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Genetic Improvement of Oil Yield and Quality in Brassica Crops under Climate Stress

Sehar Amin[1], Shayhaq Sayed[2], Samia Younas*[3], Iqra Ashrafi[4], Mohammad Fateh Sher Khan[5], Mohammad Ayoob[6], Osama Akbar[7]

[1] Centre of Agricultural Biochemistry and Biotechnology (CABB), University of Agriculture Faisalabad. seharamin393@gmail.com
[2] Govt of Balochistan Agriculture Cooperatives Department Agriculture Extension Date Farm Turbat. shayhaq.sayed@gmail.com
[3] Department of Botany, Bahauddin Zakariya University, Multan.
Corresponding Author; Samiayounas176@gmil.com
[4] Institute Department of Botany Hafiz Hayat Campus University of Gujrat. iqrachaudhary1000@gmail.com
[5] Department of Plant Breeding Genetics, University of Agriculture Faisalabad. fatehsherfatehsher891@gmail.com
[6] Department of Plant Breeding Genetics, University of Agriculture Faisalabad. ayoubkhoso992@gmail.com
[7] Department of Plant Breeding Genetics, University of Agriculture Faisalabad. osamashahwani0@gmail.com

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Abstract

Brassica oilseed crops (B. napus, B. juncea, B. rapa, B. carinata) rank as the world's second-largest source of vegetable oil, supplying 12–14% of global production and supporting food, biofuel, and industrial sectors valued at over US$67 billion. However, escalating climate stresses terminal heat, drought, salinity, and waterlogging severely impair reproductive success, seed filling, and oil biosynthesis, reducing yield and altering fatty-acid profiles toward less desirable compositions. This review synthesizes the genetic and physiological basis of oil yield and quality under stress, highlighting the polyploid complexity of U's Triangle genomes, key QTL hotspots (e.g., A09 for oil content, A06 for pod shatter resistance), and master regulators such as WRI1 and FAD genes. Advances in high-throughput genomics, GWAS, and multi-omics have pinpointed stable marker-trait associations and candidate genes, while CRISPR/Cas9-mediated editing (e.g., BnFAD2 and BnaEOD3 knockouts) has already delivered high-oleic and higher-seed-weight lines. Exploitation of crop wild relatives and landraces, combined with marker-assisted pyramiding, accelerated breeding platforms, and AI-driven predictive modeling, offers a clear pathway to climate-resilient, high-oil Brassica varieties. Recent releases such as Pusa Mustard 26 and double-zero B. juncea lines demonstrate that integrated genomic strategies can simultaneously enhance stress tolerance, oil content, and nutritional quality. Continued convergence of genome editing, spatial omics, and epigenome engineering will be essential to secure stable oil production under future climate scenarios.

Keywords: Brassica Napus, Brassica Juncea, Oil Yield, Abiotic Stress Tolerance, QTL mapping, GWAS, CRISPR/Cas9, Gene Pyramiding, U's Triangle, Crop Wild Relatives, Multi-Omics, Climate-Resilient Breeding, Fatty Acid Desaturase, WRI1

1. Introduction

The global production of oilseed crops is currently navigating a period of unprecedented volatility, driven by the dual pressures of an expanding human population and the increasingly erratic climatic conditions associated with anthropogenic environmental change (Borah et al., 2024). Brassica species, which include a diverse array of economically significant crops such as rapeseed (Brassica napus), Indian mustard (B. juncea), turnip rape (B. Rapa), and Ethiopian mustard (B. carinata), constitute the second largest source of vegetable oil worldwide (Sinha et al., 2025). These crops are not only vital for the global food supply, providing approximately 12% to 14% of the world's vegetable oil, but also serve as critical feedstocks for the biofuel, chemical, and pharmaceutical industries (Sun et al., 2026). The economic footprint of the Brassicaceae family is substantial, with the combined production value of broccoli, cabbages, cauliflower, mustard, and rapeseed estimated at approximately 67.5 billion US dollars as of 2020 (El-Esawi, 2020). However, the biological potential of these crops is increasingly constrained by abiotic stresses, including heat waves, prolonged droughts, soil salinity, and erratic waterlogging events, which threaten the stability of global oilseed yields (Shahsavari et al., 2025).

The genetic improvement of oil yield and quality under these stressors requires a sophisticated understanding of the complex interactions between plant physiology, metabolic networks, and the underlying genomic architecture (Tong et al., 2025). Oil content in Brassica is a polygenic quantitative trait governed by embryonic, cytoplasmic, and maternal genetic components, with broad-sense heritability (H2) estimates ranging from 30% to 70% (Sun et al., 2026). Achieving significant genetic gains necessitates the integration of high-throughput genomics, precise genome editing via CRISPR/Cas9, and systems biology approaches to identify and manipulate the regulatory hubs that coordinate stress resilience and lipid biosynthesis (Li et al., 2025).

2. Taxonomy and the Evolution of Brassica Oilseeds

The genus Brassica belongs to the tribe Brassiceae within the Brassicaceae family, which is one of the largest plant families, encompassing between 338 and 419 genera and upwards of 4,130 species (Raza et al., 2020). The evolutionary relationships among the primary cultivated Brassica species are traditionally described by the "U's Triangle," which illustrates the genomic connections between three diploid species B. rapa (AA, 2n=20), B. nigra (BB, 2n=16), and B. oleracea (CC, 2n=18) and their allotetraploid derivatives: B. juncea (AABB, 2n=36), B. napus (AACC, 2n=38), and B. carinata (BBCC, 2n=34) (Office of the Gene Technology Regulator, 2024).

This polyploid nature, particularly in B. napus and B. juncea, presents both opportunities and challenges for genetic improvement (Jabeen, 2020). While the presence of multiple homeologous gene copies provides a buffer against deleterious mutations and allows for sub-functionalization, it also complicates molecular breeding efforts, as targeting a specific trait often requires the simultaneous manipulation of redundant gene copies (Glombik et al., 2020). Understanding this genomic complexity is fundamental to leveraging the genetic diversity found in landraces and crop wild relatives (CWRs), which often possess rare alleles for stress tolerance that have been lost in elite modern cultivars through intensive selection for yield (Li & Gschwend, 2023). Recent multi-species graph pangenome analysis representing presence-absence variation across 41 Brassica genomes has further expanded our understanding of this genetic diversity (MacNish et al., 2025).

Table 1. Genomic Characteristics and Primary Uses of Major Cultivated Brassica Species

Species	Genome	Chromosome Number (2n)	Primary Use
Brassica rapa	AA	20	Oilseed (Turnip rape), Vegetables (El-Esawi, 2020; Office of the Gene Technology Regulator, 2024)
Brassica nigra	BB	16	Condiments (Black mustard) (Office of the Gene Technology Regulator, 2024)
Brassica oleracea	CC	18	Vegetables (Cabbage, Broccoli, Kale) (El-Esawi, 2020; Office of the Gene Technology Regulator, 2024)
Brassica juncea	AABB	36	Oilseed (Indian mustard), Condiments (El-Esawi, 2020; Office of the Gene Technology Regulator, 2024)
Brassica napus	AACC	38	Oilseed (Canola/Rapeseed), Forage (Adwiyah et al., 2025; Sun et al., 2026)
Brassica carinata	BBCC	34	Oilseed (Ethiopian mustard), Biofuel (Adwiyah et al., 2025; Sun et al., 2026)

3. Physiological Impact of Abiotic Stress on Oil Production

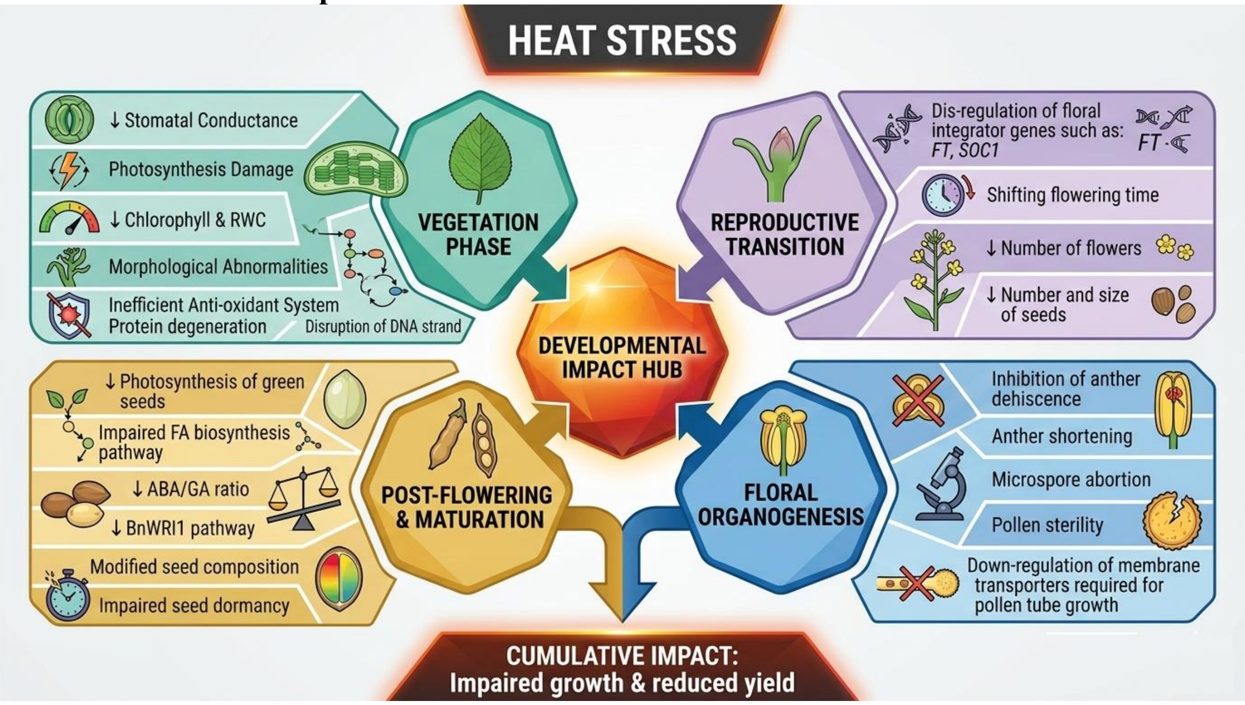
Abiotic stresses disrupt the delicate balance of carbon assimilation and resource partitioning required for optimal seed development and lipid accumulation. In Brassica crops, the reproductive phase and the subsequent seed-filling stage are the most vulnerable periods (Chen et al., 2025).

3.1 Heat Stress and Reproductive Failure

Heat stress is a major limiting factor, especially in regions experiencing terminal heat during flowering and pod-development. As C3 plants, Brassica species exhibit reduced photosynthetic efficiency and altered osmotic balance when temperatures exceed the optimal range, typically around 25 to 28 degrees Celsius (Bakhsh et al., 2025). High temperatures accelerate floral progression but significantly shorten the seed-filling duration, leading to reduced seed weight and oil content (Kumar et al., 2025).

The impact on reproductive organs is particularly severe. High temperatures during flowering cause pollen sterility and flower abortion by disrupting the accumulation of starch and sucrose in pollen grains (Pokharel, 2020). Furthermore, heat stress triggers an oxidative burst, with reactive oxygen species (ROS) accumulation detectable within 30 minutes of exposure (Kourani et al., 2022). This ROS accumulation leads to lipid peroxidation, measured by increased malondialdehyde (MDA) levels, which damages cellular membranes and inactivates enzymes essential for fatty acid synthesis (Dey et al., 2022).

Figure 1. Impact of Heat Stress on the Physiological, Developmental, and Reproductive Hubs of Oilseed Brassica Crops



3.2 Drought and Salinity: Osmotic and Ionic Challenges

Water deficit induces physiological drought by limiting the plant's ability to maintain turgor and uptake nutrients. Water movement through the soil-plant-atmosphere continuum is driven by differences in water potential (psi), comprising osmotic (psi-pi), matric (psi-m), pressure (psi-p), and gravitational (psi-g) components (Jayarathna, 2024).

Drought stress impacts development from germination through harvest. During germination, water absorption occurs in three phases: imbibition, activation, and emergence. Early-stage screening using polyethylene glycol (PEG-6000) has been used to identify drought-tolerant candidates (Bukhari et al., 2021). Salt-tolerant species like B. fruticulosa and certain B. napus cultivars manage ionic toxicity by maintaining a lower Na:K ratio in their leaves through selective K+ uptake and sequestration of Na+ in vacuoles (Dai et al., 2024).

3.3 Waterlogging and Root Hypoxia

Soil waterlogging creates a hypoxic environment in the root zone. Brassica napus is sensitive because it is unable to form aerenchyma tissue in its roots. This forces the plant to shift from aerobic respiration to less efficient fermentative pathways (Prasad & Ranjan, 2020). Waterlogging induces the expression of genes encoding fermentative enzymes, including pyruvate decarboxylase (PDC), lactate dehydrogenase (LDH), and alcohol dehydrogenase (ADH) (Ambros et al., 2022). These shifts are accompanied by the downregulation of genes involved in cell wall biogenesis, indicating suppressed growth and a reallocation of energy toward survival (Hussain, 2023).

4. Biochemical Pathways of Oil Biosynthesis and Quality

The quality of Brassica oil is determined by its fatty acid profile, particularly the proportions of oleic (C18:1), linoleic (C18:2), and linolenic (C18:3) acids (Patel et al., 2025).

4.1 Lipid Metabolism under Stress

The assembly of triacylglycerols (TAGs) involves enzymatic reactions where Fatty Acid Desaturase (FAD) genes determine the degree of unsaturation. Heat stress typically leads to a negative correlation between temperature and polyunsaturated fatty acids like C18:2 and C18:3, shifting metabolic flux toward saturated fatty acids (Adwiyah et al., 2025). CRISPR/Cas9-mediated knockout of the BnFAD2 gene has successfully produced high-oleic rapeseed lines. For industrial oils, high erucic acid (HEAR) varieties are desirable, but reaching levels beyond 50% remains a challenge (Liu et al., 2022).

4.2 Secondary Metabolites and Osmoprotectants

Brassica crops produce phytochemicals like glucosinolates, flavonoids, and carotenoids for stress mitigation. Heat stress can suppress glucosinolate biosynthesis in the silique wall to conserve energy (Borges et al., 2018). Flavonoids act as antioxidants to quench ROS generated during drought and heat. The accumulation of solutes such as proline, trehalose, and glycine betaine helps maintain cellular turgidity and protect macromolecules (Chen et al., 2025).

5. Genetic Architecture and Mapping of Stress Resilience

Mapping techniques like QTL mapping and Genome-Wide Association Studies (GWAS) are elucidating the genetic basis of oil content and tolerance (Babu et al., 2021).

- **Chromosome A09 Hotspot:** Identified as a significant region for seed quality, including color, oil, and protein. A candidate gene, BnaA09g48250D, significantly increases seed oil content when overexpressed (Li et al., 2025).
- **Pod Shatter Resistance:** A stable QTL, qSRI.A06, and its candidate gene BnaA06g27900D, involved in cell wall development, have been identified (Wang et al., 2025).
- **GWAS in Indian Mustard:** A study on 142 genotypes identified 49 marker-trait associations (MTAs) for oil content and glucosinolates, with twelve stable associations identifying 31 candidate genes involved in biosynthesis (Altaf et al., 2024).

6. Regulatory Networks and Systems Biology

Adaptation is governed by transcription factors (TFs), long non-coding RNAs (lncRNAs), and epigenetic modifications.

- **Transcription Factors:** WRINKLED1 (WRI1) is the master regulator of oil biosynthesis (Sun et al., 2026). WRKY, DREB, and NAC families orchestrate induction of genes for ABA signaling and cell wall reinforcement (Shahsavari et al., 2025).
- **Epigenetics and lncRNAs:** lncRNAs like SVALKA and CIL1 regulate temperature tolerance, while DANA2 and DRIR are involved in drought response. Alternative splicing also plays a role in forming priming-induced heat-stress memory (Dey et al., 2022).

7. Genome Editing and Precision Breeding

The development of CRISPR/Cas9 and associated technologies has revolutionized the ability to achieve precise genetic gains in Brassica crops (Goutam et al., 2026).

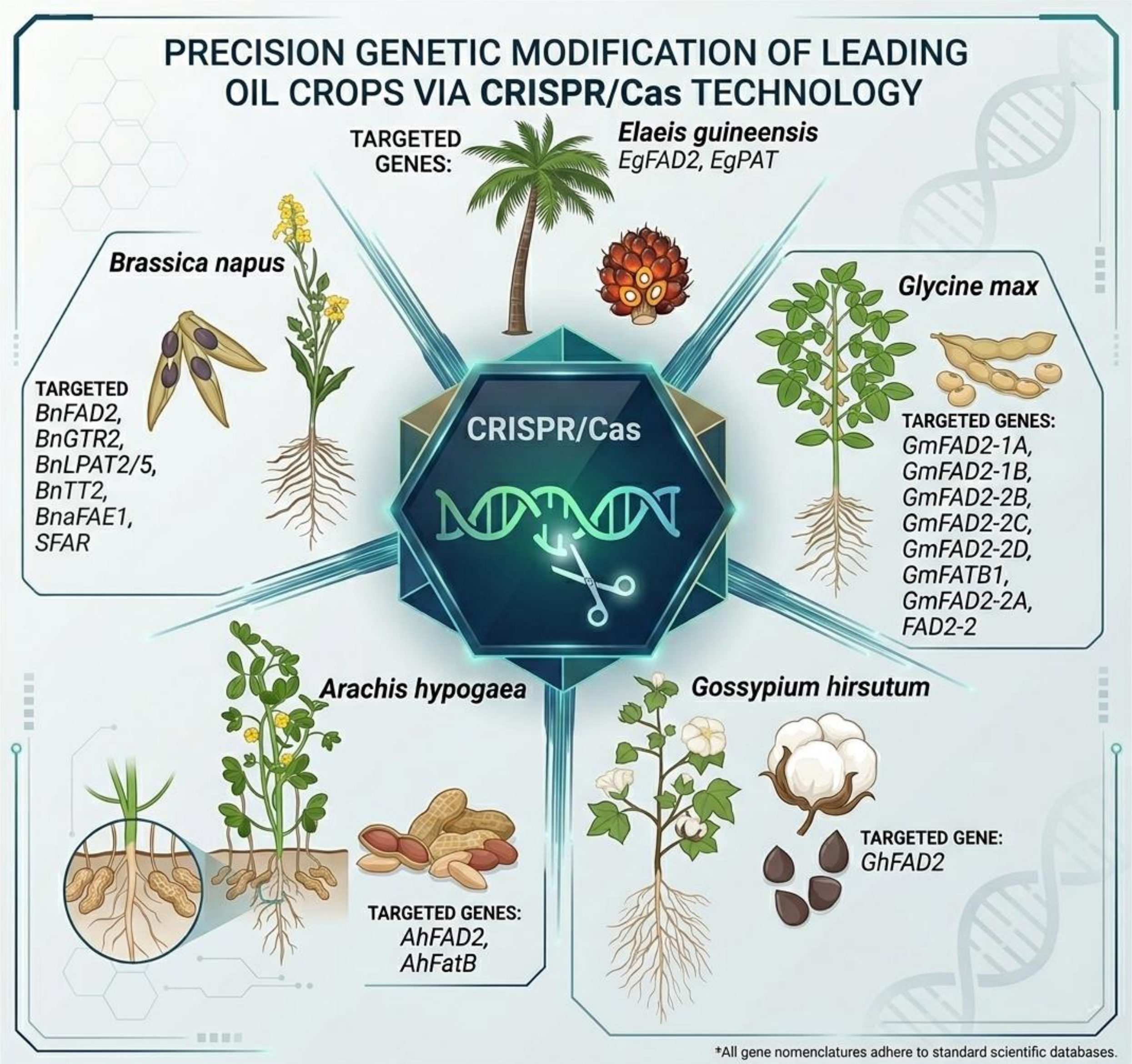
7.1 CRISPR/Cas9 Applications in Brassica

CRISPR/Cas9 is particularly valuable for polyploid species like rapeseed, where it can be used to target multiple homeologous gene copies simultaneously. Recent advancements have enabled yield improvement through the targeted mutation of BnaEOD3 copies, which resulted in a 13.9% increase in seed weight per plant (Adwiyah et al., 2025).

7.2 Integration with Modern Breeding Platforms

Modern breeding strategies, such as the Accelerated Breeding Modernization (ABM-BOx) framework, integrate CRISPR editing with genomic selection and predictive breeding. These strategies aim to increase selection intensity and accuracy while drastically shortening the breeding cycle (Sun et al., 2026).

Figure 2. Strategic CRISPR/Cas-Mediated Gene Editing Targets for Enhancing Oil Quality and Yield in Major Oilseed Species



8. Exploiting Genetic Diversity: Wild Relatives and Landraces

The narrow genetic base of elite cultivars necessitates exploring crop wild relatives (CWRs) and landraces (El-Esawi, 2020).

8.1 The Potential of Crop Wild Relatives (CWRs)

CWRs have withstood thousands of years of environmental fluctuations and possess diverse resistance genes. For example, Sinapis alba and B. fruticulosa are known for exceptional heat and salt tolerance. Interspecific hybridization is a sustainable approach to enhancing crop adaptability (Kumar et al., 2023).

8.2 Introgression Lines and Bridge Species

Interspecific hybridization, such as developing B. juncea introgression lines from B. carinata, has identified additive QTLs for drought tolerance. These segments were primarily located on the B genome of B. juncea, highlighting the importance of the BB subgenome in abiotic stress resilience (Limbalkar et al., 2023).

Table 2. Overview of Genetic Resources and Contributed Traits for Brassica Improvement

Genetic Resource	Species/Source	Contributed Trait
Wild Relatives	Brassica fruticulosa	White rust resistance, Salt-alkalinity tolerance (El-Esawi, 2020; Bayer, 2025)
Wild Relatives	Sinapis alba	Exceptional Heat and Drought tolerance (El-Esawi, 2020)
Wild Relatives	Diplotaxis tenuifolia	Salt tolerance and Early maturity (El-Esawi, 2020)
Landraces	Indian traditional (e.g., Varuna)	Adaptation to low-input and rainfed systems (El-Esawi, 2020)
Landraces	Himalayan Mustard	Cold tolerance, unique glucosinolate profiles (El-Esawi, 2020)

9. Case Studies: Developing Climate-Resilient Varieties (2020–2025)

9.1 Indian Mustard (B. juncea) Breakthroughs

In India, breakthroughs include varieties like Pusa Mustard 26 (NPJ-113), which was released for terminal heat tolerance, outyielding check varieties in multi-location trials. Additionally, the first double-zero quality varieties, Pusa Double Zero Mustard-35 and 36, maintain high yield while providing low erucic acid and low glucosinolates (Indian Agricultural Research Institute, 2024).

9.2 Global Canola (B. napus) Developments

Global canola development has produced near-homozygous cultivars like Amanda (winter) and Clearwater (spring), selected for high adaptability to dryland regions (Office of the Gene Technology Regulator, 2024). In temperate regions like Kashmir, KGS53 was consistently identified as the most stable and highest-yielding B. napus genotype across multi-year trials (Mishra et al., 2023).

10. Future Outlook and Emerging Technologies

The future of genetic improvement in Brassica will be shaped by the convergence of multi-omics, AI, and high-precision engineering (Syeda, 2025).

10.1 AI and Predictive Breeding

The integration of multi-omics data with climate models using AI-based predictive breeding will allow researchers to design "climate-smart" varieties optimized for specific future environments. AI-driven models like YOLOv5 are already being adapted for automated pest identification in the field (Bakhsh et al., 2025).

10.2 Single-Cell and Spatial Omics

Emerging tools like single-cell RNA sequencing (scRNA-seq) and spatially resolved metabolomics offer resolution to map cell-type specific responses, such as those protecting reproductive cells during heatwaves (Glombik et al., 2020).

10.3 Epigenome and 3D Genome Editing

Beyond traditional gene editing, the manipulation of the epigenome and 3D genome architecture offers a promising avenue to fine-tune the expression of metabolic genes without introducing transgenes (Li et al., 2025).

11. Conclusions

The genetic improvement of oil yield and quality in Brassica crops under climate stress has transitioned from empirical selection to precision genome engineering, offering realistic solutions to one of agriculture's most pressing challenges. By leveraging the rich allelic diversity in crop wild relatives, mapping stable QTLs and MTAs, and deploying CRISPR/Cas9 for targeted editing of key regulatory hubs (WRI1, FAD2, EOD3), breeders have already produced high-oleic, stress-tolerant, and high-yielding varieties that maintain commercial quality under heat, drought, and salinity. The polyploid nature of modern Brassica genomes, once a breeding obstacle, now provides multiple homeologous targets for simultaneous improvement of oil content, pod shatter resistance, and stress resilience. Integration of multi-omics, AI-powered predictive breeding, and spatially resolved metabolomics will further accelerate the design of "climate-smart" ideotypes tailored to specific agro-ecological zones. To realize this potential at scale, coordinated international efforts are required strengthening germplasm conservation, harmonizing regulatory frameworks for genome-edited crops, and establishing participatory seed-delivery systems for smallholder farmers. Only through such an integrated, forward-looking approach can the Brassica oilseed complex continue to underpin global food security, sustainable bioenergy, and rural economies in an increasingly unpredictable climate.2.3sFast

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