

A REVIEW: EXPLORING GENETIC VARIATION AND REGULATORY NETWORKS IN WHEAT HEAT STRESS TOLERANCE

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Abstract: *Wheat (Triticum aestivum L.) is a staple crop vital to global food security, yet rising global temperatures increasingly threaten its productivity. Heat stress (HS), particularly during critical growth phases like anthesis, disrupts physiological and biochemical processes, reducing yields and grain quality. This review explores the genetic variation and regulatory mechanisms that underpin wheat's resilience to heat stress. Advanced breeding techniques, such as genome-wide association studies (GWAS), quantitative trait loci (QTL) mapping, and next-generation sequencing, have identified key genetic factors contributing to heat tolerance. Novel biotechnological strategies, including CRISPR/Cas9 gene editing, have shown promise in introducing heat-tolerant traits by targeting specific genes. Additionally, omics approaches encompassing transcriptomics, proteomics, and metabolomics offer deeper insights into stress-responsive pathways. With machine learning and artificial intelligence integration, wheat breeding is poised to become more efficient, accelerating the development of cultivars capable of withstanding heat stress. These advancements are essential to ensure sustainable wheat production amidst the challenges of climate change.*

Keywords: CRISPR/Cas9 Gene Editing, Genome-Wide Association Studies (GWAS), Heat Stress, Omics Approaches, Wheat Resilience

Introduction

Wheat (*Triticum aestivum* L.) is one of the most commonly cultivated cereal crops globally, contributing significantly to global cereal production (28%) and trade (41.5%) (Raza et al., 2021). With the human population projected to reach 9.8 billion by 2050, an additional 198 million tons of wheat grain will be necessary to meet food demands (Raza et al., 2021). However, wheat production is increasingly vulnerable to both abiotic and biotic stresses, leading to stagnant and declining global productivity rates (Arriagada et al., 2022). The mean global temperature is expected to rise by 1.5°C within the next two decades, which poses a significant threat to wheat cultivation (Ghorbel et al., 2022). Recent analyses from scientific communities have indicated an increase in average global temperature of 1.04°C from 1880 to 2019 (Yadav et al., 2023). This elevated temperature is causing heat stress (HS), which triggers significant changes in the biological and developmental processes of wheat, ultimately leading to reductions in both grain production Lv et al. (2021) and grain quality (Su et al., 2023). Wheat is particularly susceptible to elevated temperature stress, especially during the anthesis stage, and is less likely to recover if stressed at this critical period (Mishra, 2023). Heat stress can adversely affect the growth and development of wheat by altering physiological and biochemical processes, including photosynthesis, respiration, oxidative damage, and the activity of stress-induced hormones and proteins (Qiu et al., 2021). Low-latitude zones, where approximately 100 million hectares of

wheat are cultivated, are predominantly heat-prone areas worldwide (Wang et al., 2022). Asseng et al. (2014) tested 30 wheat crop models, demonstrating that mean temperatures during the growing season ranging from 15 to 32°C can significantly impact wheat yield (Wang et al., 2021). Numerous studies have documented the detrimental effects of heat stress on wheat yield and quality. For instance, Asseng et al. (2014) found that a 1°C increase in temperature could reduce global wheat production by 6% (Wang et al., 2021). Other research has focused on specific aspects of heat stress, such as its effects on grain filling, protein quality, and bread-making properties. Heat stress during flowering can damage pollen viability and fertilization, leading to a decreased number of grains per spike (Guo et al., 2023). Additionally, high temperatures during grain filling can hinder nutrient translocation and starch accumulation, resulting in smaller and lighter grains (Aloisi, 2023). Accelerated heat stress can also cause premature leaf senescence, limiting the photosynthetic period and reducing biomass accumulation, which ultimately affects grain yield (Wang et al., 2022). Heat stress impacts wheat plants in both indirect and direct ways. Indirect injuries include poor seed germination, decreased growth, enhanced leaf senescence, and reduced photosynthesis and floret fertility (Mustafa et al., 2022; Guo et al., 2023; Tao et al., 2021). In contrast, direct injuries involve protein denaturation, increased fluidity of membrane lipids, and protein aggregation (Liu et al., 2022). The consequences of heat stress depend on the duration and

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intensity of the stress, as well as the specific genotypes of wheat (Ghorbel et al., 2022). Therefore, emphasis should be placed on sustaining wheat yields through the identification of tolerant genotypes and the promotion of breeding strategies and management practices that enhance heat stress resilience (Ahlawat et al., 2022; Wang & Chang, 2022).

Genetic variation in Wheat heat tolerance

Heat stability index (HSI) is a critical tool used to measure terminal heat stress tolerance in wheat, particularly in assessing yield reductions caused by unfavorable versus favorable environments Шаманин et al. (2022). Wheat varieties possess a vast reservoir of genetic diversity, including genes for heat tolerance. Despite extensive breeding efforts, many modern cultivars often lack sufficient heat tolerance, indicating that genetic variation within existing cultivars remains under-studied (Szerement et al., 2021). Mutation breeding techniques have successfully created new alleles for heat tolerance and resistance, with studies on induced mutants demonstrating improved heat tolerance (Sousa et al., 2021). Furthermore, the introduction of foreign genes has shown promise in enhancing heat tolerance in wheat, particularly through the expression of heat shock proteins and antioxidant enzymes (Mitura et al., 2023). Merging heat-tolerant genes and alleles from different sources can lead to the development of superior genotypes. Hybrid breeding has been successful in developing heat-tolerant varieties in crops like maize and rice, suggesting similar strategies could be applied to wheat (Vassileva, 2023). Wheat exhibits polyploidy, and crossing tetraploid wheat with *Aegilops* species can yield new genetic combinations that enhance heat tolerance (Zhu, 2023). The exploration of genetic combinations, particularly through the identification of QTLs associated with heat tolerance, is essential for advancing wheat breeding programs aimed at improving resilience to heat stress (Krishna, 2023).

Methods of Identifying Genetic Variation

Genome-wide association studies (GWAS) and quantitative trait loci (QTL) mapping are the two primary approaches utilized to dissect the genetic bases of complex traits. In wheat, the mapping approach may locate genomic regions with low resolution, often limited to the bi-parental population under study. As a complement to QTL mapping, GWAS offers a high-resolution, cost-effective method for gene discovery and molecular marker identification. GWAS is widely employed to identify genetic variants associated with complex traits such as heat tolerance. This method involves genotyping a large population of individuals with diverse genetic backgrounds and phenotyping them for the trait of interest. By correlating genetic markers with phenotypic data, GWAS can specify genomic regions associated with heat tolerance Matsuo et al. (2021). The GWAS process includes several steps: genotyping, phenotyping, statistical analysis, and candidate gene identification. However, conducting GWAS in wheat presents challenges due to the crop's large genome, incomplete genome sequence, and polyploidy, which complicates the assignment of markers to individual (A, B, and D) genomes (Lee et al., 2023). Over the years, significant advancements have been made in sequencing technologies, transitioning from first-generation sequencing (FGS) to second-generation sequencing, and now to third-

generation sequencing. Next-generation sequencing (NGS) represents a revolutionary approach that produces thousands or millions of sequences simultaneously at a fraction of the cost of traditional Sanger methods. One of the emerging applications of NGS is large-scale genetic polymorphism discovery, which facilitates the rapid and cost-effective identification of simple sequence repeat (SSR) or microsatellite loci (Wensel et al., 2022). The application of next-generation sequencing (NGS) technologies for developing simple sequence repeat (SSR) or microsatellite loci for genetic research in the botanical sciences is gaining global traction. Recent advancements in NGS, such as sequencing by synthesis (e.g., Illumina), have simplified the sequencing of large portions of plant genomes at affordable costs, enabling the rapid development of molecular markers, including microsatellites (Ermini, 2024). QTL mapping has significantly advanced the analysis of complex traits, establishing large collections of molecular/genetic markers that can be used to construct detailed genetic maps of both experimental and domesticated species (Gupta, 2024; Wei et al., 2021). These maps provide the foundation for modern QTL mapping methodologies, including single-marker mapping, interval mapping, composite interval mapping, and multiple trait mapping, which allow for statistical analyses of the associations between phenotype and genotype (Hoyer, 2024; Handy et al., 2022).

Transcriptional Regulation

Heat stress (HS) is becoming a more serious issue for food security as global warming rises. High temperatures harm wheat grain yield and quality, especially during the anthesis and post-anthesis stages of development Mahdavi et al. (2022). Abiotic stressors such as high temperatures, drought, and salinity negatively impact plant survival, development, and reproduction (Balla et al., 2021). Heat stress significantly affects wheat, altering morphological characteristics (such as seedling establishment, germination, shoot, leaf area, and root growth) and physiological factors (such as respiration, leaf senescence, photosynthesis, and water-nutrient relationships). This stress produces reactive oxygen species (ROS), which disrupt the photosystem, affect grain number, grain size, and maturity, and reduce agricultural yield (Cao, 2024). These stresses necessitate the expression of heat-responsive genes, which are regulated by a network of transcription factors, including heat shock transcription factors (HSTFs) (Tabassum et al., 2023). Heat shock response (HSR) is an important process in plants that reduces heat stress-induced damage, facilitating lifecycle stability and cellular protection. It involves the synthesis of heat shock proteins (HSPs) and other stress-responsive proteins. Heat shock transcription factors are evolutionarily conserved proteins that control plant biological activities and stress responses (Tabassum et al., 2023). Stay green (SG) wheat genotypes express senescence-related genes that maintain grain filling and photosynthesis during heat stress by delaying senescence. SG protects photosynthetic areas while reducing seed abortion, increasing nitrogen remobilization, and ensuring sugar availability in pollen and anther. According to research, SG characteristics are strongly linked with canopy temperature depression (CTD), making them appropriate selection criteria for heat stress (Kalaipandian et al., 2023).

Table of Transcription factors identified in wheat heat tolerance and their roles during heat stress

TFs	Role in Cold Tolerance	References
TaHsfA1	Increase thermo tolerance in wheat by activating HSP expression	(Wang <i>et al.</i> , 2023)
TaHsfA2–10	Involves in wheat heat stress tolerance	(Guo <i>et al.</i> , 2020)
TaHsfA2–11	Improve heat tolerance in wheat by regulating heat response genes	(Li <i>et al.</i> , 2024)
TaHsfA6b-4D	Play a role in heat stress tolerance by maintaining cellular homeostasis	(Meena <i>et al.</i> , 2022)
TaHsfC2a	Protect wheat from excessive heat during grain filling stage via ABA mediated stress regulation	(Guo <i>et al.</i> , 2020)
AtWRKY30	Overexpression of this gene increase heat tolerance in wheat	(El-Esawi <i>et al.</i> , 2019)
TaWRKY74-B and TaSnRK3.15-B	Involve in high temperature stress tolerance in wheat	(Fu <i>et al.</i> , 2024)
DREBA2	Increase thermotolerance	
TaPLC1-2B	Involves in heat stress tolerance at seedling and adult stages	(Li <i>et al.</i> , 2023)
TaNAC69-1	Increase heat tolerance in durum wheat	(Haider <i>et al.</i> , 2022a)
TaNAC2a, TaNAC4, TaNA C4a and TaNAC6	Act as transcriptional activator involved in response to high temperature	(Trono and Pecchioni, 2022)
TaOPR3	Improve heat stress tolerance in wheat by JA mediated signaling pathway	(Tian <i>et al.</i> , 2020)
DREB2A	Regulate heat stress tolerance in wheat	(Kaur <i>et al.</i> , 2019)
TaDREB3-AI	Over expression of this gene increase tolerance in wheat during heat stress	(Osipova <i>et al.</i> , 2022)
TaPEPKR2	Improve heat stress tolerance in wheat	(Sun <i>et al.</i> , 2022)
TaGATA38, TaGATA54, TaGATA57 and TaGATA60	Up regulated during heat stress and are involved in heat tolerance in wheat	(Feng <i>et al.</i> , 2022)
TaGNAC2-7D	Possess low expression level and highest heat stress response in wheat	(Guérin <i>et al.</i> , 2022)
TaNAC2L	Over expression of this transcription factor results in wheat heat tolerance	(Sun <i>et al.</i> , 2022)
TaGATA25	Increase heat stress tolerance in wheat by down regulation during high temperature	(Feng <i>et al.</i> , 2022)
TaGNAC1-7B and TaGNAC4-7D	Show highest expression during heat stress in wheat	(Guérin <i>et al.</i> , 2022)
TaASRP1	Over expression of this gene protect wheat plant from heat stress	(Huang <i>et al.</i> , 2022)
OsHAG702	Increase heat stress tolerance in wheat	(Sharma <i>et al.</i> , 2023)
TaHsaA2d or TaHsaA6f	Promote heat tolerance in wheat	(Du <i>et al.</i> , 2023)
TaMYB344, TaAIDFa, or TaAREB3	Over expression of these transcription factors improve high temperature tolerance in transgenic wheat varieties	(Du <i>et al.</i> , 2023)
TaC2H2-ZF	Improve heat stress tolerance in wheat	(Li <i>et al.</i> , 2021)
TaAP2/ERF	Up regulation of this gene helps in wheat heat tolerance	(Magar <i>et al.</i> , 2022)

Signaling Pathways in Heat Tolerance in Wheat

Calcium-dependent protein kinases (CDPKs) are pivotal signaling molecules in plants, particularly in their response to various environmental stresses, including heat stress. These kinases play a critical role in regulating reactive oxygen species (ROS) homeostasis, which is essential for protecting plant cells from abiotic stresses (Dekomah *et al.*, 2022). In wheat, a complex network of Mitogen-Activated Protein Kinases (MAPKs) is involved in transcriptional reprogramming, facilitating recovery after the perception of heat stress. MAPK-based sensors detect both internal and external stimuli, triggering specific transcription factors (TFs) and activating stress-associated genes and proteins (Iqbal *et al.*, 2022). The influx of free calcium ions, facilitated by calcium-permeable channels and calcium-

transporting proteins, is crucial for signaling the onset of stress and generating appropriate responses (Khan *et al.*, 2023). This increase in calcium concentration activates CDPKs, which in turn regulate numerous stress-responsive genes, enhancing heat stress tolerance (Zhao *et al.*, 2021). Reactive oxygen species (ROS) are also significant signaling molecules during heat stress. NADH oxidases induce hormone-activated ROS, which are involved in feedback control and signaling events that activate defense mechanisms and stress-responsive pathways (Sehar *et al.*, 2022). While excessive ROS can be detrimental to plant development, their concentration is tightly regulated by the ROS scavenging system, which promotes stress tolerance (Iqbal *et al.*, 2022).

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These signaling molecules, including ROS and various hormones, modify the plant's transcriptomics, metabolomics, and biochemical conditions to adapt to heat stress (Paul et al., 2022). Hormone-signaling pathways are integral to wheat's ability to withstand heat stress. Phytohormones such as ethylene, abscisic acid (ABA), and jasmonic acid are essential signaling molecules that mediate stress responses (Yan et al., 2023). ABA, in particular, plays a crucial role in wheat's adaptation to high temperatures by influencing stomatal closure and enhancing root water absorption, thereby maintaining physiological activities under stress (Iqbal et al., 2022).

Additionally, ABA increases the production of heat shock proteins (HSPs) and enhances the activity of antioxidant enzymes, which work synergistically to mitigate damage from ROS (Wang et al., 2023). Ethylene also regulates heat stress responses by modulating osmolyte levels (such as proline) and antioxidant systems, with hormonal pathways activated during heat stress leading to elevated concentrations of these hormones (Sehar et al., 2022). Furthermore, brassinosteroids (BR) have been shown to improve heat tolerance by enhancing photosynthetic rates and the expression of HSPs, thereby contributing to the plant's overall resilience against heat stress (Liu et al., 2021).

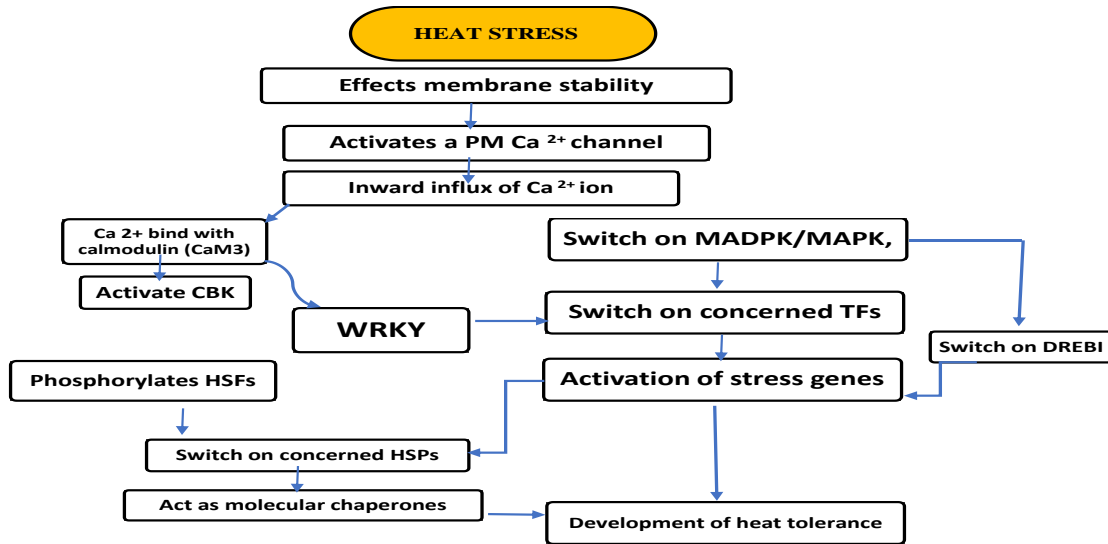


Figure 1: Flow Chart Diagram showing signaling pathways and response

Breeding and Biotechnological Strategies to Induce Tolerance

Breeding and biotechnology efforts to increase heat tolerance in wheat are becoming increasingly important as climate change causes rising temperatures and more frequent heat stress events. The response integrates traditional breeding methods with sophisticated biotechnology efforts to improve wheat crop resistance to extreme temperatures. Molecular Marker-assisted breeding program revolutionized the way of selection for plant breeding which was previously focused on phenotypic trait observation (Kumari et al., 2024) Marker-assisted selection is an efficient method of crop improvement that employs the early detection of targeted genes (QTLs) via linked markers and indirect selection in lines, cultivars, and breeding populations irrespective of the environment. MAS based approach includes Marker assisted back crossing (MABC), Marker assisted recurrent selection (MARS), Genome wide association studies (GWAS), and Genomic selection (GS) (Yadav et al., 2022).

The development of QTL-specific markers for both simple and complex traits has accelerated MAS. There are now markers for qualities in wheat such as disease resistance, heat tolerance etc, which can boost the production of heat tolerant wheat variety. Important genes can now be chosen and tracked more easily and affordably in breeding project using MAS (Pandurangan et al., 2022). Identification of QTLs in common wheat for control Heat tolerance resulted in the development of new cultivars of Durum wheat and

bread wheat, such as Faraj wheat, which thrives under heat stress. Wild relatives are excellent sources of beneficial genes for abiotic stress tolerance. For example, introgression drought-resistant QTLs from wild emmer wheat into elite durum and bread wheat boosted drought tolerance, implying that wild relatives can be used in HS wheat breeding (Yadav et al., 2022).

Hybridization and backcrossing are significantly proven techniques to get heat-tolerant wheat crops. Hybrid wheat has gained renewed interest due to its potential for improved abiotic stress tolerance, including heat stress (Alam et al., 2024). Hybridization is a process of cross fertilization among different species. To improve drought and heat tolerance in wheat and other important traits successful hybridization is proven significant particularly Durum wheat which is drought and heat resistant dominantly used for hybridization with bread wheat (Hassan et al., 2016) (Reynolds et al., 2021). Marker-assisted backcross breeding is an effective approach for introgression heat tolerance genes into elite wheat cultivars. In backcrossing, the initial cross is made between the recurrent parent (the variety that is being improved) and the donor parent (which possesses the desired trait). The resulting offspring undergo several generations of backcrossing to the recurrent parent, allowing for the gradual recovery of the recurrent parent's genome while maintaining the desired traits from the donor. A recent study used marker-assisted backcrossing to develop heat-tolerant wheat lines by targeting two QTLs linked with markers Xbarc186 and Xgwm190. Another

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study reported a background recovery of 85.35% to 95.79% after several backcross generations, highlighting the effectiveness of this approach. (P. K. C. Kumar et al., 2023). Omics based approach including Genomics, proteomics, transcriptomics, and metabolomics data, plays crucial part in identifying heat responsive genes, proteins and pathways (Sun et al., 2022). This multi-faceted approach allows researchers to connect genetic information with phenotypic outcomes, facilitating the identification of key traits related to yield, stress tolerance, and overall plant health. Transcriptomics including microarray and RNA sequencing revealed that 10.7 % of probe sets involve in heat stress. It highlights the response of homologous triplets in polyploidy wheat towards heat stress, which may enhance heat tolerance. Epigenetic modification such as DNA Methylation and non-coding RNAs involve in post transcription regulation of heat tolerance. At translation level a set of proteins involve in response to heat. According to iTRAQ findings, 256 proteins identified as differentially expressed out of which 126 up regulated and 130 down regulated. These proteins are found to be active in stimulus response, stress response, kinase activity and transference activity etc (Sun et al., 2022). Metabolomics, similarly, provide insights of plant physiology under stressful condition. In wheat plants, maintaining the yield in heat stress depends on the metabolite accumulation in grains. Stress-induced increases in the production of carbohydrates and fatty acids improve cell membrane integrity and protein stability, indicating a useful defense against heat-related damage (Sarkar et al., 2021).

Transgenic technology, which enables the transfer of desired genes to superior cultivars without the risk of linkage drag, is another way to introduce heat tolerance into wheat. These procedures enable gene transfer that is not possible through traditional breeding. Heat stress tolerance was increased in wheat and Arabidopsis plants by overexpressing the *TaPEPKR2* gene (Al-Ashkar et al., 2020). Heat-stress-tolerant transgenic wheat plants with improved leaf protein and photosynthetic membrane stability, as well as a greater rate of CO₂ fixation, were produced by overexpressing *ZmEFTu1* (elongation factor) under the *ZmUbi1* promoter (Kaur et al., 2019). A potent method for comprehending genomes and enhancing crops is genome editing. It is based on programmable nucleases, such as NHEJ, that bind and recognize target genomic loci,

use restriction endonucleases, such FokI and Cas, to induce double-strand breaks (DSBs), and then use either non-homologous end joining (NHEJ) or homology-directed recombination (HDR) to repair the breaks. ZFN, TALEN, and CRISPR/Cas are among the methods utilized to introduce or eliminate specific traits.

The CRISPR/Cas9 gene-editing technique accelerates up the advancement of agriculture by enabling the precise editing of crop species, the development of advantageous germplasm, and the establishment of more sustainable agricultural systems (M. Kumar et al., 2023). To enhance heat tolerance in wheat, the *TaMLO* gene (mildew resistance locus O) has been introduced into wheat protoplasts. Additionally, the abiotic stress-related genes Wheat ethylene-responsive factor 3 (*TaERF3*) and Wheat dehydration response element binding protein 2 (*TaDREB2*) have been targeted to strengthen crop resilience against environmental stress. When combined with advanced breeding techniques like speed breeding and omics-assisted breeding, CRISPR/Cas9 offers significant potential for increasing wheat production and ensuring food security (Yadav et al., 2023).

In wheat, severe heat can cause cellular deterioration and cell death, which can result in structural damage and compromised functionality. This degradation could negatively impact the plant's general health, especially during the stages of grain maturation and reproduction. Wheat has three strategies to cope with heat stress: escape, avoidance, or tolerance. Tolerance include canopy cooling, enhanced photosynthesis, effective radiation utilization, and extended grain filling at high temperatures. Wheat's responses to heat stress occur at morphological, physiological, and biochemical levels, with adaptation efficiency being crucial. These responses are regulated by signaling cascades involving transcription factors and signaling molecules, which ultimately influence the plant's transcriptome, proteome, and metabolome (Farhad et al., 2023). Heat stress influences several metabolic cycles, including the production of cancer-preventive agent proteins, the electron transport system, the citrus extract cycle, and glycolysis. Identifying cultivars that can withstand heat becomes less difficult by the fact that the wheat plant produces a range of metabolites that alter in response to stress (Abasi et al., 2024).

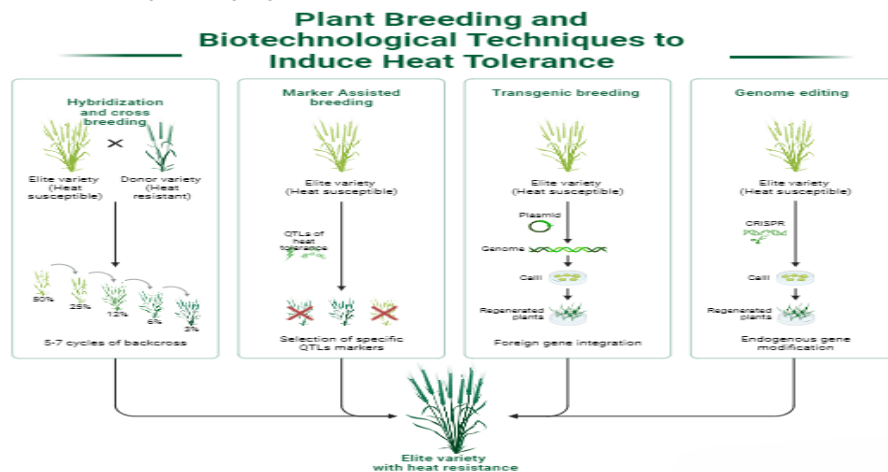


Fig.1.1: Explains some biotechnological approaches to induce heat tolerance in wheat including MAS, Hybridization and Backcrossing, Transgenesis, and Genome editing. Each approach is detailed in the sections below

Discussion

Challenges and Future Directions Heat

One of the primary challenges in wheat research is the complexity of genome and the regulatory networks that influence phenotypic traits. Despite advancements in genomic technologies, translating genetic information into practical breeding applications remains difficult, due to large number of transposable elements (Li et al., 2022). Efficiency of Genome editing from CRISPR cas9 has been constrained due to polyploid complex genome of wheat. Wheat is an allohexaploid plant with three homologous copies of the majority of genes spread over its A, B, and D genomes. It is therefore particularly difficult to target all copies at once during genome editing. A gene's leftover copies may act as a buffer to the genome, possibly preventing detectable phenotypic alterations, if all copies are not effectively knocked out (Kumar et al., 2019). Except base editing, precise editing in wheat is still a big challenge. Omics data is a good source of genome wide regulatory networks but a challenge to develop integrative network. In addition to the advancement of genome editing technologies, numerous other milestones are required, such as the development of high throughput phenotyping method, the advancement of basic genetic research, and the creation of regulatory frameworks that are favorable.

Novel technologies such as CRISPR gene editing, high-throughput genomic sequencing, and machine learning have great potential for addressing the difficulties associated with wheat breeding. The effective use of CRISPR Cas 9 for single trait genome editing in wheat has sparked interest in the development of super wheat varieties with multiple stress tolerance capabilities. (Haber et al., 2024). A promising method for increasing crop characteristics and resilience to different stress conditions is CRISPR/Cas 2. Notably, the study expanded the toolset available for precise genome changes in wheat by confirming for the first time that CRISPR/dCasII2-CBE (cytosine base editor) and CRISPR/dCasΦ2-ABE (adenine base editor) function in plants (Zhao et al., 2024). Moreover, silicon treatment used during seedling in hot season can improve wheat development and increase its ability to withstand heat. This is made possible by nanotechnology. As per Singh et al. (2023), wheat cultivars can have faster growth rate when exposed to carbon nanotubes (Singh et al., 2023).

Additionally, breeding values and trait performance under various environmental conditions can be better predicted with the application of machine learning and artificial intelligence. The analyzed research's conclusions show that artificial intelligence has significantly advanced wheat breeding. Breeding cycle length has decreased due to genomic selection, whereas phenotypic trait prediction accuracy has increased with ML algorithms. Artificial intelligence is used in high-throughput phenotyping to enable detailed analysis of plant traits in various stress conditions, which aids in the selection of robust cultivars. In addition, AI-driven models have demonstrated better-projected accuracy for disease resistance and agricultural productivity when compared to traditional techniques (Mushtaq et al., 2024).

Conclusion

In conclusion, the intricate genome and complex

regulatory networks of wheat pose significant challenges to advancing heat stress tolerance through breeding. While breakthroughs in genomic technologies such as CRISPR/Cas9 have paved the way for more targeted gene editing, the polyploid nature of wheat remains a formidable barrier, particularly when it comes to knocking out all homologous gene copies in its A, B, and D genomes. Although base editing shows promise, precise editing on a broader scale is still a challenge. The integration of omics data provides valuable insights into wheat's regulatory networks, but translating these findings into effective breeding strategies requires further refinement. Novel approaches like CRISPR/dCasII2-CBE and CRISPR/dCasΦ2-ABE offer exciting prospects for precise genome editing, potentially leading to wheat varieties that can better withstand environmental stresses. Additionally, silicon treatments and nanotechnology, such as the use of carbon nanotubes, are promising methods for enhancing heat tolerance and growth in wheat under challenging conditions. The adoption of machine learning and artificial intelligence in wheat breeding marks another transformative step, improving the accuracy of trait prediction and speeding up breeding cycles. However, the future of wheat breeding lies not only in technological innovations but also in the development of supportive regulatory frameworks, high-throughput phenotyping methods, and enhanced genetic research to fully harness these advancements. By combining cutting-edge genomic tools with AI-driven models, wheat breeding can move toward developing cultivars with improved heat stress tolerance, ensuring food security in a rapidly changing climate.

Declarations

Data Availability statement

All data generated or analyzed during the study are included in the manuscript.

Ethics approval and consent to participate

Approved by the department Concerned.

Consent for publication

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The authors declared absence of conflict of interest.

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Study Design, Review of Literature.

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Conception of Study, Development of Research Methodology Design, Study Design, Review of manuscript, final approval of manuscript.

Conception of Study, Final approval of manuscript.

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Data entry and Data analysis, drafting article.

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