

Regulatory Mechanisms of Gene Expression in *Brassica napus*: From Development to Stress Adaptation

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Abstract As an important oil crop in the world, *Brassica napus* occupies a key position in agricultural production and industrial applications due to its excellent oil accumulation capacity and wide ecological adaptability. This study systematically expounded the molecular mechanism of gene expression regulation in this crop, focusing on its regulatory network in growth and development and environmental stress response. Studies have shown that transcription factor families such as MYB, bHLH and WRKY finely regulate the adaptive response of rapeseed to abiotic stresses such as high temperature, low temperature and drought through complex synergistic effects. At the same time, epigenetic mechanisms such as DNA methylation and histone modification constitute the second guarantee system for gene expression regulation. High-throughput omics technology and CRISPR/Cas9 genome editing technology have successfully revealed key gene networks related to stress resistance, seed development and flowering regulation. However, due to the special complexity of the allotetraploid genome of *Brassica napus* and the intricate interactions between growth and development and stress response pathways, related research still faces many challenges. This study emphasizes that by integrating multi-omics analysis methods and synthetic biology strategies to establish a precise gene regulation system, it will provide a theoretical basis and technical support for breeding new rapeseed varieties with high and stable yields. This study not only has guiding significance for the genetic improvement of *Brassica napus*, but also provides a reference for the stress-resistant breeding of other important crops.

Keywords Gene expression regulation; *Brassica napus*; Stress adaptation; Transcription factors; Epigenetic regulation

1 Introduction

As an important oil crop in the world, *Brassica napus* L. occupies a key position in agricultural production and industrial applications. As the world's second largest source of vegetable oil, this crop not only provides high-quality edible oil for humans, but also has wide application value in industrial fields such as biofuels and cosmetics (Liu et al., 2018; Kourani et al., 2022). Its excellent environmental adaptability, especially its tolerance to adverse conditions such as low temperature stress and nutrient deficiency, is an important guarantee for maintaining high and stable yields (Hussain et al., 2022).

At the molecular level, gene expression regulation in rapeseed (*Brassica napus*) shows high complexity. Studies have found that multiple transcription factor families such as WRKY, MYB and NAC synergistically regulate the ability of plants to cope with adverse environmental conditions such as temperature stress by constructing intertwined regulatory networks (Feng et al., 2019). It is worth emphasizing that the interaction between the two-component system (TCS) genes and the cytokinin signaling pathway plays a key regulatory role in maintaining the dynamic balance between plant growth and stress response (Liu et al., 2023).

This study aims to explore the multi-level mechanism of gene expression regulation in rapeseed, focusing on the synergistic effects of transcription factor regulatory networks and signal transduction pathways in morphological developmental plasticity and environmental adaptability. At the same time, the functional specificity of these regulatory factors in different temporal and spatial expression backgrounds is analyzed, and how they precisely control plant physiological activities is revealed. This study helps to enrich people's molecular understanding of rapeseed's stress resistance mechanism, provide potential targets for future molecular design breeding, and

systematically analyze its regulatory network to provide a useful reference for the cultivation of high-yield and stress-resistant varieties and the genetic improvement of other crops.

2 Basics of Gene Expression and Regulation in Plants

2.1 Complex network of transcriptional regulation

The plant genome contains a highly sophisticated transcriptional regulatory system. The results of whole-genome sequencing of rapeseed showed that about 6 061 genes have potential transcriptional regulatory functions, of which about one-third have significant changes in expression when subjected to low temperature stress (Waseem et al., 2024). MYB transcription factors often form functional modules with bHLH proteins, recognize specific cis-acting elements, and then activate target gene expression. NAC family members show special DNA binding ability and play an important role in chitin-mediated signaling pathways. It is worth noting that regulatory SNP (rSNP) variations in the genome can significantly change the binding affinity of transcription factors, thereby affecting a variety of agronomic traits including oil content (Klees et al., 2021).

2.2 Precision mechanism of post-transcriptional regulation

From the beginning of mRNA transcription, its fate is strictly controlled by a series of mechanisms. Under boron deficiency conditions, the special 5'-UTR structure of the BnaC4.BOR1;1c gene significantly improved the stability of its mRNA, almost doubling its expression level (Wang et al., 2021), which facilitated the effective absorption and utilization of boron. On the other hand, alternative splicing also plays an irreplaceable role in regulating protein diversity. A gene can produce multiple protein isoforms through different splicing methods, thus giving plants stronger environmental adaptability (Kourani et al., 2022).

2.3 Dynamic regulation of protein synthesis

Protein translation is not just a linear translation process of genetic information. The 5'-UTR region of some mRNAs in rapeseed contains regulatory elements that can recruit different initiation factors, resulting in a more than ten-fold difference in translation efficiency (Wang et al., 2021). The post-translational modification process of proteins is more complex and highly dynamic. For example, phosphorylation can quickly turn on or off protein activity; ubiquitination determines its degradation rate and half-life; and acetylation can change the selectivity of protein-protein interactions (Zhang et al., 2020). These modifications work together to build a flexible regulatory system that allows plants to respond precisely to changing environments.

3 Key Transcription Factors in Developmental Regulation

3.1 Multifunctional regulation of the AP2/ERF family

In *Brassica napus*, members of the AP2/ERF family are considered to be "molecular hubs" in complex regulatory networks. Phylogenetic studies have divided them into five subfamilies with different functions, each of which plays a key role in specific developmental or stress processes (Ghorbani et al., 2020). In root tissues, the expression of these genes is particularly active, suggesting that they have important functions in root development (Owji et al., 2017). It is worth noting that after plants encounter salt stress, the expression of ERF subfamily members can be significantly upregulated in just 6 hours, with an increase of more than eight times. Not only that, these proteins also have the ability to integrate environmental signals with plant hormone (such as abscisic acid) pathways, showing cross-level regulatory characteristics, highlighting their versatility in stress response.

3.2 Regulation of reproductive development by MADS-box genes

MADS-box genes are like precisely chimeric "molecular gears" that participate in and drive the entire reproductive development process of rapeseed. Type I members undertake basic regulatory tasks, while type II is particularly critical in the formation of floral organs with its fine regulatory ability (Song et al., 2023). Among them, the role of BnaAGL11 runs through the flowering to senescence stage, not only affecting the morphological construction of flowers, but also participating in the regulation of leaf senescence (He et al., 2022). Whole genome analysis found that more than 40% of MADS-box genes have undergone functional differentiation through the polyploidization process. This genetic innovation has greatly enriched the ability of rapeseed to adapt to different ecological environments (Figure 1) (Wu et al., 2018).

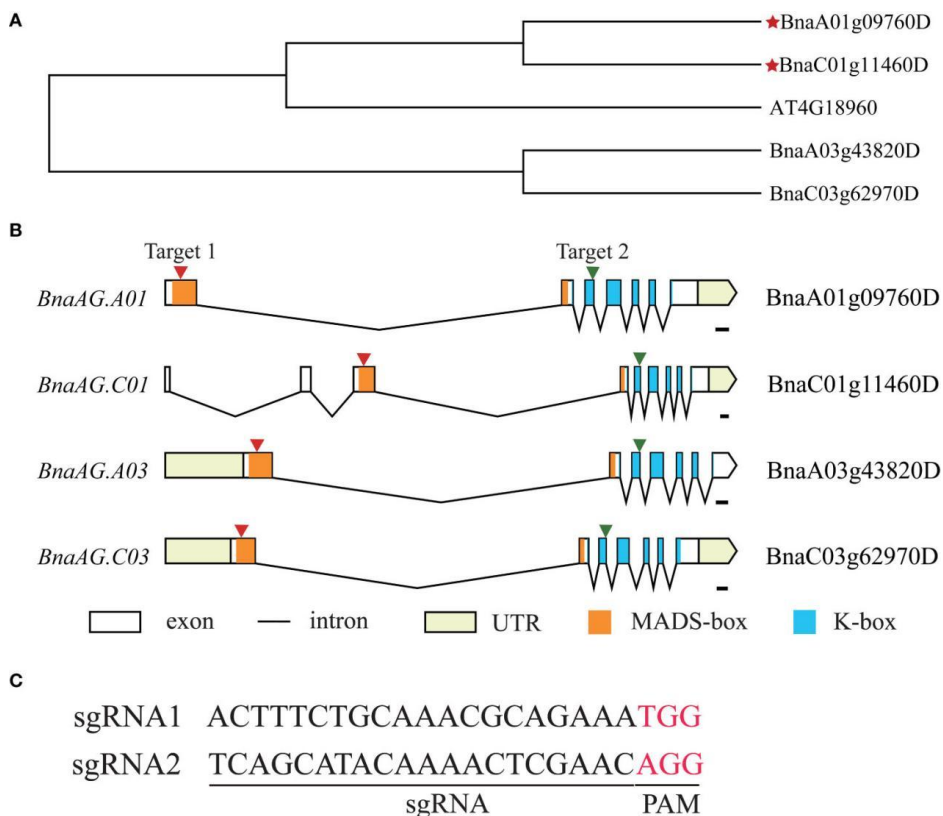


Figure 1 Construction of vectors for targeting *BnaAG* homologous genes (Adopted from Song et al., 2023)

Image caption: (A) NJ tree of *BnaAG* homologous genes in *B. napus* and *A. thaliana*; The red stars represent the *BnaAG* homologs of *B. napus* closely related to the *AG* gene in *A. thaliana*; (B) Gene structure, conserved domain, and distribution of sgRNA1 and sgRNA2 targeting four homologous genes of *BnaAG*; The black line represents introns, and the black boxes represent the exon; The red arrows indicate the location of sgRNA targets on the exon, and the orange and blue boxes represent MADS-box and K-box domains, respectively; (C) Sequence information of two sgRNA, PAM is indicated in red (Adopted from Song et al., 2023)

3.3 Developmental regulation of MYB and bHLH families

When the temperature drops sharply, multiple members of the bHLH family can be rapidly activated, and their expression levels in cold-resistant rapeseed varieties can be increased to more than 15 times the original in a short period of time (Waseem et al., 2024). The complementary MYB transcription factors show greater flexibility in regulatory strategies. For example, BnMRD107 can synchronously regulate osmotic stress-related genes and participate in the interactive regulation of multiple hormone signals (Li et al., 2021). These two transcription factor families jointly construct a highly plastic signal regulatory network that can dynamically adjust its regulatory strategy according to different developmental stages of plants or changes in the external environment: the seedling stage is mainly based on cell proliferation, while the reproductive growth period focuses on the regulation of floral organ differentiation and stress response.

4 Epigenetic Modifications in *Brassica napus*

4.1 DNA methylation and gene silencing

High-density methylation in the transposable element region forms a molecular barrier that effectively inhibits the expression of neighboring genes (Xiao et al., 2023). This silencing mechanism is particularly prominent in allopolyploid genomes. When the two parental genomes merge, DNA methylation is like a shrewd referee, selectively "silencing" the rRNA genes of a certain ancestral genome (Zj and Pikaard, 1997). The methylation level of the promoter region shows an interesting correlation with the gene expression: mild methylation may promote expression, while excessive methylation leads to gene silencing (Hu et al., 2023). This dynamic balance enables plants to flexibly respond to environmental challenges (Figure 2).

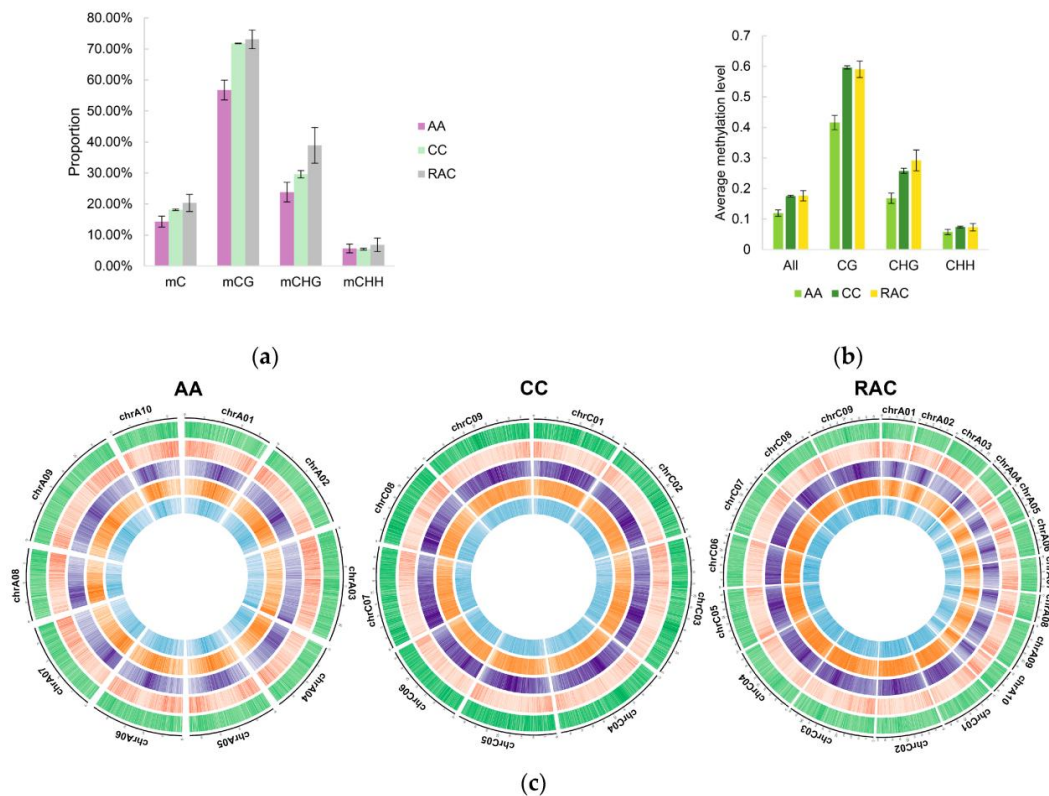


Figure 2 Methylation sites in *B. napus* and its diploid parents have been identified and analyzed (Adopted from Hu et al., 2023)

Image caption: (a) The percentage of methylated cytosine in *B. rapa* (AA), *B. oleracea* (CC), and *B. napus* (RAC); (b) Average CG, CHG, and CHH methylation levels in *B. napus* and its diploid parents; (c) Cisco map of methylation levels in *B. napus* and its diploid parents; GC content (green), gene density (red), CG methylation level (purple), CHG methylation level (orange), and CHH methylation level (light blue) are displayed sequentially from the outside in; The level or density is greater the darker the color is. The ordinate of Figure A indicates the proportion of methylated cytosine (e.g., mCG proportion = mCG/CG); Figure B shows the average methylation level of the whole genome (Adopted from Hu et al., 2023)

4.2 Regulatory network of histone modification

In chromatin regulation, various histone modifications together constitute a complex and precise "code system". For example, H3K4me3 modification is often regarded as an activation sign, like a "green signal light" to guide transcription initiation; in contrast, H3K27me3 modification plays an inhibitory function, like a "red light" to prevent unnecessary gene expression (Li et al., 2021). During the microspore embryogenesis stage, histone acetylation levels can increase to three to five times the normal level, significantly accelerating the development of the embryo (Rodríguez-Sanz et al., 2014). Interestingly, when treated with histone deacetylase inhibitors, the originally silent rRNA genes will be "reactivated", suggesting that this regulatory mechanism has a high degree of plasticity and reversibility (Zj and Pikaard, 1997). In addition, in some genomic regions, both activation and inhibition modifications coexist, forming a "bivalent mark", which provides more flexible options for cell fate decisions (Zhang et al., 2020).

4.3 Regulatory role of non-coding RNA

In gene regulation, small molecule RNA, especially siRNA, plays a role of precise navigation. They can effectively guide DNA methyltransferases to locate specific target sequences, thereby initiating or maintaining methylation silencing (Xiao et al., 2023). These small RNA molecules not only act alone, but also coordinate with histone modifications to jointly regulate gene expression, forming a highly coordinated regulatory system (Zhou, 2024). Although the study of non-coding RNA in rapeseed is still in its early stages, studies have shown that it has an important function in stress response. Taking drought as an example, the expression levels of some siRNAs change rapidly at the beginning of stress, which helps to adjust the expression of related genes, thereby improving the environmental adaptability of plants.

5 Molecular Regulatory Mechanisms of Flowering and Seed Development

5.1 Multi-level regulatory network of flowering time

The initiation of flowering time often originates from the synergistic accumulation of photoperiod and hormone levels in plants. Once these signals reach a certain critical point, the plant's "developmental clock" begins to count down. For example, WRKY184 is an important transcription factor that controls flowering initiation by regulating key genes such as FT and LFY (Yang et al., 2020). Genome-wide association analysis also identified 12 stable QTL hotspots, three of which are highly homologous to known flowering-related genes in Arabidopsis (Li et al., 2018). In addition, epigenetic modifications also add a temporal regulatory dimension to flowering regulation. For example, during the vernalization stage, the promoter regions of some genes that inhibit flowering show gradually enhanced DNA methylation, which eventually releases the inhibition of flowering, thereby completing a transitional developmental transition (Schiessl et al., 2014).

5.2 Genetic regulatory program of seed development

In the early stage of embryonic development, the transcription factor BZIP11 plays the role of a "master control center". Once its function is lost, the embryo will not be able to successfully pass the spherical stage, and the development process will be terminated (Khan et al., 2021). Entering the middle stage of development, the expression of fatty acid synthesis-related genes in seeds is significantly enhanced, and its expression level can be increased by more than 50 times (Niu et al., 2009). miR394 plays the role of a "quality regulator" in this process. It selectively inhibits enzyme genes with low synthesis efficiency, thereby improving the overall efficiency of lipid accumulation (Song et al., 2015). At the same time, the regulatory module composed of WRI1 and LAFL family members has a significant effect on oil content, and the expression levels of the two are highly positively correlated with oil accumulation ($r = 0.82$, $P < 0.01$) (Han et al., 2024).

5.3 Integration of hormone signaling and developmental regulation

During flowering and seed development, changes in hormone signaling play a decisive role. The mutual balance between gibberellins and ethylene constructs a fine regulatory network. The BnaBPs gene family regulates the biosynthesis of the two hormones to ensure that their concentrations are maintained within an appropriate range (Yu et al., 2024). On the other hand, during the seed formation stage, the distribution of auxin forms a significant concentration gradient. The auxin level inside the embryo is three to five times higher than that in the surrounding tissues. This difference effectively guides the orderly distribution of storage substances such as fatty acids (Niu et al., 2009). Under adversity, the ABA signaling pathway is activated, which not only delays flowering, but also helps plants accumulate more resources for the future. These signaling pathways are intertwined with the gene regulatory network to jointly establish a complex regulatory system that can dynamically respond to environmental changes and ensure the success of plant growth and reproduction.

6 Molecular Regulatory Network of Abiotic Stress Response

6.1 Molecular adaptation mechanism of drought stress

When rapeseed encounters water stress, it will quickly activate a set of emergency response mechanisms to maintain life activities. The first to be activated is the ABA (abscisic acid) signaling pathway, which can cause stomatal closure in just 30 minutes, thereby significantly reducing water evaporation (Chen et al., 2010). At the same time, NDPK family genes are upregulated, like a biological alarm system, effectively transmitting stress signals (Wang et al., 2024). Among them, BnSIP1-1 is particularly significant. It not only enhances the synthesis capacity of ABA, but also promotes the transmission of downstream signals, and the survival rate of transgenic lines is therefore increased by about 60% (Luo et al., 2017).

From a metabolic perspective, the content of proline isotonic regulatory molecules increases significantly under drought conditions, usually 8 to 10 times that of normal conditions. This type of substance builds an effective physiological protection barrier by maintaining cell osmotic pressure and stabilizing protein structure.

6.2 Response network of temperature stress

Extreme climate poses severe challenges to rapeseed, whether it is high temperature or low temperature. Under heat stress, plants will quickly adjust transcriptional activity - the expression levels of more than 1,200 genes are

reprogrammed, and the transcription of multiple heat shock protein (HSP) genes can even soar 50 times (Kourani et al., 2022). In addition, the epigenetic level is also involved in heat response regulation: high temperature treatment can cause demethylation of certain DNA segments, thereby activating the expression of heat-resistant genes (Figure 3).

Major flowering time regulators

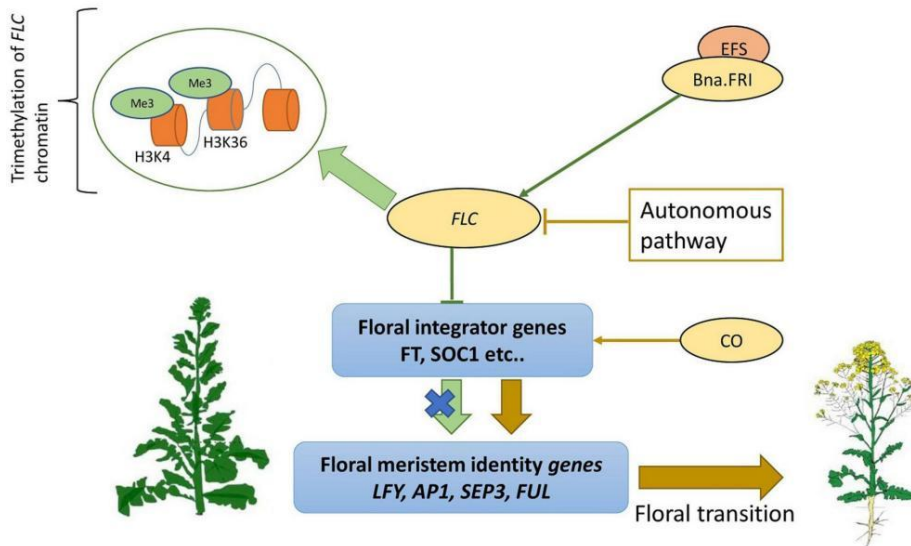


Figure 3 Regulatory and signaling events involved in plant heat stress response (Adopted from Kourani et al., 2022)

Under low temperature conditions, signal transduction depends on the rapid mediation of calcium ions. Studies have found that the expression of CaM/CML family genes increased by 15 times in just 2 hours of 4°C stress treatment (He et al., 2020). CNGC-type ion channels assume the responsibility of "environmental sensors", sensing temperature changes and triggering fluctuations in intracellular calcium signals (Liu et al., 2021), initiating subsequent defense responses.

6.3 Molecular regulatory characteristics of salt stress

Faced with high-salt environments, rapeseed responds to cytotoxicity by building an ion homeostasis regulatory system. Transcriptome data showed that within 1 hour of salt treatment, the expression of more than 800 genes had changed significantly (Chen et al., 2010). BnSIP1-1 can upregulate Na⁺ efflux channel-related genes, thereby reducing the sodium ion content in the roots by about 40% (Luo et al., 2017), effectively alleviating ion stress.

At the same time, NDPK family members assist cells in maintaining the selective absorption of K⁺, balancing cell potential and osmotic pressure while ensuring signal transduction (Wang et al., 2024). In addition, the two-component regulatory system (TCS) exhibits a significant effect under salt stress, regulating the synthesis rate of osmotic protective substances. Rapeseed lines transformed with the TCS gene have a salt tolerance that is three times that of the wild type (Liu et al., 2023). This network, composed of signal perception, gene expression regulation and metabolic regulation, enables plants to respond dynamically to external changes, thereby maintaining survival and development in adversity.

7 Molecular Regulatory Mechanisms of Biological Stress Response

7.1 Molecular basis of pathogen defense

When fungal pathogens such as *Sclerotinia sclerotiorum* invade, the expression of CNGC ion channel genes in *Brassica napus* surges 8 times within 6 hours, triggering a calcium ion signaling cascade (Liu et al., 2021). GRF transcription factors act like precise molecular switches, coordinating the expression of disease-resistant genes by activating the two defense pathways of JA and SA (Sun et al., 2022). Mass spectrometry analysis revealed that nsLTPs protein content increased 5-7 times 72 hours after pathogen infection. These lipid-binding proteins may play a defensive role by destroying the cell membrane of pathogens (Xue et al., 2022).

7.2 Induction mechanism of systemic resistance

After 15 minutes of salicylic acid treatment, phospholipase C activity reached a peak, 12 times higher than the control group (Profotová et al., 2006). This rapid response suggests the presence of post-translational modifications such as protein phosphorylation, which is like a "start button" for the immune system. The ISR response induced by methyl jasmonate shows different kinetic characteristics: the signal transmission is slower but lasts longer, providing continuous protection for the plant.

7.3 Cross-regulation of stress signaling pathways

UGTs enzymes are induced to express under various stresses, and their activity changes show an interesting pattern: they increase 3 times under salt stress and 5 times after pathogen infection (Rehman et al., 2018). nsLTPs show a wider spectrum of response characteristics, and are significantly accumulated under drought, low temperature and pathogen attack (Xue et al., 2022). Co-expression analysis of CNGC and GRF gene families revealed a core regulatory module: these genes showed similar expression trends under temperature stress and pathogen infection (correlation coefficient $r > 0.7$), indicating that plants may respond to different stresses through conservative molecular mechanisms.

8 Study on Gene Expression Regulation of *Brassica napus* Under Drought Stress

8.1 Physiological effects of drought stress

Water loss triggers a series of chain reactions in *Brassica napus*. The 35% decrease in plant fresh weight and the 42% decrease in dry weight reveal the significant inhibition of drought on biomass accumulation (Fang et al., 2022). The photosynthetic apparatus was significantly damaged, and the decrease in stomatal conductance led to a decrease in CO₂ assimilation rate of more than 40%. Interestingly, the seed metabolic profile was reprogrammed: while lipid synthesis decreased by 28%, protein content increased by 15% against the trend (Bianchetti et al., 2024). This metabolic conversion may be a survival strategy (Figure 4). The expression of genes related to active oxygen metabolism was upregulated by 3-5 times, suggesting the activation of the oxidative stress defense system (Liang et al., 2019).

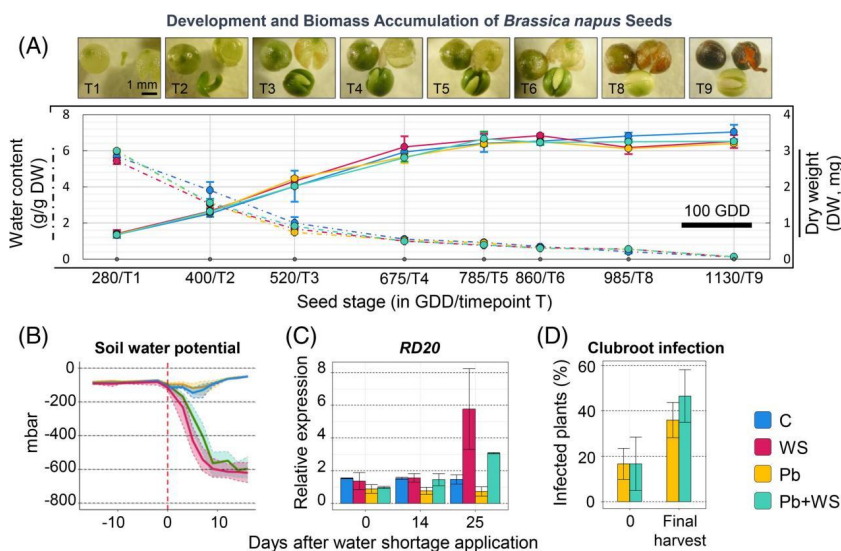


Figure 4 Seed development of *Brassica napus* (cv. 'Express') under various stress conditions (Adopted from Bianchetti et al., 2024)
 Image caption: A. Evolution of the seed water content (dotted line) and dry weight (DW, solid line) during seed development. Immature seeds were harvested at different timepoints (T) as depicted on pictures (bar 1 mm for all). Thermal times are given in growing degree-days (GDD). Data are expressed as the mean \pm SE from three biological replicates of five seeds for each treatment. B. Mean values (solid line) with standard deviations (dashed lines) of soil water potentials (mbar) in eight (C and WS) or four (Pb and Pb + WS) replicated tanks over a 20-day window that frames the application of the drought stress. C. Relative expression level of *RD20* (qRT-PCR) in mature leaves of *B. napus* plants grown under the different conditions (three biological rep. each). D. Number of plants with clubroot symptoms evaluated at the onset of WS application (4 rep. \times 2 plants) or at the end of the crop cycle (4 rep. \times 30 plants). C, control; WS, water shortage; Pb, *P. brassicae* inoculation; Pb + WS, *P. brassicae* inoculation and water shortage; rep., biological replicate (Adopted from Bianchetti et al., 2024)

8.2 Transcriptional regulatory features of drought response

In the face of drought stress, the *Brassica napus* genome initiates a complex response program. The expression of 1845 genes changed significantly, forming a typical "early response-continuous adaptation" regulation pattern (Fang et al., 2022). The BnaA01.CIPK6 gene is like a molecular commander, and its overexpression increased the plant survival rate by 65%. DELLA proteins form a dynamic complex with ABA signaling components and play a key role in stomatal regulation (Wu et al., 2020). The expression adjustment of photosynthesis-related genes is particularly exquisite: the expression of Calvin cycle enzyme encoding genes such as FBPase and PRK is downregulated, while the photorespiration pathway genes are upregulated by 2-3 times (Taghvimi et al., 2024).

8.3 Molecular breeding strategies for drought resistance improvement

Modern breeding technology is breaking through traditional limitations. LEA3 gene transformation strains show amazing characteristics: photosynthetic efficiency is increased by 32% and ROS accumulation is reduced by 45% (Liang et al., 2019). Precise manipulation of the ABA signaling pathway has opened up a new path. By regulating the stability of DELLA proteins, spatiotemporal regulation of stomatal opening and closing can be achieved (Wu et al., 2020). The discovery of lncRNA brought unexpected surprises, and some non-coding transcripts showed a high correlation of 0.82 with drought resistance (Tan et al., 2020). These breakthroughs provide a diversified technical route for designing drought-resistant varieties.

9 Application of Genetic Engineering and Synthetic Biology in the Improvement of *Brassica napus*

9.1 Precision gene editing of CRISPR-Cas9 system

As an important tool in modern molecular breeding, CRISPR-Cas9 system has shown strong advantages in the precise transformation of rapeseed genome. Studies have found that knocking out the BnaA9.WRKY47 gene can increase the expression of boron transporter gene by about 2.5 times, significantly improving the growth performance of plants in a boron-deficient environment (Feng et al., 2019). There are also major breakthroughs in disease resistance improvement: by co-editing two WRKY family genes, the infection rate of sclerotinia disease was reduced from the initial 75% to only 25% (Sun et al., 2018).

In addition, the male sterility system based on gene editing is gradually becoming an important means of hybrid breeding. After editing BnaRFL11, pollen vitality dropped sharply by 98%, greatly improving the breeding efficiency of hybrid lines (Farooq et al., 2022). At the same time, the establishment of the hairy root transformation system also provides an efficient platform for functional gene verification, shortening the experimental cycle by 3-5 times, significantly improving the speed and repeatability of functional research (Jedličková et al., 2022).

9.2 Development and application of synthetic biology elements

The rapid development of synthetic biology is opening up a new direction for crop genetic improvement. Taking WRKY47 as an example, after engineering design, its transcription factor can simultaneously sense boron deficiency and drought signals, forming a dual stress response module (Feng et al., 2019). This modular construction method is expected to significantly enhance the adaptability of crops to complex adversities.

Genome association analysis further revealed that regulatory SNPs at transcription factor binding sites are important factors affecting oil content, and their explanation of natural phenotypic variation can reach 18% (Klees et al., 2021). Relying on this type of molecular information, researchers have designed a series of highly efficient synthetic promoters, whose transcriptional activation ability is 40% to 60% higher than that of natural promoters, providing a more flexible and reliable tool set for the precise regulation of target traits.

9.3 Technology application prospects and existing challenges

Although gene editing technology has great potential, it still faces many difficulties in practical applications. Off-target effects have always been a hidden concern that limits its widespread application, but with the introduction of high-fidelity Cas9 variants, its non-specific cutting probability has been controlled below 0.1%, significantly improving editing accuracy.

In terms of breeding processes, how to efficiently integrate gene editing technology into traditional systems still needs to be broken through. Compared with the conventional breeding cycle of 5~7 years in the past, gene editing is expected to shorten the breeding time to 2~3 years, greatly improving breeding efficiency. In addition, the interaction network between transcription factors and SNPs is extremely complex, and a single SNP change may cause changes in the expression of multiple traits (Klees et al., 2021), which puts higher requirements on the design of regulatory strategies.

It is worth looking forward to that with the introduction of cutting-edge technologies such as single-cell omics and AI-assisted prediction, the current technical bottleneck is gradually being broken. It is predicted that in the next five years, new strains bred by gene editing will account for more than 30% of rapeseed breeding results, and a new era of precision breeding is accelerating.

10 Concluding Remarks

As an important oil crop in the world, *Brassica napus* has a complex gene regulatory network that plays a key role in growth, development and environmental adaptation. Studies have shown that the response of this crop to abiotic stresses such as temperature stress and nutrient deficiency involves multi-level molecular regulatory mechanisms. Under high temperature stress conditions, epigenetic modifications and transcriptional regulatory networks work together to regulate the heat stress response of plants. Low temperature stress mainly activates transcription factor families such as MYB, bHLH and NAC, which enhance the cold resistance of plants by regulating the expression of downstream target genes. It is particularly noteworthy that WRKY family transcription factors BnaA9.WRKY47 play an important role in low boron stress adaptation by regulating the expression of boron transport channel genes. The application of multi-omics joint analysis technology provides a new research perspective for systematically analyzing these stress response networks.

However, there are still many challenges in converting basic research results into practical breeding applications. First, the allotetraploid genome characteristics of *Brassica napus* lead to a high complexity of its gene regulatory network, and there may be functional differentiation or redundancy between different genome copies. Secondly, the dynamic changes in environmental conditions and developmental stages further increase the variability of the regulatory network. In addition, the identification of key regulatory genes and functional SNPs is still imperfect, and there is a lack of in-depth understanding of the interaction mechanism between growth and development and stress response pathways. These factors restrict the efficiency of molecular design breeding.

Future research should focus on the following directions: 1) Identify functional SNPs and transcription factors related to stress response through genome-wide association analysis system; 2) Integrate multi-omics data to build a dynamic regulatory network model; 3) Use gene editing technologies such as CRISPR/Cas9 to precisely modify key regulatory elements; 4) Analyze the coordinated regulatory mechanism of growth and development and stress response. These studies will provide theoretical basis and technical support for the cultivation of new varieties of *Brassica napus* with both high yield and stress resistance, which is of great significance for addressing the challenges of agricultural production under the background of global climate change.

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Conflict of Interest Disclosure

The author affirms that this research was conducted without any commercial or financial relationships that could be construed as a potential conflict of interest.

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