**Bridging the Genetic Gap: Utilization of Wild Relatives and Landraces in *Brassica juncea* Improvement Programs**

**ABSTRACT**

Brassica juncea (Indian mustard) is a vital oilseed crop cultivated extensively in South Asia and other parts of the world for its adaptability and nutritional value. However, its genetic base has been significantly narrowed due to prolonged selection for high yield and uniformity, rendering modern cultivars vulnerable to biotic and abiotic stresses. This review explores the critical role of underutilized genetic resources, specifically wild relatives and landraces in enhancing the genetic diversity and adaptive potential of B. juncea. Wild species such as Brassica fruticulosa, Sinapis alba, and Diplotaxis spp. possess genes for disease resistance, drought and salinity tolerance, and unique agronomic traits. Landraces, on the other hand, represent farmer-selected, locally adapted populations rich in resilience and quality attributes. Both genetic sources are instrumental for breeding climate-resilient and nutritionally enriched cultivars. The study discusses key breeding strategies including conventional approaches (hybridization, backcrossing, recurrent selection), molecular tools (QTL mapping, GWAS, marker-assisted selection, genomic selection), and cutting-edge biotechnologies such as CRISPR/Cas9 and omics platforms. The paper also highlights genome-wide studies that have identified domestication-related loci associated with flowering time and stress adaptation. Despite notable advances, the utilization of wild and landrace germplasm faces challenges like linkage drag, reproductive barriers, and insufficient pre-breeding infrastructure. Addressing these constraints through participatory breeding, public-private partnerships, and climate-smart breeding frameworks is essential. By integrating genetic diversity with advanced breeding tools, B. juncea improvement programs can be revolutionized to meet future demands of food security, sustainability, and climate resilience.

***Keywords****:* Brassica juncea*, genetic diversity, wild relatives, landraces, genomic breeding, climate resilience*

1. **INTRODUCTION**

Crop wild relatives are the weedy, wild relatives of domesticated plants, which usually occur and are maintained mostly in their centers of origin. They have been left unexploited in nature because of the presence of some undesirable genes/alleles contributing as yield barriers. Over the years, these wild relatives have withstood the selection pressure of various biotic and abiotic stress factors, developed the resistance mechanisms gradually and inherited it over the generations (Kashyap et al., 2022). Brassica juncea *(Indian mustard) holds a prominent place in global agriculture, not only as a key oilseed* crop but also for its multifaceted roles in nutrition, industry, and sustainability. As one of the most widely cultivated species in the Brassica genus, it is known for its adaptability to marginal environments, short growing period, and compatibility with diverse cropping systems. Over the past few decades, B. juncea has gained importance not only in traditional growing regions like the Indian subcontinent but also in countries like Canada and Australia, where it is used as an alternative to canola in water-limited areas (Yadava et al., 2012). The increasing global demand for edible oils, biofuels, and sustainable farming inputs has driven renewed attention to Brassica crops. Among them, B. juncea stands out for its ability to thrive under conditions of drought, heat, and soil salinity challenges that are becoming more pronounced due to climate change (Panjabi et al., 2019). Its naturally deep root system, early maturity, and resistance to pod shattering make it suitable for cultivation in dryland and low-input systems, especially in South Asia and Africa. Additionally, the seed meal, a byproduct of oil extraction, is rich in protein and serves as a valuable feed source, while the leaves and young shoots are used as green vegetables in several cuisines. Given its central role in food security and sustainable agriculture, especially in Asia, *B. juncea* requires a strategic approach to broaden its genetic base. The underexploited diversity in wild relatives and landraces, when coupled with advanced genomic tools, offers promising prospects for trait enhancement. Incorporating diverse gene pools through modern breeding, QTL mapping, and marker-assisted selection can lead to the development of high-yielding, climate-resilient cultivars (Bisen et al., 2025).

However, the intensification of breeding programs over the last few decades has led to the selection of a relatively narrow set of elite genotypes, often prioritizing traits such as oil content and erucic acid levels. As a result, a significant portion of the crop’s genetic diversity has been underutilized or lost. This narrowing of the gene pool has limited the scope of future genetic gains, particularly in improving resistance to pests, diseases, and emerging environmental stresses (Dormatey et al., 2020). To address this, researchers and breeders are turning toward the vast yet underexplored reservoirs of genetic diversity found in wild relatives and landraces of Brassica juncea and related species. These genetic resources often possess rare and valuable traits such as tolerance to extreme temperatures, resistance to diseases like white rust and Alternaria blight, and unique quality attributes (Bhawani et al., 2021). The challenge lies in identifying, conserving, and integrating these traits into modern breeding pipelines without compromising agronomic performance.

The integration of modern genomic tools such as genome-wide association studies (GWAS), marker-assisted selection (MAS), and genomic selection (GS) with conventional breeding and pre-breeding approaches offers new avenues for accelerating the use of wild and traditional genetic materials (Khan et al., 2024). Advances in molecular biology, particularly in genome editing and transcriptomics, have further enhanced our ability to mine, characterize, and utilize desirable genes. This review aims to explore the untapped potential of wild relatives and landraces in B. juncea improvement, focusing on their role in diversifying the genetic base, enhancing resilience, and meeting the future demands of sustainable agriculture. By leveraging these genetic resources, we can overcome current breeding limitations and develop climate-resilient, high-yielding, and nutritionally rich cultivars to support both food and economic security.

### **1.1 Importance of Brassica juncea in Global Agriculture**

Brassica juncea (Indian mustard) is a versatile and widely cultivated species of the Brassicaceae family, serving multiple roles across diverse agroecosystems as an oilseed, leafy vegetable, condiment, green manure, and fodder crop. As a resilient alternative to canola (B. napus), B. juncea exhibits exceptional tolerance to heat, drought, and pod-shattering traits that help sustain production in semi-arid and temperate regions with short growing seasons (Anjum et al., 2024). It is among the world's top three edible oilseed crops after palm and soybean with significant acreage in South Asia, especially India (over 6 million hectares), as well as expanding cultivation in Canada, Australia, and parts of Europe.

### **1.2 Economic and Nutritional Significance**

The seeds of B. juncea are rich in oil (30–45%) and protein (20–45% in meal), making it both an economically valuable and nutritionally important crop (Rai et al., 2022). Mustard oil, prized for its distinctive pungency, is extensively used in cooking, pickling, and condiment preparation, and its beneficial fatty acid profile, including omega‑3s, omega‑6s, and tocopherols supports cardiovascular health and antioxidant activity. Additionally, oil-extracted meal serves as a high-quality animal feed comparable to soybean meal, and its bioactive glucosinolates and polyphenols contribute to soil health, biopesticidal properties, and potential medicinal applications (Nehmeh et al., 2022).

### **1.3 Genetic Bottlenecks in Modern Cultivars**

Despite its agricultural prominence, B. juncea shows a limited genetic base, an outcome of its allotetraploid origin and intensive selection toward high-yielding, quality traits. Modern breeding has often focused on reducing undesired compounds like erucic acid and glucosinolates (“double-low” traits), inadvertently diminishing genetic diversity (Saini et al., 2020). Genomic studies reveal that strong selection pressure and linkage among QTLs for oil and protein content have led to genetic constraints, limiting progress in simultaneously improving yield, nutritional quality, and stress resilience (kumar et al., 2021). Moreover, yields have plateaued, with recent stagnation exacerbated by increased climate variability, emerging pests, and diseases.

**1.4 Need for Utilizing Diverse Germplasm**

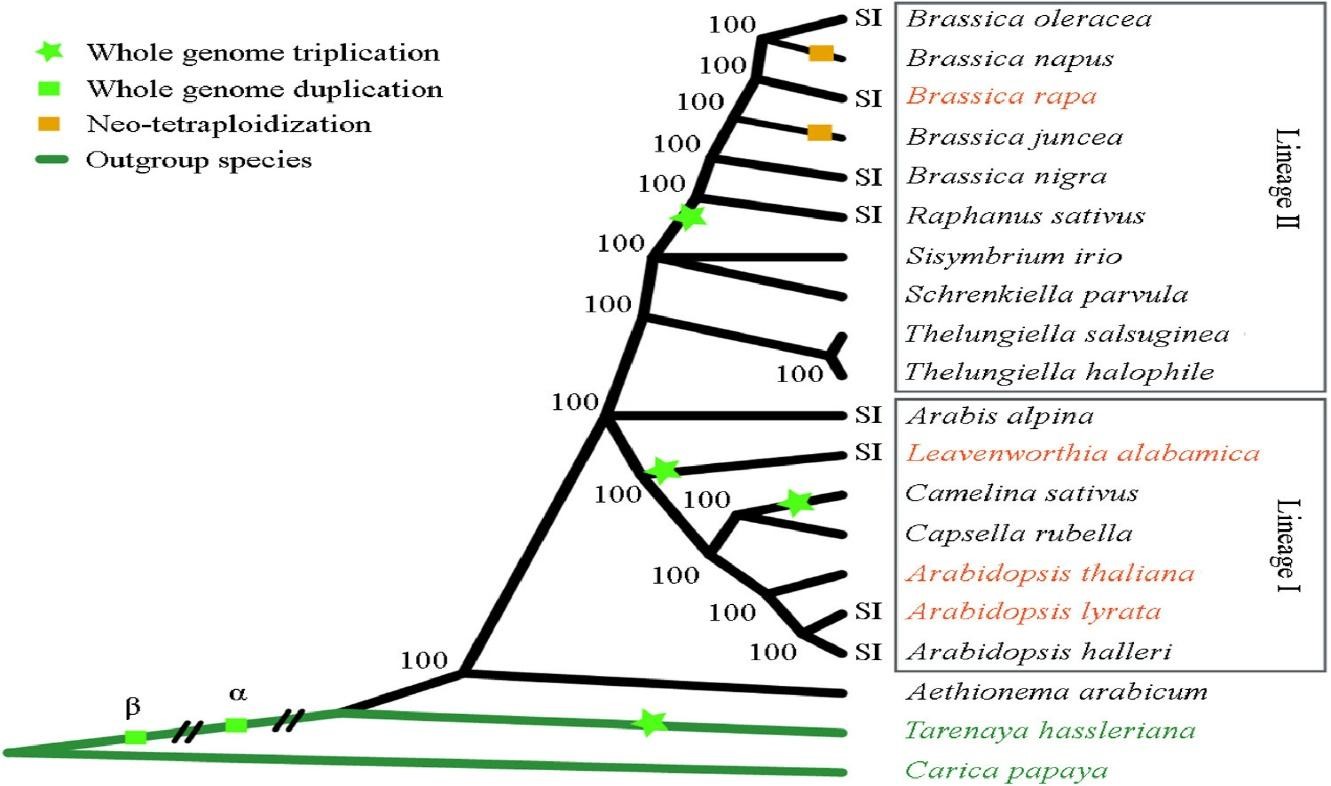
To overcome these genetic limitations, integrating genetic variation from wild relatives and landraces is essential. Wild species like B. rapa, B. nigra, and others harbor alleles associated with biotic and abiotic stress tolerance traits often absent in elite cultivars (Pant et al., 2022). Pre-breeding strategies using interspecific hybridization, embryo rescue, and introgression have successfully broadened genetic diversity, unlocking novel phenotypes for seed weight, flowering time, and stress adaptation. Additionally, landraces maintained by farmers in diverse agro-ecologies carry locally adapted traits and phytochemicals such as high tocopherol content, glucosinolates, and polyphenols that can fortify modern breeding lines (Yadav & Upsana, 2024). Thus, conserving, characterizing, and deploying this rich genetic reservoir is critical to enhancing B. juncea for resilience, productivity, and nutritional value in the face of climate change, evolving pest pressures, and global food security demands.

## 2. Genetic Diversity in Brassica juncea

### **2.1 Origin and Domestication History**

Brassica juncea is an allotetraploid species (AABB, 2n = 36) that originated from a natural hybridization between the diploid species B. rapa (AA, 2n = 20) and B. nigra (BB, 2n = 16). Genomic analyses of 480 accessions support a single origin in West Asia approximately 8,000–14,000 years ago, with at least three independent domestication events as the crop spread eastward, contributing to the evolution of diverse crop types for seed, vegetable, root, and stem uses (Zohary et al., 2012). Domestication may date back to around 3000 BC, with evidence in ancient Sanskrit and Sumerian texts. While there is some debate historical interpretations suggest both monophyletic and polyphyletic origins modern genome sequencing leans toward a primary center in West Asia followed by eastward migrations via Central Asia into China and India, leading to the emergence of secondary diversity centers.

Fig. 1 illustrates phylogenetic relationships among *Brassica* and related genera highlighting key evolutionary events, including whole-genome triplication (WGT), duplication, and neo-tetraploidization (Cui et al., 2020). The tree reveals two major lineages Lineage I (e.g., *Arabidopsis thaliana*, *Camelina sativa*) and Lineage II (e.g., *Brassica juncea*, *B. rapa*, *B. nigra*) which diverged after several shared polyploidy events. *Brassica juncea*, an allotetraploid, arose through natural hybridization between *B. rapa* (AA genome) and *B. nigra* (BB genome), as marked by neo-tetraploidization events (orange squares). The tree also shows high bootstrap support (100%) across nodes, reinforcing the robustness of inferred relationships. Outgroup species such as *Carica papaya* and *Tarenaya hassleriana* help root the phylogeny and trace genome evolution (Paterson et al., 2008). This genomic context provides critical insight into the origin and diversification of *B. juncea* within the *Brassicaceae* family, emphasizing the evolutionary mechanisms that shaped its genetic architecture.

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**Fig. 1. Phylogenetic tree showing the evolutionary relationships among Brassica species. (Source: Cui et al., 2020).**

### **2.2 Current Genetic Base of Cultivated Varieties**

Modern cultivated B. juncea exhibits measurable genetic diversity across global regions. For instance, genome resequencing of 193 accessions from China’s Yunnan‑Guizhou Plateau revealed over 1 million high-quality SNPs and more than 3 million InDels, which formed four distinct genetic groups (Yuan et al., 2023). These groupings shed light on the crop’s spread, adaptation, and trait diversification like seed color and fatty acid composition. Yet, Chinese accessions typically display higher allelic richness and private alleles compared to Indian varieties. In India, molecular marker studies using SSRs and RAPDs demonstrate structured diversity but often reveal narrow genetic differentiation among major cultivars, underscoring the influence of breeding selection and pedigree reuse (Bunjkar et al., 2024).

### **2.3 Limitations in Available Genetic Variation**

Despite some intra-specific diversity, B. juncea suffers from a relatively narrow genetic base, particularly within modern varieties. RAPD analyses of 45 genotypes showed high similarity among oilseed cultivars (similarity coefficients of 0.77–0.99), indicating low polymorphism (Kalita et al., 2007). SSR-based studies of 135 germplasm accessions confirmed limited variability in maturity-related traits but broader variation in yield components signaling that only certain traits retain adequate genetic diversity. The restricted geographical spread of breeding programs, primarily in Northern India, combined with widespread use of elite varieties like 'Varuna' in over 38 derived cultivars, has further narrowed the gene pool (Aruna et al., 2018). This bottleneck limits breeders’ ability to introduce new traits for stress tolerance, nutrition, and yield enhancement, and complicates efforts to adapt to evolving environmental and pest pressures. Together, these findings highlight both the complex domestication history and the current limitations in genetic variability within B. juncea. While population genomics has revealed valuable allelic diversity especially in regions like China concerted efforts are required to tap underutilized germplasm and introduce novel diversity into breeding pipelines. Without such actions, the crop’s capacity to adapt to future challenges will remain constrained.

## 3. Role of Wild Relatives in Crop Improvement

### **3.1 Identification of Wild Relatives and Their Traits**

Crop wild relatives (CWRs) of Brassica juncea, such as Sinapis alba, B. fruticulosa, B. tournefortii, Diplotaxis erucoides, Crambe abyssinica, and Erucastrum gallicum represent a valuable source of genetic diversity (Sharma et al., 2022). These species have evolved in diverse habitats, developing resilience to multiple stresses. For instance, S. alba and B. fruticulosa demonstrate tolerance to drought and salinity, while D. erucoides exhibits strong resistance to Alternaria brassicae due to high glucosinolate production. The identification of these species and their traits is the crucial first step toward enriching the B. juncea gene pool.

### **3.2 Traits of Interest from Wild Germplasm**

#### **3.2.1 Biotic Stress Resistance**

Wild species offer valuable resistance traits against pests and diseases that are weak or absent in elite cultivars. For example, Diplotaxis erucoides exhibits strong inducible glucosinolate-mediated defense against Alternaria blight compared to cultivated lines, making it a target for resistance breeding. Moreover, introgression lines from B. fruticulosa demonstrate significant aphid resistance, making them promising for QTL mapping and marker-assisted selection.

#### **3.2.2 Abiotic Stress Tolerance (Drought, Salinity, Temperature)**

Several wild relatives of B. juncea, including S. alba and B. fruticulosa, have adapted to habitats with water scarcity and salinity stress. These species maintain higher proline levels and exhibit lower yield loss under drought. Rooted in their ability to germinate under PEG-induced osmotic stress, they carry genes that regulate water-use efficiency and stress-responsive pathways—traits largely absent in modern cultivars.

#### **3.2.3 Novel Agronomic Traits**

Wild relatives can also contribute unique agronomic characteristics such as branching architecture, flowering time regulation, and cytoplasmic male sterility (CMS), all valuable for hybrid breeding. For example, somatic hybrids between S. alba and B. juncea have introduced CMS, enabling male sterility systems crucial for hybrid seed production (Gautam et al., 2023). Additionally, S. alba-derived candidate genes have been associated with improved branching patterns in re-synthesized lines.

### **3.3 Pre-breeding and Introgression Strategies**

Due to ploidy barriers, pre-breeding techniques like wide hybridization, embryo rescue, somatic hybridization, and protoplast fusion are often necessary. For instance, S. alba and B. fruticulosa were successfully somatically fused with B. juncea, and resistant hybrids were backcrossed to recover fertility and stress tolerance traits. Somatic hybrids provided CMS lines and maintained donor traits across backcross generations. Emerging OMICS technologies such as transcriptomics, QTL mapping, and marker-assisted breeding are critical for characterizing introgressions and efficiently transferring complex traits (Rajendra, 2025).

### **3.4 Challenges in Utilizing Wild Germplasm**

Despite their benefits, using wild genes presents significant challenges. Intergeneric crosses often suffer from hybrid sterility, abnormal meiosis, and linkage drag, unintended transfer of undesirable alleles and infertility, complicating breeding cycles. Cytogenetic instability and post-fertilization barriers frequently cause embryo abortion, necessitating laborious embryo rescue and in vitro techniques (Rogo et al., 2023). Additionally, introduced CWR traits may negatively impact agronomic performance, requiring extensive backcrossing to eliminate unwanted traits. Finally, limited characterization of wild germplasm at molecular and phenotypic levels hinders selection efficiency and integration into breeding programs.

## 4. Significance of Landraces in Brassica juncea Breeding Programs

### **4.1 Definition and Characteristics of Landraces**

Landraces are locally adapted, historically cultivated plant populations that have evolved through natural and farmer-driven selection over generations. Unlike modern hybrids or pure lines, landraces display substantial genetic heterogeneity, featuring wide variation in traits such as morphology, maturity, yield, flavor, and adaptation to local environmental stresses. Their resilience to local pests, climate, and cultural practices makes them valuable reservoirs of adaptive traits often lost in modern elite varieties.

### **4.2 Landraces as a Source of Adaptation and Resilience**

Landraces embody resilience acquired through prolonged exposure to specific agroecological conditions. In Brassica crops, traditional varieties have demonstrated tolerance to drought, temperature fluctuations, pest pressures, and low-input environments. For instance, mustard landraces conserved by Indian farmers exhibit better performance under variable rainfall and heat stress compared to uniform commercial cultivars. Such resilience traits are critically important for addressing climate variability and emerging pests, and can be effectively mobilized in modern breeding programmes.

### **4.3 Success Stories of Landrace-Based Improvement**

Several breeding success stories stem from landrace-derived traits. In India, high-yielding B. juncea varieties such as Varuna, Pusa Bold, and RH-749 have inherited earliness, stress tolerance, and improved oil quality traits originally present in traditional landraces (Raina, 2022). In broader Brassica vegetable crops, revitalization of heirloom varieties through on-farm selection and participatory breeding in Europe and North America has led to the release of locally adapted open‑pollinated varieties that meet organic farmers’ needs for flavor and regional adaptation.

### **4.4 On-farm Conservation and Participatory Breeding**

On-farm conservation of landraces, supported by participatory plant breeding (PPB), empowers farmers to maintain and evolve seed diversity in their fields, integrating traditional knowledge with scientific techniques (Fadda et al., 2020). Farmer-led selection ensures that breeding priorities align with local preferences, yield stability, taste, stress adaptation, and market needs. Case studies illustrate that farmers effectively screen for yield and consumer-preferred traits, and PPB initiatives have successfully reintroduced and scaled heritage varieties e.g., in organic tomato programmes and traditional maize cultivars. While PPB is less common in B. juncea, its relevance is growing among smallholder communities seeking seed sovereignty and agroecological resilience.

The practical utility of wild relatives and landraces in *Brassica juncea* improvement is increasingly recognized due to their ability to introduce novel alleles for stress resilience, yield stability, and nutritional quality. These genetic resources offer a rich repertoire of traits absent in modern cultivars, many of which have been narrowed through intensive selection for high yield. Wild relatives like *Brassica fruticulosa* and *Sinapis alba* have contributed resistance to white rust and tolerance to heat and drought, respectively, and have been successfully utilized in backcross breeding and pre-breeding pipelines (Verma et al., 2023). Similarly, landraces such as Indian traditional varieties (e.g., Varuna, Rohini) and Himalayan mustard populations are known for their adaptive plasticity, cold tolerance, and favorable quality traits under low-input environments. These attributes make them highly valuable for participatory breeding programs and region-specific cultivar development. The summary of these key contributions is presented in **Table 1**, which highlights the specific species, traits contributed, and their relevance in breeding programs. This compilation underscores how integrating underexploited germplasm sources with conventional and molecular tools can strategically address the current challenges of yield stagnation and climate vulnerability in mustard production.

**Table 1. Key Traits Contributed by Wild Relatives and Landraces for Genetic Improvement in** Brassica juncea

| **Genetic Resource** | **Species/Source** | **Trait Contributed** | **Application in Breeding** |
| --- | --- | --- | --- |
| **Wild Relatives** | Brassica fruticulosa | Resistance to white rust (Albugo candida) | Used in backcross breeding for biotic stress resistance |
| Sinapis alba | Heat and drought tolerance | Pre-breeding for climate resilience |
| Diplotaxis tenuifolia | Salt tolerance, early maturity | Donor for abiotic stress breeding |
| Brassica tournefortii | High oil content, pest resistance | Trait introgression under controlled conditions |
| **Landraces** | Indian traditional landraces (e.g., Varuna, Rohini) | Adaptation to low-input conditions, yield stability | Direct use in participatory breeding and stress selection |
| Himalayan mustard landraces | Cold tolerance, rich glucosinolate profile | Screening for quality traits and regional adaptation |
| Ethiopian mustard (B. carinata) | Water use efficiency, disease tolerance | Used as bridge species for interspecific hybridization |

## 5. Breeding Approaches for Genetic Enhancement

### **5.1 Conventional Breeding**

***5.1.1 Hybridization***

Traditional breeding through deliberate hybridization remains a cornerstone in Brassica juncea improvement. Crosses between elite and diverse parental lines aim to combine complementary traits such as high seed yield and stress tolerance. An example is the hybrid DMH‑11, which achieved 19–40% yield heterosis over elite varieties in multi-location trials.

***5.1.2 Backcrossing***

Backcross breeding is extensively used to introgress specific traits, such as disease resistance from donor into elite backgrounds while retaining optimum agronomic performance. Marker-assisted backcrossing integrates molecular markers to accelerate recovery of the recurrent parent genotype with the target trait.

***5.1.3 Recurrent Selection***

Recurrent selection involves selecting and intercrossing the best-performing individuals over successive generations to accumulate favorable alleles. For B. juncea, it has enabled stacking of QTLs for yield under water-limited conditions, especially when used in combination with MAS to maintain key agronomic qualities (Lokeshkumar et al., 2025).

### **5.2 Molecular Breeding Techniques**

***5.2.1 QTL Mapping & Marker-Assisted Selection (MAS)***

High-resolution linkage maps constructed with SNPs, SSRs, and AFLPs have facilitated the identification of QTLs linked to traits such as white rust resistance, seed glucosinolate content, oil composition, and seed coat colour (Yadava & Ramchiary, 2022). These QTLs are actively used in MAS to accelerate breeding cycles and efficiently integrate complex traits.

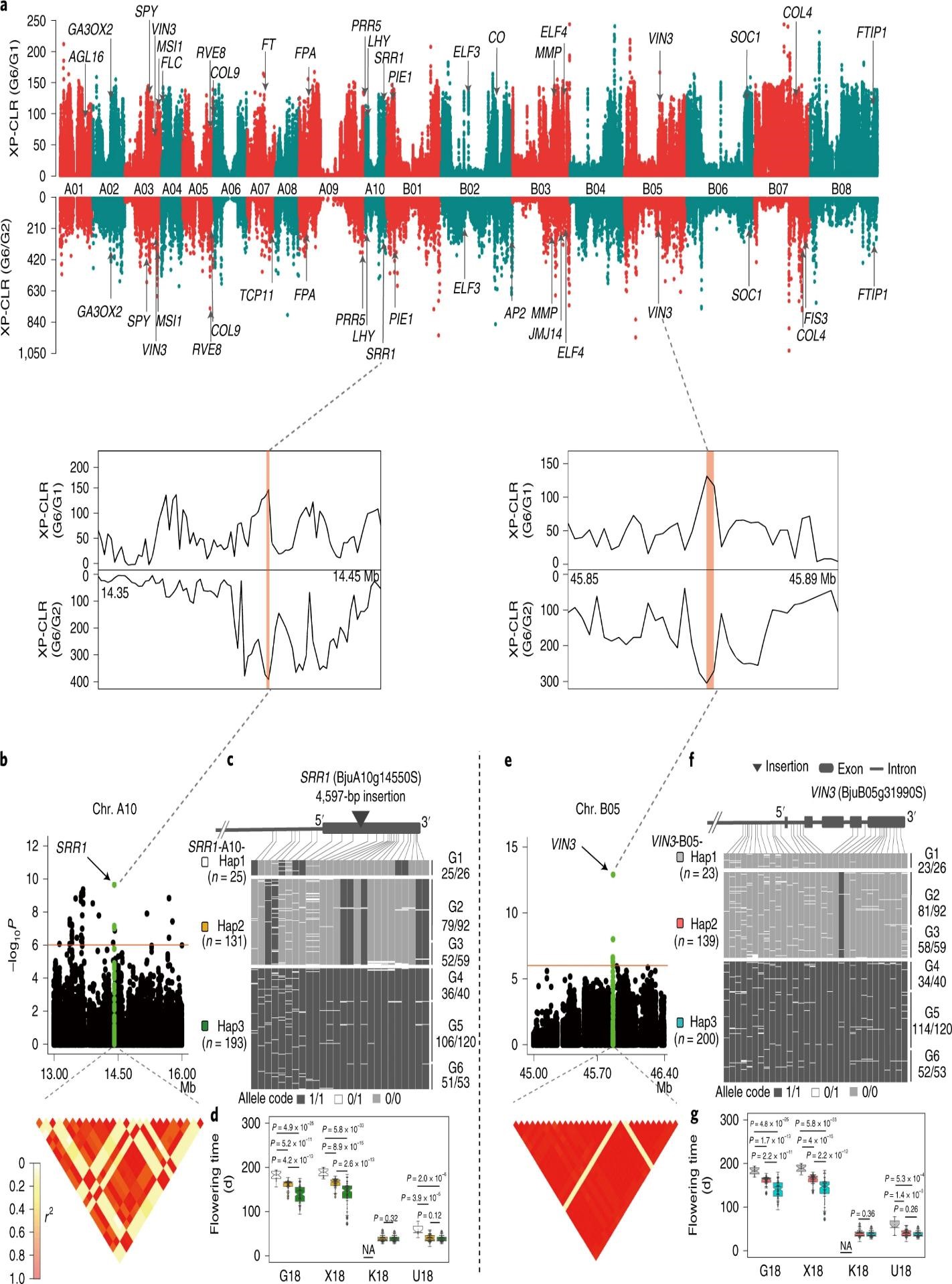
***5.2.2 Genomic Selection***

Genomic selection (GS) leverages genome-wide marker information to predict breeding values across complex traits. GS increases selection accuracy and throughput, especially for polygenic traits, outperforming traditional MAS techniques by considering the collective effect of all markers.

***5.2.3 Genome-Wide Association Studies (GWAS)***

GWAS analyzes genetic associations across diverse germplasm collections to identify marker-trait correlations. In B. juncea, GWAS has elucidated genetic loci for disease resistance, quality components, and yield traits complementing QTL mapping and enabling the inclusion of novel alleles from underexplored germplasm (Kang et al., 2022). Though still emerging in mustard, its integration with QTL data promises more precise marker development.

Fig. 2 presents a comprehensive genome-wide scan for selection signals and association with flowering time in *Brassica juncea*, based on cross-population composite likelihood ratio (XP-CLR) analysis. Panel (a) highlights the genomic regions under selective sweeps between two ecotypes (G6 and G8), with major peaks corresponding to candidate flowering-related genes such as SRR1, VIN3, FT, CO, FLC, ELF3, and LHY distributed across different chromosomes (Kang et al., 2021). These selective sweep signals indicate key domestication loci that have been under directional selection during mustard breeding. Panels (b) and (e) show Manhattan plots and LD heatmaps for the association of SRR1 on chromosome A10 and VIN3 on B05 with flowering time variation. Panel (c) reveals a structural 4,597-bp insertion in the SRR1 gene among haplotypes, while panel (f) maps similar haplotype diversity in VIN3. Panels (d) and (g) show box plots of flowering time for different haplotypes across germplasm groups, indicating significant phenotypic variation based on allelic variation at these loci. These findings demonstrate how integrating GWAS, haplotype analysis, and selective sweep detection can effectively uncover functional alleles controlling flowering time an essential trait for regional adaptation. Such markers are pivotal for genomic-assisted selection in mustard breeding programs (Kang et al., 2021, 2022).

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**Fig. 2. Genome-wide association analysis and domestication signals in Brassica juncea, showing selective sweeps, key flowering-time genes (e.g., SRR1, VIN3), haplotype structure, and flowering time associations across chromosomes. (Source: Kang et al., 2021).**

### **5.3 Biotechnological Tools**

***5.3.1 Genetic Engineering***

Transgenic approaches enable the introduction of genes conferring disease resistance, enhanced nutrient use efficiency, or modified oil composition (Pradhan et al., 2021). For example, white rust resistance and glucosinolate reduction have been successfully engineered using transgenes, though regulatory and public acceptance remain challenges.

***5.3.2 CRISPR/Cas9 Gene Editing***

CRISPR/Cas9-mediated genome editing provides precise allelic changes without introducing foreign DNA. In B. juncea, CRISPR has been deployed to knock out allergenic proteins and key metabolic genes for fatty acid biosynthesis, offering opportunities for transgene-free trait improvement with greater public acceptance (Malik, 2025).

***5.3.3 Omics Technologies***

Advanced omics genomics, transcriptomics, proteomics, metabolomics generate a comprehensive understanding of trait regulation. In B. juncea, combined QTL mapping and transcript profiling have identified candidate genes for phytonutrient traits. Metabolomic studies have similarly informed breeding for glucosinolates and antioxidants. Modern breeding in Brassica juncea blends traditional methods hybridization, backcrossing, and recurrent selection, with cutting-edge approaches like MAS, GS, GWAS, CRISPR, and omics (El-Esawi, 2024). This integrated toolkit allows breeders to efficiently deploy alleles for high yield, improved quality, and stress resilience, accelerating genetic gains while circumventing the limitations of a narrow gene pool.

## 6. Challenges and Future Prospects

### **6.1 Barriers to Wild and Landrace Germplasm Utilization**

Crop wild relatives (CWRs) and landraces, despite their immense potential, remain significantly underutilized due to practical and scientific barriers. Many wild germplasm collections are incomplete 29% of CWR taxa lack representation in genebanks, and nearly 95% are inadequately captured across environments (Thakur et al., 2024). Collecting from remote or protected regions not only incurs high logistical costs and quarantine hurdles but also raises ethical concerns around benefit-sharing with communities. Often, germplasm is gathered opportunistically without thorough characterization, limiting its immediate utility in breeding programs.

### **6.2 Genetic Incompatibility and Linkage Drag**

Wide crosses with wild species frequently face reproductive barriers such as hybrid sterility or male infusion/genetic load that complicate introgression. Even when successful, large donor genome fragments hitchhike along with target genes, resulting in linkage drag that diminishes agronomic performance in the recipient cultivars. Marker-assisted backcrossing can mitigate this by selecting against unwanted genomic segments, but such resolution is mainly effective for traits governed by major genes (Xu et al., 2012). Complex traits controlled by many small-effect loci remain a challenge to disentangle. Pre-breeding steps embryo rescue, somatic hybridization, and bridge crosses can help overcome fertility blockage, but they are labor-intensive, costly, and time-consuming.

### **6.3 Bridging Research Gaps Through Public–Private Partnerships**

Integrating CWRs and landraces into mainstream breeding requires sustained funding, technical support, and germplasm pipelines. Public–private partnerships (PPPs), such as CIMMYT–Syngenta and the APSA–WorldVeg initiatives, have achieved success in crop improvement via shared germplasm evaluation and early variety deployment (Das et al., 2019). These partnerships enable resource sharing, capacity building, and efficient pre-breeding by pooling expertise and aligning goals across sectors. Models like the PPP-specific “stage-gate” approach outline target identification, trait validation, pre-breeding, multi-location testing, and deployment stages, enhancing translational efficiency.

### **6.4 Climate-Smart Breeding Priorities**

Climate change intensifies the need to integrate adaptation traits drought tolerance, heat and cold resilience, and disease resistance, into Brassica juncea. Pre-breeding efforts must be linked to high-throughput phenotyping and genomic selection platforms capable of screening large-introgression populations across diverse environments (Cockram, 2024). Complementary strategies like rapid generation advancement, genomic prediction of complex traits, and de‑novo domestication of CWR species can significantly promote the development of climate-resilient varieties (majhi et al., 2024). Additionally, global conservation initiatives like the Crop Trust and Svalbard Global Seed Vault are essential to safeguard genetic diversity and enable future breeding needs.

Overcoming bottlenecks in CWR and landrace utilization requires a coordinated strategy, combining comprehensive germplasm collection, genetic characterization, advanced breeding techniques, and partnership-driven delivery models. By addressing genetic incompatibilities, linkage drag, and diversity gaps, while leveraging PPP frameworks and climate-smart tools, the mustard breeding community can unlock the vast untapped potential of genetic resources paving the way for resilient, sustainable, and nutritionally enhanced B. juncea cultivars (Meena et al., 2025).

### **7. CONCLUSION**

The genetic enhancement of Brassica juncea is imperative for ensuring its continued relevance in global agriculture, particularly under the looming pressures of climate change, pest evolution, and resource scarcity. This review underscores the indispensable value of underutilized genetic reservoirs namely wild relatives and landraces as critical tools for broadening the narrow genetic base of modern cultivars. Wild species resist multiple biotic and abiotic stresses, while landraces carry locally adapted traits and nutritional qualities refined over centuries of farmer selection. However, the full integration of these resources into mainstream breeding is hindered by barriers such as reproductive incompatibilities, linkage drag, and insufficient characterization. Advances in molecular breeding, including QTL mapping, GWAS, marker-assisted selection, genomic selection, and CRISPR-based genome editing, have greatly accelerated the identification and deployment of favorable alleles. These approaches, when complemented with omics technologies and pre-breeding strategies, offer unprecedented precision in trait introgression while minimizing undesirable effects. Additionally, genome-wide scans for domestication signals, such as those identifying loci like SRR1 and VIN3 have revealed critical targets for adaptation and flowering-time regulation. To fully realize the potential of wild and traditional germplasm, strong public-private partnerships, participatory breeding initiatives, and enhanced conservation efforts are essential. Bridging research, conservation, and innovation through collaborative frameworks will be key to developing climate-smart, high-yielding, and resilient B. juncea varieties.

## DISCLAIMER (ARTIFICIAL INTELLIGENCE)

Author(s) hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc) and text-to-image generators have been used during writing or editing of this manuscript.

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