International Journal of Molecular Evolution and Biodiversity, 2025, Vol.15, No.2, 84-98
http://ecoevopublisher.com/index.php/ijmeb

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Drought Tolerance in Rapeseed: Genetic Mechanisms and Breeding Strategies

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International Journal of Molecular Evolution and Biodiversity, 2025, Vol.15, No.2 doi: 10.5376/ijmeb.2025.15.0008
Received: 07 Feb., 2025
Accepted: 12 Mar., 2025
Published: 25 Mar., 2025

Preferred citation for this article:
Yu S.Y., 2025, Drought tolerance in rapeseed: genetic mechanisms and breeding strategies, International Journal of Molecular Evolution and Biodiversity, 15(2): 84-98 (doi: 10.5376/ijmeb.2025.15.0008)

Abstract Rapeseed (*Brassica napus* L.) is an important oil crop worldwide, and its yield stability is often severely affected by drought stress. This study analyzed the key role of regulatory factors such as BnA.JAZ5 and BnaA6.RGA in the ABA signaling pathway, which regulate the expression of downstream genes and mediate the response to drought stress. Studies have shown that the activation or inhibition of these genes affects the plant's ability to adapt to adversity, reflecting its important position in the molecular regulatory network. At the physiological level, drought-tolerant varieties show a series of adaptive characteristics: not only can they maintain a high level of antioxidant enzyme activity and chlorophyll content, but they can also accumulate osmotic regulatory substances including proline and soluble sugars, thereby alleviating the adverse effects of water deficit. This physiological regulation mechanism enhances its ability to survive and grow in drought environments. With the rapid development of molecular biology technology, the analysis of drought resistance mechanisms is becoming more efficient and in-depth. Genome-wide association analysis (GWAS) combined with precise gene editing technologies such as CRISPR/Cas9 provides a powerful means for the rapid identification and utilization of key drought-resistant genes. This study provides a reference for integrating traditional breeding and molecular design technology to cultivate new drought-resistant varieties, especially in improving water acquisition efficiency and regulating physiological balance.

Keywords Rapeseed (*Brassica napus*); Drought tolerance; ABA signaling; Genetic regulation; Enzymatic activity; Marker-assisted selection; Transcriptomics; Sustainable breeding

1 Introduction

As the world's third largest source of vegetable oil, rapeseed (*Brassica napus* L.) continues to gain importance at the economic and strategic levels. It is not only the main source of high-quality edible oil, but its rich unsaturated fatty acids also support human health. It also has diversified development potential in feed, industry and bioenergy (Chaghakaboodi et al., 2021). Although rapeseed has strong ecological adaptability and performs well in temperate regions, drought stress is still one of the main bottlenecks restricting its yield increase (Channaoui et al., 2019).

The effect of drought stress on the growth and development of rapeseed has systemic characteristics. From seed germination to maturity, water deficit significantly inhibits root development, reduces photosynthetic efficiency and disrupts metabolic balance (Dai et al., 2020). This multi-level stress response makes drought tolerance improvement a core goal of rapeseed breeding. Especially in rain-fed agricultural areas, improving the drought adaptability of varieties is of decisive significance to ensure yield stability (Chaghakaboodi et al., 2021).

This study will comprehensively explore the genetic mechanisms and physiological response pathways behind rapeseed drought resistance, integrate multi-omics data resources, and systematically identify metabolic pathways and key regulatory gene networks that are significantly active under drought stress. In addition, this study will evaluate a variety of drought-resistant breeding strategies from conventional breeding to molecular marker-assisted selection, and successfully screen core germplasm materials that show strong drought resistance potential. This study provides a solid theoretical support for coping with the trend of intensified drought in the future, and provides practical guidance for promoting the transformation of rapeseed production towards sustainability and efficiency.

2 Impact of Drought Stress on Rapeseed

2.1 Physiological and biochemical effects of drought on rapeseed

Drought is one of the important abiotic stress factors affecting the growth and development of rapeseed (*Brassica napus* L.). Under drought conditions, the chlorophyll content in plant leaves is often significantly reduced, and the reduction of chlorophyll directly inhibits the efficiency of photosynthesis. Due to the damage to the photosynthetic system, reactive oxygen species (ROS) are easily accumulated in cells, causing oxidative stress, thereby damaging the cell membrane system (Teymoori et al., 2020).

To alleviate this oxidative damage, plants accumulate osmotic regulating substances such as proline, betaine and trehalose. These small molecules not only help maintain the osmotic balance of cells, but also play an important role in enhancing the activity of antioxidant enzymes, which can effectively reduce the content of malondialdehyde (MDA) and hydrogen peroxide (H_2O_2) and alleviate cellular oxidative stress (Bhuiyan et al., 2019).

Drought stress profoundly affects the metabolic regulatory network of rapeseed, especially during the reproductive growth stage. When water is deficient, the oil synthesis pathway of rapeseed grains is reprogrammed, which is manifested by an abnormal increase in the proportion of long-chain fatty acids such as erucic acid, resulting in the deterioration of edible oil quality. At the same time, secondary metabolic pathways are activated, and defensive substances such as phenolic compounds and glucosinolates accumulate in large quantities. These changes may reduce the feeding value of rapeseed meal (Bouchereau et al., 1996). Physiological index monitoring shows that the proline content of rapeseed leaves increases in a dose-dependent manner under drought conditions, and its accumulation level is significantly positively correlated with biomass and yield indicators (Norouzi et al., 2008), indicating that this osmotic regulating substance has an important physiological function in drought adaptation.

2.2 Effects of water deficiency on yield and quality

Drought stress directly affects the yield components of rapeseed, among which the decline in the number of siliques and the number of grains per silique is the most prominent (Norouzi et al., 2008). In severe drought conditions, yield losses can reach significant levels, especially when water is insufficient during the flowering or silique formation period, which will adversely affect grain yield and its oil content.

The decline in oil quality caused by drought is often manifested as an increase in palmitic acid and erucic acid content, which is a disadvantage for edible oil use (Khodabin et al., 2021). Protein content will also decrease due to reduced water content, thus affecting the overall nutritional value of seeds (Germchi et al., 2010; Shekari et al., 2016).

In order to alleviate the adverse effects of drought, some studies have tried to regulate by applying trace elements. For example, spraying zinc or manganese sulfate can improve the oil composition to a certain extent, reduce the accumulation of erucic acid and glucosinolates (Khodabin et al., 2021), and thus improve the quality of oil products.

2.3 Environmental regulatory factors of drought stress intensity

There are many factors that affect the effects of drought stress, among which soil moisture, temperature and the time when water deficiency occurs are particularly critical. Especially after the plant enters the flowering period and silique development period, insufficient water supply often aggravates the negative impact on yield and quality. Climate type also has a regulatory effect on stress manifestations. For example, the Mediterranean climate is characterized by high temperatures and droughts in summer and wet winters, which makes rapeseed more susceptible to water stress in the late growth period (Teymoori et al., 2020).

Rising temperatures will accelerate transpiration, thereby increasing soil water loss and worsening drought conditions. At the same time, the effects of water stress at different growth stages vary. Early drought may have long-term effects on grain quality, while water shortage during flowering will directly weaken seed formation and yield potential (Bouchereau et al., 1996).

In order to cope with the risk of drought, some studies have proposed improving the drought resistance of rapeseed by improving soil structure. For example, the application of biochar not only improves soil water retention, but also increases soil nutrient supply, which helps maintain the normal physiological activities and yield levels of rapeseed in arid environments (Khan et al., 2021).

3 Genetic Basis of Drought Tolerance in Rapeseed

3.1 Identification and function of key genes for drought resistance

The drought resistance of rapeseed (*Brassica napus*) is determined by a complex genetic network. The latest research shows that multiple key genes regulate the plant's response to drought stress through synergistic effects. A genome-wide association analysis revealed 139 SNP loci significantly associated with drought resistance, among which genetic variation on chromosome A10 showed particularly prominent association strength (Shahzad et al., 2021). In-depth analysis found that four genes, including BnaC09.RPS6, play a core regulatory function under water stress conditions. These genes jointly maintain the physiological homeostasis of plants in drought environments by affecting different physiological and metabolic processes.

In addition, studies have shown that overexpression of the bZIP transcription factor encoding gene BnaABF2 in *Arabidopsis* can significantly enhance its drought resistance. This gene maintains cellular osmotic balance and metabolic homeostasis by upregulating the expression of stress-related genes such as RD29B, RAB18 and KIN2 (Zhao et al., 2016). These results emphasize the importance of targeting key genes for functional verification and provide basic information and potential gene resources for molecular breeding of rapeseed drought resistance.

3.2 Drought-resistant regulatory role of DREB, NAC and WRKY transcription factors

In the drought resistance regulatory network, transcription factors (TFs) play a pivotal role in signal transduction and gene expression regulation. The DREB (dehydration response element binding protein), NAC and WRKY transcription factor families are considered to be the core elements for regulating drought resistance because of their extensive involvement in drought signal transduction and response.

For example, after the DREB1A gene is heterologously expressed in sage, it can upregulate downstream genes related to stress response, photosynthesis regulation and carbohydrate metabolism, thereby improving the drought tolerance of plants (Wei et al., 2016). This mechanism provides a reference for the application of corresponding regulatory factors in rapeseed.

NAC family transcription factors play a key role in regulating plant drought response. Studies have shown that the expression profile of papaya CpNAC genes is significantly reprogrammed under water stress conditions, suggesting that they are involved in drought signal transduction (Arroyo-Álvarez et al., 2023). It is also worth noting that members of the WRKY transcription factor family, such as WRKY57, enhance plant drought resistance through a dual regulatory mechanism: on the one hand, they activate the ABA signal transduction pathway, and on the other hand, they increase the activity of antioxidant enzymes such as superoxide dismutase (Yang et al., 2020). This synergistic effect effectively removes excess reactive oxygen species in cells and reduces the damage of oxidative stress to the membrane system (Jiang et al., 2012).

3.3 Study on the localization of quantitative trait loci (QTL) for drought resistance

The localization of quantitative trait loci (QTL) provides an effective tool for analyzing the genetic mechanisms behind complex traits, especially showing great potential in revealing genomic regions related to drought resistance. In rapeseed, although the QTL research on drought resistance is still relatively limited, the existing research on waterlogging resistance provides a valuable reference for subsequent expansion. Some physiological indicators respond to both drought and waterlogging stresses, so there may be intersections between the two in some genetic pathways.

Important progress has been made in the study of rapeseed waterlogging tolerance. Through systematic analysis, 66 key QTL loci were identified, which regulate important traits such as root development and biomass accumulation (Xiaoyu et al., 2020). The study found that these loci can be clustered into 6 main functional modules, providing new targets for molecular marker-assisted breeding.

Although the current research on drought resistance QTL is still in its infancy, the integration of multi-omics data such as GWAS and transcriptome will significantly improve the efficiency of gene mining. This multidimensional data fusion strategy can not only deeply analyze the genetic basis of drought resistance traits, but also provide new ideas for precision breeding, and promote breakthrough progress in the selection and breeding of drought-resistant rapeseed varieties.

3.4 Epigenetic regulation and gene expression changes under drought stress

In a water stress environment, the response of plants to adversity not only depends on the classic transcriptional regulation pathway, but also relies deeply on the participation of epigenetic mechanisms. Such as DNA methylation, histone post-translational modification and the intervention of non-coding RNA, can regulate the expression state of stress resistance genes by regulating chromatin conformation and transcription factor accessibility. These mechanisms together build a dynamic and plastic regulatory network, enabling plants to respond quickly and maintain homeostasis under drought conditions, thereby improving their overall drought tolerance.

For example, the BnaC09.Histone gene identified in drought-related GWAS studies has attracted attention because of its close relationship with histone modification (Shahzad et al., 2021). Such modifications may regulate the open state of chromatin, thereby affecting the expression efficiency of downstream stress-resistant genes.

WRKY and NAC family transcription factors constitute the core hub of the plant drought resistance regulatory network. Studies have shown that WRKY57 activates downstream target gene expression under drought conditions by specifically recognizing the cis-acting elements of ABA-responsive genes (Jiang et al., 2012). This transcriptional regulation works synergistically with epigenetic mechanisms such as DNA methylation and histone modification, giving plants transcriptional plasticity to cope with environmental stress. This multi-level regulatory network not only enhances the accuracy of gene expression, but also improves the dynamic response ability of plants to adapt to water stress, providing important molecular targets for drought resistance breeding.

4 Molecular and Physiological Mechanisms

4.1 Water-use efficiency and root architecture adaptations

Water use efficiency (WUE), as a key indicator for measuring crop drought resistance, directly determines the survival ability and yield performance of rapeseed under drought conditions. With the increasing scarcity of global water resources, improving WUE has become an important direction for modern drought-resistant breeding. To achieve this goal, it is necessary to work together from two dimensions: genetic improvement and physiological regulation: on the one hand, optimize the genetic basis of water use-related traits through molecular breeding methods; on the other hand, use physiological regulation strategies to enhance the plant's resource conversion ability, thereby cultivating new drought-resistant varieties with efficient water use characteristics.

Among many physiological traits, the structure and distribution pattern of the root system have a direct impact on water acquisition. Some rapeseed genotypes show a deeper or more rationally distributed root system, which can more effectively absorb water from deep soil and enhance adaptability in drought environments (Araus et al., 2002; Ruggiero et al., 2017).

In addition to the root system, controlling stomatal conductance to reduce transpiration rate can also reduce water loss while maintaining photosynthesis efficiency. Simultaneously improving leaf photosynthetic capacity helps maintain high physiological activity under drought stress (Ruggiero et al., 2017; Lin et al., 2020). Whether the root system is developed or not also directly affects the ability to absorb water and nutrients, and is an important physiological indicator for measuring drought resistance.

With the continuous advancement of root phenotyping technology, it has become possible to accurately quantify the root structure. Studies have shown that in the increasingly frequent extreme climate events, the resource acquisition ability of the root system is of decisive significance for the stable yield of rapeseed (Wu et al., 2018). Therefore, incorporating root traits into the breeding evaluation system is expected to accelerate the screening and breeding process of drought-resistant varieties.

4.2 Osmotic adjustment through proline and sugar accumulation

Under drought stress conditions, plants must maintain normal water potential and metabolic activities of cells. Osmotic regulation becomes the core mechanism, among which proline and soluble sugars are the main regulatory factors. The accumulation of these two types of small molecules helps to maintain cell turgor pressure, regulate osmotic balance, and protect organelles and membrane structures. Studies have found that drought-tolerant rapeseed varieties have significantly higher levels of proline and sugar accumulation than susceptible varieties (Chaghakaboodi et al., 2021; Batool et al., 2022).

Proline can not only stabilize protein structure in cells, but also effectively scavenge free radicals and alleviate oxidative damage caused by stress. At the same time, soluble sugars not only participate in osmotic regulation, but also provide cells with necessary energy support to maintain basic metabolic functions. The enrichment of these osmotic regulating substances is usually closely related to the increase in the activity of related enzymes, thereby further enhancing the plant's resistance to drought (Batool et al., 2022). Therefore, focusing on osmotic regulation pathways and screening materials with stronger proline and sugar accumulation capabilities is one of the important strategies to improve rapeseed drought tolerance.

4.3 Antioxidant defense system and regulation of reactive oxygen species (ROS)

Under drought conditions, reactive oxygen species (ROS) often accumulate rapidly in plants. If these unstable molecules cannot be removed in time, they can easily trigger a series of oxidative stress reactions such as membrane lipid peroxidation, protein inactivation and DNA damage. To defend against this damage, plants rely on a sophisticated antioxidant enzyme system. Key enzymes including superoxide dismutase (SOD), catalase (CAT) and peroxidase are important barriers to remove ROS and maintain cellular redox balance (Batool et al., 2022).

Studies have shown that drought-tolerant rapeseed can usually maintain higher levels of antioxidant enzyme activity under drought stress, while drought-sensitive varieties are more susceptible to damage by reactive oxygen species. The enhancement of antioxidant enzymes helps maintain cell metabolic balance and alleviate the adverse effects of oxidative stress. For this reason, strengthening antioxidant defense mechanisms has become one of the important directions of current drought-resistant breeding. By regulating key genes related to the antioxidant system, enzyme activity can be increased at the molecular level, providing a new path to improve the physiological stability and survival ability of rapeseed under drought conditions.

4.4 Regulatory role of hormone signaling pathways in drought response

Plant hormones constitute a complex signal network to regulate the drought response process. ABA, as a core signal molecule, accumulates rapidly under water stress, triggering key physiological responses such as stomatal closure and osmotic regulation (Lin et al., 2020). Ethylene and cytokinin synergistically participate in this process. The former regulates the remodeling of the root system architecture, while the latter affects cell proliferation and expansion, jointly enhancing the drought resistance of plants.

The discovery of the rapeseed BnA.JAZ5 gene reveals a new mechanism of hormone cross-regulation. This gene integrates the ABA and JA signaling pathways and affects water use efficiency by regulating the dynamics of stomatal development (Cao et al., 2022). This multi-hormone synergistic action mode provides a new perspective for understanding plant environmental adaptation strategies.

Analyzing the interaction mechanism of the hormone signaling network has important application value. By targeting and regulating key node genes, precise intervention in drought response can be achieved, opening up new ways to cultivate high-yield and stable-yield rapeseed varieties.

5 Breeding Approaches for Drought Tolerance

5.1 Conventional breeding techniques and challenges

Traditional breeding methods have always occupied a core position in the cultivation of drought-resistant rapeseed varieties. Technical means such as systematic selection, recurrent selection, backcrossing and mutagenesis all use existing natural genetic diversity to improve target traits (Ashraf, 2010; Begna, 2022). For example, by selecting traits such as root morphology, leaf curling and proline accumulation, some strains have shown significant improvements in water use efficiency and stress tolerance (Ranjith and Rao, 2021).

Despite the effectiveness, traditional methods still have significant limitations. On the one hand, the entire breeding cycle often takes many years and requires a large amount of manpower; on the other hand, the genetic resources relied on are limited by the range of variation of the species itself, and it is not easy to achieve significant breakthroughs (Ashraf, 2010). More importantly, drought stress does not have a single effect, but ultimately suppresses yield potential by affecting leaf expansion, stem growth, root distribution and other pathways (Begna, 2022). Coupled with the complex interaction between genetic background and environmental conditions, breeding results are often difficult to maintain consistency under different ecological conditions (Ashraf, 2010).

Despite this, conventional breeding is still the basic pillar of drought resistance improvement, especially when combined with modern methods such as molecular assistance, it can play an important role under the premise of clear selection direction.

5.2 Gene marker-assisted selection (MAS)

Marker-assisted selection (MAS), as an important means of molecular breeding, has been widely used to improve the adaptability of rapeseed to drought environments. This method relies on molecular markers that are closely linked to the target quantitative trait loci (QTLs), which can achieve early screening of individuals before the trait is expressed (Ashraf, 2010). Compared with traditional breeding methods, MAS significantly shortens the breeding cycle and reduces the dependence on large-scale field trials to a certain extent.

In past studies, scientists have mapped several QTL maps related to drought resistance, which cover multiple key indicators such as root growth depth, osmotic regulation ability, and antioxidant enzyme activity (Cattivelli et al., 2008). These traits play an important role in improving the adaptability of rapeseed to drought stress. However, the performance differences of different genotypes in a changing environment, especially the interaction effect between genes and the environment, often affect the stability and positioning accuracy of QTLs, which brings certain challenges to practical applications.

Molecular marker-assisted selection (MAS) provides a precise technical means for drought-resistant breeding. By aggregating multiple drought-resistant gene loci, this technology can achieve the coordinated improvement of important traits and effectively improve the adaptability of rapeseed under drought conditions (Ashraf, 2010). With the advancement of molecular marker development technology, MAS is gradually becoming an important strategy for breeding drought-resistant varieties.

5.3 Integrated application of genomic selection and high-throughput phenotyping

Genomic selection (GS) represents the innovative direction of modern breeding technology. This method integrates whole genome marker information and phenotypic data to construct a predictive model to evaluate the drought resistance potential of breeding materials (Cattivelli et al., 2008). Compared with MAS, GS can more comprehensively analyze the genetic basis of complex quantitative traits and significantly improve the accuracy and stability of selection.

The rise of high-throughput phenotyping (HTP) provides a data basis for the efficient implementation of GS. With the help of remote sensing imaging, multispectral analysis and automation platforms, researchers can collect important trait data such as stomatal conductance, chlorophyll content and root morphology of crops under drought stress in a short period of time (Cattivelli et al., 2008; Wu et al., 2018). These high-resolution phenotypic information not only enriches the input variables of the prediction model, but also improves the depth of analysis of the interaction between genotype and environment.

The synergistic integration of high-throughput phenomics (HTP) and genomic selection (GS) has significantly improved the efficiency of drought-resistant breeding. This multi-omics strategy has achieved a significant shortening of the breeding cycle and a significant improvement in selection accuracy by optimizing the genotype screening process, providing technical support for the breeding of rapeseed varieties with stronger adaptability.

5.4 Integrated application of biotechnology in drought-resistant breeding

Genetic engineering technology has opened up new avenues for the precise improvement of drought-resistant traits. By targeted introduction of functional genes related to the ABA signaling pathway or osmotic regulation (Ashraf, 2010), this technology breaks through the limitations of traditional breeding. Compared with conventional hybridization methods, genetic engineering not only simplifies the multi-generation screening process, but also ensures the stable inheritance of target traits in offspring (Cao et al., 2022), showing its important application value in drought-resistant breeding.

At the same time, the CRISPR/Cas9 gene editing system has shown broad application prospects in regulating drought-responsive genes due to its high targeting and editing efficiency. By precisely knocking out or activating regulatory elements or coding regions, this technology can effectively enhance the adaptability of plants under water stress conditions (Ashraf, 2010). More importantly, CRISPR/Cas9 is not only an independent improvement tool, but its flexibility also makes it easy to integrate with traditional breeding methods, QTL positioning and genomic selection (GS) technology to build a multi-dimensional synergistic drought-resistant breeding system (Figure 1) (Cao et al., 2022). With the continuous optimization and in-depth application of these biotechnologies, rapeseed drought-resistant breeding is gradually moving towards a new stage of precision, efficiency and controllability.

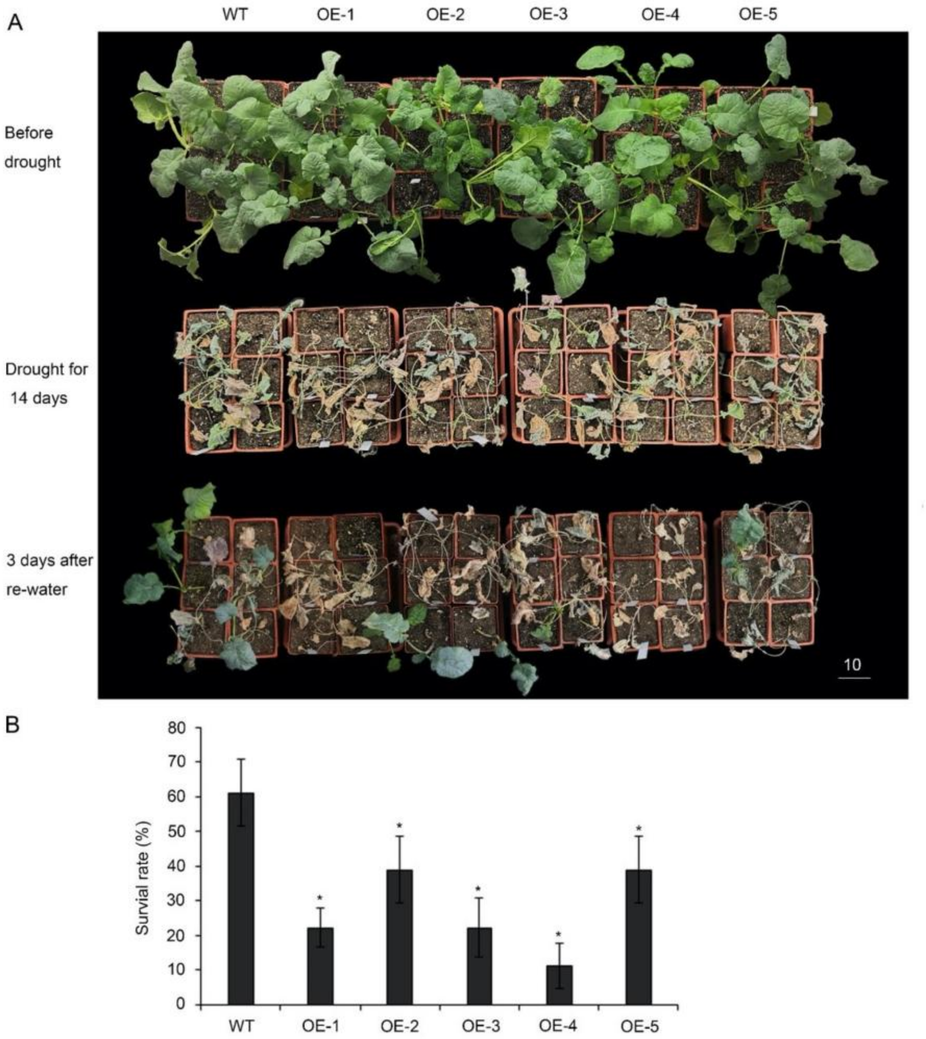

Figure 1 Drought resistance testing of *p35S::BnA.JAZ5* plants at the five-leaf stage (Adopted from Cao et al., 2022)

Image caption: (A) Drought resistance assay of five overexpressing lines. (B) Survival rates of five overexpressing lines after 3-day recovery from drought stress treatment. WT, accession K407. OE-1, OE-2, OE-3, OE-4 and OE-5, *p35S::BnA.JAZ5* plants. Asterisks indicate significant differences between wild-type and *p35S::BnA.JAZ5* lines ($P< 0.05$, Student's t-test). Scale bar, 10 cm (Adopted from Cao et al., 2022)

6 Biotechnological Interventions

6.1 Application of transgenic methods in drought resistance improvement

Transgenic technology plays a vital role in the study of improving rapeseed drought resistance. By introducing target genes with stress resistance, the drought tolerance of plants can be enhanced. Among them, the overexpression of BnaABF2 transcription factor is a representative achievement. This gene can activate stress response genes in the ABA signaling pathway, thereby improving the survival ability of plants under drought and salt stress (Zhao et al., 2016). This strategy clearly demonstrates the feasibility of improving plant stress adaptability by precisely regulating core genes.

Key research cases show that the BnA.JAZ5 gene plays a key regulatory role in rapeseed drought resistance. Related experiments have shown that overexpression of this gene triggers the interaction between the abscisic acid (ABA) and jasmonic acid (JA) signaling pathways, thereby causing an increase in stomatal density (Cao et al., 2022). This change in anatomical structure weakens the plant's ability to regulate under water stress and significantly reduces its survival level under drought conditions. This result reflects the high complexity of the intrinsic regulation of the plant hormone signaling network. When carrying out transgenic improvement, if the interaction effects between different hormones are not fully considered, unexpected phenotypic variation can easily occur. Therefore, the creation of efficient and stable drought-resistant transgenic rapeseed lines must rely on accurate gene function annotation and the construction of expression regulation systems.

6.2 Application prospects of CRISPR-Cas9 technology in rapeseed genetic improvement

The CRISPR-Cas9 system has become one of the important tools for modern plant molecular breeding due to its high targeting and editing efficiency. The gene editing operation achieved using this technology has shown great potential in the improvement of multiple target traits in rapeseed. For example, editing the EPSPS gene significantly improved the plant's tolerance to glyphosate herbicides, verifying its feasibility in actual production trait improvement (Wang et al., 2021).

In addition, CRISPR-Cas9 has also played a key role in analyzing the drought resistance mechanism of rapeseed. Taking DELLA protein as an example, by performing functional mutation treatment on its encoding gene BnaA6.RGA, researchers obtained mutants with different expression types. The results showed that the protein participates in the response regulation under drought stress by interacting with the core elements of the ABA signaling pathway. Plants with functional mutants showed stronger drought resistance, while mutants with missing functions performed relatively weaker under the same stress conditions (Wu et al., 2020). Such results not only deepen the understanding of key nodes in the regulatory network, but also provide a clear path for constructing new rapeseed germplasm with high stress resistance through gene-directed editing in the future.

6.3 Application of “omics” technology in drought resistance research

In recent years, “omics” technology has played an important role in revealing the drought resistance mechanism of rapeseed, covering multiple levels such as genomics, transcriptomics, proteomics and metabolomics. Genomic research has identified a series of key genes and their regulatory modules closely related to drought response through systematic analysis of the entire genome, providing strong support for the molecular improvement of drought resistance traits (Figure 2) (Raza et al., 2021).

At the same time, transcriptomics revealed the transcriptional response characteristics of rapeseed under drought stress, revealing the dynamic process of how plants adapt to environmental stress by regulating gene expression. These data provide important clues for understanding the transcriptional regulation strategy of adversity adaptation.

The combined analysis of proteome and metabolome provides a new perspective for revealing the mechanism of rapeseed drought resistance. Drought-resistant varieties show unique metabolic characteristics, including enhanced key enzyme activities and accumulation of osmotic regulatory substances (Batool et al., 2022). This physiological advantage is achieved through post-translational modification regulation and metabolic network reconstruction, forming a complete cell protection system that effectively responds to the physiological challenges brought about by drought stress.

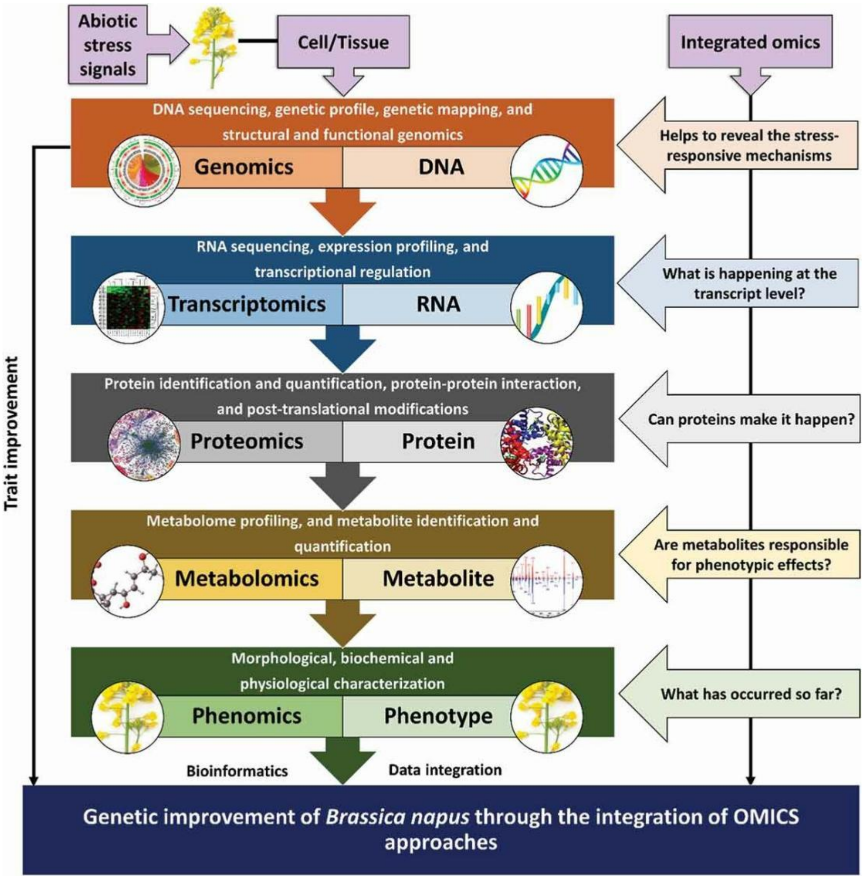

Figure 2 The central dogma of systems biology showing the flow of information from DNA to phenotype (Adopted from Raza et al., 2021)

Image caption: Step-wise presentation of OMICS approaches for studying abiotic stress responses. Ultimately, the integration of omics tools, primarily genomics (mainly single-cell/tissue-specific) leads toward the genetic improvement of rapeseed by modulating several agronomic traits such as environmental stress tolerance, yield, plant height, seed rate, flowering, photosynthesis, and respiration rate, root and shoot length, grain quality and yield, biomass production, etc (Adopted from Raza et al., 2021)

7 Case Studies

7.1 Success stories of drought-tolerant rapeseed varieties

Some rapeseed varieties have shown outstanding tolerance under drought stress conditions, providing important material resources for drought-resistant breeding. For example, JYZ 158 and FY 520 performed well in the PEG-6000 simulated drought experiment. They not only maintained a high level of antioxidant enzyme activity, but also accumulated a large amount of osmotic regulating substances such as proline and soluble sugars, which are physiological indicators that help alleviate drought-induced cell damage. In addition, these varieties maintained high chlorophyll content and low malondialdehyde (MDA) levels under water stress, indicating that they have strong photosynthetic efficiency and cell membrane stability (Figure 3) (Batool et al., 2022).

As a representative drought-resistant rapeseed variety, RGS003 shows remarkable yield stability under water-deficient conditions. Compared with ordinary varieties, this genotype has a significantly smaller yield reduction in water stress environments (Rahimi-Moghaddam et al., 2021). This excellent drought resistance stems from its unique genetic background, which enables it to maintain high physiological activity and yield potential. As a precious material for drought-resistant breeding, RGS003 provides an important genetic resource for breeding new varieties adapted to drought environments.

7.2 Comparative analysis of drought-resistant traits under different environments

The expression of drought-resistant traits in different environmental backgrounds and simulated stress conditions shows significant diversity. Taking PEG-6000 simulated drought treatment as an example, a systematic evaluation of 24 rapeseed varieties revealed obvious differentiation: outstanding varieties such as JYZ 158 and FY 520 maintained higher antioxidant enzyme activity under stress and could effectively regulate the cell osmotic state, thus showing significant advantages in cell homeostasis and metabolic balance (Batool et al., 2022). In contrast, genotypes with weaker drought tolerance accumulated more reactive oxygen products such as H_2O_2 and MDA in the body, showing obvious oxidative damage characteristics, and their growth potential and physiological activity were severely inhibited (Khan et al., 2019).

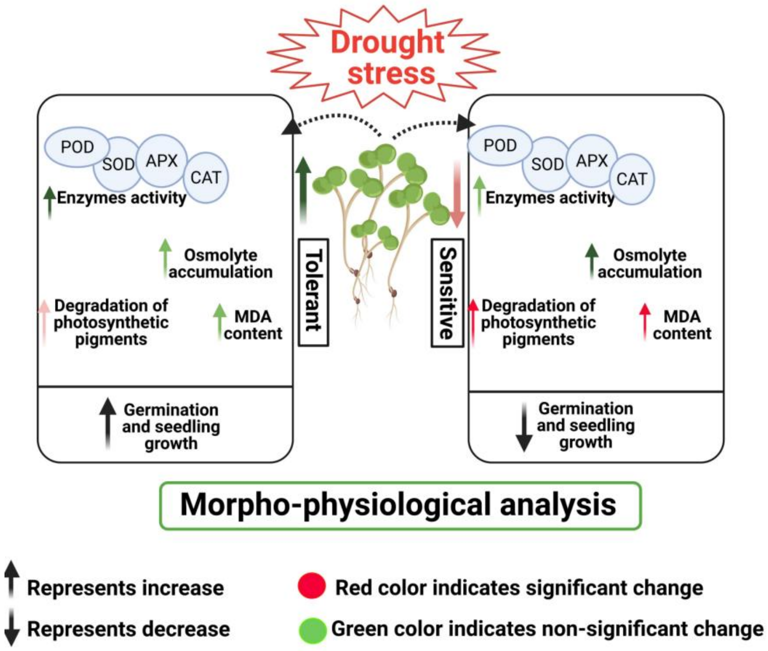

Figure 3 Comparative morphophysiological analysis of drought-tolerant and drought-sensitive rapeseed cultivars under drought stress (Adapted from Batool et al., 2022)

These observations highlight the wide variation in the response mechanism of drought resistance traits under different environments, and further illustrate that varieties with strong adaptability should be selected according to specific ecological zones to achieve the maximum balance between yield and stress resistance.

In actual field conditions, different climate zones also have a significant impact on rapeseed yield and drought resistance. Studies have shown that in temperate regions, the overall yield level of rapeseed is higher than that in tropical or arid climate zones. Under full irrigation, Hyola401 (a mid-maturing variety) achieved the highest yield. Under water-limited conditions, RGS003 had the smallest yield decrease due to its strong drought tolerance (Rahimi-Moghaddam et al., 2021). These results emphasize the importance of environment-genotype interactions, and also suggest that in actual breeding, the most suitable variety type should be selected according to the climatic characteristics of the target ecological zone to balance drought resistance and high yield potential.

8 Challenges and Future Prospects

8.1 Limitations of current breeding and biotechnological approaches

There is still a gap in the understanding of the mechanism of action of the core regulatory factors of drought resistance. Taking the BnA.JAZ5 gene as an example, although it is known to be involved in the cross-regulation of the ABA and JA signaling pathways (Cao et al., 2022), the specific downstream target gene network and regulatory cascade still need to be further analyzed. The transcriptional heterogeneity of different genotypes under drought stress (Schiessl et al., 2020) has brought challenges to the development of universal molecular markers. To establish a stable and reliable drought resistance evaluation system, large-scale multi-environment experiments combined with rigorous molecular verification are required.

There are obvious technical bottlenecks in the current drought-resistant breeding methods. Most studies focus on the improvement of a single trait or gene, which is difficult to cope with the multidimensional regulatory characteristics of the complex trait of drought resistance. Although relevant functional genes such as ROS metabolism have been identified (Schiessl et al., 2020), there is a lack of a genetic framework that systematically integrates multiple signaling pathways. The disadvantages of long traditional breeding cycles and low efficiency have seriously restricted the selection and breeding of drought-resistant varieties. This urgently requires the combination of systems biology and intelligent algorithms to promote the transformation of the breeding paradigm from experience-oriented to mechanism-driven.

8.2 Integration of interdisciplinary strategies to enhance drought resistance

Improvement of the root system provides a new breakthrough for drought-resistant breeding. As the main organ for water absorption, the root system architecture directly affects the adaptability of plants in drought environments (Wu et al., 2018). By integrating root phenotypic groups and genomic data, an accurate drought resistance prediction model can be established. This multi-omics joint combat strategy will significantly improve the scientificity and predictability of breeding selection, and provide a new technical path to break through the current bottleneck of drought-resistant breeding.

Achieving breakthrough progress in drought-resistant breeding requires multidisciplinary collaborative innovation. The integration of cutting-edge technologies such as systems biology and artificial intelligence is driving the transformation of breeding models from experience-driven to data-driven. By constructing a multidimensional database covering genomes, phenotypic groups, and environmental groups, the genetic basis of drought resistance traits can be more comprehensively analyzed, providing theoretical support for precision breeding. This interdisciplinary collaboration model will effectively solve bottleneck problems such as the long cycle and low efficiency of traditional breeding.

At the same time, the continuous advancement of molecular breeding tools has also provided higher resolution for the analysis of drought resistance mechanisms. For example, whole genome association analysis (GWAS) has been used to screen multiple SNP loci closely related to water loss rate (WLR). As an important physiological parameter for measuring crop drought resistance, the exploration of the genetic basis of WLR has expanded the understanding of the regulatory network of drought resistance traits (Shahzad et al., 2021). The identification of these candidate genes not only provides clear targets for subsequent functional research, but also lays a solid molecular foundation for precision breeding in combination with conventional breeding processes. Through this molecular-phenotypic synergistic system, it is expected to accelerate the breeding process of drought-resistant rapeseed varieties in practice.

Furthermore, building a linkage mechanism between plant physiology, genomics and agronomic management is becoming an important direction to promote the improvement of crop drought resistance. In specific practice, optimizing water management strategies for different ecological regions and matching variety genotypes with environmental adaptability can significantly enhance the yield stability and drought resistance of rapeseed under variable climate conditions (Rahimi-Moghaddam et al., 2021). The introduction of systems biology provides theoretical support for the construction of multidimensional response mechanisms, and also provides a realistic path for creating a rapeseed production system with high adaptability and sustainable production potential in the future.

8.3 Impact of climate change on rapeseed drought resistance research

Climate change is constantly reshaping agricultural ecosystems, posing unprecedented challenges to rapeseed drought resistance research. With the increasing frequency of extreme weather events, droughts are not only more sudden, but also increasingly intense. This high variability makes environmental control in traditional breeding processes more complicated, and many experimental conditions are difficult to simulate stress scenarios under future actual climates (Wu et al., 2018). Therefore, when evaluating drought-resistant varieties, single-environment testing can no longer meet the goal of adapting to future climate needs.

What's more difficult is that drought often occurs together with other abiotic stresses such as high temperature and strong radiation, forming a multi-stress superposition effect. Studies have shown that the combined stress of drought and high temperature has a significant synergistic inhibitory effect on plant growth and yield performance, which puts higher demands on stress resistance research. Therefore, drought resistance research is gradually transforming to adaptive mechanisms under the background of multiple stresses. In-depth revelation of the interactions between these stresses and exploration of the key genetic and physiological mechanisms that control multi-stress tolerance will help to develop more forward-looking breeding strategies.

8.4 Policy and economic considerations in drought-resistant rapeseed breeding

The cultivation and promotion of drought-resistant rapeseed varieties cannot be separated from the dual drive of policy support and economic guidance. Strong institutional guarantees are particularly critical, which requires government departments to take practical measures in resource allocation and mechanism design - both to increase financial support for drought resistance research and to build a dynamic regulatory framework to regulate the agricultural application of biotechnology. It is worth noting that the improvement of the intellectual property system is also crucial, which is to stimulate innovation vitality and prevent technical barriers to ensure that new varieties can enter the market smoothly (Chaghakaboodi et al., 2021).

Market acceptance determines the actual promotion effect of drought-resistant varieties, and its core lies in whether it can create sustainable and stable economic benefits for farmers. The ideal drought-resistant characteristics should not be limited to the improvement of physiological parameters in the laboratory, but should be transformed into yield stability and risk resistance in field planting. To achieve this goal, single variety improvement is obviously not enough. A multi-dimensional support system must be established: lower the planting threshold through seed price subsidies, diversify production risks with the help of drought insurance, and introduce financial instruments to alleviate transformation pressure. This synergy between policy and market will not only significantly enhance farmers' willingness to plant, but also accelerate the realization of agricultural sustainable development goals.

9 Concluding Remarks

In recent years, research on the genetic mechanism of drought resistance in rapeseed has made important breakthroughs, and the functions of multiple key regulatory factors have been revealed one after another, laying a molecular foundation for analyzing the plant drought response network. Taking BnA.JAZ5 as an example, this protein regulates stomatal dynamics through the ABA signaling pathway and directly participates in the perception and transduction process of drought signals. It is worth noting that the DELLA family member BnaA6.RGA exhibits a unique regulatory function - it can cooperate with ABA signaling molecules to activate multiple drought resistance gene expression pathways, thereby significantly improving the plant's ability to adapt to water stress environments.

In terms of physiological performance, drought-resistant rapeseed varieties show multi-dimensional advantages. Its efficient antioxidant enzyme system can remove reactive oxygen in a timely manner and effectively reduce oxidative damage. These varieties also have stronger osmotic regulation capabilities, can better maintain chlorophyll content and inhibit MDA accumulation, and ultimately show a more stable physiological state and stronger stress resistance under drought conditions.

Further transcriptome analysis showed that drought-resistant varieties constructed a more efficient defense network at the genetic level. This network not only involves the ROS removal system, but also includes the precise regulation mechanism of the plant development cycle, so as to achieve rapid perception and dynamic adaptation to the drought environment. The above results have laid a theoretical foundation for the genetic improvement of rapeseed drought resistance in the future, and also provided a practical path for building an oilseed production system with environmental resilience.

As climate change continues to drive drought frequency and intensification, building a stable and efficient drought resistance strategy has become a key direction of agricultural research. The integration of traditional breeding experience and modern molecular breeding tools constitutes a realistic path to achieve precision breeding. For example, genome-wide association analysis (GWAS) and systematic identification of key drought-resistant genotypes provide strong support for the selection of breeding materials and the cultivation of new materials.

In addition, root traits show irreplaceable importance in drought adaptation. Varieties with deep roots and well-developed root branches have stronger water and mineral nutrient absorption capacity, which helps to alleviate the adverse effects of drought on plant growth. Future breeding strategies should fully integrate the traits of root development regulation and water use efficiency to improve resource adaptability.

It is worth noting that biological control agents such as Trichoderma harzianum have shown application potential in enhancing plant drought resistance. By affecting plant hormone balance and rhizosphere microecological system, they introduce eco-friendly intervention methods for sustainable agricultural systems.

Acknowledgments

Thank you very much to the reviewers for providing detailed comments and guidance on the manuscript of this study. The reviewers' keen insights into the issues and attention to detail have greatly benefited the author.

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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