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# Germplasm Innovation and Utilization of High Yield, Disease Resistance, and Stress Tolerance Traits in Wheat

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**Abstract** Wheat is one of the most important food crops globally, and germplasm innovation plays a critical role in enhancing wheat yield and adaptability. Advances in genomics and molecular breeding technologies have opened new possibilities for achieving these goals. This study summarizes the progress of wheat germplasm innovation in improving traits such as high yield, disease resistance, and stress tolerance. It explores the discovery of efficient germplasm resources on a global scale, the application of genomic selection and molecular improvement strategies, and the innovative use of stress-resistant and disease-resistant wheat germplasm. The study also analyzes successful cases of germplasm innovation, evaluating the impact of these technologies on future agriculture and their importance in addressing climate change challenges. The research demonstrates that germplasm innovation can significantly enhance wheat yield, disease resistance, and stress tolerance, providing strong support for addressing global food security issues. The exploration of modern breeding methods, such as genomics, transgenic technologies, and gene editing, can optimize the utilization of wheat germplasm resources and promote sustainable agricultural development. This study not only advances modern breeding but also provides effective strategies for global agriculture to address climate change and disease threats.

**Keywords** Wheat; Germplasm innovation; High-Yield breeding; Disease resistance; Stress tolerance

## 1 Introduction

Wheat (*Triticum aestivum* L.) is a cornerstone of global food security, providing a significant portion of the daily caloric and protein intake for a large part of the world's population (Babu et al., 2020; Pang et al., 2021). The continuous improvement of wheat germplasm is essential to meet the increasing demands for high yield, disease resistance, and stress tolerance, especially in the face of climate change and evolving biotic stresses (Mondal et al., 2016; Kumar et al., 2022; Trono and Pecchioni, 2022). The innovation and utilization of wheat germplasm are critical for the development of cultivars that can withstand various biotic and abiotic stresses. The genetic diversity conserved in gene banks worldwide offers a rich reservoir of traits that can be harnessed to improve wheat resilience and productivity (Khadka et al., 2020a; Kumar et al., 2022). Modern breeding techniques, including genomic selection and genetic engineering, have significantly enhanced the ability to develop stress-tolerant and high-yielding wheat varieties (Mahpara et al., 2022; Trono and Pecchioni, 2022).

Wheat breeding programs aim to achieve high yield potential while incorporating traits for disease resistance and stress tolerance. High-yielding wheat varieties are essential to meet the global food demand, which is projected to increase significantly in the coming decades (Singh et al., 2007; Crespo-Herrera et al., 2018). Disease resistance, particularly against rusts and other major pathogens, is crucial to prevent significant yield losses and ensure food security (Babu et al., 2020). Additionally, the development of wheat varieties that can tolerate drought, salinity, and extreme temperatures is vital to mitigate the adverse effects of climate change on wheat production (Pang et al., 2021; Trono and Pecchioni, 2022).

Wheat breeding faces several challenges, including the complex genotype-environment interactions that affect trait expression and the limited availability of truly resistant or tolerant germplasm (Singh et al., 2007; Kumar et al., 2022). The continuous evolution of pathogens and pests necessitates the ongoing identification and deployment of effective resistance genes (Babu et al., 2020). Moreover, the integration of multiple stress resistance traits into a single variety is a time-consuming and complex process, often hindered by the limitations of conventional breeding methods (Mondal et al., 2016; Khadka et al., 2020a).

This study provides an in-depth analysis of the current status of wheat germplasm innovation and utilization, with a focus on high yield, disease resistance, and stress tolerance traits. It further explores advancements in breeding technologies and the richness of genetic resources, while emphasizing the potential of developing resilient wheat varieties that can address future food security challenges. This research holds significant importance for guiding future breeding programs and ensuring the continued production of wheat in changing environments.

## 2 Innovation and Utilization of High-Yield Germplasm in Wheat

### 2.1 Exploration of high-yield germplasm resources

The exploration of high-yield germplasm resources is a critical step in enhancing wheat productivity. Various global wheat gene pools, including cultivated varieties, landraces, and wild relatives, harbor a wealth of genetic diversity that can be harnessed for breeding high-yielding wheat cultivars. For instance, the National Genebank of India conserves an extensive collection of wheat germplasm, which includes Indian wheat landraces, primitive cultivars, and breeding lines from other countries. This diverse collection is pivotal for developing wheat cultivars with high yield potential and stress tolerance (Kumar et al., 2022). Similarly, the evaluation of germplasm pools for drought tolerance has identified several genotypes with desirable traits, which can be utilized to improve wheat yield under water-deficit conditions (Ahmed et al., 2022b).

Moreover, the identification of quantitative trait loci (QTLs) associated with yield and stress tolerance traits has been instrumental in the selection of high-yield germplasm. For example, genome-wide association studies (GWAS) have revealed significant marker-trait associations for yield-related attributes under both normal and heat-stressed environments, providing valuable insights for breeding programs aimed at enhancing wheat yield (Ahmed et al., 2022a). The integration of phenotypic and molecular data from diverse germplasm collections facilitates the identification of high-yielding genotypes, which can be further exploited in breeding programs to meet the growing food demands (Khadka et al., 2020a).

### 2.2 Application of genomic selection in high-yield breeding

Genomic selection (GS) has emerged as a powerful tool to accelerate the breeding of high-yield wheat by utilizing genomic markers and QTLs. GS involves the use of genome-wide markers to predict the breeding values of individuals, thereby enabling the selection of superior genotypes at an early stage. This approach has been particularly effective in addressing the challenges posed by genotype-environment interactions and the non-availability of reliable markers linked with significant QTLs (Kumar et al., 2022). For instance, the identification of QTLs for drought tolerance and their integration into GS models has facilitated the development of wheat varieties with enhanced yield potential under drought conditions (Khadka et al., 2020a).

The application of GS in wheat breeding programs has also been supported by advancements in high-throughput phenotyping and genotyping technologies. These technologies enable the rapid and accurate assessment of large germplasm collections, thereby enhancing the efficiency of GS. For example, the use of high-density SNP arrays in GWAS has identified several QTLs associated with heat tolerance, which can be incorporated into GS models to breed heat-tolerant, high-yielding wheat varieties (Figure 1) (Ahmed et al., 2022a). Additionally, the integration of genomic and phenotypic data from diverse germplasm pools has provided a comprehensive understanding of the genetic basis of yield traits, further enhancing the effectiveness of GS in wheat breeding (Gupta et al., 2020).

Ahmed et al. (2022a) revealed the genetic basis variations of thousand grain weight (TGW) and grain yield per plant (GYP) in wheat under different growth environments, particularly under heat stress. Compared to normal conditions, the distribution of significant SNPs for TGW and GYP under heat stress changed, indicating the influence of environmental factors on gene expression and its impact on traits. Genomic selection can be used to identify genetic markers associated with heat tolerance and high yield, accelerating the breeding of heat-tolerant, high-yielding wheat varieties. In future breeding programs, genomic selection based on such SNP information will help enhance crop adaptability and productivity in the context of global warming.

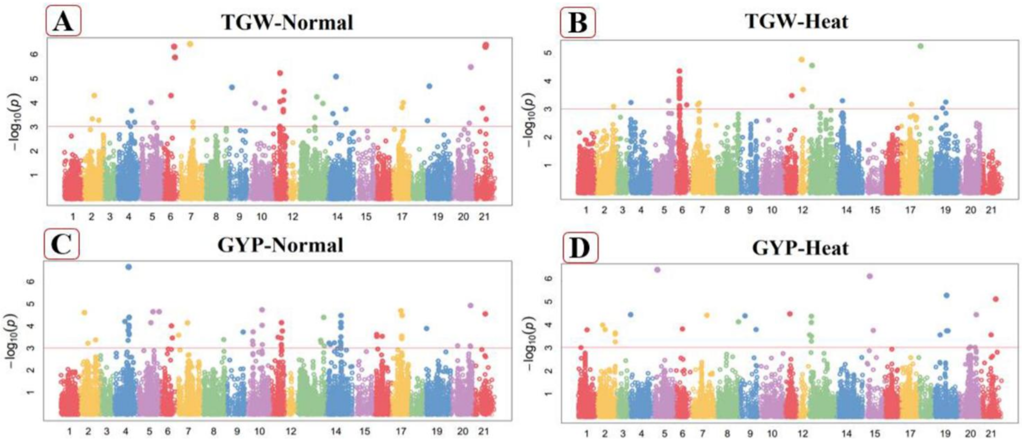

Figure 1 Manhattan plots for thousand grain weight (TGW) and grain yield per plant (GYP) under normal and heat stress conditions (Adapted from Ahmed et al., 2022a)

Image caption: The figure shows the genome-wide association study (GWAS) results for Thousand Grain Weight (TGW) and Grain Yield per Plant (GYP) under normal conditions (A, C) and heat stress conditions (B, D). The X-axis represents the wheat chromosome numbers, while the Y-axis indicates the -log10(p) values of significant SNP (Single Nucleotide Polymorphism) loci. The threshold line is used to identify significant genomic regions associated with yield traits (Adapted from Ahmed et al., 2022a)

### 2.3 Molecular improvement of high-yield germplasm

The advent of gene editing technologies, particularly CRISPR-Cas9, has revolutionized the molecular improvement of high-yield germplasm in wheat. CRISPR-Cas9 allows for precise modifications of specific genes associated with yield traits, thereby enabling the development of wheat varieties with enhanced yield potential. Recent studies have demonstrated the potential of CRISPR-Cas9 in fine-tuning the expression of genes controlling yield and stress tolerance traits, thereby improving wheat productivity under various environmental conditions (Khadka et al., 2020a). For instance, the use of CRISPR-Cas9 to edit genes involved in drought tolerance has shown promising results in enhancing wheat yield under water-deficit conditions (Dwivedi et al., 2017).

Moreover, the integration of CRISPR-Cas9 with other genomic tools, such as GWAS and QTL mapping, has further enhanced the efficiency of molecular breeding. This integrated approach allows for the identification and targeted modification of key genes associated with yield traits, thereby accelerating the development of high-yielding wheat varieties. For example, the identification of SNPs associated with heat tolerance and their subsequent editing using CRISPR-Cas9 has led to the development of wheat genotypes with improved yield under heat stress (Sall et al., 2023). The continued advancement of gene editing technologies and their application in wheat breeding holds great promise for achieving significant yield gains and ensuring food security in the face of climate change (Dwivedi et al., 2017; Khadka et al., 2020a).

## 3 Innovation and Utilization of Wheat Disease Resistant Germplasm

### 3.1 Innovation of disease resistance traits in wheat germplasm

The innovation of disease resistance traits in wheat germplasm has been significantly advanced through the identification and utilization of resistance genes against major diseases such as stripe rust and powdery mildew. The Indian Wheat Genomics Initiative has highlighted the importance of exploring the genetic diversity available in gene banks to develop stress-resistant cultivars. This initiative has focused on the molecular and phenotypic characterization of conserved genetic resources, which is essential for the improvement of wheat germplasm (Kumar et al., 2022). Additionally, the use of synthetic hexaploids, developed from the hybridization of durum wheat with *Aegilops tauschii*, has shown promise in enhancing disease resistance traits. These synthetic-derived lines have been evaluated for their agronomic potential, including resistance to biotic stresses, and have demonstrated significant improvements in grain yield and other yield components (Blanco et al., 2001).

Moreover, the integration of advanced molecular techniques such as genomic selection (GS) and genome-wide association studies (GWAS) has facilitated the identification of quantitative trait loci (QTLs) associated with disease resistance. These techniques allow for the precise selection of resistant genotypes, thereby accelerating the breeding process. For instance, the use of GWAS in durum wheat has identified several QTLs associated with heat tolerance, which can be leveraged to improve disease resistance under stress conditions. The development of kompetitive allele-specific PCR markers for these QTLs further enhances the efficiency of breeding programs aimed at improving disease resistance (Sall et al., 2023).

### 3.2 Identification and transfer of resistance genes

The identification and transfer of resistance genes in wheat have been greatly enhanced by genomics and genome-wide association studies (GWAS). These approaches have enabled the discovery of disease resistance genes and their integration into breeding materials. For example, the use of high-density SNP arrays in GWAS has revealed the genetic basis of heat tolerance in wheat, identifying significant marker-trait associations (MTAs) that can be used to develop heat-tolerant and disease-resistant genotypes (Ahmed et al., 2022a). Similarly, the assessment of functional diversity in germplasm pools through genome-wide approaches has identified alleles associated with desirable agronomic traits, including disease resistance (Dwivedi et al., 2017).

The transfer of resistance genes from wild relatives and landraces into elite cultivars has also been a key strategy. The use of synthetic hexaploids and other exotic germplasm has introduced novel alleles for disease resistance into breeding programs (Ma and Cai, 2024). For instance, the mobilization of genetic variation from gene banks has led to the identification of new allelic variations for vernalization and glutenin genes, which are crucial for disease resistance and overall plant health (Sehgal et al., 2015). The integration of these genes into breeding pipelines has been facilitated by the development of effective DNA markers, making the process of heterologous gene transfer more efficient (Shumny et al., 2016).

### 3.3 Multigene resistance strategy for disease-resistant germplasm

The multigene resistance strategy involves the integration of multiple resistance genes to develop germplasm with broad-spectrum disease resistance. Case studies have demonstrated the effectiveness of this approach in enhancing disease resistance in wheat. For example, the Indian Wheat Genomics Initiative has identified promising genotypes with high levels of biotic stress tolerance (Figure 2), which can be used to develop varieties with multigene resistance (Kumar et al., 2022). The use of genome editing technologies such as CRISPR-Cas9 has further enabled the fine-tuning of gene expression to enhance disease resistance traits. This technology allows for the precise modification of multiple genes, thereby improving the overall resistance of wheat cultivars to various diseases (Khadka et al., 2020a).

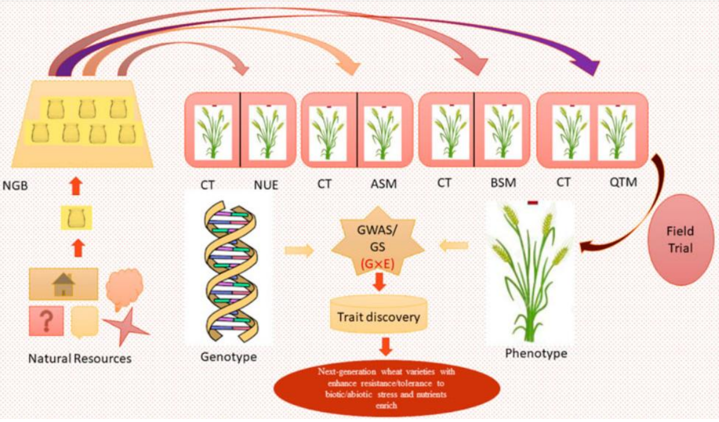

Figure 2 Workflow for trait discovery in Indian germplasm through multi-layered integration of genotypic and phenotypic analysis (Adapted from Kumar et al., 2022)

Image caption: The figure illustrates the preliminary screening of genetic resources (controlled trials, CT), including nutrient use efficiency (NUE), abiotic stress measurement (ASM), biotic stress measurement (BSM), and quality trait measurement (QTM). Genome-wide association studies (GWAS) or genomic selection (GS) are used to identify genotypes associated with specific traits, and the effects of these genotypes on phenotypes are ultimately validated through field trials (Adapted from Kumar et al., 2022)

Another case study involves the use of synthetic hexaploids to introduce multiple resistance genes into wheat. These synthetic-derived lines have shown significant improvements in grain yield and resistance to biotic stresses, demonstrating the potential of multigene resistance strategies (Blanco et al., 2001). The integration of novel alleles from wild relatives and landraces into elite cultivars has also contributed to the development of multigene resistant germplasm. For instance, the identification of new SNP variations in landraces adapted to drought and heat stress environments has opened new avenues for pre-breeding and the development of disease-resistant wheat varieties (Sehgal et al., 2015).

## 4 Innovation and Utilization of Wheat Stress Resistant Germplasm Resources

### 4.1 Exploration and application of drought- and salt-tolerant wheat germplasm

The exploration and application of drought- and salt-tolerant wheat germplasm are crucial for developing wheat varieties that can thrive in harsh environments. Recent studies have highlighted the importance of utilizing diverse germplasm collections to identify and develop drought-tolerant wheat varieties. For instance, extensive collections of genetic resources conserved in national and international genebanks have been pivotal in identifying useful genes for drought tolerance in wheat. These collections have been evaluated using advanced molecular techniques such as genotype by sequencing to identify quantitative trait loci (QTLs) associated with drought tolerance traits, which are essential for genome- and marker-assisted selection approaches (Khadka et al., 2020a). Additionally, local wheat cultivars have been screened for drought tolerance, revealing that certain cultivars, such as Barani-83 and Blue Silver, exhibit significant drought tolerance due to their ability to maintain higher shoot and root weights under stress conditions (Ghaffar et al., 2023).

Similarly, the identification and characterization of wheat germplasm for salt tolerance have been a focus of recent research. A study involving 334 internationally derived wheat genotypes identified 12 genotypes with significant salt tolerance. These genotypes demonstrated better growth under salt stress due to their ability to maintain stable osmotic potential, ion homeostasis, and efficient use of soluble sugars (Quan et al., 2021). The exploration of such germplasm resources is essential for breeding new wheat cultivars that can withstand salinity and drought, thereby ensuring food security in regions affected by these stresses.

### 4.2 Molecular breeding for stress tolerance traits

Molecular breeding has played a significant role in the discovery and application of key stress tolerance genes in wheat. The identification of over 100 genes associated with drought and salt tolerance has provided valuable insights into the mechanisms of stress tolerance. These genes are involved in various functions such as osmotic adjustment, ionic and redox homeostasis, and are crucial for the efficient selection of new tolerant genotypes through marker-assisted selection (MAS) (Urbanavičiūtė et al., 2021). The use of advanced molecular techniques, including CRISPR-Cas9 and other gene-editing technologies, has further enhanced the ability to fine-tune the expression of genes controlling drought adaptive traits, thereby improving drought tolerance in wheat (Khadka et al., 2020a).

Moreover, the genetic characterization and agronomic evaluation of wheat cultivars have identified specific genotypes with high drought tolerance. For example, Egyptian wheat cultivars such as Giza 171 and Misr 2 have been identified as valuable germplasm for breeding high-yielding, drought-tolerant wheat. These cultivars exhibited significant positive correlations between yield under drought conditions and indices such as mean productivity (MP) and geometric mean productivity (GMP), highlighting their potential for use in breeding programs (Emam et al., 2022). The integration of molecular breeding techniques with traditional breeding approaches is essential for developing wheat varieties with enhanced stress tolerance.

### 4.3 Environmental adaptability of stress tolerance traits

The performance and resource development of stress-tolerant wheat under different climate conditions are critical for ensuring the adaptability of these traits. Studies have shown that wheat germplasm with drought tolerance can maintain yield stability and performance under varying environmental conditions. For instance, the evaluation of 152 spring wheat cultivars under non-stress and drought-stress conditions revealed that certain germplasm accessions could sustain grain yield and improve drought tolerance simultaneously (Figure 3). These findings provide a theoretical basis for developing new wheat cultivars with excellent drought tolerance and high yields in diverse environments (Xu et al., 2023).

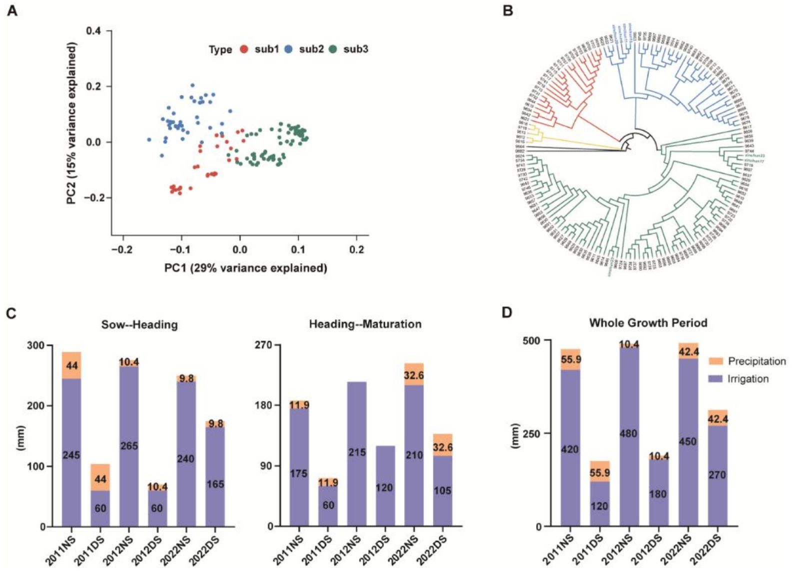

Figure 3 Wheat population structure and analysis of irrigation, precipitation, and drought resistance (Adapted from Xu et al., 2023)
Image caption: (A) Principal component analysis (PCA) divides wheat germplasm into three subpopulations (sub1, sub2, sub3), showing the genotypic differences of different subpopulations in the principal component dimensions; (B) Neighbor-joining tree analysis displays the phylogenetic relationships of different wheat varieties, with different colors representing distinct subpopulations; (C) Bar charts show precipitation and irrigation conditions during different growth stages (from sowing to jointing and from jointing to maturity) under non-stress and drought stress conditions; (D) The total amount of precipitation and irrigation throughout the growing season in different years (Adapted from Xu et al., 2023)

Xu et al. (2023) analyzed the drought resistance and water use efficiency of wheat germplasm resources. Principal component analysis and phylogenetic analysis helped in understanding the genetic differences in drought tolerance among different wheat varieties. By comparing irrigation and precipitation levels under drought and non-drought conditions, the study revealed that certain wheat varieties are capable of maintaining high yields with limited water resources. This information is of significant reference value for the future development of drought-resistant, high-yielding wheat varieties.

Additionally, the evaluation of Ethiopian and Chinese wheat germplasm for drought tolerance at the seedling stage demonstrated significant genetic variation in traits such as shoot dry weight and proline content. The identification of genotypes with strong drought resistance under both non-stress and simulated stress conditions highlights the potential for further investigation at the molecular and cellular levels to identify novel genes associated with stress response (Belay et al., 2021). The adaptability of stress tolerance traits to different climate conditions is essential for the successful development and utilization of stress-tolerant wheat germplasm in breeding programs.

## 5 Technological Advances in Wheat Germplasm Innovation

### 5.1 Application of modern molecular breeding techniques in germplasm innovation

Marker-assisted selection (MAS) has revolutionized wheat breeding by enabling the precise selection of desirable traits at the seedling stage, thus reducing costs and increasing efficiency. MAS has been successfully applied to transfer resistance genes such as Lr34, Yr36, and Pch1 into elite breeding material, demonstrating its potential in enhancing disease resistance. However, the integration of MAS in practical breeding programs faces challenges such as the small effects of individual QTLs and economic constraints (Miedaner and Korzun, 2012). Advances in high-throughput genotyping platforms and genomic selection are expected to overcome these limitations, opening new avenues for molecular-based resistance breeding (Gupta et al., 2010; Miedaner and Korzun, 2012).

Gene editing technologies, particularly CRISPR/Cas9, offer promising prospects for wheat improvement. These technologies enable precise modifications of the wheat genome, facilitating the development of disease-resistant and high-yielding varieties. The CRISPR/Cas9 system has been highlighted for its potential to assist breeders in the genetic improvement of wheat, particularly in developing resistance against major diseases (Jabran et al., 2023). The integration of MAS and gene editing technologies is anticipated to significantly enhance the efficiency and precision of wheat breeding programs (Hussain et al., 2023; Jabran et al., 2023).

### 5.2 Application of transgenic and gene editing technologies in wheat trait improvement

Transgenic and gene editing technologies have made significant strides in improving wheat traits such as disease resistance and yield (Xu and Su, 2024). The CRISPR/Cas9 system has been utilized to develop wheat varieties with enhanced resistance to fungal and nematode diseases, addressing major factors responsible for yield losses. This system, along with other molecular markers, has been instrumental in developing broad-spectrum disease resistance in wheat (Jabran et al., 2023). The advent of next-generation sequencing (NGS) technologies has further accelerated the application of transgenic and gene editing technologies in wheat breeding. The release of a fully annotated reference wheat-genome assembly has facilitated the identification and cloning of candidate genes linked to key traits, enabling precise modifications through gene editing. These technological advances have opened new opportunities for marker-assisted selection (MAS) and genomic selection (GS) in wheat, enhancing the efficiency of breeding programs aimed at improving yield and resistance to biotic and abiotic stresses (Hussain et al., 2023).

### 5.3 Integration of omics technologies

The integration of omics technologies, including genomics, phenomics, and metabolomics, plays a crucial role in wheat germplasm innovation. Genomics provides a comprehensive understanding of the wheat genome, enabling the identification of genes and QTLs associated with important traits such as drought tolerance and disease resistance. The use of advanced molecular techniques, such as genotype by sequencing, has facilitated the identification of QTLs for drought tolerance, aiding in the development of drought-tolerant wheat varieties (Khadka et al., 2020a).

Phenomics, which involves the high-throughput phenotyping of plant traits, complements genomics by providing detailed phenotypic data that can be correlated with genetic information. This integration enhances the accuracy of selection and accelerates the breeding process. Metabolomics, which involves the comprehensive analysis of metabolites, provides insights into the biochemical pathways underlying important traits, further aiding in the identification of candidate genes for breeding (Sinha et al., 2023).

The combined use of genomics, phenomics, and metabolomics in an integrated approach, known as integrated genomic selection (IGS), has been highlighted for its potential to develop climate-smart crops that can endure abiotic stresses while maintaining high yield and quality. This integrated approach leverages advanced technologies such as speed breeding, machine learning, and environmental data to enhance the efficiency and precision of wheat breeding programs (Sinha et al., 2023).

## 6 Success Stories of Germplasm Innovation in Wheat Breeding

### 6.1 Development and promotion of high-yield, disease-resistant wheat varieties

The development of high-yield, disease-resistant wheat varieties has been a cornerstone of modern wheat breeding programs. One notable success story is the Indian Wheat Genomics Initiative, which has harnessed the potential of wheat germplasm resources to breed disease-resistant, nutrient-dense, and climate-resilient cultivars. This initiative has focused on exploring the genetic diversity available in gene banks and utilizing advanced breeding technologies like genomic selection to enhance climate resilience and maximize yield potential (Kumar et al., 2022). Another significant effort is the use of synthetic hexaploid, hybrid, and transgenic wheats to expand genetic variability and select for recombinants. These methods, combined with molecular approaches such as quantitative trait locus (QTL) and association mapping, have been instrumental in improving yield potential and resistance to new pests and diseases, particularly in Asian countries (Rauf et al., 2015).

### 6.2 Commercial application of stress-tolerant wheat

The commercial application of stress-tolerant wheat varieties has shown promising results in various regions. For instance, the development of drought-tolerant wheat genotypes has been a priority due to the increasing frequency of drought events. Recent studies have identified wheat germplasm with useful genetic sources for drought tolerance and reported QTLs associated with drought tolerance traits. These efforts have facilitated genome- and marker-assisted selection approaches, accelerating the development of drought-tolerant wheat varieties (Khadka et al., 2020a). Additionally, the evaluation of newly developed wheat genotypes for water deficit stress tolerance has highlighted the importance of physio-biochemical mechanisms in breeding programs. Genotypes that maintain better water relations, photosynthetic pigments, and antioxidative defense mechanisms under limited water supply have shown better yield performance, making them suitable for commercial application in drought-prone areas (Shahid et al., 2022).

### 6.3 Development of comprehensive resistance varieties

The development of wheat varieties with comprehensive resistance to multiple diseases and environmental stresses has been achieved through various innovative breeding strategies. One such example is the identification of wheat genotypes with high levels of biotic and abiotic stress tolerance from the extensive collections conserved in national and international genebanks. These genotypes have been evaluated for trait-specific germplasm, leading to the development of varieties with combined resistance to multiple stresses (Kumar et al., 2022). Another case study involves the genome-wide association study of yield-related traits in wheat under normal and drought conditions. This study identified several QTLs and SNPs associated with yield and drought resistance, which have been transformed into kompetitive allele-specific PCR (KASP) markers. These markers facilitate the discovery of promising SNPs for yield-related traits and drought stress tolerance, accelerating the development of new wheat varieties with comprehensive resistance (Zhao et al., 2023).

## 7 Future Research Directions and Trends

### 7.1 Diversified strategies for wheat germplasm innovation

Future research should focus on integrating multiple traits and diversifying breeding strategies to enhance wheat germplasm innovation. Traditional breeding methods, such as direct hybridization and backcrossing, have been successful but are time-consuming and limited in their ability to combine multiple desirable traits (Mondal et al., 2016). Modern approaches, including high-throughput phenotyping, genome sequencing, and genomic selection, offer promising avenues to accelerate the breeding process and improve the genetic gains in wheat (Mondal et al., 2016; Dwivedi et al., 2017). Additionally, the use of cisgenic techniques to transfer beneficial alleles within related species can help achieve durable resistance to diseases like rust (Mondal et al., 2016). An integrated approach involving multiple stakeholders and disciplines, such as molecular biology, genomics, agronomy, and stress tolerance, will be essential to address the global challenges of food security and climate change (Dwivedi et al., 2017).

### 7.2 Germplasm innovation in the context of climate change

Climate change poses significant challenges to wheat production, necessitating the development of stress-tolerant germplasm. Strategies to enhance germplasm innovation in response to climate change should include the identification and utilization of genetic diversity from gene banks and wild relatives (Sehgal et al., 2015; Kumar et al., 2022). Advanced molecular techniques, such as genotype-by-sequencing and genome editing (e.g., CRISPR-Cas9), can be employed to identify and incorporate quantitative trait loci (QTLs) associated with drought and heat tolerance (Khadka et al., 2020a; Khadka et al., 2020b). High-throughput phenotyping platforms can also play a crucial role in evaluating physio-morphological traits at different growth stages, thereby improving the efficiency of breeding programs aimed at developing drought-tolerant wheat varieties (Khadka et al., 2020b). The integration of genetic, genomic, and phenotypic information will be vital for the rapid application of novel genetic discoveries in breeding programs (Dwivedi et al., 2017).

### 7.3 Integration of wheat germplasm innovation with precision agriculture

The application of digital breeding and precision agriculture technologies holds significant potential for advancing wheat germplasm innovation. Precision agriculture techniques, such as remote sensing and data analytics, can enhance the monitoring and management of crop growth and stress responses (Mondal et al., 2016). Digital breeding tools, including genome-wide association studies (GWAS) and high-density SNP arrays, can help dissect the genetic basis of complex traits like heat tolerance and yield. The integration of these technologies can facilitate the development of high-yielding, stress-tolerant wheat varieties by enabling more precise selection and breeding decisions (Ahmed et al., 2022a). Furthermore, the use of phenotypic markers, such as peduncle length and tillers per plant, can aid in the selection of disease-resistant and high-yielding genotypes (Saeed et al., 2022). By leveraging the power of precision agriculture and digital breeding, future research can significantly enhance the efficiency and effectiveness of wheat germplasm innovation.

## 8 Concluding Remarks

Germplasm innovation plays a pivotal role in enhancing wheat's yield, disease resistance, and stress tolerance. The exploration and utilization of genetic diversity within wheat germplasm collections, including landraces, wild relatives, and breeding lines, are fundamental to developing cultivars that can withstand various biotic and abiotic stresses. For instance, the Indian Wheat Genomics Initiative highlights the significance of harnessing genetic resources to breed disease-resistant, nutrient-dense, and climate-resilient wheat varieties, which is crucial for ensuring food security in stress-prone environments. Similarly, the identification and deployment of alleles associated with desirable agronomic traits through genome-wide approaches have been shown to enhance crop productivity and resilience, particularly in drought-prone environments.

The integration of advanced breeding technologies, such as genomic selection and genome editing, further accelerates the improvement of wheat by combining multiple traits, including yield potential, phenology, and stress adaptation. Studies have demonstrated the identification of quantitative trait loci (QTL) and single nucleotide polymorphisms (SNPs) associated with yield-related traits and stress tolerance, which are instrumental in developing high-yielding and stress-tolerant wheat varieties. Moreover, the evaluation of genetic variation and drought stress tolerance in different wheat genotypes underscores the importance of germplasm resources in breeding programs aimed at improving drought tolerance and yield stability.

The broad application of germplasm innovation in future agriculture holds immense potential for addressing global food security challenges. As climate change exacerbates the frequency and intensity of abiotic stresses such as drought and heat, the development of stress-tolerant wheat varieties becomes increasingly critical. The utilization of diverse germplasm collections, coupled with advanced molecular techniques, enables the identification of valuable genetic resources for breeding programs. This approach not only enhances the genetic gain of multigenic traits but also ensures the rapid and efficient development of resilient wheat cultivars.

The integration of genome engineering/editing technologies, such as CRISPR-Cas9, offers promising avenues for fine-tuning the expression of genes controlling adaptive traits, thereby improving drought tolerance and overall crop performance. Additionally, high throughput phenotyping (HTP) techniques can accelerate the selection process, facilitating the development of wheat varieties with superior stress tolerance and yield potential. The collaborative efforts of researchers, breeders, and stakeholders in managing and utilizing genetic resources will be instrumental in addressing the global challenge of ensuring food security amidst growing resource demands and climate change-induced stresses.

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### Conflict of Interest Disclosure

The authors affirm 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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