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Advances in Genomic-Assisted Breeding for High-Yield and Climate-Resilient Wheat

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Abstract: *Wheat (Triticum spp.) is a staple food crop important for global food security, providing essential calories and proteins to billions of people. However, wheat production faces numerous challenges due to climate change, in the form of droughts, heat stress, and extreme weather events. This review synthesizes advances in genomic-assisted breeding that are used to develop climate-resilient varieties of wheat for high-production. Advanced molecular breeding methods such as genomic selection, marker-assisted selection breeding, genome-wide association studies method, and CRISPR-Cas9 gene editing methods are compared with traditional methods. Advance breeding methods enhance precision in breeding, accelerate genetic gains, and target various complex traits like drought tolerance, heat resistance, disease immunity, and grain quality of crop. Further, Genetic resources from wild relatives are discussed for broadening diversity and introgression stress-resistant alleles. Case studies demonstrate successful applications, including doubled genetic gains via GS and improved yield-protein trade-offs. Challenges, such as the wheat genome's complexity, high phenotyping costs, and resource limitations in developing regions, are addressed, alongside future directions involving multi-omics integration, artificial intelligence, and global collaborations (CIMMYT). Ultimately, genomic-assisted breeding offers a transformative strategy to sustain wheat productivity amid environmental pressures, ensuring long-term food security.*

Keywords: *genomic selection (GS), genome-wide association studies (GWAS), CRISPR-Cas9, climate resilience, drought tolerance, heat stress, disease resistance, genetic diversity, landraces, wild relatives, sustainable agriculture, yield improvement, grain quality, global collaboration.*

1. Introduction

Wheat is an important staple food crop for food security globally. Wheat production is greatly affected due to climate change. Wheat supplies approximately 20% of the global population's caloric and protein diets (Erenstein *et al*., 2022). Wheat serves as highly nutritional crop and broad application of wheat in daily diet make it an important crop across the world. Apart from its significance in caloric consumption, wheat also plays a major role in global trade; approximately 25% of the world's production of wheat is exported in the global market. This indicate its indispensable role in food value chains in the world (Langridge *et al*., 2022). Despite an ever-growing world population, the global demand for wheat still increases, particularly due to its dominant position in processed foods, which are becoming increasingly ubiquitous in developing countries. This necessitates an emergency increase in wheat productivity and effective adaptation in diverse agri-food systems in the world, especially in the Global South (Erenstein *et al*., 2022). Green Revolution achievements in the past highly increased wheat productivity; however, there is an imminent need for new approaches to maintain these gains against environmental and economic threats such as water scarcity, drought, and the rising price of fertilizers and pesticides (Shiferaw *et al*., 2011). Increase in global temperatures alter the weather conditions such as precipitation that cause severe droughts affecting wheat production. For example, drought stress in wheat affects morphological and physiological characteristics, as a result, wheat productivity decreases (Bohra *et al*., 2024).The studies reveal that 60% of wheat growing would face extreme climatic events as droughts by the end of 21st century, affecting the global wheat production (Bohra *et al*., 2024; Jan et al., 2025). The impacts of climate change are spatially heterogeneous in their expression; whereas some cooler regions can witness a marginal increase in wheat yield due to an enhancement of the level of carbon dioxide, equatorial nations near the equator can expect a considerable decrease in yield, causing food insecurity in such regions (Farooq *et al*., 2023). Climate change in countries like Australia is expected to decrease the wheat-growing region and yield per hectare in some regions, thus directly jeopardizing local as well as global wheat production (Wang *et al*., 2018). Global wheat production is faced with a myriad of yield and sustainability challenges that need to be tackled to ensure food security and environmental conservation. Climate change has a profound impact on wheat production by altering patterns of weather and heightening the frequency of extreme weather events. The changes might lead to decreased yields, especially in equatorial regions, while potentially boosting yields in cooler regions due to enhanced carbon dioxide uptake (Farooq *et al*., 2023).

To manage these issues, extensive investment in research and development is necessary to improve the resistance of wheat to drought and render it more sustainable as a whole. Progress in wheat genetics, breeding technology, and the application of biotechnological innovations can help develop drought-resistant varieties and enhance the efficiency of nutrient use (Farooq *et al*., 2023). Sustainable intensification adopting technologies that enhance resistance to pests, diseases, and climatic stresses is key to maintaining wheat productivity in a rapidly evolving world (Shiferaw *et al*., 2011). Climate change adaptation requires the utilization of multiple climate models and bias correction techniques to improve projections and enable better planning (Farooq *et al*., 2023). Successful water management is key to the sustainability of wheat production. The utilization of innovative irrigation practices, such as drip irrigation and integrated deficit irrigation management, is necessary to optimize water use efficiency and adopt variable rainfall conditions. The methods are key to the maintenance of crop productivity, especially in semi-arid regions that are characterized by persistent water shortages (Hashemi *et al*., 2024; Tahir *et al*., 2024; Jan et al., 2025). The yield and quality of wheat is linked with proper use of nitrogen. Balancing the use of nitrogen is key to sustainable wheat production despite being essential for wheat production, over use of nitrogen can cause environmental impacts like eutrophication and increased greenhouse gas emissions. (Tahir *et al*., 2024). Determination of the right areas for wheat production is important to expand production and correct yield imbalances. The agro-ecological zones (AEZ) approach is a useful tool in the determination of land suitability for wheat in irrigated and rainfed conditions. For irrigated wheat, areas such as the North China Plain are prioritized, while areas in Europe are identified as good areas for the expansion of rainfed wheat production (Dadrasi *et al*., 2023). Biotechnology advancement through genetic modification and development of stress-tolerant cultivars, and eco-friendly agricultural practices such as crop rotation and integrated pest management, are the possible solutions for enhanced crop resistance and productivity. Furthermore, precision agriculture maximizes the use of resources and increases productivity through data-based management (Khan, 2024; Yang *et al*., 2021). There are enormous gaps in irrigated and rainfed wheat production in various countries. It is essential to fill these gaps in order to meet the rising food demands and to ensure global food security (Dadrasi *et al*., 2023).

2. Genetic Resources for Wheat Improvement

Genomic-assisted breeding is advantageous over traditional breeding as shown in (Table 1). Genetic wheat resources such as landraces, wild relatives, and cultivated varieties are important in wheat breeding programs. The wide genetic pool enables breeders to come up with new varieties that can resist different environmental stresses and are able to satisfy specific agricultural requirements. Landraces are traditional cultivars that developed naturally over time and possess high variability and tolerance to growing conditions in local areas. They provide a rich genetic variability that can be utilized to enhance the improvement of modern wheat cultivars. But due to long-term genetic erosion, some landraces have been reduced in diversity, highlighting the need to conserve and utilize them in breeding schemes (Mourad *et al*., 2019; Jan et al., 2025). Wild relatives of wheat are a precious source of genetic diversity for breeding, especially those characteristics that are linked to biotic and abiotic stress resistance. Wild barley-durum wheat cross that resulted in hexaploid tritordeum is a prime example of the successful utilization of wild relatives to create new crop species with favorable characteristics. The genetic variation and adaptive characteristics of the wild relatives make them most important for breeding crops with durability (Ávila *et al*., 2021).

Improved yield and quality of wheat were brought about by modern breeding but also frequently resulted in a reduced genetic base. However, the intentional introduction of new alleles of plant genetic resources (PGRs) into the contemporary gene pool is intended to enhance genetic diversity and enhance characteristics. This is done via methods such as marker-assisted selection (MAS) and genomic selection, which enable the introgression of valuable alleles from varied germplasm into elite wheat lines (Sharma *et al*., 2021; Subedi *et al*., 2023). Genetic diversity evaluations establish differences in the level of diversity between geographically disparate areas. For example, application of genetic polymorphism research in countries such as India and Turkey gives information about structures of populations, which are essential in successful breeding. There has been similar analysis of how contemporary methods of breeding can both hinder or worsen genetic erosion in crops, pointing to the importance of balanced strategies for maintaining genetic diversity (Henkrar *et al*., 2016; Khan *et al*., 2015). Influence of the untapped genetic diversity of wheat is a strategic strategy for attaining greater yields and climate resilience. Advantages of using wild relatives as well as landrace diversity is highlighted in several studies.

Table 1. Comparison between traditional breeding vs genomic-assisted breeding

Characteristics	**Traditional Breeding**	**Genomic-Assisted Breeding**
Basis of Selection	Relies on visible traits (phenotypes)	Use DNA markers and genome information
Accuracy	Lower, influenced by environment	Higher, precise identification of desirable genes
Time Required	Long (multiple generations)	Shorter (early selection possible)
Cost	Initially low, but high over long cycles	Higher initial cost, but more cost-effective long-term
Genetic Gain	Slower improvement	Faster improvement
Detection of Hidden Traits	Difficult to detect recessive or complex traits	Can identify hidden or polygenic traits
Application	Suitable for simple traits (e.g.,	Ideal for complex traits (e.g., yield, disease resistance, drought

	color, size)	tolerance)
Adaptability	Limited in rapidly changing environments	Better adaptability due to precise selection
Data Requirement	Minimal data (field trials only)	Requires genomic, phenotypic and bioinformatics data

Wild wheat relatives (WWR) hold a pool of genetic components that can maximize resistance to insects, pathogens, and abiotic stresses such as drought and salinity. Promising developments in genomic sequencing and gene editing hold the key to transferring such desirable traits to cultivated wheat (Farooq *et al*., 2025). The A.E. Watkins landrace collection exhibits high levels of genetic diversity that have not been exploited due to the fact that many modern cultivars are based on a narrow genetic base. By analyzing genomes, thousands of quantitative trait loci (QTL) and important marker-trait associations have been mapped, opening up new traits for climate-change adaptation and nutritional improvement (Cheng *et al*., 2023). Traditional breeding methods such as, hybridization and backcrossing can be augmented by newer techniques such as, high-throughput phenotyping and genomics to effectively incorporate desirable characteristics. These techniques have the potential to overcome the constraints of conventional breeding, thus driving genetic gains in yield, climate tolerance, and nutrient content (Mondal *et al*., 2016). Crop biotechnology involving gene editing technologies has the potential to increase genetic diversity and improve resilience. Although previous developments in recombinant DNA technology have yet to achieve this potential, novel gene editing approaches present huge opportunities. Such technologies must be brought from the laboratory to application, to the point where they can make an effective contribution to agricultural changes (Garland and Curry, 2022; Jan et al., 2025). Increased landscape diversity can further assist in increased resilience and stability of yields. Research has demonstrated that diversification of the landscape results in high yield gain and decreased variability of the yield. This suggests that both environmental and genetic diversity play pivotal roles in gearing up wheat production systems for coping with climate extremes (Nelson *et al*., 2022). Producing high-yielding, stress-tolerant wheat varieties necessitates strong support for breeding programs, field trials, and research. Investment and interdisciplinarity are essential for making the use of the available genetic resources present in landraces and wild relatives (Farooq *et al*., 2025).

MAS has greatly helped to enhance wheat traits through increased genetic gain, efficiency in breeding, and trait accuracy. Below a number of ways MAS has been used to enhance wheat traits, MAS plays an essential role in increasing disease resistance in wheat. It makes it possible to identify and introduce disease-resistant genes accurately at the seedling stage. In wheat, (Lr34/Yr18) and (Lr46/Yr29) genes have been efficiently utilized to enhance leaf rust and stripe rust resistance (Kuchel *et al*., 2007; Miedaner and Korzun, 2012). In addition, MAS application for quantitative disease resistances is preferred, although issues persist for QTL-controlled traits (Mapari and Mehandi, 2024). MAS offers a more effective selection procedure for quality characteristics such as, dough character and semolina quality. MAS for the selection of specific glutenin alleles has led to enhanced dough extensibility and resistance (Kuchel *et al*., 2007). MAS reduces the selection procedure for quality characteristics that are historically expensive and time-consuming to phenotype (Fiedler *et al*., 2017). For agronomic qualities like drought resistance, MAS provides a way to improve breeding programs through the association of genomic and phenotypic information. Genomic selection (GS), a relatively new method associated with MAS, permits the quick choice of traits like yield and crop stability across different environments, managing genotype by environment interactions (GEI) (Chang-Brahim *et al*., 2024; Huang *et al*., 2016). Using MAS, breeders are able to enhance the accuracy of selection and effectively transfer valuable characteristics into elite breeding lines. Forward breeding and marker-assisted backcrossing are among the techniques applied to introduce traits from donor to recipient genotypes, accelerating the breeding cycle and attaining objectives effectively (Gupta *et al*., 2009). High-throughput genotyping and automated screening methods raise the tempo and minimize the cost of MAS. These developments, complemented by artificial intelligence (AI) and genomic resources, are optimizing MAS for use in contemporary breeding programs (Landjeva *et al*., 2007; William *et al*., 2007).

GS is essential in the acceleration of wheat breeding through improved accuracy in selection and enhanced genetic gain over conventional procedures. GS builds on MAS methods by employing a statistical model for estimating genome-wide effects of markers, resulting in genomic estimated breeding values (GEBVs) for the selection of superior breeding lines even in the absence of phenotypic information (Larkin *et al*., 2019; Jan et al., 2025). One of the key benefits of GS is the possibility of realizing greater genetic gains. Conventional wheat-breeding programs, through crossing the parental lines and the resultant selfing, may take more than eight years to produce a new variety. Yet, with the use of genomic data, genetic gains through GS have been reported to triple those of phenotypic selection (Tessema *et al*., 2020). This effectiveness comes about due to GS capacity to accelerate the breeding process by minimizing cycle times, enabling quicker release of new varieties. GS do this by adopting rapid-cycle recurrent genomic selection (RCRGS), which can successfully boost grain yield and improvement of traits in a shorter time than traditional approaches (Dreisigacker *et al*., 2023).

GS is also adaptable, accommodating two-component breeding strategies that segregate into population improvement and product development. These strategies incorporate GS into different stages of the breeding pipeline to predict and select efficiently breeding lines within and between breeding cycles. This strategy maximizes parental selection and retains genetic diversity while enabling maximum cross-prediction (Merrick *et al*., 2022). GS also has the potential to predict and enhance complex traits in wheat, including disease resistance and grain quality. It has great benefits for low-heritability traits, in which conventional phenotypic selection may not be so effective. Applied properly, GS can provide very high prediction accuracy and thus is a key component of breeding approaches to enhance major traits such as grain yield, grain quality, and resistance to disease (Venske *et al*., 2019). GS implementation is also not simple and demands appropriate consideration of factors affecting prediction accuracy. These considerations involve the choice of prediction models, marker density, heritability of traits, and the connection between the training and validation sets (Crossa *et al*., 2013). These factors can be addressed in order to optimize the effectiveness of GS, thus providing effective inclusion in wheat breeding programs. These measures highlight the paramount significance of GS in transforming wheat breeding in accordance with the growing agricultural needs as well as environmental demands (Robert *et al*., 2022; Venske *et al*., 2019). Genome-wide association studies (GWAS) are useful for detecting major wheat genes and quantitative trait loci (QTLs) important for different traits, including disease resistance, drought tolerance, and agro-morphological traits. GWAS exploits large amounts of genotypic and phenotypic information to identify associations between genetic markers and target traits. In the case of wheat, GWAS has enabled the detection of major QTLs associated with stress resistance and tolerance traits like leaf rust and powdery mildew resistance and cold tolerance. For instance, a high-density GWAS revealed 153 QTLs in multiple stress resistance traits with most of these QTLs bounded to narrow genomic regions, which are valuable for genetic enhancement by fine mapping and identification of candidate genes (Pang *et al*., 2021). Additional research has mapped disease resistance genes for powdery mildew and cereal cyst nematode through the use of mixed linear models and detected novel QTLs on different wheat chromosomes. For example, QTLs located on (3A, 3B, 6D, and 7D) chromosomes for resistance to powdery mildew indicate possible new genetic markers for resistant cultivar breeding (Kang *et al*., 2019; Pariyar *et al*., 2016).

In addition, the mapping of QTLs for agro-morphological traits such as plant height and flag leaf characteristics has better elucidated the underlying genetic determinants. A systematic GWAS that was done across locations and years identified new QTLs that control these traits, which indicates the prospect that breeding programs can generate wheat with favorable plant architecture to produce higher yield potential (Subedi *et al*., 2024). GWAS has also played a key role in deciphering and enhancing drought tolerance in wheat by revealing important marker-trait associations (MTAs) for biomass attributes under drought stress (Mathew *et al*., 2019). This information helps to design strategies for marker-assisted breeding to enhance drought resistance and maximize biomass allocation towards carbon sequestration. The application of CRISPR-Cas genome editing technology has significantly advanced wheat improvement by offering precise and efficient methods for genetic modification.

This tool permits the specific alteration of those genes accountable for wanted traits, something that has historically been done at a slow pace using traditional breeding methods. CRISPR-Cas has made it possible to achieve improvements in a number of applications for wheat improvement: CRISPR-Cas technology is key to improving both biotic and abiotic stress tolerance in wheat. For example, genes governing disease resistance, drought tolerance, and salt tolerance have been specifically edited to create wheat varieties that are more resilient to environmental stresses (Erdoğan *et al*., 2023). CRISPR-Cas technology's precision enables the editing of genes influencing crop yield and quality. Through the targeting of unique genetic loci, scientists have enhanced key characteristics in wheat, including nutrient value, grain size, and general nutritional composition (Guo *et al*., 2023). The creation of CRISPR-Cas variants, including base editors and prime editors, has expanded editing precision, enabling precise alteration without triggering unintended modifications (Biswas *et al*., 2021). This specificity is important in minimizing off-target effects, making genome editing a more reliable and safer option for wheat improvement. There have been improvements in delivery systems for CRISPR-Cas, with DNA-free systems being notable. These systems enable gene editing without foreign DNA introduction, a key aspect of minimizing regulatory challenges posed by genetically modified organisms (GMOs) (Chen *et al*., 2019). CRISPR-Cas technology enables synthetic biology applications and wheat domestication. This can make possible the evolution of new traits not present in existing wheat varieties by introducing genes from wild relatives or entirely new traits (Biswas *et al*., 2021; Chen *et al*., 2019).

3. Advancements in Genomic Tools and Technologies

Successful genomic strategies for improving drought tolerance in wheat include a range of methods aimed at breeding and genetic alteration. These methods include MAS, GS and gene editing methods as given in (Table 2). MAS uses molecular markers associated with target characteristics (e.g., drought resistance) to support the selection process. In wheat, genomic locations responsible for drought tolerance have been discovered, for instance, on chromosome 4B, which controls grain yield, harvest index, and root biomass during drought (Kadam *et al*., 2012). GS, the integration of high-throughput phenotyping (HTP) and genomics, has the potential to predict drought tolerance as a complex trait more efficiently (Mohammadi, 2018). The utilization of diverse genetic resources preserved in gene banks is important for the determination of drought-tolerant traits. QTLs for drought tolerance have been identified, and large germplasm collections have contributed useful genes to breeding programs (Khadka *et al*., 2020). Genes influencing drought tolerance traits can be fine-tuned using tools such as, CRISPR-Cas9 mentioned in (Figure-1). This level of gene precision makes it easier to construct wheat varieties with improved drought tolerance (Khadka *et al*., 2020; Jan et al., 2025). Phenotypic evaluation coupled with molecular information makes it easy to screen wheat varieties comprehensively. This integration assists in the choice of varieties with favorable characteristics for drought tolerance, such as, Tunisian wheat varieties, which were tested through both agronomic and molecular markers (Guizani *et al*., 2024). Knowledge about genetic, physiological, and biochemical interactions responsible for drought resistance is important. This information can inform breeding programs in producing cultivars that are more suited to drought (Bapela *et al*., 2022). HTP technologies improve the effectiveness of choosing drought-resilience traits by allowing high-speed phenotypic analysis of high-density populations. It enables the finding of stress-resistance phenotypes and shortens breeding cycles (Mohammadi, 2018). Genomic tools have been pivotal in implementing heat tolerance in wheat, which is an essential requirement owing to rising global temperatures affecting wheat yields.

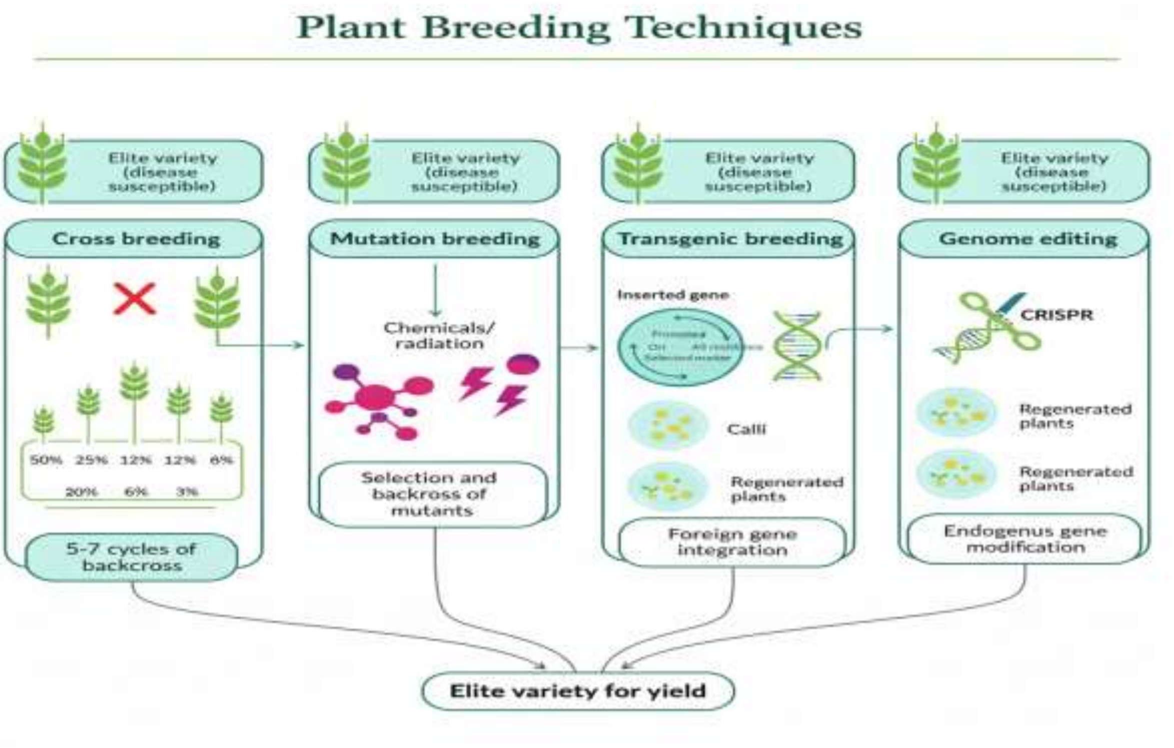
Table 2. Key tools used in wheat breeding

Tools	**Purpose in wheat breeding**
Molecular Markers (SSR, SNP, DArT, AFLP, etc.)	Marker-assisted selection (MAS); trait mapping; genetic diversity analysis
High-Throughput Genotyping (SNP arrays, GBS)	Rapid genome-wide marker profiling for large populations
QTL Mapping and GWAS	Identifying genomic regions controlling yield, stress tolerance, disease resistance
Genomic Selection (GS)	Predicting breeding values using genome-wide markers to accelerate selection

Transcriptomics (RNA-seq)	Studying gene expression under stress or developmental stages
Proteomics and Metabolomics	Linking gene function to protein/metabolite profiles influencing traits
Genome Editing (CRISPR-Cas9, TALENs, ZFNs)	Precise modification of genes for traits like disease resistance, quality improvement
Speed Breeding + Genomics	Combining rapid generation advancement with genomic tools for faster cultivar release
Pangenomics and Comparative Genomics	Capturing genetic diversity across cultivars and wild relatives to broaden gene pools
Bioinformatics	Managing large genomic datasets; predictive modeling; decision support in breeding

Following are some genomic approaches used to mitigate heat stress in wheat. QTLs and genes that control heat tolerance in wheat have been identified through recent developments. The genomic regions that map these genes can be used by scientists to select for the desirable traits that enhance heat tolerance, including better cellular membrane stability and drought-tolerant water use (Elbashir *et al*., 2017; Sun *et al*., 2021). Methods like CRISPR-Cas9 and marker-assisted selection are employed to create or improve heat resistance characteristics. For instance, scientists have been able to apply genomic editing to alter wheat genes involved in heat-stress responses, which assists in creating varieties that are able to sustain productivity under heat stress (Benavente and Giménez, 2021; Fu *et al*., 2008).

Wheat's wild relatives have natural heat tolerance and other stress resistance properties. By cross-breeding and genomic selection, these characters can be introgressed into crop wheat lines,



thus making them more heat stress resilient (Farooq *et al*., 2025). The sequences of the entire wheat genome have helped in genetic analysis of heat tolerance traits, enabling breeders to make accurate selection for tolerant genotypes. This genomic data complements traditional breeding schemes by allowing more effective integration of useful traits (Hill and Li, 2022; Yadav *et al*., 2022). Progress has also been reported in creating transgenic wheat lines that alleviate heat stress at the molecular level. For example, transgenic wheat plants carrying a maize gene encoding the EF-Tu elongation factor had improved heat stress protection through increased protein stability and photosynthetic efficiency (Fu *et al*., 2008). Combining genomic tools with physiological and biochemical approaches is an integrated method of breeding. This multi-disciplinary approach is a matter of learning the way genes perform under heat stress and making certain that these functional characteristics are efficiently expressed in field conditions (Akter and Rafiqul Islam, 2017; Ibrahim and Quick, 2001).

Figure 1. Approaches for plant breeding techniques

4. Strategies for Disease Resistance in Wheat

A number of genomic approaches have been designed to improve disease resistance in wheat, especially to major diseases, rusts and *Fusarium* head blight (FHB). Such strategies rely on several molecular and breeding methods to come up with more resistant wheat species to such diseases. One of the tools is MAS which employs the use of DNA markers to help in the indiscriminate selection of plants that have desirable characteristics e.g. disease resistance. MAS has also been applied to tagging of useful disease resistance genes in wheat that allow for even efficient and fast selection as opposed to conventional breeding techniques. An example of the successful application of MAS is the Lr34 and Yr36 genes of rust resistance and the QTL such as FHB1 (Jabran *et al*., 2023; Miedaner and Korzun, 2012). GS further develops MAS in that the effects of multiple genetic markers are jointly estimated to select breeding stock based on their profile of genome-wide marker sets. In case of quantitative traits, such as FHB resistance, this method has been able to progress in breeding different individuals whose genetic results were desirable when they did not possess any phenotypic observations (Larkin *et al*., 2019; Todorovska *et al*., 2009).

CRISP-Cas9 system gives maximum accuracy when editing particular genes linked to resistance of diseases. This technology has potential to alter the genes to increase worm resistance features of wheat to cover the issues of several pathogens (Jabran *et al*., 2023). This is done by stacking together several resistance genes in one genotype and this could be more sustainable. Nevertheless, it is a complicated and period-consuming step in case of the conventional methods, whereas molecular breeding can be used to accelerate the process (Luo *et al*., 2023; Todorovska *et al*., 2009). The presence of QTL related with disease resistance would enable the specific improvement of certain parts of the wheat genome. This has proved especially handy with traits such as FHB resistance (Steiner *et al*., 2017). GWAS allows identifying the genetic variations that are associated with a trait of resistance to disease throughout the entire genome. These experiments would assist in revealing new resistance genes and play a critical role in generating broad-spectrum resistance (Jabran *et al*., 2023). It is possible to make use of the available genetic variation of primary, secondary and tertiary pools of genes of wheat and thus use them to introduce new genes and alleles into breeding. This should provide the diversity that will enable it to come up with varieties that are able to handle the changing pathogens and stresses in the environment (Mondal *et al*., 2016).

Genomic-assisted breeding, and, specifically, through GS, has become an effective methodology to improve wheat yield potential and grain quality. This technique involves a statistical model to predict GEBVs using the marker data and thereby selecting without using massive quantities of phenotypical data. GS is adapted to wheat breeding programs that have already been used to enhance grain yield and grain quality and disease resistance to fungus, FHB (Larkin *et al*., 2019).

5. Advantages of Genome-Assisted Breeding in Wheat

The method of identification of traits such as grain yield, which are strongly affected by environmental conditions and grain quality can be efficiently addressed with optimizing prediction models, marker density, heritability of the traits, and others to ensure maximal prediction accuracy (Larkin *et al*., 2019). The MAS is synergistic with the phenotypic information in the context that it increases the preferential choice of both the desired traits like disease's resistance and grain quality traits. Such an approach makes it possible to enrich the positive alleles, which contributes to the overall breeding effectiveness of the program (Toth *et al*., 2019). The use of GS models has allowed high genetic gain rates of complex traits in shorter time than conventional approaches to breeding. Such a process is vital to aligning with the needs of global food security and MAS (Bentley *et al*., 2014; Zhang-Biehn *et al*., 2021). GS is important in enhancing heritage traits of end use quality determination of genetic variability of quality traits like gluten strength and bake-mixing time. It has led to more streamlined selection and assisted with satisfying consumer demand regarding a particular wheat product in the international market (Fiedler *et al*., 2017; Subedi *et al*., 2023; Zhang-Biehn *et al*., 2021). Through the decoding of wheat genetic architecture negative correlation between protein content and yield can be resolved thereby enhancing both at the same time. Genomic prediction can be used to guide the discovery and utilization of trait-linked metabolites that will disrupt this antagonism (Thorwarth *et al*., 2018).

The use of genomic-aided breeding has resulted in a number of interesting case studies on the production of wheat types. Such strategies have concentrated on a range of essential characteristics with a view to enhancing both wheat yields and quality. One case study has noted the success of simultaneously selecting grain yield and protein content with GS index. This method successfully managed this trade-off whereby generating varieties that have high yield and protein content through efficient utilization of the nitrogen that is available (Michel *et al*., 2019). Marker-assisted breeding is also used in Canada to develop better yielding and disease resistant hexaploid spring wheat. There has been the development of molecular markers to various traits such as resistance to various diseases and even agronomic characteristics such as plant height and vernalization. This allows the increasing of the desired allelic frequency and provides the situation of effective selection, contributing to a better efficiency of selection (Toth *et al*., 2019). GS will be used to take traditional wheat breeding programs to new heights in accentuating genetic gain. This technique has proved to be promising, whereby genetic gain has tripled in comparison to the conventional phenotypic selection. These developments facilitate the breeding process and overcome the weaknesses of the traditional breeding mechanism given in (Figure-2) (Tessema *et al*., 2020). A third paper examined how to incorporate GS with wheat breeding programs redesigning the historic pathway of breeding allowed to increase genetic gain significantly by making the decision on selection and subsequent cross-prediction more efficient. The key elements of such a two-component breeding approach (as population improvement and product development) help to release new wheat varieties quicker and with improved genetic characteristics (Merrick *et al*., 2022).

The application of genomic-assisted breeding in wheat is not without obstacles that hamper its transfer to major use. The complex nature of the wheat genome is one of the problems that cannot be ignored since it hinders the identification and use of genetic markers. The complexity of wheat compared to the other staple crops is due to it having a large and polyploid genome. This makes it more difficult, necessitating highly technology-demanding sequencing platforms and the most innovative computational applications to handle and parse genomic information (Larkin *et al*., 2019). The second obstacle is the necessity of the high-quality data on phenotype to supplement the genomic data. One of the keys to the application of genomic selection is the combination of tremendous data on genomic structures with precise phenotypic data. Such an approach is also expensive, labor-intensive, and time-consuming to gather comprehensive phenotypic data, which constrains the use of genomic-assisted approaches to breeding (Sandhu *et al*., 2022). Another big problem is the cost involved with GS implementation including cost of establishment of infrastructure, cost of staff training and possible cost of technology acquisition. In some wheat breeding programs in the developing world, because of a lack of resources and funding, it may not be possible to implement and sustain GS applications (Tadesse *et al*., 2018). Also, there are the issues of data management and data analysis. Processes of large-scale genomic data integration and analysis need sound bioinformatic skills and tools that are not readily available in all breeding facilities. This knowledge imbalance may slow down the application of genomic technologies and restrain their performance in conventional breeding programs (Luo *et al*., 2023). Moreover, there might be resistance to change, and poorly informed breeders will make the adoption slow. Traditional breeding methods are ingrained in the systems, and it will be a paradigm shift to adopt genomic-assisted methodologies which is a far cry if one is reluctant to adopt new approaches to methodologies (Todorovska *et al*., 2009). Multi-omics and AI will transform wheat breeding to bring together large biological data sets with advanced computing to speed crop improvement. Combined application of multi-omics (genomics, transcriptomics, proteomics, and metabolomics) offers a comprehensive perspective on the biology phenomenon behind wheat traits. It enables breeders to identify and directly modify major genes linked to beneficial traits, including disease resistance, drought tolerance, and improved yield, with the result that wheat varieties can be improved in effective ways (Yang *et al*., 2021; Zhang *et al*., 2022).

The computational power provided by AI improves this process by allowing it to deal with the large amount of data generated through multi-omics studies. Machine learning and deep learning technologies can read intricate patterns in the data, helping to predict which phenotype can be extrapolated out of available genotype input. This is possible because it helps in developing a more accurate selection model and decision-making framework, and, thus, enables breeding programs to be more efficient (Eftekhari *et al*., 2024; Khan *et al*., 2022). Also, the AI-multi-omics combination can assist in reducing major issues in wheat breeding like the connection between the genotype and phenotype and the streamlining of high-throughput phenotyping operations. The efficiency of the envirotype, genotype and phenotype could be improved by the usage of the AI algorithms; thereby making it more useful in breeding. The development of potentially better-adapted wheat varieties under environmental pressures and climate change can be achieved based on these advancements, which have led to faster gene identification and acceleration of wheat improvement programs (Khan *et al*., 2022). Moreover, AI-driven strategies can revolutionize wheat breeding via enhanced population selection strategies and predictive breeding. The combination of AI with systems biology and pan-omics based platforms can help to identify regulatory networks, which in turn should allow modifying them to boost the wheat resilience and productivity across various tropospheric conditions (Cembrowska-Lech *et al*., 2023). With this integration, breakthroughs can be expected not only in breeding efficiencies but also in food security of wheat, considering the effects of ushering climatic changes in the globe (Chao *et al*., 2023).

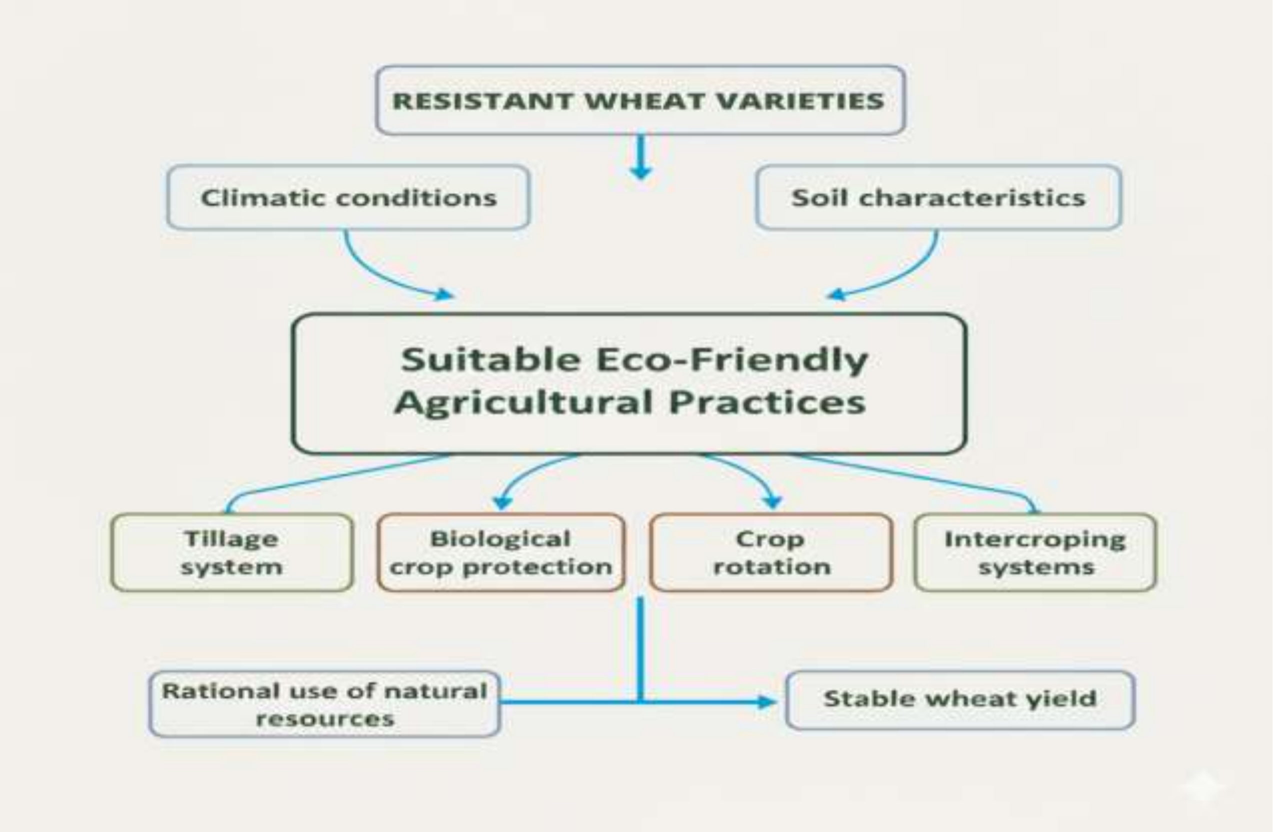


Figure 2. Strategies for resistant wheat varieties

6. Future Directions

The global collaboration and data sharing is the critical aspect of the genomic-assisted wheat improvement because there are various aspects which would facilitate the development of superior wheat cultivars and thus enhance food security in this world. The international maize and wheat improvement center (CIMMYT) is just another organization that has contributed towards the conservation and improvement of genetic resources. These include maintenance of genetic diversity, advancement of value added germplasm and strategic germplasm development. By distributing these materials, CIMMYT and other organizations allow international scientists to exchange a large number of genetic resources required in research programs. The system of the consultative group on international agricultural research (CGIAR) explains the popularity of international collaboration, and the open-source model of crop improvement is encouraged. This system promotes germplasm and international cooperation as the germplasm free exchange has been the antidote to any global food crisis and poverty and hunger alleviation according to history.

Crop improvement strategies can be accelerated with advances in genomics and bioinformatics. New technologies conceptualized through next-generation sequencing provide assistance in the production of complete reference genomes which are the basis of further genomic investigations. These tools are crucial in the conductance of advanced genome-wide association studies and functional tests that can point out important breeding-related objectives. Gene mapping has greatly enhanced insight into the quality traits of wheat including gluten proteins that are the key to end-use and health-related traits. The opportunities to share knowledge via access to collaborative genomic projects enable the sharing of this key data with the whole world, speeding access to breeding programs aimed at those respective traits The use of genetic resources in different environments in combination with genomic-based selection tools will enable robust and yield-stable wheat varieties that could satisfy the end-user requirements. This is of particular relevance to solving the two-fold dilemma of maximizing yield and conservation of quality attributes such as protein content. Collaboration distributes innovative genomic tools and breeding approaches time quickly, which makes them possible in different breeding programs. The ability to carry out all these activities together has also facilitated the production of disease resistant, climate tolerant, and high-yielding wheat varieties that are necessary to maintain agricultural productivity in the presence of globalization.

Conclusion

The global food security is the dire need of time. As climate variability and global food demands intensify, genomic-assisted breeding represents not only a technological advancement but also a strategic necessity for ensuring wheat productivity and food security worldwide. The integration of genomic-assisted breeding techniques has marked a new era in the development of high-yielding and climate-resilient wheat varieties. Breakthroughs in GWAS, GS, and CRISPR-based genome editing have significantly accelerated the pace and precision of wheat improvement. These tools have enabled breeders to more effectively harness genetic diversity and target complex traits related to yield stability, drought tolerance, and disease resistance. Despite these advancements, challenges remain in translating genomic discoveries into field-level impact, particularly in low-resource settings. Limitations in phenotyping capacity, data integration, and genotype-environment interactions continue to pose hurdles. To fully realize the potential of genomic-assisted breeding, future efforts should focus on integrating multi-omics data, developing climate-smart breeding pipelines, and fostering international collaboration among breeding programs.

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