaptive potential of FLO genotypes.

The findings serve as a theoretical platform for adapting agricultural crops to climate change, advancing MAS technologies, and developing innovative genotypes with abbreviated vegetative periods.

Keywords: *sunflower, FLO genes, literature review, SNP polymorphism, sequencing, functional genotype, early maturity, genetic markers, marker-assisted selection (MAS).*

МОЛЕКУЛЯРНО-ГЕНЕТИЧЕСКИЙ КОНТРОЛЬ ВРЕМЕНИ ЦВЕТЕНИЯ И СЕЛЕКЦИОННОЕ ЗНАЧЕНИЕ СКОРОСПЕЛОСТИ У ПОДСОЛНЕЧНИКА

Аннотация. *В данном аналитическом обзоре на основе анализа современной литературы освещаются молекулярные механизмы, обеспечивающие признак скороспелости в селекции подсолнечника (Helianthus annuus L.), в частности, функциональная роль семейства генов FLO (FLORICAULA/LEAFY). В статье обобщены исследования, проведенные мировым научным сообществом, проанализированы изменения нуклеотидной последовательности в генах FLO (SNP-полиморфизм) и их влияние на ускорение онтогенеза растений. Также проведено сравнительное изучение генетического разнообразия функциональных генотипов, выявленных с помощью технологий секвенирования, и степени их адаптивности к различным климатическим условиям. В работе обсуждаются перспективы стратегий маркер-ассоциированной селекции (MAS) в*

улучшении генофонда подсолнечника и возможности эффективного использования генов FLO в селекционном процессе. Интерпретированы результаты глобальных исследований последнего десятилетия, научно обоснована функциональная значимость SNP-маркеров (Single Nucleotide Polymorphism), возникающих в результате нуклеотидных субституций в структуре генов FLO. В обзоре освещены корреляционные связи между генетическим разнообразием линий подсолнечника различных филогенетических групп и адаптивным потенциалом генотипов FLO. Выводы исследования служат теоретической платформой для адаптации сельскохозяйственных культур к климатическим изменениям, совершенствования технологий MAS и создания инновационных генотипов с коротким вегетационным периодом.

Ключевые слова: *подсолнечник, гены FLO, обзор литературы, SNP-полиморфизм, секвенирование, функциональный генотип, скороспелость, генетические маркеры, маркер-ориентированная селекция (MAS)*

Introduction

Sunflower (*Helianthus annuus* L.) is an annual oilseed crop belonging to the Asteraceae (Compositae) family and is considered one of the plants of significant economic importance in global agriculture. According to modern systematics, the genus *Helianthus* includes more than 70 wild and cultivated species, among which *H. annuus* is the most widespread and actively utilized species in the industry. The name of the plant is associated with its large, basket-like inflorescence resembling a solar disk, as well as the phenomenon of heliotropism—the characteristic of turning toward the sun—observed during its early growth stages.

According to evolutionary and archaeobotanical data, the sunflower is a native plant of the temperate regions of North America. Wild forms are widely distributed there, having been utilized since ancient times by indigenous peoples as a source of food and oil. Researchers note that the domestication of the sunflower began approximately 3,000–5,000 years ago in North America (Blackman et al., 2011).

Sunflower was introduced to Europe in the 16th century by Spanish explorers. Although initially cultivated as an ornamental plant, its significance as an oilseed crop was discovered later.

In the early 19th century, the development of oil extraction technology from sunflower seeds by D.S. Bokarev in Russia significantly elevated the crop's agricultural status. Consequently, the first oil processing plants were established in Russia, Ukraine, and the North Caucasus, marking the beginning of sunflower breeding on a scientific basis.

Throughout the 20th century, the sunflower gene pool was substantially enriched through the breeding efforts of scientists such as L.A. Zhdanov and V.S. Pustovoit. Specifically, varieties with high oil content, low hullability, and resistance to the sunflower moth and the parasite *Orobanche cumana* were developed. These achievements laid the foundation for sunflower to become a strategic global oilseed crop.

Today, sunflower is cultivated in many countries worldwide and holds a leading position in vegetable oil production. The sharp increase in global production volume over recent decades further strengthens its importance in economic and food security.

Simultaneously, under climate change conditions, traits such as early maturity, stress resistance, and adaptability are becoming priority directions in sunflower breeding.

One of the most pressing tasks facing modern agriculture, particularly in oilseed breeding, is the development of varieties and hybrids with a short growing season that yield stably under climate change and global warming. Increasing temperatures, uneven precipitation distribution, and intensifying drought stress are becoming limiting factors for the vegetation period. Therefore, the trait of early maturity holds particular importance as an adaptive characteristic in modern breeding.

Sunflower (*Helianthus annuus* L.) is one of the world's leading oilseed crops, and its productivity largely depends on the rate of phenological development and adaptability to environmental factors. Early maturity allows the plant to complete its generative development before the onset of extreme summer heat and drought, thereby ensuring yield stability.

Consequently, studying the genetic mechanisms governing flowering time has become a crucial area of molecular breeding in recent years.

From a molecular-genetic perspective, the transition from the vegetative to the generative stage (floral transition) is controlled by a complex regulatory network within the plant. In this system, genes known as "floral integrators"—FT (*Flowering Locus T*), TFL1 (*Terminal Flower 1*), and FLO/LFY (*FLORICAULA/LEAFY*)—play a central role. The FT gene often acts as a florigen signal, synthesized in the leaves and transported through the phloem to the apical meristem to activate the flowering program. Meanwhile, FLO/LFY genes convert this signal into a meristem identity program, ensuring the transformation of the vegetative meristem into a floral meristem (Blackman et al., 2010; Blackman et al., 2011).

It has been identified that several paralogs of the FT gene (HaFT1–HaFT4) exist within the sunflower genome, formed as a result of gene duplication. These paralogs differ functionally: while some accelerate flowering, others may delay it. For instance, HaFT4 plays a role in promoting flowering, whereas the HaFT1-D allele exhibits anti-florigen properties and delays flowering. Transgenic studies conducted on the model plant *Arabidopsis thaliana* have demonstrated that the strong expression of HaFT4 accelerates flowering, while HaFT1-D can suppress its effect (Blackman et al., 2010).

Recent genomic studies confirm that the multi-copy structure and allelic diversity of these gene families are associated with variations in flowering phenology. In particular, it has been noted that SNP polymorphisms within FLO/LFY genes may influence the rate of ontogenesis and photoperiodic response (Filippi et al., 2020).

Furthermore, during the domestication and long-term breeding of sunflower, strong selective sweep signals have been identified in loci determining flowering time, indicating that these genes were actively involved in artificial selection (Mangin et al., 2017). This confirms that the molecular control of flowering time is executed through a polygenic and hierarchical system.

Thus, the functional interactions between the FT–TFL1–FLO/LFY genes constitute the primary molecular mechanisms governing early maturity in sunflower. Identifying functional polymorphisms within these genes and applying them in marker-assisted selection (MAS**)** serves as a robust scientific foundation for developing resilient, early-maturing, and high-yielding genotypes under climate change conditions.

1. Functional Divergence of the FT Gene Family and Paralogs

Modern research indicates that the FT (*Flowering Locus T*) gene is one of the primary determinants governing flowering time in sunflower (Blackman et al., 2010; Blackman et al., 2011). The sunflower genome contains four paralogous copies of the FT gene (HaFT1, HaFT2, HaFT3, and HaFT4), which originated through gene duplication during the evolutionary process (Blackman et al., 2011). Such a multi-copy gene system likely enhances the sunflower's adaptability to diverse photoperiods (day length) and various climatic conditions (Blackman et al., 2010).

Crucially, FT paralogs do not perform redundant tasks but have undergone functional differentiation. For instance, HaFT4 is actively expressed in leaf tissues and is noted to accelerate flowering; HaFT2 also leans toward a promotional role, whereas HaFT3 is described as a pseudogene that has lost its original function (Blackman et al., 2011). In contrast, in certain genetic variants, HaFT1 may exert a delaying effect on flowering (Blackman et al., 2010).

This concept is further supported by transgenic experiments: in the *Arabidopsis thaliana* model, strong expression of HaFT4 accelerated flowering, while the co-expression of HaFT1-D and HaFT4 delayed it, demonstrating that HaFT1-D can suppress the activity of HaFT4 (Blackman et al., 2010). From a breeding perspective, this is vital: to enhance early maturity, it is not enough to simply select "accelerating" alleles; the presence of inhibitory alleles must also be taken into account (Blackman et al., 2011).

FLO/LFY Genes: The Meristematic "Generative Transition"

While FT genes are often regarded as the "signal" (florigen), FLO/LFY genes play a critical role as the primary regulators that trigger the meristem's flowering program (Maizel et al., 2005). As a transcription factor, LFY/FLO activates the transition of the vegetative meristem to the floral meristem and governs the identity of floral organs.

Reviews emphasize that changes in the nucleotide sequence of FLO/LFY genes, specifically SNP polymorphisms, can influence the rate of ontogenesis and the onset of flowering (Blackman et al., 2011; Filippi et al., 2020). The functional genotypes of FLO identified through sequencing have been linked to adaptability across different climatic conditions, and the prospects for utilizing FLO genes in marker-assisted selection (MAS) have been widely discussed (Filippi et al., 2020).

Such an approach allows for the selection of early maturity based on genotype rather than relying solely on phenotype, thereby increasing the precision and efficiency of the breeding process (Blackman et al., 2011).

2. QTL Mapping, Selective Sweeps, and FT/TFL1 Loci

It has been noted that an integrated candidate gene strategy has been employed to identify genetic loci determining flowering time during sunflower domestication and breeding processes.

Research conducted using this approach has highlighted five paralogs belonging to the FT and TFL1 gene families as the primary causal QTLs (Quantitative Trait Loci) controlling flowering time.

Furthermore, the detection of strong selective sweep signals within these paralogs in cultivated sunflower varieties indicates that they underwent active selection during domestication and long-term breeding—demonstrating their strategic importance throughout breeding history.

Consequently, it is emphasized that the molecular control of flowering time is manifested on two levels: first, at the level of gene families and paralogs through the duplication and functional differentiation of FT and TFL1 genes; and second, at the population level through genomic signatures formed as a result of QTL analysis and selective sweeps (Blackman et al., 2011; Mangin et al., 2017).

3. FLO/LFY Genes and the Rate of Ontogenesis

The rate of plant ontogenesis—specifically the pace of transition from vegetative to generative development—is a decisive factor in ecological adaptability and yield formation. At the molecular level, this process is controlled by regulatory genes that govern meristem activity, among which the FLO/LFY (FLORICAULA/LEAFY) genes are recognized as the primary "master-regulator" genes determining floral meristem identity (Weigel & Nilsson, 1995; Maizel et al., 2005). The LFY gene was first described in the model plant *Arabidopsis thaliana*, and its function is linked to initiating the transformation of the vegetative meristem into a floral meristem.

When LFY is activated, the meristem switches from a "leaf-producing mode" to a "floral organ-producing mode"; hence, LFY is often regarded as the "key gene triggering flowering." The FLO gene is a homolog of LFY and performs a similar function in plants belonging to the Asteraceae family, including sunflower (Maizel et al., 2005).

In sunflower, FLO/LFY genes form a functional network with FT genes that determine flowering time. The FT protein, synthesized in the leaves as a florigen signal, migrates to the apical meristem, where FLO/LFY converts this signal into a meristem identity program, effectively launching the flowering process. Therefore, the coordinated expression between these genes is a crucial mechanism determining the rate of ontogenesis (Blackman et al., 2011). Recent molecular studies indicate that SNP (Single Nucleotide Polymorphism**)** variations observed in FLO genes can directly affect the pace of ontogenesis. Small substitutions in the nucleotide sequence can alter gene expression levels, protein function, or the activity of regulatory regions, resulting in the acceleration or delay of flowering onset (Filippi et al., 2020).

Functional genotypes of FLO identified through sequencing technologies have also been linked to adaptability across various climatic conditions. It has been observed that early-maturing genotypes exhibit early and stable expression of FLO genes, whereas in late-maturing genotypes, the activation of these genes may be delayed. This demonstrates that FLO genes act as fine-tuned regulators of ontogenesis speed (Filippi et al., 2020). From a breeding perspective, FLO/LFY genes are highly promising as they directly influence the formation of the flowering meristem.

Utilizing SNP markers linked to FLO genes in marker-assisted selection (MAS) programs allows for the prediction of early maturity at the genotypic level, providing faster and more reliable results compared to phenotypic evaluation (Blackman et al., 2011).

Furthermore, FLO/LFY genes are associated with ecological adaptability. In regions with harsh climates, early flowering and a short ontogenesis period provide the plant with a "stress escape" strategy. Consequently, it is natural that functional polymorphisms in FLO genes undergo selection during evolutionary and breeding processes (Weigel & Nilsson, 1995; Blackman et al., 2011). In summary, FLO/LFY genes are central regulators of ontogenesis rate, flowering time, and ecological adaptability in sunflower, and studying their molecular diversity serves as a vital

scientific foundation for developing early-maturing, climate-resilient, and high-yielding genotypes.

4. Gene Duplication and Selective Sweeps

The evolution of plant genomes is largely determined by gene duplication processes.

Duplication results in additional copies of genes, which over time can evolve in different directions to acquire new functions (neofunctionalization) or partition existing functions among themselves (subfunctionalization). Consequently, gene duplication is regarded as a primary mechanism of adaptive evolution (Lynch & Conery, 2000). In sunflower, it has been demonstrated that the gene families governing flowering time, specifically FT and TFL1, expanded precisely through duplication. The existence of multiple FT paralogs enhances the sunflower's adaptability to various photoperiodic and climatic conditions, while the divergence in the expression profiles and functional directions of each paralog ensures precise genetic control over flowering time (Blackman et al., 2011).

During domestication and long-term breeding, beneficial alleles undergo artificial selection, a process that leaves selective sweep signatures in the genome. A selective sweep is characterized by a reduction in genetic diversity in genomic regions adjacent to a beneficial allele due to its rapid spread within a population; in other words, strong selection causes the segment of the genome surrounding the "beneficial" allele to become fixed as well (Maynard Smith & Haigh, 1974). QTL analysis of loci controlling flowering time in sunflower has shown that several paralogs of the FT and TFL1 families are the primary causal loci. The identification of selective sweep signatures in the regions where these genes are located, particularly in cultivated sunflower varieties, confirms their significant role in breeding history (Blackman et al., 2011; Mangin et al., 2017).

This phenomenon is also understandable from an evolutionary perspective: while flowering time in wild sunflowers varies across a wide range to adapt to natural environments, varieties with uniform phenological traits—such as early and synchronous flowering—are preferred in agricultural settings. As a result, the alleles providing these traits are repeatedly selected during breeding and become dominant in the population (Blackman et al., 2011). Gene duplication and selective sweeps function as interconnected processes: duplication creates the genetic "raw material," while selection filters and strengthens beneficial variants. This leads to the formation of complex gene networks governing flowering time, causing cultivated sunflowers to develop a phenological profile distinct from their wild ancestors during domestication (Lynch & Conery, 2000; Blackman et al., 2011).

Modern genomic studies utilize SNP density, haplotype blocks, and nucleotide diversity metrics to identify selective sweeps. Such analyses allow for the "reading of breeding history at the genomic level," making the detection of selective sweeps important not only for fundamental evolutionary research but also for optimizing practical breeding programs (Mangin et al., 2017).

Practically, genes identified with selective sweep signatures are considered priority candidates for breeding because they have "proven" their agronomic utility through historical selection. Therefore, genomic regions associated with flowering genes such as FT, TFL1, and FLO require special attention in marker-assisted selection (MAS) (Blackman et al., 2011).

In summary, while gene duplication created the genetic diversity controlling flowering time in sunflower, selective sweeps acted as one of the primary evolutionary forces that sorted beneficial variants from this diversity to shape the cultivated sunflower phenotype (Lynch & Conery, 2000; Blackman et al., 2011).

Marker Technologies: SSR and SNP

In modern plant breeding, molecular markers are essential tools for determining genetic diversity, identifying loci associated with important agronomic traits, and accelerating the targeted selection process. This is because they provide stable genetic information that is less dependent on environmental influences compared to phenotypic evaluation (Gupta & Varshney, 2000; He et al., 2014). Particularly in cross-pollinated crops like sunflower (Helianthus annuus L.), controlling genetic purity, reliably identifying parental lines, and confirming the authenticity of hybrids are key factors determining breeding efficiency. Molecular marker technologies offer a significant advantage in performing these tasks (Mandel et al., 2011).

SSR (Simple Sequence Repeat) markers, due to their high polymorphism, co-dominant inheritance, and reproducibility, are widely used in sunflower for genetic mapping, studying population structure, and verifying the genetic purity of hybrids. They allow for the precise differentiation of parental forms based on allele sizes (Gupta & Varshney, 2000). However, in recent years, with the advancement of high-throughput sequencing technologies, SNP (Single Nucleotide Polymorphism) markers have become the dominant platform for genome-wide analysis, association mapping (GWAS), and genomic selection programs. SNP markers are densely distributed throughout the genome, enabling high-precision analysis of complex traits (He et al., 2014).

Large-scale SNP panels and high-density genetic maps developed for the sunflower genome facilitate the identification of QTLs associated with critical traits such as flowering time, oil content, and disease resistance (Mandel et al., 2011). Thus, SSR and SNP markers serve as complementary platforms in sunflower breeding, creating a robust molecular foundation for assessing genetic diversity and effectively implementing Marker-Assisted Selection (MAS) and genomic selection strategies.

SSR Markers: High Polymorphism and Identification Precision

SSR (Simple Sequence Repeat) or microsatellite markers are based on short repetitive nucleotide motifs (e.g., di-, tri-, or tetranucleotide repeats) within the genome. Due to their co-dominant inheritance, high polymorphism, and high reproducibility, they are extensively utilized in molecular breeding. SSR markers clearly indicate differences between genotypes through variations in allele fragment length and allow for the differentiation between heterozygous and homozygous states (Gupta & Varshney, 2000; Semagn et al., 2006).

Research in sunflower has demonstrated that genetic inheritance between parental lines and hybrids can be confirmed with high precision using SSR markers. Markers with a high PIC (Polymorphism Information Content) coefficient, such as ORS-453 and CO-306, have been noted for their high informativeness in genotype differentiation (Tang et al., 2003). SSR markers perform several vital functions in breeding, including verifying hybrid authenticity, monitoring genetic purity, characterizing gene pool collections, and optimizing the selection of parental pairs.

Therefore, they are regarded as reliable diagnostic tools in sunflower seed production and hybrid breeding (Gupta & Varshney, 2000).

However, SSR markers also have certain limitations. Their relatively narrow coverage of the genome, the limited number of available markers, and their lower compatibility with high-throughput genotyping platforms compared to SNP markers have somewhat reduced their share in modern genomic research (Semagn et al., 2006).

5. SNP Markers: Genome-Wide High Precision

SNP (Single Nucleotide Polymorphism) markers are based on variations at the level of a single nucleotide within the genome. As the most abundant type of genetic polymorphism, they are widely distributed across the entire genome, making them an ideal molecular tool for high-resolution genetic analysis (Rafalski, 2002). Using modern genotyping platforms—such as SNP-arrays, genotyping-by-sequencing (GBS), and Next-Generation Sequencing (NGS) technologies—it is possible to analyze thousands or even millions of SNP loci simultaneously, enabling the study of complex traits at the genomic scale (He et al., 2014).

SNP genotyping studies conducted on sunflower populations show that long-term breeding and domestication processes have significantly altered the molecular structure of populations.

Specifically, a reduction in allelic diversity, an increase in homozygosity, and genetic differentiation between populations are interpreted as genomic signatures of breeding pressure (Mandel et al., 2011). The extensive genome coverage, high precision, stability, and compatibility of SNP markers with automated high-throughput analysis, as well as QTL mapping and Genome-Wide Association Studies (GWAS**)**, have established them as the priority platform in modern breeding (Rafalski, 2002; He et al., 2014).

Consequently, SNP markers play a vital role in identifying complex traits such as early maturity, flowering time, and abiotic stress resistance, and are widely utilized in genomic selection and marker-assisted selection programs (Filippi et al., 2020).

Integrated Approach and Prospects for MAS

In contemporary breeding practice, the integrated use of SSR and SNP markers is regarded as one of the most effective strategies. While SSR markers are convenient for rapid identification, hybrid authenticity testing, and genetic purity monitoring, SNP markers provide a high-precision platform for genome-wide association studies, QTL mapping, and genomic selection. As a result, the combined application of these two marker types increases the precision and efficiency of the breeding process (Collard & Mackill, 2008; He et al., 2014).

The use of markers linked to genes governing flowering time in Marker-Assisted Selection (MAS) programs significantly shortens the breeding cycle, allows for the identification of promising genotypes at early stages, and reduces reliance on phenotypic evaluation. This is a crucial advantage, especially for complex traits requiring multi-environment trials (Collard & Mackill, 2008). In the context of climate change, molecular markers are becoming strategic tools for developing rapidly adaptable, early-maturing, and stress-resistant genotypes, as they allow breeding decisions to be substantiated with genomic evidence (He et al., 2014; Filippi et al., 2020).

In summary, SSR and SNP markers serve as a solid scientific foundation for effectively managing genetic resources in sunflower breeding, targeted selection for critical traits like early

maturity and flowering time, and creating a sustainable long-term gene pool. Their importance is expected to grow further as they become more integrated with genomic selection in the future (Filippi et al., 2020).

Conclusion

This literature review provides a comprehensive overview of the molecular-genetic control of flowering time in sunflower (*Helianthus annuus* L.) and the breeding significance of the early maturity trait. The analysis demonstrates that the regulation of flowering time occurs through a multigenic and interconnected regulatory system, in which FT, TFL1, and FLO/LFY genes play a central role. In particular, the duplication of the FT gene family and the functional differentiation of its paralogs emerge as a vital evolutionary mechanism that ensures the sunflower's adaptability to diverse photoperiodic and climatic conditions.

The FLO/LFY genes, acting as "master-regulators" of the transition to generative development, play a decisive role in determining the rate of ontogenesis and the onset of flowering. Modern genomic research confirms that SNP polymorphisms in these genes significantly impact the pace of ontogenesis and are closely linked to early maturity and ecological adaptability.

Furthermore, QTL analysis and selective sweep signatures indicate that the genes controlling flowering time were actively selected during domestication and long-term breeding, confirming the targeted formation of phenological traits in cultivated sunflower. While gene duplication provided the genetic diversity, selective sweeps emerged as one of the primary evolutionary forces that fixed agronomically beneficial variants from within this diversity.

Molecular marker technologies, specifically SSR and SNP platforms, provide powerful instruments for identifying and controlling loci associated with flowering time and early maturity.

While SSR markers are effective for genetic purity and identification, SNP markers provide high-precision analysis at the genomic scale. Their integrated application enhances the efficiency of Marker-Assisted Selection (MAS) and shortens the breeding cycle. Overall, an in-depth study of the molecular-genetic foundations of flowering time establishes a robust scientific platform for developing early-maturing, climate-resilient, and high-yielding sunflower varieties.

Future Perspectives

In recent years, the rapid advancement of plant genomics and bioinformatics has enabled a deeper exploration of the genetic mechanisms governing flowering time and early maturity in sunflower. In the future, utilizing high-precision sequencing technologies (whole-genome sequencing, pan-genome analysis) to fully map the allelic diversity of the FT, TFL1, and FLO/LFY gene families, identify their regulatory regions, and isolate functional variants remains a priority.

Additionally, transcriptomic epigenomic and approaches are expected to play a crucial role in understanding how flowering time genes respond to environmental factors. For instance, the fine-tuned regulation of gene expression through DNA methylation, chromatin structure, and small RNAs may reveal additional regulatory layers in the formation of the early maturity phenotype.

In the coming years, genomic selection (GS) and prediction models based on artificial intelligence could significantly accelerate breeding processes.

By integrating large-scale phenotypic and genotypic data, it will be possible to predict complex traits such as flowering time, ontogenesis rate, and stress resistance with high accuracy, reducing dependence on traditional multi-year field trials.

Moreover, gene-editing technologies (CRISPR/Cas) allow for the targeted modification of flowering genes to create new phenological types. This approach is particularly promising for developing flexible, early-maturing, and stable genotypes for regions with extreme climate variability. Under climate change, the focus of sunflower breeding should be on maintaining the balance between early maturity, yield, and stress resistance. Therefore, future research should be directed toward studying multigenic regulatory networks through a systems biology approach.

In conclusion, the integration of molecular genetics, genomics, and digital breeding technologies is expected to elevate sunflower breeding to a new level, contributing to the creation of resource-efficient, climate-resilient, and high-productivity varieties.

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