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Genomic Tools in Mustard Breeding for the Enhancement of Yield, Oil Quality and Stress Tolerance

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Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

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ABSTRACT

Mustard (*Brassica* species) plays a crucial role in global agriculture due to its high oil content and economic significance. However, challenges such as limited genetic diversity, disease susceptibility, and environmental stressors hinder the potential of mustard crops. Genomic tools have emerged as powerful tools to enhance mustard breeding by improving key traits such as yield, oil quality, and disease resistance. Marker-Assisted Selection (MAS) has been widely applied to select for desirable traits, including oil content and disease resistance, by targeting specific genes like *FAD2* and *FAD3*, which are involved in fatty acid composition. Additionally, Quantitative Trait Loci (QTL) mapping has identified genomic regions associated with yield components like seed size, weight, and pod number, facilitating the selection of high-yielding varieties. Genomic Selection (GS) has also accelerated breeding programs by enabling the prediction of complex traits with high accuracy.
Genomic approaches are further improving stress tolerance in mustard, with research focusing on

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genes related to drought, heat, and salinity resistance. The use of genomics to reduce glucosinolate levels in mustard has also improved seed meal quality, making it more suitable for animal feed. The application of CRISPR-Cas9 genome editing holds great potential for modifying genes responsible for oil content, disease resistance, and stress tolerance. As genomic resources for mustard continue to grow, the integration of these tools will revolutionize breeding practices, resulting in faster development of resilient, high-yielding, and high-quality mustard varieties. These advancements will address global agricultural challenges, benefiting both producers and consumers by ensuring a more sustainable and efficient mustard production system.

Keywords: Agricultural genomics; diseaseresistance; genomic breeding; oil content; stress tolerance.

1. INTRODUCTION

Mustard crops, particularly those of the *Brassica* species, are integral to global agriculture due to their dual purpose as oilseed and forage crops. Among the various *Brassica* species, *Brassica juncea* (yellow or brown mustard), *Brassica nigra* (black mustard), and *Brassica rapa* (field mustard) are the most cultivated for oil production (Sharma et al., 2024). Mustard oil, extracted from seeds, is widely consumed in culinary practices, especially in South Asia, and has industrial uses in biofuels and cosmetics (Aslan,2023). Additionally, the by-product, mustard seed meal, serves as a high-protein feed for livestock.

Several studies have demonstrated the successful use of these genomic tools to identify and introgress genes related to oil content, disease resistance, drought tolerance, and seed quality into elite mustard cultivars. High-throughput sequencing technologies and bioinformatic platforms now allow breeders to dissect complex traits and associate them with specific loci or candidate genes, thereby improving the accuracy and speed of selection.

The cultivation of mustard crops also plays a critical role in sustainable agricultural practices by serving as an effective rotational crop. As a member of the *Brassicaceae* family, mustard helps enhance soil fertility through its nitrogen-fixing capabilities (Salmasi et al.,2024). With the increasing global demand for vegetable oils, the significance of mustard in agriculture continues to grow, particularly in the context of improving oilseed yields to meet the needs of both human consumption and industrial applications (Sachan,2024). Consequently, the improvement of key agronomic traits such as oil content, seed size, disease resistance, and stress tolerance in mustard is of paramount importance (Gill et al*.,* 2012).

The global demand for mustard products necessitates continued research efforts to improve the yield and quality traits of mustard crops. Specifically, enhancing oil content is critical for meeting both food and biofuel requirements (Akhatar et al*.,* 2025). In addition to oil content, factors such as disease resistance and stress tolerance (to conditions like drought, heat, and salinity) are vital to ensure consistent and high-quality production in the face of climate change. Advances in breeding strategies, particularly those that utilize genomic tools, offer new avenues for improving these essential traits in mustard crops (Gupta et al*.,*2024).

1.1 Need for Genetic Improvement

Despite the significant agricultural potential of mustard crops, conventional breeding methods used to improve yield and quality face several limitations. Traditional breeding techniques often rely on phenotypic selection, which is time-consuming, resource-intensive, and prone to environmental variability (Thriveni et al*.,*2024). Additionally, breeding programs for mustard are constrained by the relatively narrow genetic base of commercially cultivated varieties, which restricts the introduction of novel, beneficial traits. This limitation in genetic variability presents a major challenge to improving traits such as high oil content, disease resistance, and stress tolerance (Meena et al.,2025).

The long breeding cycles required for achieving significant improvements in mustard yield and quality further hinder the progress of conventional breeding programs. These cycles, often spanning several years (Yadava et al*.,* 2024), make it difficult to rapidly respond to changing environmental conditions and evolving disease pressures. Additionally, the lack of comprehensive genomic resources for mustard has slowed the adoption of more efficient molecular breeding techniques (Gupta et al*.,* 2024).

To overcome these challenges, the integration of genomic tools into mustard breeding programs holds considerable promise. Advances in molecular genetics, such as the identification of genetic markers linked to desirable traits, offer the potential to accelerate the breeding process. Genomic tools like Quantitative Trait Loci (QTL) mapping, Marker-Assisted Selection (MAS) and Genomic Selection (GS) have the potential to identify and select for specific genes associated with improved yield, oil quality, and disease resistance (Kumar et al*.,* 2024). By enabling breeders to more precisely target genes of interest, these genomic techniques can significantly reduce the breeding cycles and enhance the overall efficiency of mustard breeding programs. Moreover, the use of these tools can help address the issue of limited genetic variability by facilitating the incorporation of novel genes from wild relatives or exotic germplasm, thus broadening the genetic base of cultivated mustard crops.

2. GENOMIC TOOLS IN MUSTARD BREEDING)

2.1 Marker-Assisted Selection (MAS)

Marker-Assisted Selection (MAS) is a molecular breeding approach that uses genetic markers linked to desirable traits to facilitate the selection of specific genotypes (Priyatham et al*.,*2025). This method has proven to be a valuable tool in mustard breeding, especially for improving traits such as yield, disease resistance, and oil quality. MAS leverages the identification of markers that are closely associated with genes controlling key agronomic traits, enabling breeders to select for these traits early in the breeding cycle, even before the traits are phenotypically expressed (Salgotra & Stewart, 2020).

In mustard breeding, MAS has been widely applied to enhance oil content, one of the most important traits for oilseed crops. For example, the *FAD2* gene, which influences the balance of oleic and linoleic acid in mustard oil, has been targeted using MAS (Yashpal et al., 2020). Increased oleic acid content is desirable due to its health benefits and higher oxidative stability, which extends the shelf life of mustard oil (Syed,2016). Markers linked to this gene facilitate the selection of varieties with higher oleic acid content, improving both the quantity and quality of oil extracted from mustard seeds.

MAS has also been used to improve seed size and weight, traits directly related to yield potential. Through the identification of markers linked to these traits, breeders can accelerate the development of varieties with larger seeds, which are often associated with higher oil content and improved overall yield (Arabzai & Gul, 2021). This approach has also been applied to enhance disease resistance in mustard, particularly to diseases such as white rust (*Albugo candida*) and downy mildew (*Peronospora parasitica*) (Meena & Rai ,2023). The identification of molecular markers linked to resistance genes for these diseases enables the development of resistant varieties, which helps reduce the reliance on chemical pesticides and improve crop sustainability (Luo et al.,2023).

2.2 Quantitative Trait Loci (QTL) Mapping

Quantitative Trait Loci (QTL) mapping is a powerful technique used to identify and locate specific genomic regions associated with complex traits, which are often controlled by multiple genes (Aguet et al*.,*2023). Unlike simple Mendelian traits, quantitative traits such as yield, oil content, and glucosinolate levels in mustard are influenced by numerous genes, each contributing to a small effect (Kumar et al.,2022). QTL mapping helps to uncover these genetic regions, providing valuable information for breeders to select individuals with favorable alleles for improved traits.

In mustard, QTL mapping has been instrumental in identifying genetic loci responsible for oil content, a critical trait for oilseed production. Various studies have mapped QTLs associated with oil content on different chromosomes, providing breeders with molecular markers that can be used for selecting high-oil cultivars (Singh et al.,2022). Additionally, QTLs associated with seed size, seed weight, and fatty acid composition have been identified, further enhancing the precision of selection for improved yield and oil quality (Bilgrami et al*.,*2022).

Another important trait for mustard quality is glucosinolate content. High levels of glucosinolates in mustard seeds can be undesirable due to their bitter taste and Impact on the meal's nutritional value for animal feed (Grygier,2023). QTL mapping has been used to identify regions in the mustard genome associated with glucosinolate biosynthesis, providing breeders with the tools to select for low-glucosinolate varieties (Rout et al*.,*2015).

Table 1. Summary of key genomic tools used in mustard breeding

Genomic Tool	Application	Key Benefits	References
Marker-Assisted Selection (MAS)	Selection for oil content, seed size, disease resistance	Accelerates breeding process by targeting specific genes	(Henkrar & Udapa, 2020)
Quantitative Trait Loci (QTL) Mapping	Identification of genomic regions linked to yield traits, oil content, glucosinolate levels	Allows for simultaneous improvement of multiple traits	(Zhao et al.,2022)
Genomic Selection (GS)	Prediction of complex traits like yield, oil content, stress tolerance	Reduces breeding cycle time by predicting genetic potential	(Sharma et al.,2022)
CRISPR-Cas9 Genome Editing	Precise modification of genes for oil content, disease resistance, and stress tolerance	Enables precise trait modifications without introducing foreign DNA	(Saraswathy et al.,2025)

This has significant implications for the quality of mustard meals, as reducing glucosinolate content can improve the nutritional value of the meal.

QTL mapping has also played a pivotal role in identifying genes involved in disease resistance. For example, QTLs for resistance to white rust and downy mildew have been identified in mustard, providing essential information for breeding disease-resistant cultivars. These QTLs serve as important markers for breeders aiming to develop mustard varieties that can withstand these common diseases, thereby reducing crop loss and the need for chemical control measures (Singh et al.,2021).

2.3 Genomic Selection (GS)

Genomic Selection (GS) is an advanced breeding technique that uses high-density molecular markers across the entire genome to predict the genetic potential of individuals for complex traits (Kumar,2024). Unlike traditional methods that rely on phenotypic selection, GS allows for the early selection of individuals based on their genomic data, without the need for phenotypic expression. This approach is particularly useful for traits with complex inheritance, such as yield, oil content, and stress tolerance, where traditional selection methods can be slow and less accurate.

In mustard breeding, GS has shown significant promise for improving traits such as yield, oil content, and stress tolerance. Since these traits are controlled by multiple genes with small effects (Singh et al.,2022), GS enables breeders to select for desirable genotypes that carry the right combination of alleles, even before phenotypic evaluation (Voss-Fels et al.,2019). This results in faster breeding cycles, as the need for extensive phenotypic screening is reduced. GS is particularly beneficial in improving traits that are influenced by environmental conditions, such as stress tolerance, where phenotypic selection can be influenced by fluctuating environmental factors.

Advancements in high-throughput sequencing and genotyping technologies have facilitated the integration of GS into mustard breeding programs. Recent studies have applied GS to improve both yield-related traits and oil quality in mustard (Singh et al.,2022). By combining genomic data with phenotypic data from field trials, breeders can make more accurate predictions about a plant's performance under different growing conditions, which is crucial for developing mustard varieties that perform well in diverse environments (Zandberg et al.,2022).

Moreover, GS is increasingly being used to improve stress tolerance in mustard, particularly in relation to drought, heat, and salinity. These stressors are becoming more prevalent due to climate change, making the development of stress-resistant crops essential. Through GS, breeders can select genes that confer resistance to these environmental stresses, ultimately leading to the development of mustard varieties that are better equipped to thrive in a changing climate. The ability to predict the performance of genotypes for stress tolerance traits in advance accelerates the breeding process and enhances the overall efficiency of breeding programs.

In conclusion, the integration of Genomic Selection (GS) into mustard breeding programs is a promising advancement that can accelerate the improvement of complex traits. Alongside MAS and QTL mapping, GS offers the potential for more efficient and precise breeding, enabling the development of mustard varieties that are high-yielding, disease-resistant, and resilient to environmental stresses. These genomic tools hold the potential to significantly enhance the productivity and sustainability of mustard crops in the face of global challenges.

3. ENHANCING YIELD IN MUSTARD THROUGH GENOMICS

3.1 Yield-related Traits

Yield improvement is a primary objective in mustard breeding, as it directly influences the economic viability of mustard production. The yield of mustard crops is determined by several key agronomic traits, including seed size, plant height, pod number, and seed weight (Akhatar, 2025). These traits are complex and often controlled by multiple genes, making their improvement through traditional breeding methods time-consuming and challenging. However, genomic tools such as Marker-Assisted Selection (MAS), Quantitative Trait Loci (QTL) mapping, and Genomic Selection (GS) have significantly enhanced the precision and efficiency of selecting these yield-related traits.

Seed size is one of the most directly correlated traits with yield potential in mustard. Larger seeds not only contribute to greater oil content but also result in higher yields per unit area. Genomic studies have identified several QTLs associated with seed size in mustard (Kumar et al.,2022). These QTLs are spread across different chromosomes, and markers linked to them can be used to select for larger seeds early in the breeding process. The identification of these QTLs has enabled breeders to accelerate the selection of high-yielding mustard varieties with larger seeds (Sachan et al.,2024).

Plant height is another important yield-related trait in mustard. Taller plants generally have higher potential for producing more pods, leading to increased seed yield. However, excessive plant height can sometimes result in lodging, particularly under heavy rainfall or windy conditions. Thus, a balance between plant height and structural stability is necessary for optimal yield. Genomic tools have been employed to map the genetic loci associated with plant height in mustard, allowing for the selection of varieties with optimal stature that maximize pod number and seed yield while minimizing lodging risks (Bhujbal et al., 2025).

Pod number and **seed weight** are critical yield components that influence overall mustard production. The number of pods per plant and the number of seeds per pod directly affect total seed production. Studies have identified key QTLs for pod number in mustard, and these QTLs have been used in MAS to select for varieties with a higher pod count (Kaur et al.,2020). Similarly, seed weight is influenced by both genetic factors and environmental conditions (Manojkumar et al.,2020). Genomic tools have identified QTLs for seed weight, enabling breeders to select larger, heavier seeds that contribute to improved yield (Luo et al.,2023). By targeting these key yield-related traits using genomic tools, mustard breeders can significantly increase productivity, ensuring a more sustainable and profitable crop.

3.2 Stress Tolerance

As climate change continues to impact agriculture, the ability to develop crop varieties that are resilient to abiotic stresses, such as drought, heat, and salinity, is becoming increasingly important (Rivero et al.,2022). Mustard, like many other crops, is highly susceptible to these stressors, which can drastically reduce both yield and quality (Pillai & Walia,2024). Genomic approaches have emerged as powerful tools for improving stress tolerance in mustard by identifying and targeting specific genes and pathways involved in stress response mechanisms.

Drought tolerance is a critical trait for mustard, particularly in regions where water scarcity is a growing concern (Singh et al.,2022). Drought stress negatively impacts plant growth, seed development, and ultimately yield. Genomic studies have identified several key genes involved in drought tolerance in Brassica species, including those related to the regulation of stomatal closure, osmotic adjustment, and cellular protection (Batool et al.,2022). For example, the DREB (Dehydration Responsive Element Binding) genes are a well-known group of transcription factors involved in the regulation of drought-responsive genes (Manna et al., 2021). These genes are activated under water stress and help plants conserve water by regulating stomatal behavior and enhancing the synthesis of osmolytes. By using genomic tools to identify and select for alleles of DREB genes, breeders can develop mustard varieties with enhanced drought tolerance (Raza et al., 2023).

Heat tolerance is another critical trait for mustard, especially in regions that experience high temperatures during the growing season. Heat stress can lead to poor pollination, reduced seed setting, and lower oil content. Genomic studies have revealed the involvement of several genes in heat tolerance, including heat shock proteins (HSPs)(Kashyap et al.,2023), which play a pivotal role in protecting plant cells from heat-induced damage. HSPs act as molecular chaperones, stabilizing proteins and ensuring cellular integrity under high-temperature stress. The identification of genomic regions linked to HSP expression has enabled breeders to select mustard varieties with better heat tolerance (Pal et al.,2024).

Salinity tolerance is also becoming an increasingly important trait as soil salinization affects large areas of arable land worldwide (Negacz et al.,2022). Salt stress interferes with water uptake, disrupts cellular functions, and hampers seed development. Genomic approaches have identified several genes associated with salinity tolerance, including those involved in ion transport and osmotic regulation (Kumar et al.,2022). The SOS (Salt Overly Sensitive) pathway is a well-characterized mechanism for salinity tolerance in plants, involving the regulation of sodium and potassium ion transporters (Atta et al.,2023).

Table 2. Major yield traits in mustard and genomic tools used

Yield Trait	Genomic Tools	Impact of Improvement
Seed Size	MAS, QTL Mapping	Increased seed size improves oil content and yield
Plant Height	MAS, QTL Mapping	Taller plants increase pod number but must be optimized for lodging
Pod Number	MAS, QTL Mapping	Higher pod number leads to increased seed production
Seed Weight	MAS, QTL Mapping, GS	Larger seeds contribute to higher yield and oil content

Table 3. Genes and pathways for stress tolerance improvement in mustard

Stress Type	Gene/Pathway Involved	Genomic Tools	Impact of Improvement	References
Drought	DREB (Dehydration Responsive Element Binding)	MAS, GS, Gene Editing (CRISPR-Cas9)	Improved water retention and osmotic adjustment	(Pérez Martí,2023)
Heat	Heat Shock Proteins (HSP)	MAS, GS, Gene Editing	Enhanced protein stability under heat stress	(Pandey et al.,2024)
Salinity	SOS (Salt Overly Sensitive) Pathway, NHX genes	MAS, GS, Gene Editing	Improved ion transport and cellular function under saline conditions	(Yousefi et al., 2024)

Additionally, NHX (Na+/H+ exchanger) genes have been implicated in maintaining cellular ion homeostasis under salt stress (Rahman et al., 2022). Using MAS and QTL mapping, breeders can select mustard varieties that possess alleles conferring enhanced salinity tolerance, enabling the crop to thrive in saline environments.

By leveraging genomic approaches to improve drought, heat, and salinity tolerance, mustard breeding programs can develop varieties that are better equipped to withstand environmental stresses. The identification and utilization of genes and pathways involved in stress responses, such as DREB, HSPs, and SOS/NHX pathways, have the potential to significantly enhance the resilience of mustard crops, ensuring stable production in the face of unpredictable and challenging climatic conditions (Singh et al.,2019).

4. IMPROVING QUALITY TRAITS IN MUSTARD

4.1 Oil Quality and Quantity

Oil content is one of the most critical quality traits in mustard breeding, as mustard oil is highly valued for both culinary and industrial applications. Enhancing oil yield and quality is essential for meeting the increasing global demand for vegetable oils. Mustard seeds contain oil in varying amounts, with oil content directly influencing the economic value of the crop. The oil composition, which includes the balance of different fatty acids, is equally important in determining the quality of mustard oil, especially in terms of its nutritional profile and industrial suitability.

Genomic approaches to enhance oil content in mustard seeds focus primarily on manipulating the biosynthesis pathways involved in fatty acid production. The *FAD2* and *FAD3* genes play pivotal roles in determining the fatty acid composition of mustard oil (Porokhovinova et al.,2022), particularly the levels of oleic and linoleic acids, which are crucial for oil quality. The *FAD2* gene encodes fatty acid desaturase 2, an enzyme responsible for converting oleic acid into linoleic acid, while the *FAD3* gene is involved in the production of alpha-linolenic acid, a polyunsaturated fatty acid. High oleic acid content in mustard oil is particularly desirable due to its stability and health benefits, including lower levels of saturated fats (Martinović et al., 2020).

In addition to improving the fatty acid profile, genomic tools have been employed to identify and select for higher oil content in mustard seeds. QTL mapping has pinpointed genomic regions associated with oil yield, providing breeders with molecular markers to select for varieties with higher oil content. These approaches, combined with the understanding of fatty acid biosynthesis pathways, allow for the simultaneous improvement of both oil quantity and quality in mustard crops.

4.2 Glucosinolate Content

Glucosinolates are sulfur-containing compounds found in mustard seeds that have both beneficial and undesirable effects on the crop(Miękus et al.,2020). These compounds are well-known for their health-promoting properties, as they have been shown to possess anti-cancer and antimicrobial activities. However, high glucosinolate levels can negatively impact the quality of mustard seed meal, a by-product of oil extraction, making it less desirable as animal feed due to its bitter taste and potential toxicity (Lietzow,2021). Thus, controlling glucosinolate content is crucial for improving the overall quality of mustard crops, especially for the feed industry.

In addition to reducing total glucosinolate content, genomic approaches are also being used to improve the composition of glucosinolates, shifting the balance toward types that are less bitter and more beneficial (Fatima et al.,2024). This work is crucial to improving the quality of mustard seed meal, making it more suitable for animal feed and enhancing its overall economic value.

4.3 Disease Resistance

Mustard crops face a range of diseases that can significantly impact yield and quality, reducing the profitability of production. Major diseases affecting mustard include white rust (*Albugo candida*), downy mildew (*Peronospora parasitica*), and Alternaria blight (*Alternaria brassicae*), (Meena et al.,2023) among others. These diseases can cause severe damage to mustard crops, leading to reduced seed production, lower oil quality, and compromised plant health. As a result, developing mustard varieties with improved disease resistance is a key goal in breeding programs.

Table 4. Genes involved in oil quality improvement in mustard

Gene	**Trait Affected**	**Impact of Modification**	**Reference**
FAD2	Oleic to Linoleic acid ratio	Higher oleic acid improves oil stability and shelf life	(Yashpal et al.,2020)
FAD3	Alpha-linolenic acid content	Modifies polyunsaturated fatty acid composition, enhancing oil quality	(Rajwade et al.,2014)

Table 5. Glucosinolate content and genomic approaches in mustard

Trait	**Importance**	**Genomic Approaches**	**Impact of Improvement**	**Reference**
Glucosinolate Content	Affects seed meal quality, particularly in animal feed	QTL Mapping, Gene Editing (e.g., CRISPR-Cas9 to reduce glucosinolate levels)	Reduced glucosinolate levels lead to better seed meal quality and improved feed value	(Manikandan et al.,2024)

Table 6. Major diseases in mustard and genomic approaches for resistance

Disease	**Genomic Approaches**	**Impact of Resistance**	**References**
White Rust (*Albugo candida*)	MAS, QTL Mapping	Reduced crop loss and pesticide use	(Sran et al.,2024)
Downy Mildew (*Peronospora parasitica*)	MAS, QTL Mapping	Enhanced resilience to fungal infection	(Kaur et al.,2024)
Alternaria Blight (*Alternaria brassicae*)	MAS, GS	Reduced disease impact, increasing yield and quality	(Munir et al.,2020)

Genomic tools have been instrumental in improving disease resistance in mustard by enabling the identification of resistance genes and the development of resistant cultivars. Marker-Assisted Selection (MAS) has been used extensively to identify molecular markers linked to disease resistance genes (Amas et al.,2023). For example, studies have identified QTLs associated with resistance to white rust and downy mildew. These QTLs, when tagged with molecular markers, allow breeders to select resistant mustard plants early in the breeding process, reducing the reliance on chemical pesticides and improving the sustainability of mustard farming (Devi et al.,2022).

Furthermore, the application of gene editing technologies such as CRISPR-Cas9 holds significant promise for directly modifying genes associated with disease resistance. For example, researchers are exploring the potential of editing genes involved in the plant’s immune response to enhance resistance to fungal and bacterial diseases. This precise modification of resistance genes offers the possibility of developing mustard varieties with durable resistance to major diseases, which is crucial for maintaining high yields and reducing the need for chemical treatments.

5. CHALLENGES AND FUTURE DIRECTIONS

5.1 Challenges

The integration of genomic approaches into mustard breeding, while promising, is not without its challenges. One of the primary difficulties is the limited genomic resources available for *Brassica* species, particularly mustard. Although the genomes of some Brassica species have been sequenced, the availability of comprehensive and high-quality genomic resources for mustard (particularly for *Brassica juncea*, the most widely cultivated mustard species) remains limited. This gap in genomic knowledge hinders the full potential of genomic tools such as Marker-Assisted Selection (MAS) and Genomic Selection (GS), as the lack of high-quality reference genomes and well-annotated gene sequences limits the identification of key genes and markers associated with desirable traits. Furthermore, without a sufficiently detailed understanding of the mustard genome, it is challenging to accurately predict the effects of genomic variations on traits such as yield, oil content, and disease resistance.

Another significant challenge in applying genomic tools to mustard breeding is the difficulty in translating genomic findings into practical applications. While genomic data can provide valuable insights into the genetic basis of desirable traits, the process of translating these findings into effective breeding strategies is often slow and complex. For example, the identification of genes associated with specific traits, such as drought tolerance or oil content, is just the first step(Tyagi et al**.,**2025). The implementation of this knowledge into breeding programs requires the development of reliable molecular markers, validation of their effectiveness in diverse genetic backgrounds, and incorporation into breeding populations.

Additionally, genetic diversity in mustard crops remains relatively low compared to other major crops like maize or wheat, which further complicates breeding efforts. Limited genetic variability reduces the ability to introduce novel traits from wild relatives or other Brassica species, which could enhance the resilience and productivity of mustard crops.

5.2 Future Prospects

Despite existing challenges, genomic research in mustard breeding holds significant promise, with several advancements on the horizon. The growing availability of high-quality genomic resources will allow for better gene identification, QTL mapping, and the application of Marker-Assisted Selection (MAS), enhancing the development of improved mustard varieties with better yield and quality. CRISPR-Cas9 genome editing offers precise modifications of key genes, such as those involved in oil biosynthesis (*FAD2* and *FAD3*) and stress tolerance (e.g., drought, heat resistance), enabling the creation of mustard varieties that can withstand adverse environmental conditions.

The integration of high-throughput phenotyping with genomic selection will accelerate the development of resilient mustard varieties by improving predictions of plant performance across diverse environments. Furthermore, advanced genomic breeding strategies like multi-trait selection, genomic prediction, and the incorporation of AI will revolutionize the breeding process, allowing for the simultaneous enhancement of multiple traits, including yield, quality, disease resistance, and stress tolerance.

For stress tolerance, future genomic research will focus on improving drought, heat, and salinity resistance in mustard by fine-tuning key genes. The combination of CRISPR-Cas9 and high-throughput phenotyping will enable the rapid development of mustard varieties that can thrive under changing climate conditions, ensuring food security and agricultural sustainability.

6. CONCLUSION

The integration of genomic tools into mustard breeding represents a transformative approach to enhancing yield, oil quality, disease resistance, and stress tolerance. The advancements in Marker-Assisted Selection (MAS), Quantitative Trait Loci (QTL) mapping, and Genomic Selection (GS) have significantly improved breeding efficiency and precision. These tools enable breeders to select beneficial traits with greater accuracy, reducing breeding cycles and allowing for faster responses to emerging challenges in mustard cultivation.

Beyond the immediate improvements in mustard production, genomic approaches have profound implications for agricultural sustainability. By enhancing disease resistance, drought tolerance, and heat resilience, mustard varieties developed through genomic tools can thrive under the increasingly erratic climate conditions associated with global climate change. This resilience not only ensures a stable supply of mustard for food and industrial uses but also reduces reliance on chemical inputs like pesticides and fertilizers, contributing to more sustainable and eco-friendly farming practices.

Furthermore, the reduction of glucosinolate levels in mustard seed meals through genomic tools enhances its nutritional value for animal feed, fostering a more efficient circular economy in agricultural systems. With the growing global demand for vegetable oils and animal feed, developing high-quality mustard varieties through genomic methods is critical for addressing food security and promoting sustainable agricultural practices.

In conclusion, the application of genomic tools in mustard breeding is poised to revolutionize both the productivity and sustainability of mustard crops. By fostering the development of varieties that are more resilient, productive, and environmentally friendly, these innovations will help meet the growing global demand for mustard products while minimizing the ecological footprint of production. The continued integration of genomics into breeding practices will play an essential role in shaping the future of global agriculture, making it more resilient and sustainable in the face of pressing environmental and economic challenges.

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 the writing or editing of this manuscript.

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COMPETING INTERESTS

Authors have declared that no competing interests exist.

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