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UNVEILING THE EFFECT OF DROUGHT AND GENETIC RESOURCES ASSOCIATED WITH DROUGHT TOLERANCE IN WHEAT

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Drought is one the gravest aspect of the climate change in the present decade. This kind of climate change neither allow the farmers to prepare itself in advance nor it can escape the season once the sowing is completed. The impact is so widespread that it causes huge crop losses and poses serious threat to food security globally. Wheat being the third most staple crop around the world after rice and maize, has been severely affected by this climatic menace. Drought tolerance has become an important part of the today's research and development of drought resilient lines in wheat is the current breeding trait of interest for plant breeders. Identification for novel genetic resources and associated genomic region clarifies the mechanisms behind drought tolerance and its regulation. The biochemical & physiological aspects associated with the said trait and their interface with the associated genomic regions, identified using genome wide associated studies (GWAS), provides deep insights for drought tolerance & its mechanism. Several significant genetic resources have been identified in the recent past which has proved their worth in development of drought tolerant lines in wheat. This review highlights the latest research and facts associated with several aspects of drought tolerance in wheat and provide profound solutions that are significant for the future wheat breeding programs.

Keywords: Drought, Wheat, Climate change, Physiology**,** GWAS

Introduction

Wheat (*Triticum aestivum* L.), being one of the major agricultural crop worldwide, is referred as "king of grains", serving a huge population of around one third of the human population[1]. It ranks as the second most extensively produced cereal globally and represents the largest crop in terms of cultivated land area[2]. Wheat contributes approximately 70% of caloric intake and 80-85% of dietary protein in human diets, primarily through wheat-based products such as bread[3]. Wheat grain is composed of approximately 60-80% starch, about 2% minerals, 2% lipids, 2.2% crude fiber, B-complex vitamins, 8-17% proteins, vitamin E, and almost all essential amino acids nutritionally[4]. Global wheat production attained about 757 million metric tons in 2017[5]. The percent of wheat consumption to the total cereal consumed in the world is 41-74% in developed countries and 35% in developing areas and serves as one of the basic human food sources[6]. It is the second most-consumed staple cereal in the world after rice[7]. About 68% of the total amount produced is utilized for human food, 19% goes to feeding cattle, and the rest is used industrially, for instance, in the manufacture of ethanol[8]. About 68% of the total amount produced is utilized for human food, 19% goes to feeding cattle, and the rest is used industrially, for instance, in the manufacture of ethanol[8]. Demand for wheat in Sub-Saharan Africa has grown by 2-3% annually, reflecting its position as one of the more important food grains of the world[9].

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Sophisticated biochemical defense mechanisms in wheat plants underpin adaptation to episodes of water scarcity. Increased generation of reactive oxygen species (ROS), leading to oxidative damage of essential cellular constituents, characterizes drought stress[10,11]. To counter the reactive oxygen species (ROS), the wheat plant has devised an antioxidant defense system, constituting of catalase (CAT), peroxidase (POD), and superoxide dismutase (SOD)[12]. During oxidative injury resulting from dehydration, the plant accumulates glutathione, glycine betaine, polyamines, and soluble sugars, which acts as a protection pathway[13]. Generally, the resilience in plant during water stress occurs through two ways i.e. drought avoidance, and dehydration tolerance[14]. Avoiding drought results through suitable root architecture, efficiency of water utilization and phenological changes for optimum use of rainfall[15]. Dehydration tolerance results from the plant's efficiency of withstanding the partial desiccation.

Response of plant against such stress is influenced by gen*etic factors, gene expression patterns, photosynthetic activity, respiratory changes, intensity, and duration of stress. The huge complexity within the plant life underscores the need to uncover the genomic basis and expression of the same during water fluctuations. This has resulted in researchers identifying various genomic loci associated with wheat's adaptability for drought[16]. The water crisis is managed via Ethylene Response Factors (ERFs) and likewise various other transcription factors. As overexpression of pathogen inducible ethylene responsive factor in *Triticum aestivum* (TaERF3) enhances proline and chlorophyll content during the stressful conditions of drought for adaptability[17]. Likewise, overexpression of TaERF1 leads to activation of other related genes imparting salinity, cold and drought tolerance in wheat[18,19].

Genomic overexpression, induction has been studied widely for the associated trait in wheat, however genetic repression is of equal importance in regulating the expression of mechanism involved in drought conditions. The discovery of crucial regulatory elements has facilitated the application of chromatin modifiers and transcriptional co-repressors for the repression of genes[20]. For example, the EAR motif is widely used as an active transcriptional repression domain in many plant species[21,22]. Recent advances in technologies dealing with molecular markers have revolutionized plant breeding and opened up new ways to speed up the process of developing drought-tolerant wheat genotypes[23]. Marker-assisted breeding has been making use of quantitative trait loci (QTLs) [24] associated with drought tolerance through DNA markers. The DNA markers allow genome mapping and tagging of traits that improve the identification of elites within the breeding lines[25]. Techniques such as single nucleotide polymorphisms (SNPs), amplified fragment length polymorphisms (AFLPs), and simple sequence repeats (SSRs) are likely to be integrated into improving the effectiveness of the breeding approach to drought tolerance[26]. Genetic markers associated with drought tolerance at particular growth stages and morphological traits are being investigated[27]. Despite the difficulties in yield measurement and the establishment of the role of individual genes, many studies have reported drought-responsive genetic markers in various stages of development[27,28,29].

Morphological adaptation is also a key aspect of wheat drought stress response[30] . Knowledge of how drought affects leaf and root traits, growth stages, and plant architecture is essential for genetic improvement of drought resistance[31] . Recent works revealed relations among length, senescence[32] and biomass roots, leaves size and shape under water limited conditions. During water limited conditions, there is a coordinated pathway of responses in wheat plant which

maintains a stable hormonal state, plant water relationship, and nutrient uptake efficiency[33].

A major mechanism devised for drought adaptability is regulating stomatal opening, which is dependent on abscisic acid dependent signals. Simultaneously, there is another mechanism utilizing antioxidant related defensive approach for overcoming oxidative stress[34]. With this, there are changes to nutrient uptake and transportation which increases the tolerance in wheat[35]. Ongoing research aims to develop agricultural practices that minimize water requirements while maximizing crop productivity, thereby strengthening local food security and ecosystem stability[36]. In this view, this review aims at discussing the physiology of wheat under heat stress and explores the major QTL/SNP/MTAs related to drought tolerance in wheat.

Heat Stress Constraint on Wheat

Among all the factors, particularly abiotic ones, periodic or continuous heat stress (HS) is a significant constraint on wheat production, especially in subtropical areas, and is regarded as a major threat to wheat[37]. The significant impacts of heat stress on the duration and rate of grain setting ultimately result in a decrease in grain yield is determined by its timing duration, and intensity[38]. At all stages of development, heat stress can impact wheat growth, and future modelling scenarios predict temperatures that are considerably highest[39]. The average temperature increases by 0.3°C per decennium globally[40], and the report published by the Intergovernmental Panel on Climatic Change (IPCC 2014) indicated that temperatures would increase by approximately 0.3°C by 2025 and by 1°C by 2100. In tropical and subtropical regions, wheat yield may decrease by 3% to 20% for each degree increase in ambient temperatures[41-43]. The rising temperature alters the seasons of the crops, leading to early crop maturation[44,45]. The ability of a plant to sustain growth, survive, and procreate under situations of restricted water availability[46] or during times of periodic water scarcity is known as drought tolerance. Drought has an impact on various factors such as plant growth, production levels, membrane integrity, osmoregulation, pigment content, water relations, and photosynthesis activity[47]. According to some researchers, heat stress can alter the water relation of the plant[48]. Heat stress can cause hormonal changes[49]. HS can lead to a reduction of metabolic activities[50] and the synthesis of reactive oxygen species[51-53]. It can also cause an increase in pollen mortality, promote ethylene production in wheat and reduce pollen tube development [54]. Many of the traits that contribute to heat tolerance under terminal heat stress are heritable, additive, and variable, suggesting that wheat improvement is possible[55,56].

Two markers, Xpsp3094 and Xgwm282, were found to be significantly associated with variation in TGW between optimally and late-sown RILs, as determined by regression analysis. The coefficients of determination (R2) for these markers were 0.14 and 0.11, respectively. It might account for the differences in the phenotypes of RILs. The R2 values indicated that Xpsp3094 and Xgwm282 were responsible for 14% and 11% of total phenotypic variation in heat tolerance within the RILs population, respectively[57].

Physiological Characteristics Linked to Heat Stress and Drought

Physiological traits refer to an individual's physical characteristics. In plants, these can be described as hormones and other growth regulators produced by the plants that act as signals within their tissues to elicit a physiological response.

Leaf Senescence

As leaves undergo senescence, certain structural alterations occur in the chloroplasts, such as vacuolar collapse, disruption of cellular homeostasis, and

plasma membrane integrity loss[58]. The photosynthetic machinery gets abrupted due to heat stress at the maturation phase[59]. Normalized Difference Vegetation Index (NDVI) has proven to be a reliable phenotyping tool to screen and discover gene associated with heat tolerance[60]. This approach is reliable as it depends on the greenness in wheat which takes in account of chlorophyll. Increased temperature of more than 34°C fastens the process of senescence via disruption of chlorophyll[61]. Since heat stress has a grim impact on photosynthesis setup of the plant, which eventually restricts the leaf surface area and finally leads to yield losses[62,63].

Spike Fertility

Decrease in the number of grains, reduction in grain size and biomass are major concerns of heat stress[64]. The major involvement of ethylene during the stress leads to programmed cell death and eventually grain loss[65,66]. The stress leads to fluctuations in metabolic pathways, chemical imbalances, and the pollen numbers[67]. Moreover, heat stress damages the female reproductive organs, by hindering the meiosis, resulting abnormal ovary and fast growth of stigma and ovule[67,68].

Starch Accumulation

A study[69] has highlighted that even with the presence of assimilates, exposure to temperature around 40°C leads to reduction in starch deposition in the grain by almost 30%. This occurs in the early stage of grain filling, which is highly sensitive and equally important stage in grain weight determination[69]. Since starch accumulation plays crucial role in total yield of the cereal, targeting the enzymes involved in starch biosynthesis may play an important part for wheat resilience in ever increasing temperature factor. Enzymes such as ATPase, granule-bound starch synthase, soluble starch synthase, branching and debranching enzymes, and plastidial starch phosphorylase are the key enzymes. With increase in temperature to 40°C, the plant activity in grains were hindered up to 97% [69]. Heat stress restricts starch production in wheat grains while significantly increasing the total protein and soluble sugar content[70]. During the seedling stage, stress caused by rising temperatures will lead to a reduction in biomass and soluble sugar content[53].

Canopy Temperature (CT)

The canopy temperature is closely associated with the development of stress due to drought and heat, and these two conditions appear to share a common genetic foundation[71]. Lopes and Reynolds asserted in 2010 that recent studies indicate that in times of drought and heat stress, the temperature of the canopy correlates with deeper roots[72]. The cooler canopy is linked to genetic differences in stomatal conductance under heat, and canopy temperature selection can help improve heat tolerance[73].

Membrane Thermostability

It was discovered that the thermostability of membranes is a heritable trait in 1998 [74]. Heat shock causes protein denaturation and increases the unsaturation of fatty acids, which subsequently hinders the movement of water, ions, and organic solutes across membranes, thereby disrupting cellular activity. “In plant swelling, certain characteristics of thylakoid membranes can be observed, such as the physical separation of the chlorophyll light harvesting complex 2 from the PS2 core complex 2 from the PS2 core complex. This results in increased leakiness and disruption of PS2-mediated electron transport” [74].

Chlorophyll Fluorescence and Chlorophyll Content

It has been recommended to consider chlorophyll fluorescence (CFL) in grain productivity under water stress conditions when choosing heat and drought resistant wheat stress genotypes. The CFL is a direct consequence of production; therefore, genotypes with larger yields will have

higher CFL values, suggesting that the CFL can be used to screen for tolerant genotypes. In wheat genotypes, CFL can serve as an indirect determinant of photosynthetic efficiency. The characteristics of CFL, Chl, and TGW were analyzed in RIL mapped populations by crossing heat sensitive genotypes with heat-tolerant ones. This analysis revealed that 17 out of 112 RILs exhibited a heat susceptibility index (HSI) of less than 1 for all characteristics[75].

Water Relation

An indicator for dehydration tolerance is Relative water content (RWC), which represents the internal status of water and the metabolic activities within the plant tissue. While facing drought stress, a continuous drop in RWC was recorded in various plant[76]. As described by[74], comparisons between fully hydrated leaves and those subjected to water deficit conditions show that patterns of water loss from excised leaves can be used to indirectly evaluate relationships among leaf structure, cuticular thickness, and transpiration rates. Traits that maintain a balance between transpiration and water retention are considered advantageous for drought resistance, as such leaves experience reduced water loss through evapotranspiration and retain hydration for longer periods[77]. In addition, dehydration tolerance is closely associated with the activation of antioxidant systems, which are induced under heat and drought stress as a consequence of increased osmotic potential in stressed leaf tissues[78]. Heat stress increases the hydraulic conductivity of cell membranes and plant tissues due to elevated aquaporin activity[79], with this effect being more pronounced in water of lower viscosity [80].

Osmotic Balance

The accumulation of low molecular weight organic solutes may lead to osmotic adjustment in plants suffering from drought. To uphold osmotic balance, plants will gather and generate suitable solutes like amino acids, sugars, and polyols as a reaction to drought stress[81]. Sugars, to a much greater extent than proline, have emerged as a vital substitute for water in cases of acute dehydration, leading to the creation of a hydration shell around proteins[82].

Hormonal Effect

According to Thompson, abscisic acid production can affect drought adaptation through two mechanisms: the avoidance of dehydration and the tolerance of dehydration[83]. Abscisic acid (ABA) is acknowledged as a chemical signal from root to shoot, restraining leaf growth and initiating short term reactions like stomatal closure. Moreover, in drought-stressed wheat, yield is closely associated with ABA, which has been identified as a promoter of root development [84]. Several additional growth regulators, including auxin, cytokinin, gibberellins, steroids, jasmonic acid, ethylene, as well as other factors such as nitrogen and pH levels, are synthesized or broken down in response to osmotic stress[85]. Prior studies have shown that ABA is generated in xylem tissues during periods of drought, and this production affects grain filling by influencing the expression of genes related to glucose metabolism and cell division; it is subsequently transported to reproductive organs. Drought causes an increase in ABA accumulation in leaves, stems and root exudates, while simultaneously decreasing leaf cytokinin levels[86].

Oxidative Damage

Plant exposed to heat and drought typically produce reactive oxygen species (ROS) that are highly detrimental, including singlet oxygen molecules, superoxide radicals, hydrogen peroxide, and hydroxyl radicals (OH)[35,87]. A complete havoc occurs to plant's lipid membrane, proteins, nucleic acids and pigments for photosynthetic activity, resulting in cell death and eventually the entire plant and its

productivity[88]. Conversely, the determination effects of drought stress are influenced by its duration, timing and intensity [88]. The level of water stress is responsible for peroxidation of membranes and organelles, activation or inactivation of enzymes, and destruction of nucleic acids, with these effects being proportional to the amount of ROS generated[89]. Malonic dialdehyde (MDA) has been considered a reliable sign of membrane degradation for a long time. A previous study indicated that the level of lipid peroxidation caused by ROS is mirrored in membrane stability[90].

Photosynthesis and Gaseous Exchange

In plants subjected to water stress, the primary indicator for assessing the level of photosynthesis is the fluctuation of photosynthetic pigment concentration. The drought rate is inversely related to the photosynthetic rate of cereals, indicating that drought reduces the photosynthetic rate in cereals[91]. In 2015, Panday and Shukla, reported that carbon dioxide diffusional limitations arise when stomata close prematurely in response to drought-induced turgor loss[92]. This led to a reduction in the activity of photosynthetic enzymes, and triosephosphate formation components, as well as a decrease in the photochemical efficiency of photosystem 2-these are the primary factors constraining the rate of photosynthesis[92]. When comparing the limitations of photosynthesis to those caused by droughts resulting from metabolic distortions, it becomes evident that the latter are more complex than those of stomata, which are primarily due to a reduced production of photosynthetic pigments[93]. As a reaction to drought, both mesophyll conductance and stomatal conductance to CO_2 decline. Heat stress has a significant effect on photosynthesis, resulting in a reduction due to reduced leaf surface area expansion, malfunctioning photosynthetic machinery, premature leaf aging, and a related decline in wheat yield[94,94].

The biochemical Underpinning of Wheat's drought Tolerance Mechanisms

Numerous biochemical processes help wheat and other plants become more drought-tolerant. Some of these include decreased Rubisco efficiency, elevated stress-related chemicals such as glutathione MDHA, and the activation of antioxidant enzymes (SOD, POD, CAT, APX, GR, GST, MDHAR). Plant's mechanism of antioxidants to counter ROS (like-hydrogen peroxide, superoxide anions, singlet oxygen, and hydroxyl radicals) helps as biochemical strategy for coping the drought conditions[11,12]. Biochemical changes within the plant's pathways helps in removal of theses ROS, which may otherwise leas to oxidative injury[96]. Soluble sugars, inorganic ions functions as osmotic regulators during water uptake within the cell[97-99]. Investigation in wheat has led to findings that genotypes with higher levels of osmo-protectants and lower level of malondialdehyde favours drought tolerance[100,101]. In periods of water stress, polyamines (PAs) play a crucial role in maintaining the integrity of cell membranes and nucleic acids [13]. Studies carried out show that higher polyamine levels promote crop growth under water stress, corroborated by previous research[102]. During drought, the activity of CAT, a quickly reversible protein found in leaf cells, diminishes, as seen under stress conditions[103].

Enhancement of Gene Expression and Gene Repression in Response to Drought Stress

It is well known that plants respond to stress with transcription factors of the AP2/ERF family. They are categorized into subfamilies in wheat, comprising DREB, ERF, AP2, and RAV. During stress [104], ERFs are activated quickly, and their study has been the focus of researchers enhancing drought tolerance through overexpression. Superior amount of chlorophyll and proline, along with the triggering of downstream genes by binding to cis-

elements of the GCC-box, are likely responsible for this[17]. TaERF1 from wheat overexpression enhances salt resistance, cold, and drought by triggering stress-related Erb origin[18]. At ERF019, orthologs could strengthen wheat's aridity toleration manufacture[105].

Although researchers have thoroughly investigated the activation of genes, our comprehension of how gene are deactivated due to environmental change is limited. It was discovered that certain molecular patterns play a role in the inhibition of gene transcription[106]. The ethylene responsive element binding factors is linked to the EAR motif [107], the TLLLFR motif[108] , the R/KLFGV motif [109], and the LxLxPP motif [110]. These patterns attract co-repressors and chromatin modifiers, aiding in the reduction of gene expression[21]. To date the ERF motif is the most commonly identified active transcriptional repression motif in plants.

Table 1: Genomic regions associated with drought tolerance, identified in wheat using different GWAS models, their algorithms, and precision.

Algorithm/ Software Used	**Category**	**Primary function or typical use in GWAS Context**	**Typical Strength/ Maintained**	**QTL/MTA/SNP marker for drought tolerance in wheat**
TASSSEL-MLM[113]	Single-locus MLM (QTL)	Investigate SNP-trait associations for drought indices (SSI/STI, root/shoot attributes) while keeping kinship and population structure under control, generates Manhattan/Q-Q for claming MTAs.	Kinship+PCA has good control over false positives; it is frequently used and simple to comprehend for candidate gene lookup around important SNPs. (Used in a 90K marker drought study conducted in 2024).	90K SNPs array(Illumina 90K iSelect) ; BS00086777_51, wsnp_BE426418A _Ta_2_1
BLINK[114]	Multi-locus/ LD-informed selection	Finds stable drought-associated SNPs by selecting markers using LD+BIC to identify MTAs with greater power and fewer false positive for dense SNP panels.	More statistical power and quicker runtimes on dense SNP data compared to earlier MLMMs; often used in conjunction with FarmCPU to cross-validate signals in 2024-2025 investigations.	GWAS analyses using 25K/35K/array and /GBS SNP set
FarmCPU[114]	MLMM/ multi-marker associatio n (SNP)	Boost the complex's power, polygenic drought feature by minimizing structural confounding and confounding and concurrently fitting several associated indications.	Superior power compared to single-marker MLM for moderate effect loci; FarmCPUpp is popular in the 2024-2025 wheat GWAS because it speeds up memory and computation for high SNP counts.	GWAS studies with Infinium arrays-25K/35K/GBS datasets
rrBLUP[115]	QTL (Genomic prediction and	Predict breeding values during drought and calculate marker	Robust for polygenic traits and breeding applications (GS); enhances GWAS by	wsnp_CAP12_c948 _496702, BS00023006_51, Kukri_rep_c10155

	marker-effect estimation [GS])	effects (complements GWAS) in drought studies to assess the precision of WUE, GY, and drought index predictions.	allowing selection even in cases where individual MTAs are modes and by sorting marker by effect	0_113, Excalibur_c59090_145
GAPIT (R package: MLMM/ BLINK/ FarmCPU wrappers)[114]	Multi-method GWAS framework (SNP)	Make many GWAS algorithms (MLM, MLMM, FarmCPU and BLINK) and plotting/post-GWAS reporting easily accessible. This is helpful when authors test multiple methods on the same wheat drought dataset.	Flexibility-allows for reproducible runs of various models, effective plotting, and model comparison (which is why numerous 2024-25 paper utilize multiple methods through GAPIT)	25K-90K arrays, GBS (used as analysis framework)
k-mer/ alignment-free GWAS[116]	Sequence-based (k-mer) association mapping captures SNPs, indel, PAVs not on arrays	Identify variants (structural and presence/absence) that array SNPs miss and uncover novel drought-related loci not included in SNP arrays	Effective for capturing non-SNP variation (PAV, gene presence) and identifying novel loci beyond array coverage; valuable in diverse germplasm panels. (Newly developed approach in wheat studies of 2025)	GBS miss Structure variants
CMLM[117]	QTL	It combines fixed SNP markers and random effects within a compressed framework to effectively identify marker-trait association.	Lessens the need for computation and manages false positives more effectively than basic MLM	M788, M1576 and M7199
PLINK[118]	QC/ basic association pipeline (GLM/MLM/CMLM/SUPER)	Before the plant GWAS pipeline, genotype QC, filtering, LD trimming and basic association testing are frequently utilized.	Quick, reliable file conversions and genotype QC_ a crucial pre-GWAS phase.	Downstream GWAS; primary SNP
EMMA[119]	Mixed model association; SNP	Effective exact/approximate mixed model tests that manage kinship; serves as a substitute for GEMMA/EMMA	Significantly quicker than the previous version of EMMA; suitable for extensive SNP collections	Exact genome-wide association analysis

GWAS and QTL/MTA/SNP Markers for Drought Tolerance in Wheat

Developments in high-throughput genotyping technologies together with enhanced computational capabilities have allowed researchers to carry research for genome-wide association studies, which fundamentally transform quantitative trait mapping. The scientific community previously employed linkage mapping methods, which had low resolution and required extensive time for mapping biparental populations, but GWAS enables the detection of genetic markers that link to various traits across multiple populations[111]. High-density genotyping combined with high-throughput phenotyping enables GWAS to detect single nucleotide polymorphisms (SNP) and quantitative trait loci (QTLs) linking to beneficial traits across diverse genetic populations. GWAS provides better resolution through the recognition of candidate genes along with their associated single nucleotide polymorphisms from historical recombination events which enables the study of natural diversity in various populations[112]. The unravelling of complex plant traits through genome-wide association studies (GWAS) brings new hope for scientists to establish detailed maps of genetic loci controlling specific traits. GWAS have proven effective for identifying gene candidates and genetic markers that are responsible for wheat tolerance to heat stress and drought (Table 1).

Effect of Climate Change on Wheat

According to the Intergovernmental Panel on Climate Change (IPCC)[120], there is a likelihood that the earth's temperature may rise by 6.4 °C if human activity continues to contribute to global warming in the current trajectory. As a result, sea levels will increase by much to 59 centimetres by the end of the twenty-first century due to glacier melting. Natural disasters like floods, droughts, storms, cyclones, and altered precipitation patterns are all made more likely by climate change. Temperature, humidity, and rainfall changes have a negative effect on crop plant yield since agriculture is highly climate dependent and sensitive to agro-climatic conditions[121,122,123]. The Food and Agriculture Organization (FAO) and the Organization for Economic Co-operation and Development (OECD) have predicted that extreme abiotic stressors like drought, high temperatures, salt, etc. may cut wheat output by 20-30%, particularly in developing nations [124]. Furthermore, a number of biotic (such wheat blast disease [125,126] and unfriendly climatic phenomena (including drought, heat stress, unpredictable rain, hailstorms, and salt) brought on by global climate change have resulted in yield loss[124]. Additionally, a meta-analysis revealed that yield loss could happen in temperate and subtropical locations for every 2 °C increase in temperature[127]. According to a different study, Asseng et al. [128] calculated that every 1 °C increase in temperature would result in a 6% decrease in wheat yield, or roughly 42 million tons of wheat[124]. The intensity of the drought has a notable effect on wheat productivity among other abiotic stresses [124,129]. Crop growth is harmed by drought stress at every stage. Drought during the early stages of wheat growth results in poor seedling stand establishment and fewer tillers per unit area.

Conclusions

After rice and maize, wheat is the most significant staple cereal. Due to the growing population's need for food, the demand for wheat is rising daily in both developed and developing nations. According to estimates, wheat production in developing countries could rise by 60% by 2050 in order to meet the growing demand from the world's expanding population. Abiotic stressors like heat, cold, salinity, and drought also cause a 20-30% reduction in wheat productivity, especially in underdeveloped nations. Therefore, innovative methods are needed for sustainable wheat production to

mitigate the negative effects on wheat productivity and guarantee the food and nutritional security of the growing population.

Most breeding efforts worldwide prioritize increasing yield, but the current breeding pipelines are not optimized for choosing drought-adaptive and constitutive characteristics and yield. Integrating advanced phenotyping assays across multiple environments, coupled with high-throughput phenotyping technologies, can enhance selection accuracy for complex quantitative traits, and expedite the development of drought-tolerant cultivars. Modern breeding approaches increasingly rely on molecular markers and genomic tools to identify quantitative trait loci (QTLs) and candidate genes associated with drought tolerance in wheat. Drought responsive genomic loci encoding for gene of interest through various approaches like QTL mapping, Single nucleotide polymorphism detection, genome-wide association studies (GWAS) will enable researchers to precisely impart resilience in existing elite wheat cultivars through breeding. High-throughput methods for genome sequencing with advances in technology, enables researchers to mine for better genomic loci and genes involved in regulation during drought stress. Integration of genomic understanding with plant's physiological resilience acts as effective strategy for the development and improvement of climate resilient wheat lines, capable to counter drought and heat stress.

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