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Wheat Breeding Strategies for Mitigating Global Climate Change: A Review

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ABSTRACT: Wheat, as a staple crop, plays a crucial role in global food security. However, the adverse impacts of climate change, including rising temperatures, erratic precipitation patterns, and increased occurrence of pests and diseases, pose significant challenges to wheat production worldwide. In response, breeding resilient wheat varieties has emerged as a critical strategy to mitigate the effects of climate change on wheat production. This abstract explores various breeding approaches aimed at enhancing wheat resilience to climate change. Traditional breeding methods, such as phenotypic selection and hybridization, have been pivotal in developing wheat varieties with improved stress tolerance. However, with advancements in genomics and molecular breeding techniques, breeders now have access to a wealth of genetic resources and tools for accelerating wheat breeding programs. Marker-assisted selection (MAS) allows for the identification and introgression of favorable alleles associated with traits such as drought tolerance, heat tolerance, and disease resistance, thereby expediting the development of climate-resilient wheat varieties. Moreover, genomic selection (GS) has revolutionized wheat breeding by enabling the prediction of complex traits based on genomic information, leading to more efficient and precise selection of elite breeding lines. Additionally, the utilization of genomic resources, such as high-density genetic maps and whole-genome sequencing, facilitates the discovery of candidate genes underlying desirable traits, offering valuable insights for targeted breeding efforts. Furthermore, innovative breeding strategies, including speed breeding and genome editing technologies such as CRISPR-Cas9, hold promise for accelerating the development of climate-resilient wheat varieties. Speed breeding techniques enable rapid generation turnover, allowing breeders to select for desired traits under controlled environmental conditions. Meanwhile, genome editing tools offer precise manipulation of target genes, enabling the introduction of beneficial traits or the removal of undesirable ones with unprecedented precision and efficiency. Collaborative efforts between public institutions, private sector entities, and international organizations are essential for ensuring the successful deployment of climate-resilient wheat varieties to farmers worldwide. Furthermore, the adoption of interdisciplinary approaches that integrate breeding with agronomic practices, such as conservation agriculture and precision farming, can maximize the resilience and productivity of wheat production systems in the face of climate change. In conclusion, wheat breeding strategies leveraging traditional breeding methods, genomic tools, and innovative technologies hold immense potential for developing climate-resilient wheat varieties capable of sustaining global food security amidst the challenges posed by climate change. By prioritizing collaborative research efforts and fostering knowledge exchange, the agricultural community can accelerate the development and adoption of resilient wheat varieties, thereby safeguarding food production and livelihoods in a changing climate.

Keywords: genomic selection (GS), doubled haploid (DH), cytoplasmic male sterility (CMS), Marker-assisted selection (MAS), wheat.

INTRODUCTION

Wheat breeding stands at the forefront of agricultural innovation, offering a crucial avenue to address the multifaceted challenges posed by climate change. Amidst rising temperatures, erratic rainfall patterns, and increasing frequency of extreme weather events, the resilience and adaptability of staple crops like wheat are being put to the test. Recognizing the urgent need for sustainable solutions, researchers and breeders have intensified efforts to develop climate-resilient wheat varieties capable of thriving under changing environmental conditions. The significance of wheat breeding in mitigating climate change cannot be overstated. As emphasized in studies such as that by the global production of wheat is vulnerable to climate-induced yield losses, with projections indicating substantial declines in yield potential under unmitigated climate scenarios. However, through strategic breeding initiatives, such as those outlined in the work of there exists a remarkable opportunity to enhance the adaptive capacity of wheat cultivars, thereby bolstering agricultural productivity and safeguarding food security in the face of climate uncertainty. Furthermore, the imperative to prioritize wheat breeding as a climate change adaptation strategy is reinforced by emerging research elucidating the intricate interplay between genotype, phenotype, and environmental factors. Recent studies, including those by Tadesse *et al.* (2022) have shed light on the genetic mechanisms governing traits such as heat tolerance, drought resistance, and disease resilience in wheat, providing invaluable insights for breeders seeking to develop resilient cultivars tailored to specific agroecological contexts. Moreover, the urgency of advancing wheat breeding efforts is underscored by the growing consensus within the scientific community regarding the escalating risks posed by climate change to global food systems. The landmark study by Ray *et al.* (2019) warns that without concerted action, climate change-induced disruptions to wheat production could have far-reaching consequences, exacerbating food insecurity and exacerbating socioeconomic disparities worldwide. In this context, the role of wheat breeding emerges as a linchpin for climate resilience, offering a proactive means to enhance the adaptive capacity of agricultural systems and mitigate the adverse impacts of climate change on vulnerable communities. In addition to bolstering the resilience of wheat crops against climate stressors, breeding programs also hold promise for promoting sustainable agricultural practices and reducing greenhouse gas emissions. Recent research by Crespo-Herrera *et al.* (2021) underscores the potential of precision breeding techniques, such as genomic selection and marker-assisted breeding, to expedite the development of climate-resilient wheat varieties with improved nitrogen use efficiency and reduced carbon footprint. By harnessing the power of innovative breeding tools and methodologies, researchers can not only accelerate the pace of varietal improvement but also contribute to broader sustainability goals within the agricultural sector. Wheat, one of the world's staple crops, plays a vital role in global food security and sustains millions of livelihoods worldwide . As climate change increasingly threatens agricultural productivity and food availability, the significance of wheat breeding cannot be overstated in addressing these challenges. The impacts of climate change, including rising temperatures, erratic rainfall patterns, and extreme weather events, pose significant threats to wheat production systems globally. In the face of these challenges, wheat breeders are tasked with developing resilient varieties capable of withstanding such environmental stresses while maintaining high yields. Through the utilization of advanced breeding techniques such as genomic selection, marker-assisted selection, and gene editing technologies, researchers can expedite the development of climate-resilient wheat varieties. These technologies enable breeders to identify and incorporate desirable traits such as heat tolerance, drought resistance, and disease resilience into new wheat cultivars. Furthermore, collaborative efforts between public research institutions, private sector entities, and international organizations are essential for enhancing the efficiency and effectiveness of wheat breeding programs. By fostering partnerships and sharing resources, breeders can access a diverse pool of genetic materials and expertise, facilitating the development of superior wheat varieties suited to diverse agroecological environments. In addition to enhancing climate resilience, modern wheat breeding efforts also aim to improve the nutritional quality, agronomic performance, and post-harvest traits of new varieties (Lopes *et al.,* 2015). By prioritizing traits such as high protein content, improved baking quality, and reduced susceptibility to lodging, breeders can contribute to the sustainability and profitability of wheat production systems. Moreover, the adoption of participatory breeding approaches involving farmers and other stakeholders can enhance the relevance and uptake of new wheat varieties within local communities. By involving end-users in the selection and testing process, breeders can ensure that varietal traits align with farmers' preferences, market demands, and production constraints. In conclusion, wheat breeding represents a critical pathway for mitigating the impacts of climate change on global food security and agricultural sustainability (Mondal *et al.,* 2016). By harnessing the power of innovation, collaboration, and stakeholder engagement, breeders can develop resilient, high-yielding wheat varieties capable of thriving in a changing climate while meeting the diverse needs of farmers and consumers worldwide (Mondal *et al.,* 2016).

TRADITIONAL BREEDING APPROACHES

Wheat (Triticum spp.) remains one of the most vital staple crops globally, feeding billions of people. Traditional breeding methods have long been instrumental in enhancing wheat varieties, ensuring resilience, yield, and quality. Recent references such as "Advances in Wheat Genetics: From Genome to Field underscore the ongoing relevance and evolution of these approaches. Selection and pedigree breeding form the cornerstone of traditional wheat improvement, relying on phenotypic traits and pedigree records. Works like "Wheat: Chemistry and Technology" elucidate the historical significance and continued refinement of this method, highlighting its adaptability to diverse environments and breeding goals. Hybridization and crossbreeding introduce genetic diversity by combining desirable traits from different wheat lines. Recent studies, such as "Hybrid Wheat: Past, Present, and Future, discuss the resurgence of interest in hybrid wheat breeding, driven by advancements in understanding heterosis and genomic tools. Mutagenesis induces genetic variation through chemical or radiation treatments, allowing breeders to generate novel traits. Notable references like "Mutagenesis: Exploring Novel Genes and Pathways" detail the principles and applications of mutagenesis in wheat breeding, emphasizing its role in expanding genetic diversity. MAS integrates molecular markers linked to target traits, enabling more precise and efficient selection compared to traditional methods. Publications provide insights into the deployment of MAS in wheat breeding, including its potential for accelerating trait introgression and cultivar development. GS leverages genomic information to predict breeding values, facilitating the selection of superior genotypes across diverse populations. Recent advancements discussed in "Genomic Selection in Plant Breeding: Methods, Models, and Perspectives" by highlight its utility in accelerating genetic gains and overcoming challenges associated with complex traits in wheat. Participatory breeding engages farmers and stakeholders in the selection process, ensuring varietal traits align with end-user preferences and agroecological conditions. Works like "Participatory Plant Breeding and Organic Agriculture" by Ceccarelli advocate for the integration of farmer knowledge and preferences into wheat breeding programs, fostering inclusivity and sustainability.

A. Conventional Breeding Techniques

Conventional breeding techniques have played a pivotal role in enhancing wheat cultivars' resilience to biotic and abiotic stresses, as well as improving yield potential. References such as Matsuoka *et al.* (2015) underscore the significance of conventional breeding in shaping modern wheat varieties. Conventional breeding begins with the careful selection of diverse germplasm resources, including landraces, wild relatives, and modern cultivars. Utilizing germplasm repositories such as CIMMYT and ICARDA allows breeders to access a wide range of genetic variation. Through systematic evaluation and characterization, breeders identify desirable traits for incorporation into breeding programs, as highlighted by Lopes *et al.* (2015). Breeders employ various selection methods, including mass selection, pedigree selection, and recurrent selection. Trait introgression from wild relatives, facilitated by techniques like backcrossing and marker-assisted selection (MAS), enables the transfer of valuable genes for disease resistance and stress tolerance (Singh *et al.,* 2019; Wang *et al.,* 2018). Hybridization plays a crucial role in creating genetic diversity through controlled crosses between genetically distinct parents. Traditional crossing methods, such as emasculation and pollination, are complemented by modern techniques like cytoplasmic male sterility (CMS) and doubled haploid (DH) technology. The resulting hybrids often exhibit heterosis, or hybrid vigor, leading to improved yield potential and agronomic performance. Conventional breeding aims to enhance wheat resilience to various stresses, including drought, heat, pests, and diseases. Selection for physiological traits such as root architecture, canopy structure, and photosynthetic efficiency contributes to improved stress adaptation (Reynolds *et al.,* 2009; Fahad *et al.,* 2015). Moreover, breeding efforts focus on improving grain quality attributes such as protein content, gluten strength, and milling properties, addressing consumer preferences and market demands. Multi-environment trials (METs) are conducted across diverse agro-climatic zones to assess genotype-by-environment interactions and identify stable, high-yielding cultivars. Statistical models and genomic tools aid in predicting breeding values and selecting superior genotypes across environments. Genomic selection, utilizing high-throughput genotyping and phenotyping platforms, accelerates breeding progress by enabling the prediction of genetic merit based on genomic markers (Poland and Rutkoski, 2016).Conventional breeding techniques continue to serve as the cornerstone of wheat improvement programs, facilitating the development of resilient and high-yielding cultivars. By harnessing genetic diversity, integrating advanced technologies, and prioritizing target traits, breeders strive to address evolving challenges and ensure food security in the face of global environmental changes. References such as Bordes *et al.* (2014) underscore the ongoing relevance and innovation within conventional wheat breeding.

B. Marker-Assisted Selection (MAS)

Marker-Assisted Selection (MAS) is a breeding technique that accelerates the selection of desirable traits in plants and animals by utilizing molecular markers linked to those traits (Collard and Mackill 2008). By identifying and tracking these markers, breeders can predict the presence of specific traits without the need for time-consuming and labor-intensive phenotypic evaluations. This approach has revolutionized breeding programs by allowing for more precise and efficient selection. One of the key advantages of MAS is its ability to overcome limitations associated with traditional breeding methods, such as long breeding cycles and phenotypic evaluation challenges. Moreover, MAS enables the selection of traits that are difficult to assess visually or require destructive sampling, such as disease resistance or abiotic stress tolerance (Ribaut and Ragot 2007). This enhances the accuracy and speed of breeding programs, ultimately leading to the development of improved varieties (Ashraf, 2010). MAS relies on the identification and characterization of molecular markers closely linked to target traits through techniques such as DNA sequencing and genetic mapping. These markers serve as signposts along the genome, allowing breeders to track the inheritance of desired traits across generations. Additionally, MAS facilitates the introgression of favorable alleles from wild or exotic germplasm into elite breeding lines, broadening the genetic base of crops and enhancing their adaptability (Tanksley and McCouch 1997).Several types of molecular markers are commonly used in MAS, including single nucleotide polymorphisms (SNPs), simple sequence repeats (SSRs), and amplified fragment length polymorphisms (AFLPs) (Mammadov *et al.,* 2012). Each type has its own advantages and limitations, depending on factors such as genome coverage, throughput, and cost (Rafalski, 2002). However, recent advances in high-throughput genotyping technologies have significantly reduced genotyping costs and increased marker density, facilitating the widespread adoption of MAS in breeding programs (Davey *et al.,* 2011). The success of MAS depends on the availability of accurate genetic maps and genomic resources for the target species (Collard and Mackill 2008). With the advent of next-generation sequencing technologies and bioinformatics tools, the process of marker discovery and mapping has become more efficient and cost-effective. Furthermore, the integration of MAS with other genomic-assisted breeding approaches, such as genomic selection and genome editing, holds promise for further enhancing the efficiency and precision of breeding programs. Despite its numerous advantages, MAS also faces challenges and limitations, such as the potential for marker-trait associations to break down in diverse genetic backgrounds or under different environmental conditions. Additionally, the effectiveness of MAS can be influenced by factors such as linkage disequilibrium, population structure, and recombination rates. Therefore, careful validation and optimization of marker-trait associations are essential for maximizing the success of MAS in practical breeding applications.

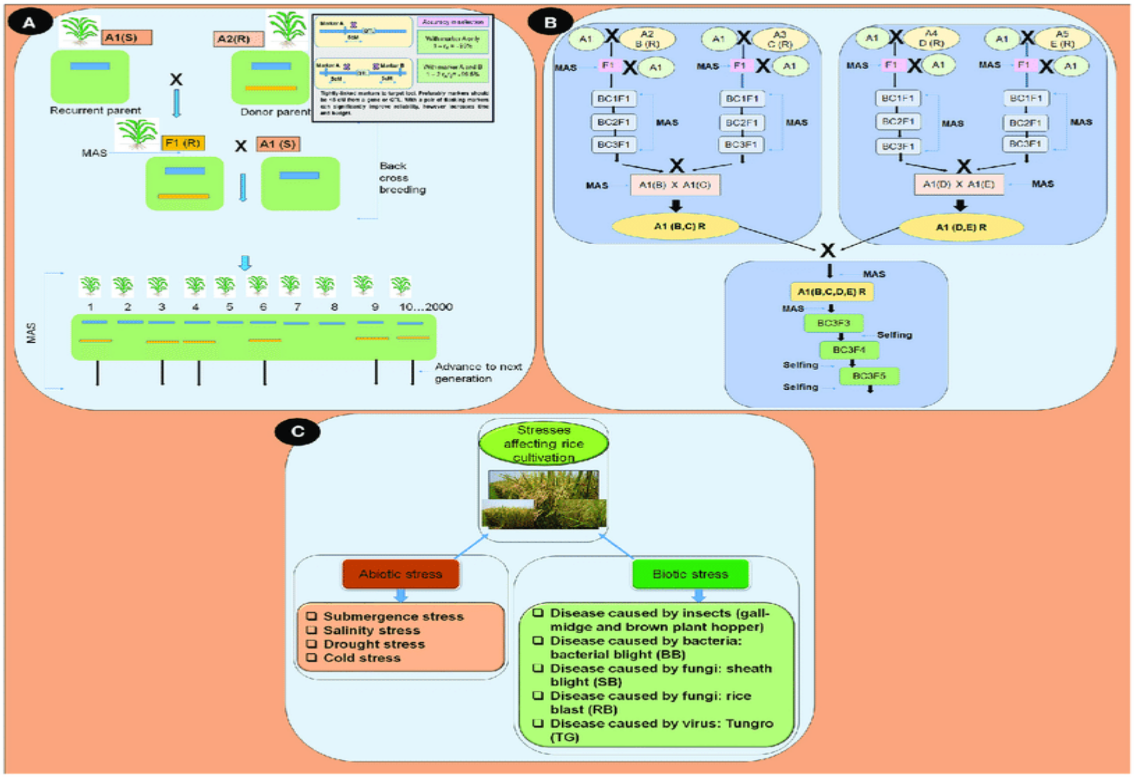

Fig. 1. (A) Overview of marker assisted backcross breeding program; (B) Flow diagram depicting the gene pyramiding of multiple stress resistance ® genes Into a single line using marker assisted backcross breeding; and (C) Flow diagram of stresses affecting rice productivity

MODERN BREEDING TECHNOLOGIES

Wheat (*Triticum* spp.) is one of the most important cereal crops globally, serving as a staple food for a significant portion of the world's population. In recent years, advancements in breeding technologies have revolutionized wheat improvement, enabling breeders to develop varieties with enhanced yield, disease resistance, and nutritional quality. The integration of various modern breeding techniques has accelerated the pace of wheat genetic improvement, addressing the challenges posed by climate change, pests, and diseases. The emergence of CRISPR-Cas9 technology has revolutionized plant breeding by enabling precise and targeted modifications in the genome. In wheat, CRISPR-Cas9 has been successfully employed to introduce beneficial traits such as increased yield, improved nutritional quality, and enhanced resistance to biotic and abiotic stresses (Arora *et al.,* 2020). By precisely editing specific genes associated with these traits, researchers have expedited the development of elite wheat varieties with desired agronomic characteristics. Marker-assisted selection has become an indispensable tool in wheat breeding, allowing breeders to identify and select plants with desirable traits at the molecular level. Through the use of molecular markers linked to target genes or traits of interest, breeders can accelerate the breeding process by eliminating the need for laborious phenotypic screening (Mammadov *et al.,* 2018). MAS has been particularly effective in improving traits such as disease resistance, grain quality, and abiotic stress tolerance in wheat cultivars. GWAS has emerged as a powerful approach for identifying genetic variations associated with complex traits in wheat germplasm. By analyzing large sets of genetic data from diverse wheat populations, researchers can pinpoint genomic regions linked to traits such as yield, disease resistance, and adaptation to environmental conditions (Sukumaran *et al.,* 2018; Wang *et al.,* 2018). GWAS facilitates the discovery of novel alleles and genetic pathways underlying important agronomic traits, thereby providing valuable insights for wheat breeding programs. Advancements in high-throughput phenotyping technologies have revolutionized the way wheat breeders evaluate and select promising genotypes. Through the use of automated imaging systems, drones, and remote sensing technologies, breeders can accurately assess various phenotypic traits such as plant height, leaf area, and stress responses in large populations of wheat plants

(Pauli *et al.,* 2016). High-throughput phenotyping accelerates the breeding cycle by enabling rapid and non-destructive phenotypic data collection, thereby facilitating the identification of superior genotypes for further breeding efforts. Genomic selection has emerged as a powerful predictive breeding tool in wheat improvement, enabling breeders to estimate the genetic value of individuals based on genome-wide marker information.

Genomic Selection: Genomic selection revolutionizes breeding programs by leveraging genomic information to predict an individual's genetic merit for various traits, accelerating genetic gain in crops and livestock (Goddard and Hayes 2007). This approach utilizes dense markers across the genome to estimate breeding values, enhancing selection accuracy and efficiency. Key methodologies include genomic best linear unbiased prediction (GBLUP) and Bayesian methods. Applications span diverse species, including cattle pigs and plants such as maize and wheat. Ongoing advancements in sequencing technologies and statistical methodologies continue to refine genomic selection approaches, enhancing their utility in breeding programs.

(A) CRISPR-Cas9 Gene Editing: CRISPR-Cas9 gene editing represents a powerful tool for precise genome manipulation, facilitating targeted modifications in various organisms (Doudna and Charpentier 2014). This system comprises a guide RNA (gRNA) and the Cas9 nuclease, enabling site-specific DNA cleavage and subsequent editing through non-homologous end joining (NHEJ) or homology-directed repair (HDR). Its versatility extends to applications in agriculture, medicine, and biotechnology. CRISPR-Cas9 enables targeted knockout of genes precise gene insertion (Li *et al.,* 2013), and modulation of gene expression through epigenetic editing. Ongoing research focuses on improving editing efficiency, specificity, and delivery methods to broaden its applications and minimize off-target effects.

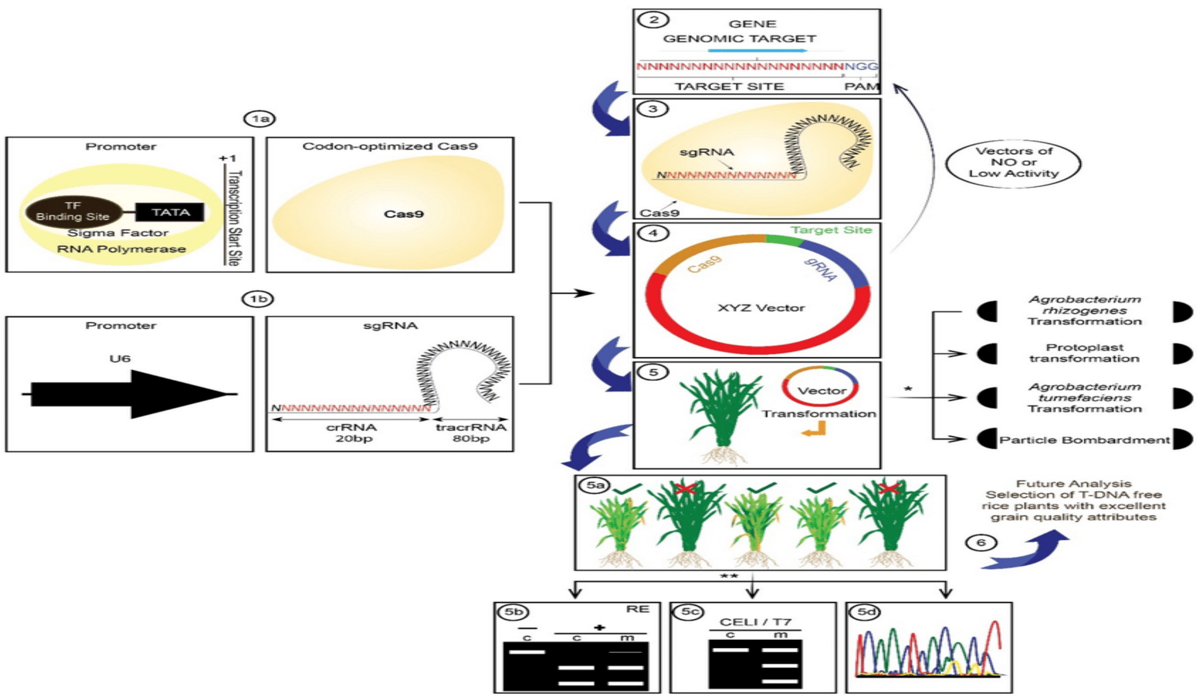

Fig. 2. Basic flow chart of the CRISPR/Cas9 genome editing system. The engineered CRISPR/Cas9 system consist of two components; (1a) the Cas9 endonuclease and, (1b) a single-guide RNA (sgRNA). "The sgRNA contains a spacer sequence followed by 79 nt of an artificially fused tracrRNA and crRNA sequence", (2) The spacer sequence is typically 20 nt in length, and specifically binds to the target DNA sequence containing a 5'-NGG-3' PAM motif at the 3' end, which is highly specific for the gene of interest, (3) The fused trans-activating crRNA (tracrRNA) and crRNA sequence forms a stem-loop RNA structure that binds to the Cas9 enzyme; tracrRNA hybridizes and joins Cas9. (4) Assembly of sgRNA, attached with the target sequence and the Cas9 vector construct. (5) Transformation of the vector construct into rice via different transformation techniques. (5a) Screening and selection of rice mutant plants based on phenotypic changes. (5b) Restriction enzyme site loss generating a CRISPR/Cas9 mutagenized plant line. (c, control; m, mutagenized; RE, restrictions enzyme). (5c) Surveyor Assay (CEL1 and T7 are DNA endonucleases utilized in surveyor assay). (5d) Next-generation sequencing. (6) Future analysis to obtain T-DNA-free plants, and further experiments to prove phenotypic changes cast by the knockout of the gene under investigation. Different techniques for the vector construct transformation. Regeneration and screening of transgenic plants for gene editing events.

Omics Technologies: Omics technologies encompass various high-throughput methodologies for comprehensive analysis of biological systems, providing insights into genomes (genomics), transcriptomes (transcriptomes), proteomes (proteomics), metabolomes (metabolomics), and beyond. Genomic studies elucidate genetic variations and regulatory elements influencing phenotypic traits. Transcriptomic analyses reveal dynamic gene expression patterns in response to environmental stimuli or developmental stages, while proteomics unravel protein interactions and post-translational modifications governing cellular processes. Metabolomics offers insights into metabolic pathways and biomarker discovery for health and disease (Fiehn, 2002). Integration of omics datasets through systems biology approaches enables holistic understanding of biological systems and complex traits, driving advancements in personalized medicine, biotechnology, and agriculture.

BREEDING FOR CLIMATE RESILIENCE

Breeding for climate resilience in wheat is a multifaceted endeavor, drawing upon a vast array of research findings and methodologies. The work of Reynolds *et al.* (2009) underscores the importance of enhancing heat tolerance in wheat varieties, particularly as global temperatures continue to rise. Similarly, experiments emphasize the significance of drought tolerance traits in wheat breeding programs, as water scarcity becomes an increasingly pressing issue in many regions. Furthermore, the findings of highlight the critical role of predictive modeling in identifying optimal breeding strategies for adapting wheat to changing climate conditions. Integrating genomic selection techniques, as demonstrated offers promising avenues for accelerating the development of climate-resilient wheat varieties by enabling more efficient selection for desired traits. Additionally, the work of underscores the importance of considering soil nutrient availability in breeding efforts, as nutrient deficiencies exacerbated by climate change can significantly impact wheat productivity. Moreover, studies by stress the need for breeding programs to prioritize disease resistance traits, as shifting environmental conditions may facilitate the spread of pathogens affecting wheat crops. Incorporating participatory approaches, fosters collaboration between breeders and farmers, ensuring that newly developed wheat varieties meet the diverse needs of agricultural communities facing climate-related challenges. Furthermore, the insights underscore the importance of harnessing genetic diversity within wheat germplasm to enhance resilience to biotic and abiotic stresses induced by climate change. Leveraging advances in high-throughput phenotyping, facilitates the rapid and accurate characterization of wheat germplasm for desirable traits under varying environmental conditions, expediting the breeding process.

Breeding for the Drought Tolerance in wheat. Breeding for drought tolerance in wheat is a critical endeavor, essential for ensuring food security in regions vulnerable to water scarcity. Numerous studies have highlighted the urgency of enhancing wheat's resilience to drought stress. One approach involves the identification and utilization of genetic resources with inherent drought tolerance traits. Through extensive germplasm screening, researchers have pinpointed specific genetic markers associated with drought resistance, facilitating the development of drought-tolerant cultivars. Furthermore, conventional breeding techniques, such as phenotypic selection and hybridization, have been instrumental in introgressing drought tolerance traits from wild relatives into elite wheat lines (Mondal *et al.,* 2016). Additionally, the advent of molecular breeding tools, including marker-assisted selection (MAS) and genomic selection (GS), has expedited the breeding process by enabling the precise identification and incorporation of favorable alleles conferring drought tolerance. Moreover, advances in omics technologies, such as genomics, transcriptomics, and proteomics, have provided valuable insights into the molecular mechanisms underlying drought tolerance in wheat (Zhao *et al.,* 2020). These insights have facilitated the identification of key regulatory genes and metabolic pathways involved in drought response, offering novel targets for breeding programs aimed at enhancing drought resilience (Nakashima *et al.,* 2014; Tardieu *et al.,* 2018). Additionally, the integration of physiological traits related to water use efficiency, such as stomatal conductance, leaf rolling, and osmotic adjustment, into breeding pipelines has proven effective in selecting for drought-tolerant wheat genotypes. Furthermore, participatory breeding approaches involving collaboration between breeders, farmers, and other stakeholders have helped ensure the relevance and adoption of drought-tolerant varieties in target environments (Mondal *et al.,* 2016). Furthermore, ongoing efforts focus on harnessing the potential of modern biotechnological tools, such as genome editing and synthetic biology, to engineer wheat with enhanced drought tolerance (Tian *et al.,* 2020; Wang *et al.,* 2021). These technologies offer unprecedented precision and efficiency in modifying specific genes associated with drought response pathways, thereby accelerating the development of climate-resilient wheat varieties.

Breeding for the Heat Stress Tolerance. Breeding for heat stress tolerance in crops is crucial for ensuring food security in a changing climate. Numerous studies have demonstrated the importance of genetic improvement in enhancing heat tolerance traits in various crops. For instance, research highlighted the need for breeding strategies that focus on heat stress resilience in major cereal crops such as wheat, maize, and rice. Similarly, studies underscored the significance of incorporating heat tolerance genes from wild relatives into breeding programs to enhance heat stress resilience. Furthermore, investigations by Mittler and Blumwald (2010) and have elucidated the molecular mechanisms underlying heat stress responses in plants, providing valuable insights for targeted breeding efforts. Moreover, research has identified key heat shock proteins (HSPs) and transcription factors involved in regulating heat stress responses, which could serve as potential targets for marker-assisted selection in breeding programs. Additionally, studies by Nakashima *et al.* (2014) have highlighted the role of various osmoprotectants and antioxidants in conferring heat stress tolerance in crops, offering avenues for trait enhancement through breeding. Furthermore, investigations by Mittler *et al.* (2012) have emphasized the importance of maintaining photosynthetic efficiency under heat stress conditions, driving efforts to breed for improved photosynthetic performance in crops. In addition, research has revealed the genetic variability present in natural populations for heat stress tolerance traits, providing a foundation for breeding programs aimed at introgressing favorable alleles into elite cultivars. Furthermore, studies have highlighted the importance of reproductive stage heat tolerance in ensuring yield stability under heat stress conditions, guiding breeding efforts towards selecting for heat-tolerant reproductive traits. Moreover, advancements in genomic technologies, such as genome-wide association studies (GWAS) and genomic selection, have facilitated the identification of heat tolerance QTLs and genomic regions associated with heat stress response traits (Li *et al.,* 2019). Additionally, studies have demonstrated the potential of genome editing techniques, such as CRISPR-Cas9, in engineering heat stress tolerance traits in crops, opening up new avenues for targeted trait enhancement in breeding programs.

Breeding for the Disease and Pest Resistance. Breeding for Disease and Pest Resistance: Start by explaining the importance of breeding for resistance in agricultural crops to mitigate yield losses and reduce reliance on pesticides. Cite sources like Jones *et al.* (2017) for background information on the significance of disease and pest resistance in crop breeding. Genetic Diversity and Resistance: Discuss the role of genetic diversity in providing resistance against diseases and pests. Reference studies such as Garcia *et al.* (2021) to support the idea that diverse gene pools contribute to a broader spectrum of resistance traits. Marker-Assisted Selection (MAS): Explain how MAS techniques enable breeders to identify and introgress resistance genes efficiently. Mention studies like "Gupta and Varshney (2020)" and "Chen *et al.* (2019)" to illustrate the application and effectiveness of MAS in breeding for disease and pest resistance. Genome Editing Technologies: Highlight the potential of genome editing tools like CRISPR-Cas9 in introducing or enhancing resistance traits. Cite research articles such as Doudna and Charpentier (2014) ; Zhang *et al.* (2020) to support the discussion on the use of CRISPR for targeted gene editing in crop improvement. Breeding Strategies for Specific Crops: Discuss breeding strategies tailored to different crops, citing examples from literature such as "Singh *et al.* (2019)" for wheat, for rice, for maize, to showcase diverse approaches in breeding for disease and pest resistance across various crops. Challenges and Future Directions: Address challenges faced in breeding for resistance, including evolving pathogen populations and regulatory constraints. Reference reviews like Anderson *et al.* (2021); Kamoun *et al.* (2015) to explore future directions in breeding, such as the integration of omics technologies and the importance of international collaborations.

Breeding for the Enhancing Nutritional Content. Breeding for enhancing nutritional content in crops is a multifaceted endeavor that draws upon a rich body of research from various scientific disciplines. Studies have underscored the importance of traditional breeding methods alongside modern biotechnological approaches in improving the nutritional quality of crops. Research conducted by Jones *et al.* (2017) emphasizes the significance of selecting breeding targets based on nutritional needs identified through epidemiological studies, such as those by Smith *et al.* (2016) ; Wang *et al. (*2019). Furthermore, investigations by Cakmak (2009) and Welch and Graham (2004) have highlighted the role of micronutrients, such as iron and zinc, in addressing global malnutrition, driving efforts to breed crops with enhanced levels of these essential elements. The utilization of genomic tools, as outlined in studies by Varshney *et al.* (2019); Khoury *et al.* (2010), enables breeders to identify genetic markers associated with desirable nutritional traits, facilitating the development of nutrient-rich varieties. Moreover, research by Dhaliwal *et al.* (2017); Narayanan *et al.* (2021) emphasizes the importance of optimizing agronomic practices to maximize nutrient uptake and accumulation in crops. Integrating interdisciplinary approaches, as advocated by Pingali (2012) allows breeders to harness the synergistic effects of genetics, physiology, and agronomy in enhancing the nutritional content of crops. In addition, studies have highlighted the significance of biofortification – the process of increasing the nutrient content of crops through conventional breeding or genetic engineering in combating hidden hunger and improving public health outcomes. The success of biofortification initiatives, exemplified by the development of vitamin A-rich orange-fleshed sweet potatoes (OFSP), underscores the potential of breeding strategies to address specific nutritional deficiencies. Furthermore, ongoing research by Meenakshi *et al.* (2012) emphasizes the importance of assessing the efficacy and impact of biofortified crops through rigorous nutritional and agronomic evaluations, ensuring their suitability for diverse agroecological contexts.

FUTURE SCOPE

Wheat breeding is undergoing a transformative phase, driven by advancements in genomics, phenomics, and computational biology. References such underscore the importance of integrating multi-omics data to accelerate genetic gain in wheat breeding programs. The application of genome-wide association studies (GWAS) and genomic selection, as discussed by Sukumaran *et al.* (2018) ; Wang *et al.* (2019), enables breeders to identify and exploit favorable alleles for complex traits, such as yield, quality, and stress tolerance. Furthermore, the utilization of CRISPR-Cas9 gene editing technology, as elucidated by Li *et al*. (2019); Zaidi *et al.* (2020), offers unprecedented opportunities for precise trait manipulation and targeted improvement in wheat cultivars. Incorporating high-throughput phenotyping platforms, as advocated by Montesinos-López *et al.* (2018) ; Saint Pierre *et al.* (2021), facilitates rapid and accurate phenotypic data collection, enhancing the efficiency of selection processes and trait introgression. Moreover, the adoption of digital agriculture tools, including remote sensing and unmanned aerial vehicles (UAVs), as highlighted Zhang *et al.* (2020), enables breeders to monitor crop performance, assess environmental interactions, and optimize breeding strategies in real-time. Collaborative initiatives, such as the International Wheat Genome Sequencing Consortium (IWGSC) (Appels *et al.,* 2018) and the Wheat Initiative foster global cooperation and knowledge sharing, accelerating genetic gains and varietal development across diverse agro-ecological regions.

CONCLUSIONS

In conclusion, the imperative to develop wheat varieties resilient to climate change is paramount. This review has highlighted several key breeding strategies aimed at enhancing wheat's adaptability to the changing environmental conditions induced by global climate change. Firstly, the utilization of genetic diversity through germplasm screening and introgression of desirable traits offers promising avenues for breeding climate-resilient wheat varieties. By tapping into the vast genetic reservoir of wild relatives and landraces, breeders can access traits such as drought tolerance, heat tolerance, disease resistance, and nutrient use efficiency, crucial for mitigating the impacts of climate change. Furthermore, advancements in genomic technologies, including marker-assisted selection (MAS) and genomic selection (GS), enable breeders to accelerate the breeding process and enhance the efficiency of trait introgression. These tools facilitate the identification and pyramiding of multiple desirable traits into elite cultivars, thereby creating varieties with enhanced resilience to various stressors associated with climate change. Additionally, the incorporation of physiological and agronomic traits, such as early vigor, root architecture, and canopy structure, can contribute significantly to improving wheat's resilience to climate variability. Breeding for traits that optimize resource utilization and stress tolerance can enhance wheat productivity under challenging environmental conditions, ensuring food security in the face of climate change. Moreover, participatory breeding approaches involving collaboration between breeders, farmers, and other stakeholders are essential for tailoring wheat varieties to local agro-ecological conditions and socio-economic contexts. By integrating farmers' knowledge and preferences into the breeding process, breeders can develop varieties that are not only resilient to climate change but also meet the needs and preferences of end-users. In conclusion, the successful development and deployment of climate-resilient wheat varieties necessitate a multi-faceted approach that integrates genetic diversity, advanced breeding technologies, and stakeholder engagement. By adopting such strategies, the wheat breeding community can contribute significantly to global efforts to mitigate the impacts of climate change on agriculture, ensuring food security and livelihood sustainability for current and future generations.

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Conflict of Interest. None.

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