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Review Article

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Comprehensive review on the consequences and omics approaches for boosting wheat production under drought stress

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Abstract

Plants are subjected to a number of abiotic stresses in the field, many of which are detrimental to plant development and output. Drought is one of the most detrimental environmental conditions for crop cultivation. Wheat, a major crop is severely affected by drought stress. Wheat production declines due to drought are likely to have significant losses from all other factors. There are big consequences of drought stress on wheat's physiological, biochemical, and morphological properties, as well as the effects on growth, water relations, and photosynthesis. Drought stress causes changes in leaf size, stem length, and root multiplication, as well as an imbalance in plant-water relationships and a decrease in water efficiency. Drought stress causes alterations in the wheat plant, which are being investigated through physiological investigations. One of the most effective strategies to make wheat plants drought tolerant is to boost their antioxidant defense system to minimise oxidative stress. Plant biologists are developing novel techniques to increase the antioxidant defense system in order to mitigate the impacts of drought-induced plant damage. Drought tolerance in plants is conferred via a number of genes and their overexpression. Recent advances in wheat genomic, transcriptomic, proteomic, and metabolomic research under varying levels of drought give critical information for generating drought-tolerant wheat cultivars. This overview aims to summarise and update understanding on drought stress's impacts on wheat and tolerance mechanisms, as well as the omics approach to wheat plant drought stress adaptation.

Keywords

Wheat;
Drought stress;
Consequences;
Omics approaches;
Agriculture productivity

1. Introduction

Wheat (*Triticum aestivum*) is the world's most frequently farmed food crop, and it is endangered by climate change in the future (Pequeno *et al.,* 2021). By mid-century, climate change is expected to reduce world wheat production by 1.9% (Pequeno *et al.,* 2021). The poor nations in tropical regions are expected to bear the brunt of the negative consequences. African countries' productivity are expected to reduce 15% by 2050, while yields in Southern Asia are expected to fall 16% (Pequeno *et al.,* 2021). Plants are subjected to a variety of abiotic stresses in the field, all of which are detrimental to plant growth and development. Because of the extreme and rapid worldwide climatic changes, the simultaneous occurrence of abiotic stress, particularly drought stress in plants, might alter the morphological, physiological, and molecular responses in plants (Hussain *et al.,* 2018). As a result of the drought, maize, peanut, wheat, sunflower, sugarcane, and cotton yields and yield components have all decreased significantly (Furlan *et al.,* 2012; Tahir *et al.,* 2002; Barnabas *et al.,* 2008; Vasantha *et al.,* 2005; Kamara *et al.,* 2003).

Wheat production has always been subject to several constraints, resulting in the formation of biotic and abiotic limitations, among them, drought is a major concern. Due to global climate change, drought stress is becoming increasingly severe and frequent in the Indo-Gangetic floodplain, particularly during the winter wheat growing season (Shekhar and Paul, 2012).

Drought stress is characterised by a shortage of water that results in morphological, biochemical, physiological, and molecular changes (Sallam *et al.,* 2019).Photosynthesis, chlorophyll production, nutrient metabolism, ion absorption and translocation, respiration, and carbohydrates metabolism are all affected by drought stress in plants (Li *et al.,* 2011; Farooq *et al.,* 2009; Oyiga *et al.,* 2020). The immediate result is decreased organ output, greater flower abortion, and a shorter grain filling time, all of which have an impact on crop yield (Koua *et al.,* 2021).Drought stress, along with high temperatures during the reproductive stage (ultimate development phase), is a major contributor to low wheat production in the tropics and subtropics (Sattar *et al.,* 2020).

Wheat must adapt to drought conditions in order to survive, and numerous resistant genotypes have been developed to assist preserve soluble sugars, proline content, amino acids, chlorophyll content, as well as enzymatic and nonenzymatic antioxidant activities (Abid *et al.,* 2016).Wheat has enhanced its drought tolerance mechanisms; nevertheless, these mechanisms differ and are dependent on the crop kinds and cultivars (Tefera *et al.,* 2021). Durum wheat was discovered to be able to survive water stress better than bread wheat (Tefera *et al.,* 2021).Drought stress reduced the grain filling period by 15–24% and grain production by 11–34% (Islam *et al.,* 2021).When compared to irrigated circumstances, yield decreased by 3.09t ha^{-1} (-46.8%) under semiarid conditions in winter wheat (Neha *et al.,* 2021). Yield and kernel per meter square decreased by 68.71% and 66.05% respectively (Koua *et al.,* 2021). Moreover, plant height, the number of spikelets spike^{-1}, spike length, chlorophyll content, and relative water were all reduced by 26%, 23%, 9%, 11%, and 16%, respectively under drought stress (Tefera *et al.,* 2021). Thus, to maintain food security under the changing climatic conditions, the development of stress tolerance in wheat might be a promising approach.

An overview of omics technologies, such as transcriptomics, metabolomics, and proteomics, is currently used to gain an in-depth, precise, and systemic understanding of key biological and cellular pathways engaged by agricultural plants during stress (Zargar *et al.,* 2022). Mutant libraries, cDNAs, expression profiles, sequence data sets, and quantitative trait loci (QTLs) are all valuable resources in structural and genomics research (Jiang *et al.,* 2011). Cloning of many genes and discovered QTLs were significant for drought tolerance (Vikram *et al.,* 2012). To address the complicated nature of drought stress and mitigating mechanisms for tolerating drought stress, a large number of QTLs were found (Fleury *et al*., 2010). In addition, numerous QTLs responsible for increased grain output and other secondary traits that allow rainfed uplands and lowlands to tolerate drought stress have been found (Bernier *et al*., 2007; Venuprasad *et al*., 2009). Under drought conditions, different QTL performance has been seen in upland and lowland habitats. Under drought conditions, different QTL performance has been seen in upland and lowland habitats. Finally, the best QTLs for the ecosystems, genetic background, and environmental conditions are chosen. Furthermore, marker assisted back crossing (MABC) has been successfully used in crop plants to generate high yielding cultivars. MABC has been used to boost the yield of crop varieties in Thailand's north-eastern provinces (Kanjoo *et al*., 2012). Applications of molecular breeding techniques such as marker-assisted selection (MAS), SNP marker applications, and genome wide assisted selection (GWAS) are expected to pave the way for understanding the molecular mechanisms underlying crop plant resilience to a wide range of environmental challenges, such as drought stress, in the near future.

1.1. Consequences of drought on wheat

Drought causes plants to undergo a number of physiological and molecular changes, the majority of which aid in their adaptation to the harsh environment. Drought stress has both direct and indirect effects on plant metabolism. Drought-induced stress changes the morpho-anatomical, physiological, and biochemical composition of plants, reducing transpiration and improving the efficiency with which the plants use the water they have stored. Leaf water deficits come from constant water loss through transpiration. Drought stress, on the other hand, has a variety of effects, ranging from lesions to confusion (Bijalwan *et al*., 2022). Some consequences are discussed below-

1.1.1. Morphological effect

As a response to drought stress, wheat undergoes morphological changes such as reduced plant size, early maturity, decreased leaf area, reduced yield, limited leaf extension, small leaf size, reduced number of tillers, reduced leaf longevity, reduced total shoot length, decreased plant height, increased leaf rolling, and reduced plant biomass (Rijal *et al.,* 2021). Drought stress has a substantial impact on seed germination, seedling development, dry matter partitioning, root growth, root depth, and extension (Lonbani and Arzani, 2011). The root is the first organ to be influenced by drought stress (Shimazaki *et al.,* 2005). Under water stress, the root grows in order to find water, while the growth of the shooting component is stunted (Ahmad *et al.,* 2018). The fall in biomass (Wang *et al.,* 2005), grain number (Dolferus *et al.,* 2011), is mostly caused by terminal drought, which results in a large reduction in wheat output. One of the most visible symptoms of leaf senescence is chlorosis, which causes a reduction in photosynthesis (Ali *et al*., 2020). Wheat grown in extreme drought circumstances can bring the entire plant to senescence, but it also improves the mobilisation of stored carbohydrates from the stem and leaves to forming grains during parenthesis, so compensating the yield loss incurred by senescence during drought stress (Nawaz *et al.,* 2013; Farooq *et al.,* 2014).

Drought stress requires specific physiological changes in the plant in order to mitigate the effects of drought stress (Vinocur and Altman, 2005). Adaptation mechanisms in wheat for dealing with drought stress include osmotic root adjustment, greater root penetration into the soil, increased root density, and increased root to shoot ratio (Ali *et al.,* 2020). The relevance of root angle in irrigated settings and roots per shoot in drought situations for boosting grain production might be crucial for designing drought-tolerant cultivars was concluded by Neha *et al.,* (2021).

Canopy stay green traits aided in the selection of drought-tolerant genotypes, since they may confer longer photosynthesis, nutrient, and water absorption under stress (Lopes and Reynolds, 2012). The use of an RGB-based vegetation index to characterize canopy green area dynamics might reduce selection time and improve precision (Neha *et al.*, 2021).

1.1.2. Physiological effect

Drought stress has been linked to a wide range of physiological responses. Drought stress on wheat crops is mitigated by a variety of physiological characteristics (Rijal *et al.*, 2021). The availability of water has a direct link with the functioning of many physiological processes in plants. These physiological processes are disrupted when water availability is reduced, and plants are unable to create appropriate amounts of dry matter (Barbeta *et al.*, 2015). Water deficit causes a decrease in water status during crop growth, soil water potential, and plant osmotic potential for water and nutrient absorption, which reduces leaf turgor pressure, causing plant metabolic processes to be disrupted (Mehraban and Miri, 2017). Drought significantly impacts water relations, nutrient absorption, growth, and yield in wheat at later stages (6 weeks after emergence) than at earlier stages (3 weeks after seedling emergence) (Nawaz *et al.*, 2014). In comparison to their individual impacts, combined drought and heat shocks had the most devastating consequences on plant relative water relations except turgor potential (Sattar *et al.*, 2020). Plants restrict their stomata (perhaps via ABA signalling) when the volume of available water decreases, reducing CO_2 input. CO_2 reduction not only reduces carboxylation but also directs additional electrons to generate reactive O_2 species (Ahmad *et al.*, 2018). Closing of stomata, a reduction in photosynthetic activity, the onset of oxidative stress, changes in cell wall integrity, and the formation of toxic compounds that lead to plant death are some of the physiological changes (Alghabari and Ihsan, 2018). Different abiotic stressors attack biological membranes first and foremost. The durability of maintenance membranes under water stress is thought to be a key component of drought resistance in plants. Drought stress damages membrane integrity (Almeselmani *et al.*, 2012). Drought stress also affects the electron transport chain, resulting in the generation of reactive oxygen species (ROS) that are detrimental to plant cells and organelles such as mitochondria, chloroplasts, and peroxisomes (Farooqi *et al.*, 2020).Under drought conditions, RuBisCO (ribulose-1, 5-bisphosphate carboxylase/oxygenase) enzyme activity is inhibited, resulting in a decrease in photosynthetic amount and the generation of ATP (Dulai *et al.*, 2006).

Plants must adapt to drought conditions in order to survive, and several tolerant genotypes have been developed to assist preserve soluble sugars, proline content, amino acids, chlorophyll content, enzymatic and non-enzymatic antioxidant activities (Abid *et al.*, 2016). When compared to leaf water potential, relative water content (RWC) is an effective predictor of water status in drought conditions (Lugojan and Ciulca, 2011), as it decreases when leaf exposed to drought (Nayyar & Gupta, 2006) and it has also been used to find drought-tolerant cultivars (Bayoumi *et al.*, 2008). These several forms of plant drought tolerance mechanisms aid in the understanding of the physiological response that aids in the maintenance of growth and productivity during times of stress (Rijal *et al.*, 2021). Similarly, these qualities are important in breeding projects aimed at developing drought-tolerant cultivars that can thrive in areas where water is scarce.

1.1.3. Biochemical effect

Reduced efficiency of Rubisco, photochemical, accumulation of stress metabolites (glybet, glutathione, and polyamines), antioxidant enzymes [peroxidase (POD), superoxide dismutase (SOD), ascorbate peroxidase (APX), catalase (CAT)], and reduced ROS accumulation are some of the biochemical effects in plants due to water stress (Nezhadahmadi *et al.*, 2013). Drought stress has a deleterious impact on total soluble sugar (TSS), total carbohydrate (TC), and enzyme activity in wheat (Hammad and Ali, 2014). The culm reserves, or water-soluble carbohydrates (WSCs), contributed less to the grains as a result of the stress (Islam *et al.*, 2021). When the generation and build-up of ROS increases, it affects cellular processes such as protein degradation, enzyme inhibition, oxidative damage to DNA and RNA, and membrane lipid peroxidation, all of which lead to cell death (Ishikawa *et al.*, 2010; Huseynova, 2012).

Wheat plants mostly in the heading stage, accumulate proline content to a greater extent than any other osmoregulators due to a shortage of water (Maralian *et al.*, 2010). Tefera *et al.*, (2021) stated that wheat in response to drought increases proline and total soluble sugar by 28% and 6% respectively and biochemical parameters need to be considered as a better option for the selection process under drought stress. Todorova *et al.*, (2021) conclude that Serrate (selective herbicide) affects the biochemical reactions of drought-stressed wheat seedlings and after the combined herbicide+drought treatment, stress indicators, the enzymatic and non-enzymatic antioxidant defense were also elevated throughout the stress phase.

As the production of ROS increases in stress (Farooqi *et al.*, 2020), enzymatic and non-enzymatic systems get activated to detoxify the toxic level of ROS (Caverzan *et al.*, 2016). This reaction is also influenced by other aspects such as tissue type, stress duration, and intensity, and developmental stage, demonstrating the intricacy of the process of ROS formation and detoxification, as well as the impact of ROS on the antioxidant mechanism (Caverzan *et al.*, 2016). Hussain *et al.*, (2021) remarked that the increase in output was attributed to the wheat genotype's improved drought tolerance, as ABA (a form of abscisic acid) aids the plant in water-saving because an increase in the concentration of ABA near the guard cell causes the closer of stomata (Sourour *et al.*, 2017). Silicon application (anthesis stage- foliar spray, tillering stage- fertigation) enhances plant biochemical characteristics, nutrient absorption, and growth rate, all of which aid the plant in mitigating drought-stressing impacts (Bukhari *et al.*, 2021). The latest findings by Gyugos *et al.*, (2021) of far-red light's adaptive adjustment of glutathione and amino acid levels during drought, which can be used as a foundation for spectrum-dependent modification of crops' defensive metabolites (glutathione, proline) to prevent stress-induced damage.

2. Omics approaches for increasing productivity of wheat under drought stress

Omics, or the study of an organism's genes, transcripts, proteins, and metabolites, decodes the complete genome in order to get a better knowledge of plant molecular reactions and develop precise crop development tactics (Jain *et al.*, 2019). The key requirement for demonstrating the exact link between genotype and phenotype is the integration of crop functional genomics and phenomics data (Yang *et al.*, 2020). One of the reasons for the limited contribution of genomics-assisted selection-based production of drought-tolerant wheat cultivars might be the polygenic nature of drought tolerance and the huge genome size of wheat (Mwadzingeni *et al.*, 2016). Koobaz *et al.*, (2020) used metabolomics and proteomics to investigate the mechanism behind wheat desiccation tolerance, as well as the function of several stress-responsive proteins and metabolites. **Figure 1** represents an overview of the integrated multi-omics approach for crop improvement. Combining multi-omics and systems biology to construct a top-down (phenotype to genotype) and bottom-up (genotype to phenotype) model for crop breeding improvement under environmental difficulties could be beneficial (Yang et al. 2021). The drought signalling route in wheat is depicted in **Figure 2**.

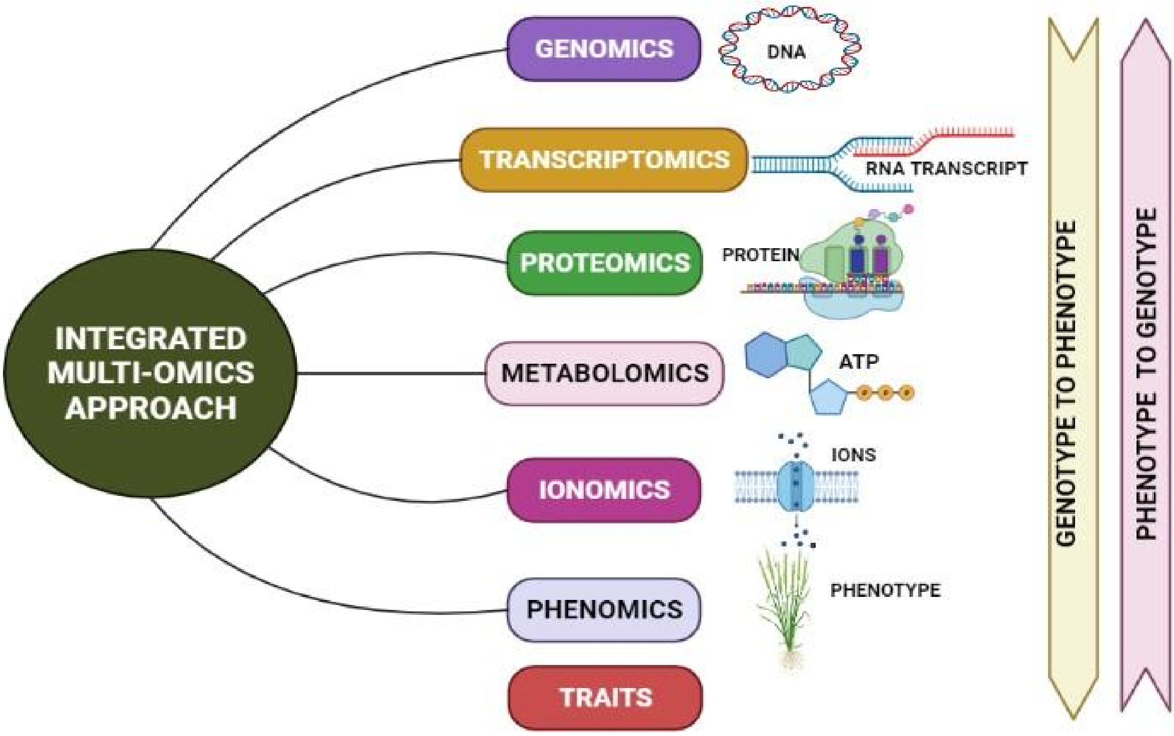

Figure 1: Integrated multi-omics approaches

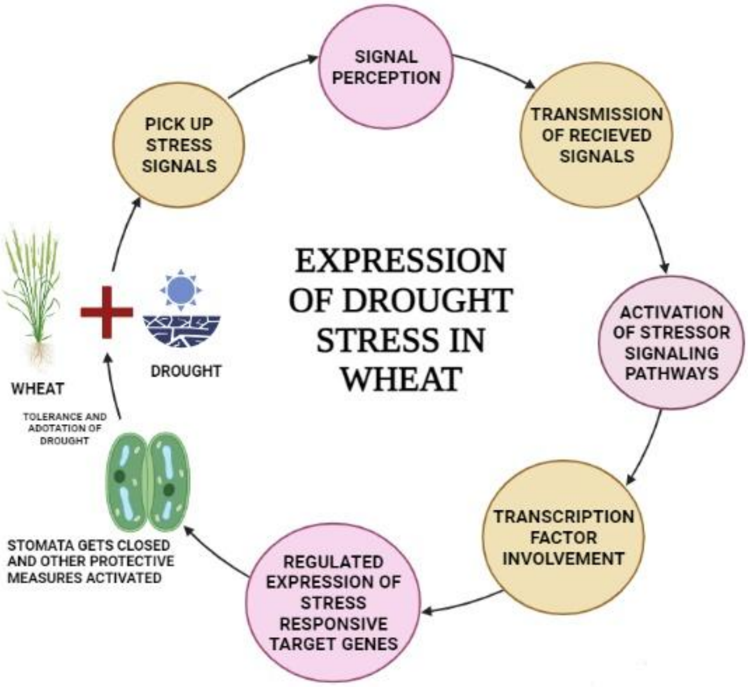

Figure 2: Drought signalling pathway in wheat.

2.1. Genomics approach

Genomics focuses on the structure, function, evolution, mapping, epigenomic, metagenomic, and genome editing aspects of genes and genomes (Muthamilarasan *et al.,* 2019). To enhance drought tolerance, several methods like quantitative trait locus (QTL) mapping, marker aided breeding, and introgression of a gene from a wild gene pool have been used (Merchuk-Ovnat *et al.,* 2016; Mwadzingeni *et al.,* 2016). Pour-Aboughadareh *et al.,* (2017) suggest that wild cousins of wheat might be used to increase stress tolerance. Khanna-Chopra *et al.,* (2020) discovered notable QTLs on chromosome 3B regarding cell membrane stability as well as on chromosome 2D for flag leaf influencing factors (area, breadth, and length). A key yield QTL (Qyld.csdh.7AL) was recently incorporated in four elite Indian wheat lines to create drought-tolerant genotypes with good yielding qualities under stressed conditions (Gautam *et al.*, 2020). Zandipour *et al.*, (2020), found a QTL hotspot for nine key characters (grain number per spike, spike length, spike weight, plant height, biological yield, grain yield, stem weight, and thousand-grain weight) on wheat chromosome 1B under terminal drought stress. Table 1 shows all recently developed QTLs and related traits for drought tolerance.

Molecular markers have greatly aided us in improving desired qualities, such as drought tolerance, with more efficacy and dependability (Budak *et al.,* 2015). The development of sequence-based simple sequence repeats (SSRs) and single nucleotide polymorphisms (SNPs) markers has been aided by recent advances in DNA sequencing and genotyping techniques (Pascual *et al.*, 2020), mostly SNPs due to their abundance in nature (Winfield *et al.*, 2016). Hua *et al.*, (2019) found target genes in wheat that might be used to increase drought resistance through genetic engineering. By studying the expression of wheat genes P5CS and P5CR during drought stress, Karolina *et al.*, (2019) discovered that they play a significant role in determining tolerance to water deficiencies. According to Neha *et al.*, (2021), *TaCwi*.4A genetic marker for drought tolerance was highly associated with grain yield in wheat under water stress and also suggested it for use in future breeding programs. **Figure 3** provides a percentage of QTLs with related trait and their presence in chromosome responsible for drought tolerance in wheat.

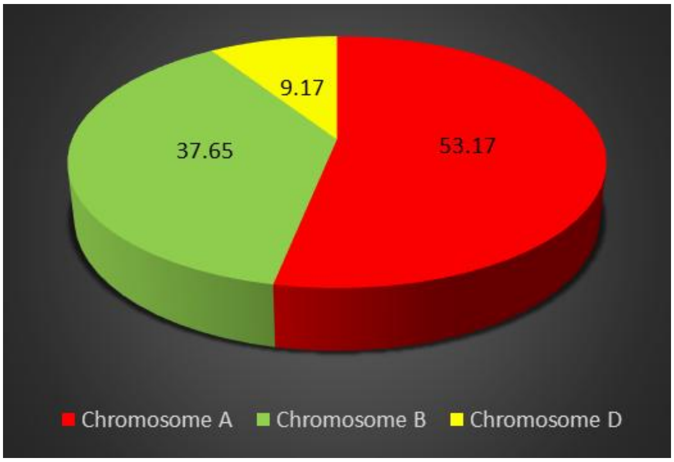

Figure 3: Graphical representation of percentage of drought responsible QTLs in chromosomes of wheat according to the work of previous researchers (Gahlaut *et al.*, 2017; Xu *et al.*, 2017; Ayalew *et al.*, 2018; Condorelli *et al.*, 2018; Fatima *et al.*, 2018; Sukumaran *et al.*, 2018; Dolferus *et al.*, 2019; Liu *et al.*, 2019; Goel *et al.*, 2019; Li *et al.*, 2019; Touzy *et al.*, 2019; Tura *et al.*, 2020; Ballesta *et al.*, 2020; Koua *et al.*, 2021).

Table 1. Genes/Transgenes responsible for drought tolerance in wheat

S. No	*Genes/Transgenes*	*Source*	*Putative function/Improved traits*	*Reference*
1.	*ERF1-V*	Wheat	Induce biochemical and molecular changes in transgenic wheat plants during salt and drought stress	(Xing *et al*., 2017)
2.	*SeCspA*	*E. coli*	More grain weight, yield, proline content, less reduction in chlorophyll content	(Yu *et al*., 2017)
3.	*TaODORANT1*	Wheat	Under salt and drought stress, an R2R3-MYB gene increases the expression of ROS and stress-related genes in transgenic tobacco	(Wei *et al*., 2017)
4.	*TaFER-5B*	Wheat	Enhance temperature and drought tolerance, improve ROS and leaf iron content	(Zang *et al*., 2017)
5.	*TaDrSR1 and TaDrSR2*	Wheat	Wheat drought tolerance proteins with differing levels of abundance	(Wang *et al*., 2018)
6.	*TaPEPKR2*	Wheat	Enhance root length and drought tolerance	(Zang *et al*., 2018)
7.	*TaSHN1*	Wheat	Enhance recovery from stress and lowers leaf water loss and stomatal density	(Bi *et al*., 2018)
8.	*TaWRKY2*	Wheat	Higher soluble sugar, proline, chlorophyll and survival rate	(Gao *et al*., 2018)
9.	*CIPK23*	Wheat	Enhanced ABA sensitivity, higher survival rate, increased osmolyte, stomata closure	(Cui *et al*., 2018)
10.	*TabZIP2*	Wheat	More single seed weight, less spikes and seed	(Luang *et al*., 2018)
11.	*TaCML20*	Wheat	In transgenic wheat, a CaM-like gene boosts water-soluble carbohydrate levels and yield	(Kalaipandian *et al*., 2019)
12.	*TaH2B-7D*	Wheat	Knock-down wheat plants were used to investigate its involvement in drought tolerance transmission	(Wang *et al*., 2019)
13.	*TaCOMT*	Wheat	In transgenic *Arabidopsis*, increases melatonin content and enhances drought tolerance	(Yang *et al*., 2019)
14.	*TaDr1*	Wheat	A transcriptional repressor that is co-expressed in wheat with TaFT1 and TaVrn1 in response to drought stress	(Zotova *et al*., 2019)

15.	*TaSIM*	Wheat	Reduces water loss and improves soluble sugar, proline, and stress-sensitive gene expression in transgenic *Arabidopsis* under drought stress	(Yu *et al.*, 2019)
16.	*TdPIP2;1*	Wheat	In transgenic wheat plants, an aquaporin gene engaged in salt and drought tolerance is found	(Ayadi *et al.*, 2019)
17.	*TaMYBsm3*	Wheat	In transgenic *Arabidopsis* plants, a MYB-CC transcription factor increases DT by upregulating the expression of stress-related genes (P5CS1, DREB2A, and RD29A)	(Li *et al.*, 2019)
18.	*OTS1*	*Arabidopsis*	More RWC, photosynthesis, and antioxidants , delayed senescence	(Li *et al.*, 2019)
19.	*AtWRK30*	*Arabidopsis*	Induces gas-exchange properties, osmolytes biosynthesis, antioxidant system, and stress-responsive gene expression in transgenic wheat plants, as well as heat and drought tolerance	(El-Esawi *et al.*, 2019)
20.	*TdSHN1*	Wheat	In transgenic tobacco plants, a transcription factor that increases salt and drought tolerance	(Djemal and Khoudi, 2019)
21.	*SBPase*	*Brachypodium*	Fully driven GUS expression promoted	(Alotaibi *et al.*, 2019)
22.	*HaHB4*	Sunflower	More water use efficiency and yield	(González *et al.*, 2019)
23.	*GmDREB1*	Soybean	Drought tolerance in transgenic wheat plants is improved.	(Zhou *et al.*, 2020)

2.2. Transcriptomics approach

Transcriptomics is concerned with the transcriptome, which is the total collection of RNA transcripts generated by an organism's genome in a cell or tissue (Raza *et al.*, 2021). With more whole-genome transcriptomic studies the genes linked to downstream signalling, production of stress response molecules, are undermined (Zang *et al.*, 2020). The transcriptome analysis based on microarray and RNA sequencing (RNA-seq) has been used to deconstruct the wheat drought tolerance (Liu *et al.*, 2015).

Drought-stressed wheat at the reproductive stage was studied using RNA-seq, and 309 drought-responsive differentially expressed genes (DEGs) linked to photosynthetic activity, floral development, and stomatal movement were discovered (Ma *et al.*, 2017). Liu *et al.*, (2017) investigated the transcriptome of wheat during the early grain-filling stage of drought and discovered 566 DEGs related to signal transduction, metabolism, and transcription. They also looked at the involvement of phenylalanine metabolism and flavonoid production in wheat spikes under drought tolerance. Plant development has been found to be aided by the use of laser irradiation under various abiotic stress situations and with the use of RNA-seq based transcriptome analysis Qui *et al.*, (2017) explored He–Ne radiation’s role in wheat drought tolerance and found that the irradiation promoted 820 DEGs in wheat under water stress. Transcriptome profiling was done in roots of wheat under water stress using RNA-seq based transcriptome analysis by Hu *et al.*, (2018). The discovery of 45139 DEGs, 13820 transcription factors, and 288 miRNAs by RNA-seq of drought-stressed roots of tolerant (NI543941) and sensitive (WL711) wheat genotypes further highlighted the applicability of RNA-seq data in the dissection of particular QTL (Iquebal *et al.*, 2019).

2.3. Proteomics approach

Proteomics is a technique for profiling the total expressed protein in an organism and it is separated into four parts: sequence, structural, functional, and expression proteomics (Mosa *et al.*, 2017; Aizat and Hassan, 2018).The amino acid sequences are determined using sequence proteomics by High-Performance Liquid Chromatography (HPLC; Twyman, 2013). The structure of proteins is studied in structural proteomics to better understand their possible activities using computer-based modelling, and experimental methods including crystallization, nuclear magnetic resonance (NMR), X-ray diffraction of protein crystals, and electron microscopy (Woolfson, 2018).Functional proteomics identifies a protein's activities, which are then investigated using a variety of techniques such as yeast-one or two hybrids and protein microarray profiling (Lueong *et al.*, 2014).

Wheat's different organs' proteomic responses to drought stress have been extensively studied, including seedling leaves and roots (Cheng *et al.*, 2015; Hao *et al.*, 2015), glume and awn development (Deng *et al.*, 2019), flag leaves (Deng *et al.*, 2018; Zhu *et al.*, 2020), and grain development (Ge *et al.*, 2012; Deng *et al.*, 2018; Duan *et al.*, 2020). Subcellular proteomics has recently been established to decode several organelle proteins involved in abiotic stress defense, such as those found in the plasma membrane, endoplasmic reticulum, mitochondria, and chloroplast (Zhang *et al.*, 2021; Zhu *et al.*, 2021).

Drought stress had a negative impact on the Bahar leaf proteome, resulting in a significant drop in total protein content, mostly due to deficiencies in photosynthetic proteins and enzymes associated with sugar and nitrogen metabolism, as well as the ability to detoxify toxic compounds, according to a study conducted on two spring wheat cultivars (Kavir, drought-tolerant; Bahar, drought-susceptible). On the other hand, relatively little protein alterations were seen in Kavir stressed leaves (Michaletti *et al.*, 2018).

Comparative proteomics to evaluate and analyse the wheat types Chinese Spring and *D. villosum* (a species of *Triticeae*) discovered a total of 883 distinct abundant proteins (DAPs) (Wang *et al.*, 2021). Many proteins associated in defense/stress change radically between *D. villosum* and the wheat variety Chinese Spring, including the G_α subunit, zinc finger protein family, PR1, HSP family, LEA protein, and serpin family (Wang *et al.*, 2021). This discovery has paved the way for more research into the molecular mechanisms of wheat resilience and quality, as well as the development of wheat varieties based on wild relatives of wheat (Wang *et al.*, 2021).

In the cell nucleus subproteome of wheat growing grains, using label-free quantitative proteomic analysis Li *et al.*, (2021) found 398 water-deficit sensitive DAPs out of which 146 up-regulated DAPs were mostly engaged in oxidation-reduction and stress response, whereas 252 down-regulated DAPs were mostly involved in translation, oxidation-reduction, and cellular amino metabolic pathway. The wheat grain nuclear sub proteome’s metabolic route in response to water shortage was hypothesised, providing new knowledge from a subcellular proteome level for understanding the molecular processes of plant drought stress response (Li *et al*., 2021).

2.4. Metabolomics approach

Metabolomics is a powerful method for obtaining detailed data on metabolite profiling and metabolic network analysis (Kumar *et al.*, 2021). It also provides information on metabolites that have been identified as well as those that have yet to be identified (Kumar *et al.*, 2021). Metabolite profiling techniques have been frequently utilized to analyse plant molecular responses to drought stress and assess metabolite levels in a specific metabolite class or pathway (Kusano *et al.*, 2007). Proteomics simply detects gene products, but metabolomics may reveal how proteins are expressed metabolically and uncover biochemical processes that are critical for gene function (Lindon and Nicholson, 2008). Genome sequencing techniques like next-generation sequencing (NGS) and metabolite measurement through mass-spectrometry (MS) are used collectively to generate crop-improvement strategies (Pandey *et al.*, 2016). In order to correctly identify and evaluate metabolites, accurate annotation and reporting of metabolomics data are critical. Alseekh *et al.*, (2021), recently published standards for annotation and quantification of gas/liquid chromatography-mass spectrometry (GC/LC-MS) based metabolomics data reporting to maintain transparency and avoid misinterpretation of metabolite data.

Drought stress responses of spring wheat leaf tissue are revealed by metabolomics and proteomics, which provide a better framework for understanding the mechanisms that drive plant cell responses to drought stress and knowledge of chemicals that can be exploited in crop improvement programmes (Michaletti *et al.*, 2018). Drought stress had a significantly higher negative impact on the distribution and accumulation of metabolites in JD8 than in JD17, according to a study conducted on shoots of two wheat genotypes (JD17- drought tolerant, JD8- drought sensitive), and GC-MS was recommended as an effective approach for understanding plant biochemistry under water stress (Guo *et al.*, 2018).

Using GC/MS, researchers discovered that lysine, asparagine, methionine, serine, and glutamine are the major metabolites involved in drought resistance in wheat leaves (Yadav *et al.*, 2019). Beside this GC-MS analysis of wheat roots and leaves under drought stress revealed that tryptophan and valine, as well as other metabolites such fumaric acid, malic acid, and citric acid, are the primary metabolites connected to drought tolerance (Kang *et al*., 2019). Guo *et al.*, (2020) examined the metabolome of drought tolerant (HX10) and sensitive (YN211) wheat genotypes using ultra-performance liquid chromatography-mass spectrometry (UPLC-MS). In response to drought stress, there was a difference in the levels of 56 metabolites between these genotypes. Future QTL or Genome-Wide Association Studies (GWAS) research might leverage this metabolome data to discover locus (loci) or gene(s) linked with these metabolic traits (s), and therefore offer gene(s) or trait-specific marker(s) for crop improvement was further remarked.

2.5. Ionomics approach

Ionomics is a method for studying the molecular systems underlying critical mineral nutrient and trace element composition in biological systems through high-throughput elemental profiling (Michaletti *et al.*, 2018). Inorganic components of cellular and organismal systems are also represented by this term (Michaletti *et al.*, 2018). It has several uses in forward and reverse genetics, mutant screening, ion absorption, compartmentalization, transport, and exclusion processes, and therefore aids in the understanding of drought and other abiotic stress mechanisms in plants (Shelden and Roessner, 2013). Integration of ionomics with other omics, such as genomics or metabolomics, might help researchers find possible genes and networks that increase crop resilience to physiological and environmental stress (Colmsee *et al.*, 2012; Satismruti *et al.*, 2013; Singh *et al.*, 2013; Wu *et al.*, 2013; Huang and Salt, 2016; Guo *et al.*, 2017).

Ionomics investigations in wheat under drought stress is yet to be published (Budak *et al.,* 2015). Ionomics is a relatively new functional genomics approach with a small number of research accessible, but spatial and technologically advanced ion profiling will be critical in the future to understand drought tolerance signalling networks (Budak *et al.,* 2015; Shah *et al.*, 2018).

2.6, Phenomics approach

Phenomics is described as the collecting of high-dimensional phenotypic data on an organism-wide scale to characterise phenotypes (Houle *et al.,* 2010). Plant phenomics is a fast-growing subject that includes anything from high-throughput field phenotyping to cellular imaging (Kaur *et al.*, 2021). Field-based high-throughput phenotyping (HTP) has received greater attention in the previous decade, especially to forecast agronomic and physiological features (Crain *et al.*, 2018). The new phenomics era has given scientists the tools they need to decode the data encoded in plant genomes (Finkel, 2009; Yang *et al.*, 2020). The capacity to collect comprehensive sets of field data and the fast speed of plant phenotyping based on phenomics has enhanced the selection phenomena of possible elite advanced lines that perform well under stress situations (Montes *et al.*, 2007).

The new phenomics era has given scientists the tools they need to decode the data encoded in plant genomes (Finkel, 2009; Yang *et al.*, 2020). Handheld infrared thermometers were used to assess canopy temperature in a high-throughput manner to avoid plot-to-plot fluctuation by Deery *et al.*, (2016) along with thermal imaging sensors in wheat for water and heat stress. The ability of several sensors to predict drought tolerance capacities of genotypes using water stress indices was tested by Becker *et al.*, (2017) utilizing passive and active hyperspectral reflectance sensors in wheat under drought stress. The usage of Unmanned Aerial Systems (UAS)-based HTP as a technique for collecting high-spatiotemporal data is quickly expanding (Haghighattalab *et al.*, 2016). Using an unmanned aerial vehicle (UAV) imagery system in 248 elite durum wheat Condorelli *et al.*, (2018) measured leaf chlorophyll content, leaf rolling, dry biomass, Normalized Difference Vegetation Index (NDVI), and QTLs for NDVI under water deficit conditions. Bhandari *et al.*, (2021) concluded that the combination of UAS-based remote sensing, agronomy, wheat breeding, and data analytics might lead to the development of digital tools that could be used to select genotypes for drought resistance and increase wheat breeding programmes' genetic gain.

3. Conclusion

Global climate change has resulted in the emergence of complex stress combinations and their effects on crop growth and production in modern agriculture. Climate change is a multifaceted issue with long-term consequences in the form of many abiotic pressures. Among them, water scarcity is receiving attention as abiotic stress because of its negative impact on plant growth and development, as well as a considerable loss in plant yield and biomass, resulting in worldwide food insecurity. Drought is one of the primary issues for attaining the potential yield since most of the worldwide wheat production area is in arid and semi-arid regions. It limits plant growth and development, which delays fruiting and grain filling, resulting in smaller and fewer wheat grains. Drought reduces wheat yields by altering the balance between the formation of ROS in plant cells, resulting in ROS overproduction and oxidative stress. Drought-induced ROS damage a wide range of macromolecules, including proteins and nucleic acids, causing plant death. It has an overall effect on plant production by interfering with physiological, metabolic, and biochemical processes. Certain breeding approaches, molecular and genomics views, with a specific emphasis on the omics technology modification, i.e., metabolomics, proteomics, genomics, transcriptomics, glycomics, and phenomics approaches, are of considerable use in improving drought stress tolerance in plants. However, a combination of advanced technologies and technical improvements is required for a better understanding of drought tolerance mechanisms and the development of drought tolerant wheat plants.

To fully comprehend complex abiotic stress tolerance features, more research is needed to combine data from omics investigations. As a result, investigations in genomics, transcriptomics, proteomics, metabolomics, and, particularly, phenomics, should focus more on the response to abiotic stressors.

Compliance with Ethical Standards

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References

Abid M, Tian Z, Ata-Ul-Karim S et al (2016) Nitrogen nutrition improves the potential of wheat (*Triticum aestivum* L.) to alleviate the effects of drought stress during vegetative growth periods. Frontiers in Plant Science, 7:981 https://doi.org/10.3389/fpls.2016.00981

Ahmad Z, Waraich EA, Akhtar S et al (2018) Physiological responses of wheat to drought stress and its mitigation approaches. Acta Physiologiae Plantarum, 40 (4), https://doi.org/10.1007/s11738-018-2651-6

Aizat WM, Hassan M (2018) Proteomics in Systems Biology. In: Aizat W, Goh HH, Baharum S (eds) Omics Applications for Systems Biology. Advances in Experimental Medicine and Biology, vol 1102. Springer, Cham. https://doi.org/10.1007/978-3-319-98758-3_3

Alghabari F, Ihsan MZ (2018) Effects of drought stress on growth, grain filling duration, yield, and quality attributes of barley (*Hordeum vulgare* L.). Bangladesh J. Bot. 47, 421–428. https://doi.org/10.3329/bjb.v47i3.38679

Ali M, Gul A, Hasan H et al (2020) Cellular mechanisms of drought tolerance in wheat. Climate change and food security with emphasis on wheat. 155–167. https://doi.org/10.1016/b978-0-12-819527-7.00009-1

Almeselmani BM, Saud A, Zubi KA et al (2012) Physiological performance of different durum wheat varieties grown under rainfed condition. Global Journal of Science Frontier Research Agriculture & Biology, 12 (1):1–11

Alotaibi S, Alyasi H, El-Shehawi A et al (2019) Functional analysis of SBPase gene promoter in transgenic wheat under abiotic stresses. Biotechnology 18(1):15–23. https://dx.doi.org/10.3923/biotech.2019.15.23

Alseekh S, Aharoni A, Brotman Y et al (2021) Mass spectrometry-based metabolomics: a guide for annotation, quantification and best reporting practices. Nat. Methods 18, 747–756. https://doi.org/10.1038/s41592-021-01197-1

Ayadi M, Brini F, Masmoudi K (2019) Overexpression of a wheat Aquaporin Gene, TdPIP2; 1, enhances salt and drought tolerance in transgenic durum wheat cv. maali. *Int. J. Mol. Sci. 20*(10), 2389. https://doi.org/10.3390/ijms20102389

Ayalew H, Liu H, Börner A et al (2018) Genome-Wide Association Mapping of Major Root Length QTLs Under PEG Induced Water Stress in Wheat. Front. Plant Sci. 9:1759. https://doi.org/10.3389/fpls.2018.01759

Ballesta P, Mora F, Pozo AD (2020) Association mapping of drought tolerance indices in wheat: QTL-rich regions on chromosome 4A. Scientia Agricola 77(2). https://doi.org/10.1590/1678-992X-2018-0153

Barbeta A, Mejia-Chang M, Ogaya R et al (2015) The combined effects of a long-term experimental drought and an extreme drought on the use of plant-water sources in a Mediterranean forest. Global Change Biology, 21(3):1213–1225. https://doi.org/10.1111/gcb.12785

Barnabás B, Jäger K, Fehér A (2008) The effect of drought and heat stress on reproductive processes in cereals. Plant Cell Environ. 31(1):11-38. https://doi.org/10.1111/j.1365-3040.2007.01727.x

Bayoumi TY, Eid MH, Metwali EM (2008) Application of physiological and biochemical indices as a screening technique for drought tolerance in wheat genotypes. J Biotechnol 7(14):2341–2352. https://doi.org/10.5897/AJB2008.000-5059

Becker E, Schmidhalter U (2017) Evaluation of yield and drought using active and passive spectral sensing systems at the reproductive stage in wheat. Front. Plant Sci. 8, 379. https://doi.org/10.3389/fpls.2017.00379

Bernier J, Kumar A, Venuprasad R (2007) A large effect QTL for grain yield under reproductive-stage drought stress in upland rice. Crop Sci. 47, 507–516. https://doi.org/10.2135/cropsci2006.07.0495

Bhandari M, Baker S, Rudd JC (2021) Assessing the Effect of Drought on Winter Wheat Growth Using Unmanned Aerial System (UAS)-Based Phenotyping. Remote Sens. 13, 1144. https://doi.org/10.3390/rs13061144

Bi H, Shi J, Kovalchuk N et al (2018) Overexpression of the TaSHN1 transcription factor in bread wheat leads to leaf surface modifications, improved drought tolerance, and no yield penalty under controlled growth conditions. Plant Cell Environ. 41(11):2549-2566. https://doi.org/10.1111/pce.13339

Bijalwan P, Sharma M, Kaushik P (2022) Review of the Effects of Drought Stress on Plants: A Systematic Approach. Preprints 2022020014. doi: 10.20944/preprints202202.0014.v1

Budak H, Hussain B, Khan Z, Ozturk NZ, Ullah N (2015) From genetics to functional genomics: improvement in drought signaling and tolerance in wheat. Front. Plant Sci. 6: 1012. https://doi.org/10.3389/fpls.2015.01012

Bukhari MA, Ahmad Z, Ashraf MY et al (2021). Silicon Mitigates Drought Stress in Wheat (*Triticum aestivum* L.) Through Improving Photosynthetic Pigments, Biochemical and Yield Characters. Silicon 13, 4757–4772. https://doi.org/10.1007/s12633-020-00797-4

Caverzan A, Casassola A, Brammer SP (2016) Antioxidant responses of wheat plants under stress. Genetics and Molecular Biology, 39 (1)1–6. https://doi.org/10.1590/1678-4685-GMB-2015-0109

Cheng Z, Dong K, Ge P et al (2015) Identification of leaf proteins differentially accumulated between wheat cultivars distinct in their levels of drought tolerance. PLoS One 10:e0125302. https://doi.org/10.1371/journal.pone.0125302

Colmsee C, Mascher M, Czauderna T et al (2012) OPTIMAS-DW: a comprehensive transcriptomics, metabolomics, ionomics, proteomics and phenomics data resource for maize. BMC Plant Biol. 12:245. https://doi.org/10.1186/1471-2229-12-245

Condorelli GE, Maccaferri M, Newcomb M et al (2018) Comparative Aerial and Ground Based High Throughput Phenotyping for the Genetic Dissection of NDVI as a Proxy for Drought Adaptive Traits in Durum Wheat. Frontiers in Plant Science. 9:893.https://doi.org/10.3389/fpls.2018.00893

Crain J, Mondal S, Rutkoski J, Singh RP, Poland J (2018) Combining high-throughput phenotyping and genomic information to increase prediction and selection accuracy in wheat breeding. *Plant Genome*, *11*(1), [170043]. https://doi.org/10.3835/plantgenome2017.05.0043

Cui XY, Du YT, Fu JD et al (2018) Wheat CBL-interacting protein kinase 23 positively regulates drought stress and ABA responses. BMC Plant Biology. 18(1):93. https://doi.org/10.1186/s12870-018-1306-5

Deery DM, Rebetzke GJ, Jimenez-Berni JA et al (2016) Methodology for High-Throughput Field Phenotyping of Canopy Temperature Using Airborne Thermography. Front. Plant Sci. 7:1808. https://doi.org/10.3389/fpls.2016.01808

Deng X, Liu Y, Xu X et al (2018) Comparative Proteome Analysis of Wheat Flag Leaves and Developing Grains Under Water Deficit. Front Plant Sci. 10;9:425. https://doi.org/10.3389/fpls.2018.00425

Deng X, Zhen S, Liu D et al (2019) Integrated proteome analyses of wheat glume and awn reveal central drought response proteins under water deficit conditions. J. Plant Physiol. 232, 270–283. https://doi.org/10.1016/j.jplph.2018.11.011

Djemal R, Khoudi H (2019) Combination of the endogenous promoter-intron significantly improves salt and drought tolerance conferred by TdSHN1 transcription factor in transgenic tobacco. Plant Physiol. Biochem. 139: 435–445. https://doi.org/10.1016/j.plaphy.2019.04.009

Dolferus R, Thavamanikumar S, Sangma H, et al (2019) Determining the genetic architecture of reproductive stage drought tolerance in wheat using a correlated trait and correlated marker effect model. G3: Genes, Genomes, Genetics 9(2): 473-489. https://doi.org/10.1534/g3.118.200835

Dolferus R, Ji X, Richards RA et al (2011) Abiotic stress and control of grain number in cereals. Plant Science : an International Journal of Experimental Plant Biology. 181(4):331-341. https://doi.org/10.1016/j.plantsci.2011.05.015

Duan W, Zhu G, Zhu D, Yan Y (2020) Dynamic proteome changes of wheat developing grains in response to water deficit and high-nitrogen fertilizer conditions. Plant Physiol. Biochem. 156, 471–483. https://doi.org/10.1016/j.plaphy.2020.08.022

Dulai S, Istvan M, Prónay J et al (2006) Effects of drought on photosynthetic parameters and heat stability of PSII in wheat and in Aegilops species originating from dry habitats. Acta Biol Szeged, 50(1-2):11-17.

El-Esawi MA, Al-Ghamdi AA, Ali HM, Ahmad M (2019) Overexpression of AtWRKY30 transcription factor enhances heat and drought stress tolerance in wheat (*Triticum aestivum* L.). Genes. 10 (2): 163. https://doi.org/10.3390/genes10020163

Farooq M, Hussain M, Siddique KHM (2014) Drought stress in wheat during flowering and grain-filling periods. Critical Reviews in Plant Sciences, 33 (4), Pp. 331–349. https://doi.org/10.1080/07352689.2014.875291

Farooq M, Wahid A, Kobayashi N et al (2009) Plant drought stress: effects, mechanisms and management. Agron. Sustain. Dev. 29, 185–212. https://doi.org/10.1051/agro:2008021

Farooqi ZUR, Ayub MA, Zia ur Rehman M et al (2020) Regulation of drought stress in plants. In Plant Life Under Changing Environment. INC. https://doi.org/10.1016/B978-0-12-818204-8.00004-7

Fatima S, Chaudhari SK, Akhtar S et al (2018) Mapping QTLS for yield and yield components under drought stress in bread wheat (*Triticum aestivum* L.). Applied Ecology and Environmental Research 16(4): 4431-4453.

http://dx.doi.org/10.15666/aeer/1604_44314453

Finkel E (2009) With phenomics, plant scientists hope to shift breeding into Overdrive. Science 325:380-381. https://doi.org/10.1126/science.325_380

Fleury D, Jefferies S, Kuchel H, Langridge P (2010) Genetic and genomic tools to improve drought tolerance in wheat. J. Exp. Bot. 61, 3211–3222. https://doi.org/10.1093/jxb/erq152

Furlan A, Llanes A, Luna V, Castro S (2012) Physiological and biochemical responses to drought stress and subsequent rehydration in the symbiotic association peanut *Bradyrhizobium* sp. ISRN Agron. 1–8. https://doi.org/10.5402/2012/318083

Gahlaut V, Jaiswal V, Tyagi BS et al (2017) QTL mapping for nine drought-responsive agronomic traits in bread wheat under irrigated and rain-fed environments. PLOS One. 12: e0182857. https://doi.org/10.1371/journal.pone.0182857

Gao H, Wang Y, Xu P, Zhang Z (2018) Overexpression of a WRKY transcription factor TaWRKY2 enhances drought stress tolerance in transgenic wheat. Front. Plant Sci. 9, 997. https://dx.doi.org/10.3389%2Ffpls.2018.00997

Gautam T, Amardeep, Saripalli G et al (2021) Introgression of a drought insensitive grain yield QTL for improvement of four Indian bread wheat cultivars using marker assisted breeding without background selection. J. Plant Biochem. Biotechnol. 30, 172–183. https://doi.org/10.1007/s13562-020-00553-0

Ge P, Ma C, Wang S et al (2012) Comparative proteomic analysis of grain development in two spring wheat varieties under drought stress. Anal. Bioanal. Chem. 402, 1297–1313. https://doi.org/10.1007/s00216-011-5532-z

Goel S, Singh K, Singh B et al (2019) Analysis of genetic control and QTL mapping of essential wheat grain quality traits in a recombinant inbred population. PLOS One. 14: e0200669. https://doi.org/10.1371/journal.pone.0200669

González FF, Capella M, Ribichich KK et al (2019) Field-grown transgenic wheat expressing the sunflower gene HaHB4 significantly outyields the wild type. J. Exp. Bot. 70(5), 1669–1681. https://doi.org/10.1093/jxb/erz037

Guo R, Shi LX, Jiao Y et al (2018) Metabolic responses to drought stress in the tissues of drought-tolerant and drought-sensitive wheat genotype seedlings. AoB PLANTS 10: ply016. https://doi.org/10.1093/aobpla/ply016

Guo R, Shi L, Yan C et al (2017) Ionomic and metabolic responses to neutral salt or alkaline salt stress in maize (*Zea mays* L.) seedlings. BMC Plant Biol. 17:41. https://doi.org/10.1186/s12870-017-0994-6

Guo X, Xin Z, Yang T et al (2020) Metabolomics response for drought stress tolerance in chinese wheat genotypes (*Triticum aestivum*). Plants (Basel). 9(4):520. https://dx.doi.org/10.3390%2Fplants9040520

Gyugos M, Ahres M, Gulyás Z et al (2021) Light spectrum modifes the drought induced changes of glutathione and free amino acid levels in wheat. Acta Physiologiae Plantarum 43:90 https://doi.org/10.1007/s11738-021-03253-x

Haghighattalab A, González Pérez L, Mondal et al (2016) Application of Unmanned Aerial Systems for High Throughput Phenotyping of Large Wheat Breeding Nurseries. Plant Methods 12, 35. https://doi.org/10.1186/s13007-016-0134-6

Hammad SA, Ali OA (2014) Physiological and biochemical studies on drought tolerance of wheat plants by application of amino acids and yeast extract. Annals of

Agricultural Sciences, 59(1), 133-145. https://doi.org/10.1016/j.aoas.2014.06.018

Hao P, Zhu J, Gu A et al (2015) An integrative proteome analysis of different seedling organs in tolerant and sensitive wheat cultivars under drought stress and recovery. Proteomics 15(9), 1544–1563. https://doi.org/10.1002/pmic.201400179

Hu L, Xie Y, Fan S et al (2018) Comparative analysis of root transcriptome profiles between drought-tolerant and susceptible wheat genotypes in response to water stress. Plant Sci. 272:276–293. https://doi.org/10.1016/j.plantsci.2018.03.036

Hua Y, Zhang C, Shi W, Chen H (2019) High-throughput sequencing reveals micro RNAs and their targets in response to drought stress in wheat (*Triticum aestivum* L.). Biotechnology and Biotechnological Equipment; 33(1):465-471 https://doi.org/10.1080/13102818.2019.1586586

Huang XY, Salt DE (2016) Plant ionomics: from elemental profiling to environmental adaptation. Mol. Plant 9(6):787–797. http://dx.doi.org/10.1016/j.molp.2016.05.003

Huseynova IM (2012) Photosynthetic characteristics and enzymatic antioxidant capacity of leaves from wheat cultivars exposed to drought. Biochimica et Biophysica Acta (BBA)-Bioenergetics, 1817(8):1516-1523. https://doi.org/10.1016/j.bbabio.2012.02.037

Hussain HA, Hussain S, Khaliq A et al (2018) Chilling and Drought Stresses in Crop Plants: Implications, Cross Talk, and Potential Management Opportunities. Front. Plant Sci. 9:393. https://doi.org/10.3389/fpls.2018.00393

Hussain S, Mushtaq MN, Bakhsh A et al (2021) Drought stress mitigation in wheat (*Triticum aestivum* L.) through physiological enhancements. Pakistan Journal of Agricultural Research, 34(2): 424-430. http://dx.doi.org/10.17582/journal.pjar/2021/34.2.424.430

Iquebal MA, Sharma P, Jasrotia RS et al (2019) RNAseq analysis reveals drought-responsive molecular pathways with candidate genes and putative molecular markers in root tissue of wheat. Sci. Rep. 9: 13917. https://doi.org/10.1038/s41598-019-49915-2

Ishikawa T, Takahara K, Hirabayashi T et al (2010) Metabolome analysis of response to oxidative stress in rice suspension cells overexpressing cell death suppressor Bax inhibitor-1. Plant and cell physiology, 51(1):9-20. https://doi.org/10.1093/pcp/pcp162

Islam MA, De RK, Hossain MA et al (2021) Evaluation of the Tolerance Ability of Wheat Genotypes to Drought Stress: Dissection through Culm-Reserves Contribution and Grain Filling Physiology. Agronomy 11(6), 1252. https://doi.org/10.3390/agronomy11061252

Jain D, Ashraf N, Khurana JP, Shiva Kameshwari MN (2019) The 'Omics' Approach for Crop Improvement Against Drought Stress. In: Rajpal V., Sehgal D., Kumar A., Raina S. (eds) Genetic Enhancement of Crops for Tolerance to Abiotic Stress: Mechanisms and Approaches, Vol. I. Sustainable Development and Biodiversity, vol 20. Springer, Cham. https://doi.org/10.1007/978-3-319-91956-0_8

Jiang Y, Cai Z, Xie W et al (2011) Rice functional genomics research: progress and implications for crop genetic improvement. Biotechnol. Adv.30(5): 1059–1070. https://doi.org/10.1016/j.biotechadv.2011.08.013

Kalaipandian S, Xue GP, Rae AL et al (2019) Overexpression of TaCML20, a calmodulin-like gene, enhances water soluble carbohydrate accumulation and yield in wheat. Physiol. Plant. 165(4): 790–799.

https://doi.org/10.1111/ppl.12786

Kamara AY, Menkir A, Badu–Apraku B, Ibikunle O (2003) The influence of drought stress on growth, yield and yield components of selected maize genotypes. J. Agric. Sci. 141, 43–50. https://doi.org/10.1017/S0021859603003423

Kang Z, Babar MA, Khan N et al (2019) Comparative metabolomic profiling in the roots and leaves in contrasting genotypes reveals complex mechanisms involved in post-anthesis drought tolerance in wheat. PLoS ONE 14, e0213502. https://doi.org/10.1371/journal.pone.0213502

Kanjoo V, Punyawaew K, Siangliw JL et al (2012) Evaluation of agronomic traits in chromosome segment substitution lines of KDML105 containing drought tolerance QTL under drought stress. Rice Sci. 19(2): 117–124. https://doi.org/10.1016/S1672-6308(12)60030-4

Karolina D, Magdalena Z, Andreas B et al (2019) Analysis of wheat gene expression related to the oxidative stress response and signal transduction under short-term osmotic stress. Scientific Reports; 9(1):2743. https://doi.org/10.1038/s41598-019-39154-w

Kaur B, Sandhu KS, Kamal R et al (2021) Omics for the Improvement of Abiotic, Biotic, and Agronomic Traits in Major Cereal Crops: Applications, Challenges, and Prospects. Plants 10, 1989. https://doi.org/10.3390/plants10101989

Khanna-Chopra R, Singh K, Shukla S et al (2020) QTLs for cell membrane stability and flag leaf area under drought stress in a wheat RIL population. J. Plant Biochem. Biotechnol. 29:276–286. https://doi.org/10.1007/s13562-019-00534-y

Koobaz P, Ghaffari MR, Heidari M et al (2020) Proteomic and metabolomic analysis of desiccation tolerance in wheat young seedlings. Plant Physiol. Biochem. 146: 349–362. https://doi.org/10.1016/j.plaphy.2019.11.017

Koua AP, Oyiga BC, Baig MM, Léon J, Ballvora A (2021) Breeding Driven Enrichment of Genetic Variation for Key Yield Components and Grain Starch Content Under Drought Stress in Winter Wheat. Front. Plant Sci. 12:684205. https://doi.org/10.3389/fpls.2021.684205

Kumar M, Kumar Patel M, Kumar N et al (2021) Metabolomics and Molecular Approaches Reveal Drought Stress Tolerance in Plants. Int. J. Mol. Sci. 22(17), 9108. https://doi.org/10.3390/ijms22179108

Kusano M, Fukushima A, Arita M et al (2007) Unbiased characterization of genotype-dependent metabolic regulations by metabolomic approach in Arabidopsis thaliana. BMC Syst. Biol. 21;1, 53. https://doi.org/10.1186/1752-0509-1-53

Le Roux ML, Kunert KJ, van der Vyver C et al (2019) Expression of a Small Ubiquitin-Like Modifier Protease Increases Drought Tolerance in Wheat (*Triticum aestivum* L.). Front. Plant Sci.10, 266. https://doi.org/10.3389/fpls.2019.00266

Li L, Mao X, Wang J, Chang X, Reynolds M, Jing R (2019) Genetic dissection of drought and heat-responsive agronomic traits in wheat. Plant, cell & environment, 42(9):2540–2553. https://doi.org/10.1111/pce.13577

Li T, Zhu D, Han Z et al (2021) Label-Free Quantitative Proteome Analysis Reveals the Underlying Mechanisms of Grain Nuclear Proteins Involved in Wheat Water-Deficit Response. Front. Plant Sci. 12:748487. https://doi.org/10.3389/fpls.2021.748487

Li C, Jiang D, Wollenweber B et al (2011) Waterlogging pre-treatment during vegetative growth improves tolerance to waterlogging after anthesis in wheat. Plant Sci. 180(5):672–678. https://doi.org/10.1016/j.plantsci.2011.01.009

Li Y, Zhang S, Zhang N et al (2019) MYB-CC transcription factor, TaMYBsm3, cloned from wheat is involved in drought tolerance. BMC Plant Biol. 19:143. https://doi.org/10.1186/s12870-019-1751-9

Lindon JC, Nicholson JK (2008) Analytical technologies for metabonomics and metabolomics, and multi-omic information recovery. Trends Anal. Chem. 27(3):194–204. https://doi.org/10.1016/j.trac.2007.08.009

Liu C, Mi H, Liu H et al (2017) Response to water deficit in glume of wheat: expression profiling by microarray analysis. Euphytica. 213: 26. https://doi.org/10.1007/s10681-016-1827-7

Liu C, Sukumaran S, Claverie E et al (2019) Genetic dissection of heat and drought stress QTLs in phenology-controlled synthetic-derived recombinant inbred lines in spring wheat. Mol. Breed. 39: 34. https://doi.org/10.1007/s11032-019-0938-y

Liu Z, Xin M, Qin J et al (2015) Temporal transcriptome profiling reveals expression partitioning of homeologous genes contributing to heat and drought acclimation in wheat (*Triticum aestivum* L.). BMC Plant Biol. 15: 152. https://doi.org/10.1186/s12870-015-0511-8

Lonbani M, Arzani A (2011) Morpho-physiological traits associated with terminal drought stress tolerance in triticale and wheat. Agronomy Research, 9(1-2), 315-329.

Lopes MS, Reynolds MP (2012) Stay-green in spring wheat can be determined by spectral reflectance measurements (normalized difference vegetation index) independently from phenology. J Exp Bot. 63(10):3789–98. https://doi.org/10.1093/jxb/ers071

Luang S, Sornaraj P, Bazanova N et al (2018) The wheat TabZIP2 transcription factor is activated by the nutrient starvation-responsive SnRK3/CIPK protein kinase. Plant Mol. Biol. 96, 543–561. https://doi.org/10.1007/s11103-018-0713-1

Lueong SS, Hoheisel JD, Alhamdani MSS (2014). Protein microarrays as tools for functional proteomics: achievements, promises and challenges. J. Proteomics Bioinform. 7:1–10. http://dx.doi.org/10.4172/jpb.S7-004

Lugojan C, Ciulca S (2011) Evaluation of relative water content in winter wheat. J Hortic For Biotechnol 15:173–177

Ma J, Li R, Wang H et al (2017) Transcriptomics analyses reveal wheat responses to drought stress during reproductive stages under field conditions. Front. Plant Sci. 8: 592. https://doi.org/10.3389/fpls.2017.00592

Maralian H, Ebadi A, Haji B (2010) Influence of water deficit stress on wheat grain yield and proline accumulation rate. African Journal of Agricultural Research, 5(4): 286–289.

Mehraban A, Miri M (2017) Effect of drought stress on cell membrane stability, relative water content and some characteristics of crop pants. Chemistry Research Journal 2(3): 85–90.

Merchuk-Ovnat L, Barak V, Fahima T et al (2016) Ancestral QTL alleles from wild emmer wheat improve drought resistance and productivity in modern wheat cultivars. Front. Plant Sci. 7: 452. https://doi.org/10.3389/fpls.2016.00452

Michaletti A, Naghavi MR, Toorchi M et al (2018) Metabolomics and proteomics reveal drought-stress responses of leaf tissues from spring-wheat. Scientific Reports 8:5710. https://doi.org/10.1038/s41598-018-24012-y

Montes JM, Melchinger AE, Reif JC (2007) Novel throughput phenotyping platforms in plant genetic studies. Trends in Plant Science 12(10): 433–436.

https://doi.org/10.1016/j.tplants.2007.08.006

Mosa KA, Ismail A, Helmy M (2017) Omics and System Biology Approaches in Plant Stress Research. In: Plant Stress Tolerance. Springer Briefs in Systems Biology. Springer, Cham. https://doi.org/10.1007/978-3-319-59379-1_2

Muthamilarasan M, Singh NK, Prasad M (2019) Multi-omics approaches for strategic improvement of stress tolerance in underutilized crop species: a climate change perspective. Adv. Genet. 103, 1–38. https://doi.org/10.1016/bs.adgen.2019.01.001

Mwadzingeni L, Shimelis H, Dube E et al (2016) Breeding wheat for drought tolerance: progress and technologies. J. Integrative Agri. 15: 935–943.

Nawaz A, Farooq M, Cheema SA et al (2013) Stay green character at grain filling ensures resistance against terminal drought in wheat. Int. J. Agric. Biol., 15 (6):1272–1276.

Nawaz F, Ashraf M, Ahmad R et al (2014) Selenium (Se) Regulates seedling growth in wheat under drought stress. Advances in Chemistry, 2014. https://doi.org/10.1155/2014/143567

Nayyar H, Gupta D (2006) Differential sensitivity of C3 and C4 plants to water deficit stress: association with oxidative stress and antioxidants. Environmental and Experimental Botany, 58(1-3): 106- 113. https://doi.org/10.1016/j.envexpbot.2005.06.021

Nehe AS, Foulkes MJ, Ozturk I et al (2021) Root and canopy traits and adaptability genes explain drought tolerance responses in winter wheat. PLoS ONE 16(4): e0242472. https://doi.org/10.1371/journal.pone.0242472

Nezhadahmadi A, Prodha ZH, Faruq G (2013) Drought Tolerance in Wheat. The Scientific World Journal, Vol 2013, pp 1-12. https://doi.org/10.1155/2013/610721

Oyiga BC, Palczak J, Wojciechowski T et al (2020) Genetic components of root architecture and anatomy adjustments to water-deficit stress in spring barley. Plant Cell Environ. 43(3):692–711. https://doi.org/10.1111/pce.13683

Pandey MK, Roorkiwal M, Singh VK et al (2016) Emerging genomic tools for legume breeding: current status and future perspectives. Front. Plant Sci. 7:455. https://doi.org/10.3389/fpls.2016.00455

Pascual L, Ruiz M, Lopez-Fernandez M et al (2020) Genomic analysis of Spanish wheat landraces reveals their variability and potential for breeding. BMC Genomics. 21: 122. https://doi.org/10.1186/s12864-020-6536-x

Pequeno DNL, Hern´andez-Ochoa IM, Reynolds M et al (2021) Climate impact and adaptation to heat and drought stress of regional and global wheat production. Environ. Res. Lett. 16 054070. https://doi.org/10.1088/1748-9326/abd970

Pour-Aboughadareh A, Ahmadi J, Mehrabi AA et al (2017) Physiological responses to drought stress in wild relatives of wheat: implications for wheat improvement. Acta Physiol. Plant. 39: 106. https://doi.org/10.1007/s11738-017-2403-z

Qiu Z, Yuan M, He Y et al (2017) Physiological and transcriptome analysis of He-Ne laser pretreated wheat seedlings in response to drought stress. Sci. Rep. 7(1): 6108. https://doi.org/10.1038/s41598-017-06518-z

Raza A, Tabassum J, Kudapa H, Varshney RK (2021) Can omics deliver temperature resilient ready-to-grow crops? Crit. Rev. Biotechnol. 41(8):1209-1232. https://doi.org/10.1080/07388551.2021.1898332

Rijal B, Baduwal P, Chaudhary M et al (2021) Drought Stress Impacts on Wheat And Its Resistance Mechanisms. Malaysian Journal of Sustainable Agriculture, 5(2): 67-76.

http://doi.org/10.26480/mjsa.02.2021.67.76

Sallam A, Alqudah AM, Dawood MFA et al (2019) Drought stress tolerance in wheat and barley: Advances in physiology, breeding and genetics research. International Journal of Molecular Sciences, 20 (13). https://doi.org/10.3390/ijms20133137

Satismruti K, Senthil N, Vellaikumar S et al (2013) Plant ionomics: a platform for identifying novel gene regulating plant mineral nutrition. Am. J. Plant Sci. 04, 1309–1315. http://dx.doi.org/10.4236/ajps.2013.47162

Sattar A, Sher A, Ijaz M et al (2020) Terminal drought and heat stress alter physiological and biochemical attributes in flag leaf of bread wheat. PLoS ONE 15(5): e0232974. https://doi.org/10.1371/journal.pone.0232974

Shah T, Xu J, Zou X et al (2018) Omics Approaches for Engineering Wheat Production under Abiotic Stresses. Int. J. Mol. Sci. 19(8): 2390. https://doi.org/10.3390/ijms19082390

Shekhar I, Paul S (2012) Rice and Wheat Crop Productivity in the Indo-Gangetic Plains of India: Changing Pattern of Growth and Future Strategies. Ind. J. Agric. Econ. 67(2):238–252. http://dx.doi.org/10.22004/ag.econ.204809

Shelden MC, Roessner U (2013) Advances in functional genomics for investigating salinity stress tolerance mechanisms in cereals. Front. Plant Sci. 4:123. https://doi.org/10.3389/fpls.2013.00123

Shimazaki Y, Ookawa T, Hirasawa T.(2005) “The root tip and accelerating region suppress elongation of the decelerating region without any effects on cell turgor in primary roots of maize under water stress,” Plant Physiology, 139(1):458–465. https://doi.org/10.1104/pp.105.062091

Singh UM, Sareen P, Sengar RS, Kumar A.(2013). Plant ionomics: a newer approach to study mineral transport and its regulation. Acta Physiol. Plant 35, 2641–2653. https://doi.org/10.1007/s11738-013-1316-8

Sourour A, Afef O, Mounir R, Mongi BY (2017) A review: morphological, physiological, biochemical and molecular plant responses to water deficit stress. Int J Eng Sci, 6, 1-4. https://doi.org/10.9790/1813-0601010104

Sukumaran S, Reynolds MP, Sansaloni C (2018) Genome-wide association analyses identify QTL hotspots for yield and component traits in durum wheat grown under yield potential, drought, and heat stress environments. Frontiers in Plant Sciences 9: 81. https://doi.org/10.3389/fpls.2018.00081

Tahir MHN, Imran M, Hussain MK (2002) Evaluation of sunflower (*Helianthus annuus* L.) inbred lines for drought tolerance. Int. J. Agric. Biol. 3, 398–400.

Tefera A, Kebede M, Tadesse K, Getahun T (2021) Morphological, Physiological, and Biochemical Characterization of Drought-Tolerant Wheat (*Triticum* spp.) Varieties. International Journal of Agronomy vol(2021) 8811749 https://doi.org/10.1155/2021/8811749

Todorova D, Sergiev I, Katerova Z et al (2021) Assessment of the Biochemical Responses of Wheat Seedlings to Soil Drought after Application of Selective Herbicide. Plants 10(4):733. https://doi.org/10.3390/plants10040733

Touzy G, Rincent R, Bogard M et al (2019) Using environmental clustering to identify specific drought tolerance QTLs in bread wheat (*T. aestivum* L.). Theoretical and Applied Genetics 132(10): 2859-2880. https://doi.org/10.1007/s00122-019-03393-2

Tura H, Edwards J, Gahlaut V et al (2020) QTL analysis and fine mapping of a QTL for yield-related traits in wheat grown in dry and hot environments. Theoretical and Applied Genetics 133(1): 239-257. https://dx.doi.org/10.1007%2Fs00122-019-03454-6

Twyman RM (2013) Principles of Proteomics. Abingdon: Garland Science Press.

Vasantha S, Alarmelu S, Hemaprabha G, Shanthi RM (2005) Evaluation of promising sugarcane genotypes for drought. Sugar Technol. 7, 82–83. https://doi.org/10.1007/BF02942536

Venuprasad R, Dalid CO, Del Valle M et al (2009) Identification and characterization of large-effect quantitative trait loci for grain yield under lowland drought stress in rice using bulk segregant analysis. Theor. Appl. Genet. 120(1):177–190. https://doi.org/10.1007/s00122-009-1168-1

Vikram P, Kumar A, Singh AK, Singh NK (2012) "Rice: genomics assisted breeding for drought tolerance," in Improving Crop Tolerance to Abiotic Stress, eds S. S. Tuteja, A. F. Gill, and R. Tiburico (Germany: Wiley-VCH Verlag GmbH & Co. KGaA), 715–731. https://doi.org/10.1002/9783527632930.ch31

Vinocur B, Altma A (2005) Recent advances in engineering plant tolerance to abiotic stress: achievements and limitations. Current Opinion in Biotechnology, 16 (2):123–132. https://doi.org/10.1016/j.copbio.2005.02.001

Wang FZ, Wang QB, Kwo, SY et al (2005) Enhanced drought tolerance of transgenic rice plants expressing a pea manganese superoxide dismutase. Journal of plant physiology, 162(4):465-472. https://doi.org/10.1016/j.jplph.2004.09.009

Wang G, Li X, Dong J et al (2021) Proteomics unravels new candidate genes of *Dasypyrumvillosum* for improving wheat quality. Journal of Proteomics, 245, 104292. https://doi.org/10.1016/j.jprot.2021.104292

Wang X, Ren Y, Li J et al (2019) Knock-down the expression of TaH2B-7D using virus-induced gene silencing reduces wheat drought tolerance. Biol. Res. 52: 14. https://doi.org/10.1186/s40659-019-0222-y

Wang X, Xu Y, Li J et al (2018) Identification of two novel wheat drought tolerance-related proteins by comparative proteomic analysis combined with virus-induced gene silencing. IJMS. 19: 4020. https://doi.org/10.3390/ijms19124020

Wei Q, Luo Q, Wang R et al (2017) A wheat R2R3-type MYB transcription factor TaODORANT1 positively regulates drought and salt stress responses in transgenic tobacco plants. Front. Plant Sci. 8: 1374. https://doi.org/10.3389/fpls.2017.01374

Winfield MO, Allen AM, Burridge AJ et al (2016) High density SNP genotyping array for hexaploid wheat and its secondary and tertiary gene pool. Plant Biotechnol. J. 14(5):1195–1206. https://doi.org/10.1111/pbi.12485

Woolfson M (2018) The development of structural x-ray crystallography. Phys. Scr. 93(3):1–32. https://doi.org/10.1088/1402-4896/aa9c30

Wu D, Shen Q, Cai S et al (2013) Ionomic responses and correlations between elements and metabolites under salt stress in wild and cultivated barley. Plant Cell Physiol. 54(12):1976–1988. https://dx.doi.org/10.1093/pcp/pct134

Xing L, Di Z, Yang W et al (2017) Overexpression of ERF1-V from *Haynaldiavillosa* can enhance the resistance of wheat to powdery mildew and increase the tolerance to salt and drought stresses. Front. Plant Sci. 8: 1948. https://doi.org/10.3389/fpls.2017.01948

Xu YF, Li SS, Li LH (2017) QTL mapping for yield and photosynthetic related traits under different water regimes in wheat. Molecular Breeding 37(3): 34. https://doi.org/10.1007/s11032-016-0583-7

Yadav AK, Carroll AJ, Estavillo GM et al (2019) Wheat drought tolerance in the field is predicted by amino acid responses to glasshouse-imposed drought. J. Exp. Bot. 70(18):4931–4948. https://doi.org/10.1093/jxb%2Ferz224

Yang Y, Saand MA, Huang L et al (2021) Applications of Multi-Omics Technologies for Crop Improvement. Front. Plant Sci. 12:563953. https://doi.org/10.3389/fpls.2021.563953

Yang WJ, Du YT, Zhou YB et al (2019) Overexpression of TaCOMT improves melatonin production and enhances drought tolerance in transgenic Arabidopsis. IJMS. 20(3): 652. https://doi.org/10.3390/ijms20030652

Yang W, Feng H, Zhang X et al (2020) Crop phenomics and high-throughput phenotyping: past decades, current challenges and future perspectives. Mol. Plant. 13: 187–214. https://doi.org/10.1016/j.molp.2020.01.008

Yu TT, Xu ZZ, Guo JJ et al (2017) Improved drought tolerance in wheat plants overexpressing a synthetic bacterial cold shock protein gene SeCspA. Sci. Rep. 7, 44050. https://doi.org/10.1038/srep44050

Yu Y, Bi C, Wang Q, Ni Z (2019) Overexpression of TaSIM provides increased drought stress tolerance in transgenic Arabidopsis. Biochem. Biophys. Res. Commun. 512(1):66–71. https://doi.org/10.1016/j.bbrc.2019.03.007

Zandipour M, Hervan EM, Azadi A et al (2020) A QTL hot spot region on chromosome 1B for nine important traits under terminal drought stress conditions in wheat. Cereal Research Comm. 48: 17–24. https://doi.org/10.1007/s42976-020-00017-0

Zang X, Geng X, He K et al (2018) Overexpression of the wheat (*Triticum aestivum* L.) TaPEPKR2 gene enhances heat and dehydration tolerance in both wheat and Arabidopsis. Front. Plant Sci. 9, 1710. https://doi.org/10.3389/fpls.2018.01710

Zang X, Geng X, Wang F et al (2017) Overexpression of wheat ferritin gene TaFER-5B enhances tolerance to heat stress and other abiotic stresses associated with the ROS scavenging. BMC Plant Biol. 17, 14. https://doi.org/10.1186/s12870-016-0958-2

Zargar SM, Mir RA, Ebinezer LB et al (2022) Physiological and Multi-Omics Approaches for Explaining Drought Stress Tolerance and Supporting Sustainable Production of Rice. Front. Plant Sci. 12:803603. https://doi.org/10.3389/fpls.2021.803603

Zhang JW, Liu DM, Zhu D et al (2021) Endoplasmic reticulum subproteome analysis reveals underlying defense mechanisms of wheat seedling leaves under salt stress. Int. J. Mol. Sci. 22(9):4840. https://doi.org/10.3390/ijms22094840

Zhang M, Hong LZ, Gu MF et al (2020) Transcriptome analyses revealed molecular responses of *Cynanchum auriculatum* leaves to saline stress. Sci. Rep. 10(1): 1–11. https://doi.org/10.1038/s41598-019-57219-8

Zhou Y, Chen M, Guo J et al (2020) Overexpression of soybean DREB1 enhances drought stress tolerance of transgenic wheat in the field. J. Exp. Bot. 71(6): 1842–1857. https://doi.org/10.1093/jxb/erz569

Zhu D, Luo F, Zou R et al (2021) Integrated physiological and chloroplast proteome analysis of wheat seedling leaves under salt and osmotic stresses. J. Proteomics 234, 104097. https://doi.org/10.1016/j.jprot.2020.104097

Zhu D, Zhu G, Zhang Z et al (2020) Effects of independent and combined water-deficit and high-nitrogen treatments on flag leaf proteomes during wheat grain development. Int. J. Mol. Sci. 21(6):2098. https://doi.org/10.3390/ijms21062098

Zotova L, Kurishbayev A, Jatayev S et al (2019) The general transcription repressor TaDr1 is co-expressed with TaVrn1 and TaFT1 in bread wheat under drought. Front. Genet. 10: 63. https://doi.org/10.3389/fgene.2019.00063

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