Among other environmental instabilities, drought stress is the primary limitation to cereal crops growth, development and productivity. In the context of continuing global climate change, breeding of drought resistant crop cultivars is the most economical, effective and sustainable strategy for adapting the crop production system and ensuring food security for the growing human population. Additionally, there is need for improving management practices. Whereas conventional breeding has sustained crop productivity gains in the past century, modern technological advancements have revolutionized our identification of important drought tolerance genes and underlying mechanisms, and accelerated new cultivar development. Large-scale high throughput sequencing, phenotyping, ‘omics’ and systems biology, as well as marker assisted and quantitative trait loci mapping based breeding approaches have offered significant insights into crop drought stress tolerance and provided some new tools for crop improvement. Despite this significant progress in elucidating the mechanisms underlying drought tolerance, considerable challenges remain and our understanding of the crop drought tolerance mechanisms is still abstract. In this chapter, therefore, we highlight current progress in the identification of drought tolerance genes and underlying mechanisms, as well as their practical applications. We then offer a holistic approach for cereal crops adaptation to future climate change exacerbated drought stress.

Keywords: drought stress, drought tolerance, cereal crops, omics approaches, phenotyping, genetic engineering, climate change, conservation agriculture

1. Introduction

Drought stress is the primary environmental factor influencing the growth, development and productivity of crops and its significance is expected to increase in the wake of global climate change [1–4]. This presents a serious challenge to the food and nutrition security of an ever-rising world human population. Moreover, the current transition from carbon/fossil intensive fuel driven economies to modern climate-smart low-carbon economies further strains our crop production systems [5]. Adapting field crops to drought stress therefore becomes critical for sustainable agricultural production under such climate change scenario [6]. To achieve that goal, breeding drought resilient crop cultivars that maintain yield stability under such conditions befits the most economical, effective and sustainable strategy. This is particularly relevant for cereal grain crops.

Cereal grain crops, chiefly rice (*Oryza sativa* L.), wheat (*Triticum aestivum* L.), maize (*Zea mays* L.), sorghum (*Sorghum bicolor* (L.) Moench), barley (*Hordeum vernum* L.), and buckwheat (*Fagopyrum esculentum* L.) are the principal crops grown worldwide, and over 80% of the world’s cereal production is concentrated in the developing world [7].
**Abiotic Stress in Plants**

*Abiotic Stress in Plants*

2. **Drought stress effects in cereal grain crops**

A decrease in water inputs into an agro/ecosystem over time that is sufficient to cause soil water deficit (SWD) is often termed drought, and this encompasses various forms such as rainfall anomalies, irrigation failure, seasonal or annual dry spells [16]. In agricultural context, drought signifies a period of below-average precipitation when the available soil water in the plant rhizosphere drops beyond the thresholds for efficient growth and biomass production [17]. The resultant oxidative stress emanating from such SWD is dubbed drought stress.

Numerous research reports have reflected on the effects of drought stress on cereal crops. Drought stress effects span from morphological to molecular levels, and are exhibited at all phenological growth stages at whatever stage the water deficit takes place. Generally, drought stress impairs seed germination resulting in poor crop stand establishment [1, 18]. Drought stress reduces the plant cellular water potential and turgor pressure, thereby increasing the cytosolic and extracellular matrices solute concentrations. Resultantly, cell growth is diminished due to the reduction in turgor pressure [19]. Additionally, abscisic acid (ABA) and compatible osmolytes such as proline are excessively accumulated, causing plant wilting. Simultaneously, reactive oxygen species (ROS) such as $\text{H}_2\text{O}_2$ are overly produced. Although they function as signal transduction molecules, over-accumulation of ROS could result in extensive cellular oxidative damage and inhibition of photosynthesis [20].

Moreover, when moisture deficit becomes severe, cell elongation becomes inhibited by the interruption of water flow from the xylem vessels to the surrounding elongating cells [21]. Consequently, vegetative growth, dry matter partitioning,
reproductive organ development and reproductive processes, grain filling and grain quality are disrupted [22]. In cereal grain crops, reproductive processes and grain filling are more susceptible to water deficit stress, with optimum and ceiling temperatures that are relatively lower than those for seedling and vegetative growth stages [21, 23–25]. Moisture deficit stress reduces yield by delaying silking, thus increasing the anthesis-to-silking interval [11]. Drought stress at flowering period is critical as it can increase pollen sterility resulting in hampered grain set [26].

Drought stress induced yield reduction in cereal crops depends upon the severity and duration of the stress period. The reduction in photosynthesis, emanating from the decrease in leaf expansion, impaired photosynthesis machinery, premature leaf senescence and related food production decreases, is the major contributing factor on yield reduction [21, 23]. Drought stress induced yield reductions have been reported and reviewed in maize [1, 21, 26–29], wheat [26, 27, 30, 31], rice [1], sorghum [32–33] and pearl millet [25].

3. Plants drought stress responses and resistance mechanisms

Plants have evolved numerous dynamic acclimation and adaptive ways of responding to and surviving short-term and long-term drought stresses [34]. The physiology of plants’ drought response at the whole plant level is complicated as it encompasses lethal and adaptive alterations. Moreover, how plants respond to drought stress differ significantly at various organizational levels, and this is generally dependent on plant species; the nature, duration and intensity of the drought stress; plant growth and phenological state at the time of stress exposure [19].

Drought stress triggers a wide range of plant structural changes which are essential for plants to respond to such drought stress conditions. These adjustments include morphological adaptations such as reduced growth rate, deepened rooting system, and root-to-shoot ratio modifications. The increased root-to-shoot ratio under drought stress conditions enables water and nutrient uptake and maintenance of osmotic pressure [19, 26, 35]. Additionally, in their response to moisture fluctuations in the soil rhizosphere, plants alter their physiology, modify their root growth and architecture, and regulate the closure of stomata on their aboveground structures. Such tissue-specific responses adjust the cell signals flux, consequently inducing stunted growth or premature flowering, and generally reduced yield [36]. Thus, drought stress is associated with alterations in leaf anatomy and ultrastructure. Reduced leaf size, decreased number of stomata; thickened leaf cell walls and induced premature senescence are some of those morphological changes [19].

Plants resist drought stress through a combination of strategies, which have been widely classified as drought escape, drought avoidance and drought tolerance [18, 21, 37, 38]. Drought escape is achieved by matching the duration of the crop cycle to water supply through genetic variation in phenology [39]. Plants prioritize early flowering and completing their life cycles before the effects of drought cause harm [21].

Drought avoidance denotes plant’s ability to maintain high tissue water potential under drought conditions. Usually, plants achieve drought avoidance through morphological and physiological alterations, including reduced stomatal conductance, decreased leaf area, promotion of extensive rooting systems and increased root to shoot ratios [38]. Drought avoidance mechanisms help in maintaining favorable cellular water balance, by enhancing water absorption, decreasing water loss, or allowing desiccation tolerance at low leaf water potential [34]. Stomatal closure, reduction of leaf growth and increased root length and density all contribute to increased water use efficiency under drought stress conditions. Further, water flux into the plant is reduced or water uptake enhanced to achieve drought avoidance [19].
On the other hand, plants attain a state of drought tolerance by cell and tissue specific physiological, biochemical, and molecular mechanisms. Drought tolerance is a complex trait which refers to the capacity of the plant to be more productive under drought stress [40]. In other words, it denotes the potential of crop plants to maintain their growth and development under drought stress [21]. The main aspects of plant drought tolerance mechanism include homeostasis maintenance, via ionic balance and osmotic adjustment; ROS scavenging and antioxidant enzyme activation; growth regulation and recovery by way of phytohormones; specific gene expression; and accumulation of specific stress responsive proteins [1, 2, 19, 21, 26].

To protect themselves against ROS induced oxidative stress and photo inhibition, plants activate an efficient antioxidant (enzymatic and non-enzymatic) defense system [17, 18, 21, 41]. Enzymatic antioxidant enzymes include superoxide dismutase (SOD), catalase (CAT), ascorbate peroxidase (APX), glutathione peroxidase (GPX) and glutathione S-transferase (GST) among others. SOD acts as the first line of defense by converting singlet oxygen into $\text{H}_2\text{O}_2$. APX and GSTs then detoxify $\text{H}_2\text{O}_2$ [42]. Non-enzymatic antioxidants including glutathione (GSH), ascorbic acid (AsA), carotenoids, tocopherols and flavonoids are also crucial for ROS homeostasis in plants [43].

At the molecular level, our current knowledge thus far regarding drought stress response pathway suggest that, sequentially, the stress is relayed through the following chain: signal perception, signal transduction, transcriptional control by way of transcription factors (TFs), stress responsive genes activation, and in-turn activation of physiological and metabolic responses [1, 19, 37, 44].

Stress signal perception in plants has revealed the role of plasma membrane in perceiving and transmitting signals to the cell interior, where molecules such as receptor-like kinases and G-proteins function as primary receptor molecules [45]. The roles of Ca$^+$ and ROS as secondary messengers in stress perception and signaling have also been well acknowledged [4]. These secondary messengers adjust the calcium levels and activate protein phosphorylation. Then, phosphorylation of inactive proteins may be directly involved in cellular protection by protein folding or activation of stress specific genes. The dominant plant signal transduction pathways involve the mitogen activated protein kinase (MAPK) and calcium dependent protein kinases (CDPK) cascades, and their role in abiotic stress response have been well reviewed [38, 42, 46].

Upon drought exposure, the resulting signal transduction triggers the production of several biochemicals, including phytohormones, to respond and adapt to the ensuing drought stress [47]. Phytohormones are molecules produced in low concentrations but are critical in regulating plant growth, development, response to biotic and abiotic stresses, and other physiological processes [48]. These phytohormones include ABA, salicylic acid (SA), ethylene (ET), cytokinins (CKs), gibberellin acid (GA), jasmonic acid (JA) and brassinosteroids (BRs) among others. Among these, ABA is the key and most extensively studied hormone that regulates drought resistance in plants [38, 49]. ABA acts as the second messenger coordinating hormonal cross-talk between several stresses signaling cascades, thereby leading to adaptations to changing physiological and environmental conditions [50]. Additionally, SA, ET, JA, CKs, GA, and BRs play vital roles in regulating various phenomena in plants acclimatization to drought stress [51].

At the molecular level, plants institute stress responsive proteins, TFs and signaling pathways among other strategies. Several studies [52, 53] have identified conserved and species-specific drought responsive genes, including membrane stabilizing proteins and late embryogenic abundant (LEA) proteins, which increase cells’ water binding capacity [1, 14]. Several heat shock proteins (HSPs), which play a major role in stabilizing protein structure, were also identified [54, 55]. The HSPs are chiefly
involved in unwinding some folded proteins and averting protein denaturation under abiotic stress conditions. The membrane stabilizing proteins, LEA proteins, detoxification enzymes, water channel proteins and ion transporter genes all constitute a group of functional proteins, that is, a group of important enzymes and metabolic proteins which directly function to protect cells from stress [37, 56]. Besides functional genes, regulatory genes are also critical for drought tolerance. These encode various regulatory proteins such as transcriptional factors (TFs), protein kinases and protein phosphatases – involved in regulating signal transduction and gene expression in response to stress [57, 58]. Several TFs that regulate a large spectrum of downstream stress-responsive genes and provide adaptive response under drought stress have been identified and reviewed, including myeloblastosis (MYB), abscisic acid responsive elements binding factor (ABF), ABRE binding (AREB), dehydration responsive element binding (DREB), C-repeat binding factor (CBF), [NAM, ATAF1/2, and CUC2 containing proteins] (NAC) and WRKYs [59–63].

Additionally, protein kinases and protein phosphatases mediate phosphorylation and dephosphorylation of proteins, respectively. In several signal transduction pathways; they are vital and an effective mechanism for stress signal relaying [19, 56, 63]. At the phosphorylation cascade terminals, protein kinases or phosphatases activate or suppress TFs, respectively. The TFs further specifically bind to cis-elements in the promoters of stress responsive genes, thereby modulating their transcription [64]. The TFs are further subjected to post translational modifications (PTMs), including ubiquitination and sumoylation, thereby forming an intricate regulatory network to modulate stress responsive genes, which consequently trigger the activation of appropriate physiological and metabolic responses [62, 65].

4. Approaches for deciphering drought stress responsive genes, proteins and metabolic pathways: where are we?

The recent convergence of crop physiology, next generation sequencing and molecular biology approaches has offered us convenience in deciphering mechanisms underlying plants’ response to various abiotic stresses [13, 15, 66]. Whereas plant physiology enhances our understanding of the complex network of traits related to drought tolerance and improving selection efficiency, genomics and molecular biology methods identify the candidate genes and quantitative trait loci (QTLs) underlying these traits [11, 13]. The classical cDNA and oligonucleotide microarrays have been widely employed to identify candidate genes for drought tolerance in several cereal grain crops including maize [67, 68], rice [69, 70] and barley [71]. Additionally, the use of tilling microarrays has allowed for the identification of differentially expressed DNA sequences at the whole genome level [72]. Other techniques such as differential display; cDNA amplified fragment length polymorphism (cDNA-AFLP); and serial analysis of gene expression (SAGE) have been essential in analyzing global gene expression profiles in functional genomics studies [56, 73–74].

Analysis of large scale, high throughput sequencing data is now facilitating the identification and cloning of important genes at target QTLs. Additionally, the ‘omics’ analysis approaches are showing monumental capacity to quicken and broaden our understanding of the molecular, genetic and functional basis of crop drought stress tolerance [12, 75]. Encouragingly, some novel insights meant to help us develop new drought tolerant cultivars are being generated [76]. Due to its low cost, high-throughput, and high sensitivity, RNA sequencing (RNA-seq) has offered us breakthrough in performing transcriptome analysis of plants’ drought stress responses [77]. Resultantly, we have obtained transcripts from RNA in a tissue- or cell-specific manner, and transcribed at a different developmental stage.
or functional state; this has been fundamental to fishing out functional genes [78]. Therefore, our knowledge pertaining to gene expression networks modulating drought stress tolerance has been significantly improved. RNA-seq technology has been used in several drought stress response studies in cereal crops and numerous genes have been identified [79–81].

Recently, large scale, high-throughput proteomics has become a very powerful tool for performing comprehensive analysis of crop proteins and identification of stress responsive proteins in comparative abiotic stress studies [82, 83]. Proteomic approaches, particularly gel free methods, that is, those involving digestion of intact proteins into peptides prior to separation, have now become very popular in proteome profiling, comparative expression analysis of two or more protein samples, localization and identification of post translational modifications (PTMs) [14]. For instance, isobaric tags for relative and absolute quantitation (iTRAQ) and isotope-coded affinity tags (ICAT) based methods have become widely used in descriptive and comparative drought stress proteomic studies in cereals [84–87]. The iTRAQ-based method allows for the time-dependent analysis of plant stress responses or biological replicates in a single experiment [88]. Besides, proteomics offers complementarity to genomics; providing clues on the molecular mechanisms underlying plant growth and stress responses, as well as being a crucial link between transcriptomics and metabolomics [82]. Moreover, genomics based methods offer access to agronomically desirable alleles localized at QTLs that affect particular physiological responses. This helps us to effectively improve the drought resilience and yield of crops. Additionally, MAS has aided us in improving drought-related traits [12, 89].

Further, a systems biology approach, premised on the advancement and integration of omics (genomics, transcriptomics, metabolomics, phonomics and proteomics) methods to establish a meaningful relationship between the genotype, phenotype and subsequent abiotic stress tolerance, has also become prominent [76]. Integrated knowledge of the morphological, physiological, biochemical, genetic and molecular events in plants allows for in depth understanding of the complex physiological and cellular processes involved in drought stress adaptation. Thus, meaningful interpretations from complex networks and component integrations can be developed from voluminous omics data, which helps us better decipher the mechanisms underlying cereal crops drought tolerance [63].

Meanwhile, the physiological analysis on contrasting genotypes provides information on the mechanisms underlying drought tolerance and aids as a useful screening strategy for drought tolerance [41]. Therefore, it is important to realize that physiological analysis remains essential in corroborating the molecular analyses in abiotic stress response studies. Thus, it would be essential that, going forward, we build on the progress made to date by harnessing the full potential of genomics-assisted breeding, and integrating our knowledge on the physiological and molecular basis of drought tolerance. This calls for crop physiologists, molecular geneticists, breeders and cytogeneticists to collaborate in a multidisciplinary manner [12].

5. Some identified key drought tolerance mechanisms, genes and metabolic pathways

By applying genetic, biochemical and molecular approaches, we have identified essential genes central in plant responses to drought stress. For instance, several physiological responses contributing to drought tolerance in cereal crops have been identified including thermal dissipation of light energy, stomatal closure, decreased hydraulic conductance, altered source-sink relations and carbon partitioning, ABA biosynthesis, among others (Table 1).
Besides the mechanisms highlighted in Table 1, several drought responsive genes have been identified and validated in different crop species. For instance, recent excellent reviews [4, 26, 102–106] provide highly informative details about some crop drought tolerance conferring genes that have been functionally validated to date. Some of these genes are listed in Table 2.

Further, several metabolic pathways implicated in drought stress tolerance in cereal grain crops have been identified through comparative physiological and omic analysis approaches. Chief among these pathways are those related to photosynthesis, secondary metabolites biosynthesis, plant hormone signaling, starch and sucrose metabolism, and nitrogen metabolism. Chloroplasts, particularly the thylakoid membranes—PSII reaction centers, are one of the organelles most influenced by drought stress [123, 124]. Photosynthesis (antenna protein) pathway related genes *lhcb5-1* and *lhcb5-2* are part of the light harvesting complexes (LHCs) and the electron transport components of the PSII of the plant photosynthesis machinery, where they participate...
Abiotic Stress in Plants

Table 2.
Examples of drought tolerance conferring genes that have been functionally validated in cereal crops.

| No. | Gene name | Donor | Host | Physiological change | References |
|-----|-----------|-------|------|----------------------|------------|
| 1   | ZmVPP1    | Arabidopsis thaliana L. (Arabidopsis) | Maize | Enhanced photosynthetic efficiency and root development | [81, 107] |
| 2   | ZmPP2C-A10 | Arabidopsis | Maize | ABA signaling | [108] |
| 3   | Zeaxanthin epoxidase (ZEP) | Arabidopsis | Maize | Improved ABA biosynthesis | [104, 109] |
| 4   | Mannitol-1-phosphate dehydrogenase (mtlD) | Escherichia coli | Wheat | Improved fresh and dry weights, plant height, and flag leaf length | [110] |
| 5   | AtNF-YB1  | Arabidopsis | Maize | Higher photosynthesis capacity | [102, 111] |
| 6   | AtABF3    | Arabidopsis | Rice | Higher Fv/fm | [112] |
| 7   | OsDREB1A  | Arabidopsis | Rice, wheat | Shoot growth retardation at the expense of root growth | [102] |
| 8   | AtHARDY   | Arabidopsis | Rice | Enhanced WUE and photosynthesis efficiency | [113] |
| 9   | OsWRKY11  | Rice | Rice | Sluggish water loss and lessened leaf wilting | [114] |
| 10  | AtLOS5 (LOSS/ABA3) | Arabidopsis | Maize | Increased ABA biosynthesis | [115] |
| 11  | HVA1      | Barley | Rice | Enhanced WUE | [116] |
| 12  | HVA1      | Barley | Wheat | Enhanced biomass accumulation and WUE | [26, 117] |
| 13  | Beta      | Escherichia coli | Wheat | Accumulation of glycine betaine | [118] |
| 14  | Nicotiana protein kinase (NPK1) | Tobacco | Maize | Preventing dehydration damage to the photosynthesis machinery | [119] |
| 15  | AtSNAC1   | Arabidopsis | Rice | ABA-hypersensitive, stomatal shutdown | [120, 121] |
| 16  | ShER2–1   | Sorghum | Maize | Increased Pn rate and higher WUE | [122] |
| 17  | Light harvest complex related genes (LHCA1, LHCB, LHCA3, LHCA2) | Maize | Maize | Balancing light capture in the PSII | [91, 93] |

as peripheral antenna systems enabling more efficient absorption of light energy [125, 126]. Further, Lhch5-1 is involved in the intracellular non-photochemical quenching and the cysteine biosynthesis processes [91]. Previously, the photosynthesis pathway
has been significantly enriched in drought stress response in maize, with chlorophyll a-b binding proteins being up-regulated in an ABA-dependent manner [87, 91], and pearl millet [127]. This photosynthesis related pathway plays a critical role in balancing light capture and utilization to avoid photo-inhibition of the PSI [87].

Phenylpropanoid metabolism is the first step of the secondary metabolites (flavonoids, phenylpropanoids, phenolic compounds and lignin) biosynthesis and phenylpropanoids act as antioxidants to protect plants against oxidative damage [128, 129]. Flavonoids play different molecular functions in plants, including stress protection. All these compounds are widely synthetized in response to several abiotic stresses, including drought [130]. In wheat leaves, an increase in flavonoid and phenolic acids content was shown together with stimulation of genes involved in flavonoid biosynthesis pathway in response to drought stress [131]. Moreover, secondary metabolites biosynthesis related pathways were found to be significantly enriched in response to drought stress in maize [80] and sorghum [37], suggesting their involvement in plant protection. A coordinated reaction of the genes and pathways involved in secondary metabolite biosynthesis is therefore vital for improved drought stress tolerance in plants [80]. Plant hormone signaling pathway participates in drought stress response via either ubiquitin-mediated proteolysis or ABA-mediated response [132], and was observed to be significantly enriched in pearl millet response to drought stress [127].

Sucrose is widely acknowledged to play a crucial role as a key molecule in energy transduction and as a regulator of cellular metabolism [130]. Additionally, sucrose and other sugars are energy and carbon sources required for defense response and are necessary for plant survival under drought stress conditions [133]. Further, sucrose can act as primary messenger controlling the expression of several sugar metabolism related genes [134]. Nitrogen metabolism pathway, being the most basic and central physiological metabolic process during plants’ growth period, directly influences the formation of cellular components and regulation of cellular activities, as well as the transformation of photosynthetic products, mineral nutrient absorption and protein synthesis. It therefore follows that the nitrogen pathway is directly affected by drought, hence its significant enrichment under such conditions [80, 127]. These key identified drought responsive pathways should be used as targets for future genetic engineering of drought stress tolerant genotypes.

6. QTL mapping for drought tolerance in cereals

Most yield-related traits in cereal crops are quantitative. Therefore, cloning of the causal genes and deciphering the underlying mechanisms influencing these traits remains critical for continuous genetic improvement [135]. Precisely, drought tolerance is a complex quantitative trait that is multi-genic in its expression and one of the most challenging traits to study and characterize [11]. In comparison to conventional approaches, genomics offers unparalleled opportunities for dissecting quantitative traits into their single genetic determinants, known as QTL, thereby facilitating MAS, gene cloning and their direct manipulation via genetic engineering [12]. Through advances in next generation sequencing, identification of major QTLs regulating specific drought responses has been made possible, via the development of large numbers of genetic markers such as single nucleotide polymorphisms (SNPs) and insertion-deletions (InDels), thereby opening the doors for an efficient way to improving drought tolerance in cereal crops [89]. Additionally, large-scale genome-wide association studies (GWAS) have been conducted to detect genomic regions and candidate genes for various agronomic traits, including drought tolerance in cereals [13, 136, 137]. Resultantly, hundreds of studies reporting thousands of major drought-responsive genes and QTLs in cereal grain crops
Abiotic Stress in Plants

can be found in the literature, including those for maize [13, 138–140], rice [12, 13, 105, 138, 141, 142], wheat [13, 31, 137, 138, 143], sorghum [138, 144, 145], barley [138, 146], and pearl millet [136, 147, 148]. The high number of studies on QTL mapping suggests that for the past decade, QTL has been the focal target of research to identify the genetic loci regulating the adaptive response of crops to drought stress. Although several QTLs for drought tolerance have already been mapped in these cereal crops, there has been little success in introgression of those QTLs and the number of causal genes that have been confirmed within these QTL regions remains relatively small as compared to Arabidopsis and rice [11, 106].

Going forward, MAS remains a useful tool for major QTL, whereas QTL cloning is increasingly becoming a more routine activity. This has been necessitated by increased use of high-throughput sequencing, precise phenotyping and identification of appropriate candidate genes through omics approaches [89, 136, 137]. Cloned QTL facilitate a more targeted search for novel alleles and will offer novel insights for genetic engineering of drought resilient cereal crops [13]. Moreover, compared to other crops, research in millets is still lagging behind. However, with millets considered predominantly climate resilient crops, millets could serve as valuable source of novel genes, alleles and QTLs for drought tolerance. Therefore, the identification and functional characterization of these genes, alleles and QTLs in millets is critical for their introgression and drought tolerance improvement in cereal grain crops [89].

7. Phenotyping for drought tolerance in cereal grain crops

Phenotyping has become an integral component of the crop improvement programme by contributing towards understanding of the genetics behind crop drought tolerance [105, 149]. Since many component traits of drought tolerance are controlled quantitatively, improving the accuracy of phenotyping has become more important to improve the heritability of the traits, and the target traits would require rapid and precise measurement [106]. High throughput phenotyping now provides an essential link in translating laboratory research to the field. This is vital in developing novel genotypes that incorporate gene(s) expressing promising trait(s) into breeding lines adapted to target field environments [150].

Auspiciously, the recent advances in phenotyping technology and robotics for measuring large number of plants means that large numbers of genotypes could be readily phenotyped [34, 151–153]. More promising approaches that target complex traits tailored to specific requirements at the different main crop growth stages are now available [150]. Precise phenotyping of drought-related physiological traits often requires the utilization of sophisticated and expensive techniques. These include magnetic resonance imaging (MRI) and positron emission tomography (PET), near-infrared (NIR) spectroscopy on agricultural harvesters, canopy spectral reflectance (SR) and infrared thermography (IRT), nuclear magnetic resonance, hyperspectral imaging, laser imaging, 3D imaging and geographical information systems (GIS), among others [34, 138, 154, 155]. For example, 3D visual modeling can be used to determine the plasticity of the canopy architecture, and to evaluate the architectural and physiological characteristics that contribute to the higher productivity of the super rice varieties under drought stress conditions [156]. Though currently expensive, up scaling the use of these phenotyping platforms will eventually enhance our understanding of crop growth kinetics and aid us improve crop models for systems biology and drought tolerance breeding programs.

Selection of primary (grain yield and yield contributing traits) and secondary agronomically important traits (ASI, root architecture, stay green, etc.) is the way to achieve drought tolerance in cereal grain crops [31, 35, 106, 152]. Yield and yield
attributing factors are targeted for direct selection whilst secondary traits are vital in conferring drought tolerance and contributing to final yield indirectly [157]. Crucially, considering that under drought stress conditions, the genetic correlation between grain yield and some secondary traits increases meaningfully, and the heritability of some secondary traits remains high, identification and selection of those highly heritable secondary traits that are positively correlated with yield related traits in the target environment, and responsive to high throughput phenotyping, will be critical in achieving the desired drought tolerance goals [11, 152, 158]. Managed stress screening approaches through the utilization of phenomics offers an opportunity to keep heritability high and phenotyping under controlled environments can be helpful in large-scale characterization studies such as trait mapping experiments [13]. However, great caution needs to be taken when phenotyping for drought stress tolerance since controlled environments may fail to mimic the real field conditions, thereby becoming less useful to study the genotype × environment interactions which are very essential to dissect the drought tolerance mechanisms [106].

8. Genetic engineering of drought tolerant cereal crops

The development of tolerant crops by genetic engineering requires the identification of key genetic determinants underlying stress tolerance in plants, and introducing these genes into crops [159, 160]. The momentous progress garnered in abiotic stress response research in the model plant Arabidopsis has created an avenue for the identification of drought tolerance conferring genes and the development of transgenics carrying these genes in other crop species. Therefore, genetic engineering approach has opened the door to the development of new crop genotypes with improved drought tolerance [103]. Over the past decade, numerous articles and reviews on drought stress tolerant transgenic crop species have been gathered [4, 26, 102–106, 160]. A selected list of transgenic cereal grain crops, which includes information on transgenes used for the transformations and the resultant drought stress tolerance mechanisms, has already been provided above in Table 2. Despite the availability of numerous reports in the scientific literature of transgenic approaches to improving drought tolerance, restrictions on the establishment of transgenic plants in the field presents a bottleneck in true testing of the effectiveness of transgenic approaches to improve crop drought tolerance [161].

In recent years, transgenesis has taken center stage in our crop improvement efforts. Advances in genome engineering has made it possible to precisely alter DNA sequences in living cells, providing unprecedented control over a plant’s genetic material [162]. The genome engineering approaches, also known as gene editing or genome editing techniques, involve the use of programmable site-directed nucleases (SDNs) engineered to modify target genes at desirable locations on the genome [163]. These SDNs cleave the double-stranded DNA at a particular location by means of clustered regularly interspaced short palindromic repeats and CRISPR-associated protein 9 (CRISPR/Cas9), zinc finger nucleases (ZFNs), or transcriptional activator-like effector nucleases (TALENs). The double-stranded DNA break then undergoes natural reparation either via homologous recombination or non-homologous end joining [105, 164]. The restoration of the DNA break can be directed to create a variety of targeted DNA sequence modifications such as DNA deletions or insertions of large arrays of transgenes [162].

Among the several genome editing methods developed to date, CRISPR-Cas9 is the most advanced and has received much attention because of its great accuracy, quickness, adaptability and simplicity [165, 166]. This technique has been successfully used in major food crops [167–169]. Whereas convectional genomics and breeding
approaches alone cannot resolve the global food security challenge [170], genetic engineering approaches have great potential to improve crops that feed the burgeoning populations of developing countries [162, 166, 171]. However, the extent of regulation imposed upon crop cultivars generated through genetic engineering will have a huge impact on the cost of their development itself and how rapidly they will be deployed into the food supply chain. Linked to that, the readiness with which the public will accept food products made from genetically engineered crops will also play a role in the extent to which this new technology will be fully utilized for crop improvement, particularly in the developing countries where cereal grain crops are staple diets [162].

9. Field management of crops in the context of climate change

Genetic and management strategies that are aimed at improving grain yields under water constrained environments target three variables, which are the amount of water captured by the plant (W), the efficiency with which that water is converted to biomass (water use efficiency, WUE), and the harvest index (HI) or the proportion of biomass forming grain. Interestingly, each of these variables can be altered [172]. For instance, WUE can be maximized by early planting of crops, and by maintaining healthy leaves with high levels of nutrients [173]. Additionally, extending leaves’ longevity through selection for delayed leaf senescence is commonly regarded important for maintaining WUE and root health, as well as increasing the kernel filling duration [172]. Supplementation of irrigation, where available, would be the major means for combating drought stress condition, besides being a prime approach to the intensification of agriculture and the generation of stable income for farmers [174]. However, its uptake will depend on various environmental, economic and social factors on both micro and macro levels [175].

Additionally, agronomic interventions, that is, improved crop management methods can complement the use of drought tolerant cultivars, contributing meaningfully to enhanced and stabilized yields under water constrained environments. Conservation agriculture (CA), a collection of practices embodying the use of reduced tillage and mulch to reduce evaporation of soil water, is an obvious means of increasing water available to the plants [172, 176]. Scaling up CA, which has recently gained wider acceptance in developing countries, offers a great potential of increasing drought resilience and sustainability of cropping systems and ensuring food security. The use of plastic mulch in semi-arid cooler areas on the Loess Plateau of China has significantly increased WUE in maize [177]. Moreover, CA has become the cornerstone of dryland systems in some regions of USA, Canada and Australia [174]. Recently, the application of melatonin with date (Phoenix dactylifera L.) residue and wheat straw biochars has enhanced biochar efficiency for drought tolerance in maize cultivars [178]. This can be a game changer in CA farming systems where biochar is a key component for ground cover. Therefore, the management of a sustainable dryland farming system would require that farmers apply good agronomic practices (GAPs) such as improved soil and water conservation and the associated reduced tillage practices, holistic weed and pathogen control, soil fertility management with respect to water regimes, optimized plant population densities and effective control of soil biotic stress factors that may inhibit root development, as well as practicing crop diversification in order to reduce the risks associated with farming in unpredictable environments. Further, governments should increase investments in weather forecasting and cloud seeding.

All these approaches and decision support systems, when integrated, would birth a more holistic strategy for adapting cereal grain crops to future climate change induced drought stress as summarized in Figure 1.
10. Future outlook

Currently, crop improvement efforts are shifting focus from solely yield, quality, or abiotic stress resistance to a holistic approach integrating breeding for a combination of these factors. For example, targeting breeding for combined drought and heat stress tolerance \[179, 180\], drought tolerance and nutritional quality \[161\] or drought tolerance and disease resistance \[3, 181\] are being underlined. Drought-tolerant micro-nutrient dense cereal crop cultivars have been developed \[8\]. In that regard, future-proofing of global food security would call for double-pronged transformation aimed at developing high yielding cultivars possessing both adaptability to abiotic or biotic stresses and higher nutritional quality. Thus, going forward, it is necessary that more breeding programs use high-priority abiotic stresses in their portfolios \[11\]. In the wake of addressing malnutrition challenges in developing countries, breeding for bio-fortified drought tolerant cultivars should be strengthened \[8, 182\]. In addition, promising genotypes in trials for fall armyworm \((Spodoptera frugiperda\ L.)\) resistance, once approved, should be screened for drought tolerance and improved cultivars harboring both traits be developed. Though seemingly a daunting task, combined efforts from crop physiologists, molecular geneticists, breeders and pathologists would make this a reality.

In our ‘omics research’, future proteomics studies should intensify the identification, quantification and analysis of stress-responsive proteins PTMs, since PTMs can affect protein functions, interactions, subcellular targeting and stability \[183\]. Moreover, breeding for resource use efficiency, for instance, nitrogen use efficiency (NUE) should be integrated in future drought tolerance breeding programs. Previously, researchers have revealed that improving NUE in crops such as paddy rice and cotton will be critical in greenhouse gas emission management \[184–188\]. Additionally, application of biochar, either singly \[189\] or in combination with \[190\] has been shown to alleviate heat-induced oxidative stress damage on the cellular physiological processes in rice plants. Thus, as we navigate the future, breeding for NUE and its proper management in the field remains essential in helping adapting crop plants to abiotic stresses such as drought.
Another area of focus will be crop physiology. Since photosynthesis is the basis of plant growth, improving photosynthesis can significantly contribute towards greater food security in the future. Multiple targets for manipulation of crop photosynthesis have been extensively reviewed. These include improving Rubisco kinetic properties and improving canopy architecture to enhance light penetration [191]. Therefore, harnessing the benefits of improved photosynthesis for greater yield potential will require that we intensify manipulation of these targets.

Furthermore, the microbes resident in the rhizosphere can potentially improve plant growth and enhance crop resilience to abiotic stresses [192]. For instance, phosphate-solubilizing bacteria can nullify the antagonistic effect of soil calcification on bioavailable phosphorus in alkaline soils, and thus, can be one of the best options for improving soil P nutrition [193]. It would be crucial to investigate, understand and quantify the complex feedback mechanisms occurring between root and microbial responses to drought stress, particularly in cereal crops. Integrating crop ecology, physiology and molecular methodologies in a multi-disciplinary approach would be central [194].

In the short to medium term, exogenous application of plant growth regulators at different crop growth phases would be an important strategy in inducing drought resistance. In a very short term, seed priming will be of value [3]. The crucial roles of plant phytohormones and growth-promoting rhizobacteria in abiotic stress responses have been extensively reviewed [195–197]. Particularly, the exogenously applied plant growth regulators can enhance morpho-physiological, growth and abiotic stress responses of crops such as rice [198–203]. Recently, Saleem et al. [204] have shown that exogenously applied gibberellic acid (GA3) can reduce metal toxicity induced oxidative stress in jute (C. capsularis L.) seedlings. Moreover, exogenous application of salicic acid (SA) has been shown to ameliorate the adverse effects of salinity on maize plants [205]. Further, silicon (Si) application improved plant water relations, photosynthesis and drought tolerance in Kentucky bluegrass [206, 207], and Si enhanced germination, growth, P and arsenic uptake in rice [208]. Therefore, targeting the modification of hormone biosynthetic pathways may be a gateway to the development of drought tolerant transgenic plants.

Meanwhile, the potential of transgenic technologies across developing countries, particularly in Sub-Saharan Africa, is being hampered by uncoordinated over-regulation by authorities. Unfortunately, the biosafety framework leading to ordered testing and deregulation in such countries is being developed on individual countries basis, instead of a more efficient resource-use regional approach. More so, present systems are modeled on overestimated, not science-evidence-based risks [172]. There is need for policy makers to revisit their stance on genetically modified organisms (GMOs) with science guaranteed evidence, not political grand-standing, guiding formulation, adoption and utilization of GMO related polices for food and nutritional security.

11. Conclusion

Though a daunting task, breeding for drought tolerance in cereal crops remains the most economical, effective and sustainable strategy for ensuring food security for the ever increasing human population. While a significant progress has been made to date towards achieving that goal, our understanding of the mechanisms underpinning plant drought stress tolerance remains fragmentary. In the face of global climate change, a multi-disciplinary research strategy becomes obligatory to integrate physiological, genotypic, omics and epigenetics data essential to dissect the complex networks regulating plant drought tolerance, which can then be manipulated through genetic engineering to develop drought resilient
crops. Additionally, cereal crop breeding programs should integrate high-priority abiotic stresses, particularly drought and heat, with other goals such as resource use efficiency, biotic resistance, and nutritional improvement. Further, formulation and effective deployment of efficient screening and precise phenotyping approaches at both laboratory and field levels to identify drought tolerant genotypes or mutants remains critical. Promisingly, our new cultivar development thrusts are now endowed with some innovative methodologies that include high-throughput phenotyping, doubled haploidy, mutation and speed breeding, as well as CRISP-Cas 9 technologies. Going forward, we should harness the potential of these technologies. Eventually, our understanding of the crop drought tolerance mechanisms will be quickened and broadened, greatly assisting our development of new drought-resilient cereal crop cultivars. This should be supported by robust, science-evidence-based and progressive policy frameworks that recognize the centrality of GMOs and modern biotechnology in increasing food production. Consequently, this would lead to improved sustainable crop productivity and global food security.

Acknowledgements

We acknowledge the funding received from the National Key Research and Development Project of China (Selection and Efficient Combination Model of Wheat and Maize Water Saving, High Yield and High Quality Varieties; Grant No. 2017YFD0300901).

Conflict of interest

Authors declare that they have no conflict of interests.

Author details

Tinashe Zenda¹²³, Songtao Liu¹²³ and Huijun Duan¹²³*

1 State Key Laboratory of North China Crop Improvement and Regulation, Hebei Agricultural University, Baoding, China

2 North China Key Laboratory for Crop Germplasm Resources of the Education Ministry, Hebei Agricultural University, Baoding, China

3 Department of Crop Genetics and Breeding, College of Agronomy, Hebei Agricultural University, Baoding, China

*Address all correspondence to: hjduan@hebau.edu.cn

IntechOpen

© 2020 The Author(s). Licensee IntechOpen. This chapter is distributed under the terms of the Creative Commons Attribution License (http://creativecommons.org/licenses/by/3.0), which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.
References

[1] Farooq M, Wahid A., Kobayashi N, Fujita D, Basra SMA. Plant drought stress: Effects, mechanisms and management. Agron. Sustain. Dev. 2009;29(1):185-212. DOI: 10.1051/agro:2008021

[2] Feller U, Vaseva II. Extreme climatic events: Impacts of drought and high temperature on physiological processes in agronomically important plants. Front Environ Sci. 2014;2:39. DOI: 10.3389/fenvs.2014.00039.

[3] Fahad S, Bajwa AA, Nazir U, Anjum SA, Farooq A, Zohaib A, Sadia S, et al. Crop production under drought and heat stress: Plant responses and management options. Front. Plant Sci. 2017;8:1147. DOI: 10.3389/fpls.2017.01147

[4] Kumar S, Sachdeva S, Bhat KV, Vats S. Plant responses to drought stress: Physiological, biochemical and molecular basis. In: S Vats (ed.) Biotic and Abiotic Stress Tolerance in Plants. Springer Nature, Singapore Pte Ltd. 2018; pp. 1-25. DOI: 10.1007/978-981-10-9029-5_1

[5] Schils R, Olesen JE, Kersebaum K, Rijk B, Oberforster M, et al. Cereal yield gaps across Europe. Eur J Agron. 2018;101:109-120. DOI: 10.1016/j.eja.2018.09.003

[6] Prasad P VV, Staggenborg SA. Impacts of drought and/or heat stress on physiological, developmental, growth, and yield processes of crop plants. 2008. ASA, CSSA, SSSA, 677 S. Segoe Rd., Madison, WI 53711, USA

[7] Cordain L. Cereal grains: Humanity’s double-edged sword. In: Simopoulos AP (ed.) Evolutionary aspects of nutrition and health diet, exercise, genetics and chronic disease. World review of nutrition and dietetics. 1999;19-73. Basel, Switzerland: Karger.

[8] Curiel R, Domínguez L, Donovan M, Doody A, Johnson J, Listman GM, MacNeil M, et al. The cereals imperative of future food systems. Seeds of Change Annual Report 2019. CIMMYT (International Maize and Wheat Improvement Center), Mexico. 2020;pp.18-19.

[9] Shiferaw B, Prasanna BM, Hellin J, Bänziger M. Crops that feed the world 6. Past successes and future challenges to the role played by maize in global food security. Food Sec. 2011;3:307-327. DOI: 10.1007/s12571-011-0140-5.

[10] Ray DK, Mueller ND, West PC, Foley JA. Yield trends are insufficient to double global crop production by 2050. PLoS One. 2013;8: e66428.

[11] Maazou ARS, Tu JL, Qiu J, Liu ZZ. Breeding for drought tolerance in maize (Zea mays L.). American Journal of Plant Sciences. 2016;7:1858-1870.

[12] Tuberosa R, Salvi S. Genomics-based approaches to improve drought tolerance of crops. Trends in Plant Science. 2006;11(8):405-412. DOI: https: 10.1016/j.tplants.2006.06.003.

[13] Choudhary M, Wani SH, Kumar P, Bagaria PK, Rakshit S, Roorkiwal M, Varshney RK. QTlian breeding for climate resilience in cereals: progress and prospects. Funct Integr Genomics. 2019;19:685-701. DOI: 10.1007/s10142-019-00684-1

[14] Ghatak A, Chaturvedi P, Weckwerth W. Cereal crop proteomics: Systemic analysis of crop drought stress responses towards marker-assisted selection breeding. Front. Plant Sci. 2017;8:757. DOI: 10.3389/fpls.2017.00757.

[15] Bokszczanin KL, SPOT-ITN Consortium, Fragkostefanakis S. Perspectives on deciphering
Adapting Cereal Grain Crops to Drought Stress: 2020 and Beyond
DOI: http://dx.doi.org/10.5772/intechopen.93845

mechanisms underlying plant heat stress response and thermotolerance. Front. Plant Sci. 2013;4:315. DOI: 10.3389/fpls.2013.00315

[16] Gilbert ME, Medina V. Drought adaptation mechanisms should guide experimental designs. Trends in Plant Sci. 2016;21:8. DOI:10.1016/j.tplants.2016.03.003

[17] Osmolovskaya N, Shumilina J, Kim A, Didio A, Grishina T, Bilova T, et al. Methodology of Drought Stress Research: Experimental Setup and Physiological Characterization. Int. J. Mol. Sci. 2018;19:4089. DOI: 10.3390/ijms19124089.

[18] Anjum SA, Xie XY, Wang LC, Saleem MF, Man C, Lei W. Morphological, physiological and biochemical responses of plants to drought stress. Afr. J. Agric. Res. 2011;6:2026-2032.

[19] Lisar SYS, Motafakkerazad R, Hossain MM, Rahman IMM. Water stress in plants: causes, effects and responses. Introductory Chapter. In: Rahman IMM, Hasegawa H, editors. Water Stress. IntechOpen. 2012;pp. 1-14. DOI: 10.5772/39363

[20] Choudhury FK, Rivero RM, Blumwald E, Mittler R. Reactive oxygen species, abiotic stress and stress combination. The Plant Journal. 2017;90:856-867. DOI: 10.1111/tpj.13299

[21] Aslam M, Maqbool MA, Cengiz R. Drought stress in maize (Zea mays L.): Effects, resistance mechanisms, global achievements and biological strategies for improvement. SpringerBriefs in Agriculture. Springer Cham. 2015. ISBN 978-3-319-25440-1. DOI:10.1007/978-3-319-25442-5

[22] Boyer JS, Westgate M E. Grain yield with limited water. J. Exp. Bot. 2004;55:2385-2394. DOI: 10.1093/jxb/erh219

[23] Sehgal A, Sita K, Siddique KH, Kumar R, Bhogireddy S, Varshney RK, Hanumanth Rao B, et al. Drought or/and heat-stress effects on seed filling in food crops: Impacts on functional biochemistry, seed yields, and nutritional quality. Front. Plant Sci. 2018;9:1705. DOI: 10.3389/fpls.2018.01705

[24] Reddy AR, Chaitanya KV, Vivekanandam D. Drought-induced responses of photosynthesis and antioxidant metabolism in higher plants. J Plant Physiol. 2004;161:1189-1202

[25] Yadav RS, Hash CT, Bidinger FR, Devos KM, Howarth CJ. Genomic regions associated with grain yield and aspects of post flowering drought tolerance in pearl millet across environments and tester background. Euphytica. 2004;136:265-277

[26] Farooq M, Hussain M, Wahid A, Siddique KH. Drought stress in plants: An overview. In: RAroca, editor. Plant responses to drought stress: From morphological to molecular features. Springer-Verlag Berlin Heidelberg. 2012;1-36. DOI: 10.1007/978-3-642-32653-0_1

[27] Daryanto S, Wang L, Jacinthe PA. Global synthesis of drought effects on maize and wheat production. PLoS ONE. 2016;11:e0156362. DOI: 10.1371/journal.pone.0156362.

[28] Lobell DB, Burke MB. On the use of statistical models to predict crop yield responses to climate change. Agricultural and Forestry Meteorology. 2010;150:1443-1452.

[29] Gammans M, Mérel P, Ortiz-Bobea A. Negative impacts of climate change on cereal yields: Statistical evidence from France. Environ. Res. Lett. 2017;12:054007.

[30] You L, Rosegrant MW, Wood S, Sun D. Impact of growing
season temperature on wheat productivity in China. Agric. For. Meteorol. 2009;149:1009-1014.

[31] Khadka K, Earl HJ, Raizada MN, Navabi A. A physio-morphological trait-based approach for breeding drought tolerant wheat. Front. Plant Sci. 2020;11:715. DOI: 10.3389/fpls.2020.00715

[32] Assefa Y, Staggenborg SA, Prasad VPV. Grain sorghum water requirement and responses to drought stress: A review. [Online]. Crop Management. 2010. DOI:10.1094/CM-2010-1109-01-RV

[33] Jabereldar AA, El Naim AM, Abdalla AA, Dagash YM. Effect of water stress on yield and water use efficiency of sorghum (Sorghum bicolor L. Moench) in semi-arid environment. International Journal of Agriculture and Forestry. 2017;7(1):1-6. Doi: 10.5923/j.ijaf.20170701.01

[34] Badigannavar A, Teme N, Costa de Oliveira A, Li G, Vaksman M, Viana VE, et al. Physiological, genetic and molecular basis of drought resilience in sorghum [Sorghum bicolor (L.) Moench]. Ind J Plant Physiol. 2018;23(4):670-688. DOI: 10.1007/s40502-018-0416-2

[35] Calleja-Cabrera J, Boter M, Oñate-Sánchez L, Pernas M. Root growth adaptation to climate change in crops. Front. Plant Sci. 2020;11:544. DOI: 10.3389/fpls.2020.00544

[36] Gupta A, Rico-Medina A, Caño-Delgado AI. The physiology of plant responses to drought. Science. 2020;6488:266-269. Doi:10.1126/science.aaz7614

[37] Goche T, Shargie NG, Cummins I, Brown AP, Chivasa S, Ngara R. Comparative physiological and root proteome analyses of two sorghum varieties responding to water limitation. Scientific Reports. 2020;10:11835. DOI: 10.1038/s41598-020-68735-3

[38] Basu S, Ramegowda V, Kumar A, Pereira A. Plant adaptation to drought stress [version 1; referees: 3 approved] F1000 Research. 2016;5 (F1000 Faculty Rev):1554. DOI: 10.12688/f1000research.7678.1

[39] Shavrukov Y, Kurishbayev A, Jatayev S, Shvidchenko V, Zotova L, Koekemoer F, et al. Early flowering as a drought escape mechanism in plants: How can it aid wheat production? Front. Plant Sci. 2017;8:1950. DOI: 10.3389/fpls.2017.01950

[40] Ribaut JM, Betran J, Monneveux P, Setter T. Drought tolerance in maize. In: Handbook of maize: its biology. Springer, New York. 2009;311-344.

[41] Bhargava S, Sawant K. Drought stress adaptation: metabolic adjustment and regulation of gene expression. Plant Breeding. 2013;132:21-32. DOI: 10.111/pbr.12004.

[42] You J, Chan Z. ROS regulation during abiotic stress responses in crop plants. Front. Plant Sci. 2015;6:1092. DOI: 10.3389/fpls.2015.01092

[43] Gill SS, Tuteja N. Reactive oxygen species and antioxidant machinery in abiotic stress tolerance in crop plants. Plant Physiol. Biochem. 2010; 48:909-930. DOI: 10.1016/j.plaphy.2010.08.016

[44] Upadhyaya H, Sahoo L, Panda SK. Molecular physiology of osmotic stress in plants. In: Rout GR, Das AB. (Eds.). Molecular Stress Physiology of Plants. 2013;179-193. Springer, India. DOI: 10.1007/978-81-322-0807-5_7

[45] Tuteja N, Sopory SK. Plant signaling in stress, G-protein coupled receptors, heterotrimeric G-proteins and signal coupling via phospholipases. Plant Signal Behav. 2008;3(2):79-86.
[46] Zhu JK. Abiotic stress signaling and responses in plants. Cell. 2016;167:313-324. DOI: 10.1016/j.cell.2016.08.029.

[47] Fahad S, Ullah A, Ali U, Ali E, Saud S, Hakeem KR, Alharby H, et al. Drought tolerance in plants role of phytohormones and scavenging system of ROS. In book: Plant Tolerance to Environmental Stress: Role of Phytoprotectants. CRC Press. 2019; 103-113.

[48] Wani SH, Kumar V, Shriram V, Sah SK. Phytohormones and their metabolic engineering for abiotic stress tolerance in crop plants. The Crop Journal 4. 2016;1 6 2 – 1 7 6.

[49] Aimar D., Calafat M., Andrade A.M., Carassay L., Abdala G.I., Molas M.L. Drought tolerance and stress hormones: From model organisms to forage crops. Plants and Environment. 2011;137-164. DOI: 10.5772/24279.

[50] Basu S, Rabara R. Abscisic acid — An enigma in the abiotic stress tolerance of crop plants. Plant Gene. 2017;11:90-98.

[51] Ullah A, Manghwar H, Shaban M, Khan AH, Akbar A, Ali U, Ali E, Fahad S. Phytohormones enhanced drought tolerance in plants: a coping strategy. Environ Sci Pollut Res. 2018. Springer-Verlag, part of Springer Nature, GmbH, Germany. DOI: 10.1007/s11356-018-0858-7.

[52] Hanin M, Brini F, Ebel C, Toda Y, Takeda S, Masmoudi K. Plant dehydrins and stress tolerance versatile proteins for complex mechanisms. Plant Signal. Behav. 2011;6:1503-1509. DOI: 10.4161/psb.6.10.17088.

[53] Kosova K, Vitamvas P, Prasil IT. Wheat and barley dehydrins under cold, drought, and salinity—What can LEA-II proteins tell us about plant stress response? Front. Plant Sci. 2014;5:343. DOI:10.3389/fpls.2014.00343.

[54] Wang W, Vinocur B, Shoseyov O, Altman A. Role of plant heat-shock proteins and molecular chaperons in the abiotic stress response. Trends Plant Sci. 2004;9:244-252. DOI: 10.1016/j.tplants.2004.03.006.

[55] Zhang X, Lei L, Lai J, Zhao H, Song W. Effects of drought stress and water recovery on physiological responses and gene expression in maize seedlings. BMC Plant Biol. 2018;18:68. DOI: 10.1186/s12870-018-1281-x.

[56] Harb A. Identification of candidate genes for drought stress tolerance. In: Hossain MA, Wani SH, Bhattacharjee S, Burritt DJ, Tran L.SP. (Eds). Drought stress tolerance in plants. Springer Cham, Switzerland. 2016;2:385-414. DOI:10.1007/978-3-319-32423-4_14.

[57] Shinozaki K, Yamaguchi-Shinozaki K, Sekiz M. Regulatory network of gene expression in the drought and cold stress responses. Curr. Opin. Plant Biol. 2003;6:410-417. DOI: 10.1016/S1369-5266(03)00092-X.

[58] Ciarmiello LF, Woodrow P, Fuggi A, Pontecorvo G, Carillo P. Plant genes for abiotic stress. 2011;283-308. DOI: 10.5772/22465.

[59] Singh D, Laxmi A. Transcriptional regulation of drought response: A tortuous network of transcriptional factors. Front. Plant Sci. 2015;6:895. DOI: 10.3389/fpls.2015.00895.

[60] Mun BG, Lee SU, Park EJ, Kim HH, Hussain A, Imran QM, Lee IJ, Yun BW. Analysis of transcription factors among differentially expressed genes induced by drought stress in Populus davidiana. 3 Biotech. 2017;7:209. DOI: 10.1007/s13205-017-0858-7.

[61] Wang CT, Ru JN, Liu YW, Yang JF, Li M, Xu ZS, Fu JD. The maize WRKY transcription factor ZmWRKY40 confers drought resistance in transgenic Arabidopsis. Int. J. Mol.
Abiotic Stress in Plants

Sci. 2018;19:2580. DOI: 10.3390/ijms19092580.

[62] Wang H, Wang H, Shao H, Tang X. Recent advances in utilizing transcription factors to improve plant abiotic stress tolerance by transgenic technology. Front. Plant Sci. 2016;7:67. DOI: 10.3389/fpls.2016.00067.

[63] Jogaiah S, Govind SR, Tran LS. Systems biology-based approaches toward understanding drought tolerance in food crops. Crit. Rev. Biotechnol. 2013;33:23-39. DOI: 10.3109/07388551.2012.659174.

[64] Pérez-Clemente RM, Vives V, Zandalinas SI, López-Climent MF, Muñoz V, Gómez-Cadenas A. Biotechnological approaches to study plant responses to stress. Biomed Res Int. 2013;654120. DOI: 10.1155/2013/654120.

[65] Hirayama T, Shinozaki K. Research on plant abiotic stress responses in the post-genome era: past, present and future. Plant J. 2010;61:1041-1052. DOI: 10.1111/j.1365-313X.2010.04124.x

[66] Andorf C, Beavis WD, Hufford M, Smith S, Suza WP, Wang K, Woodhouse M, et al. Technological advances in maize breeding: past, present and future. Theoret. App.Gen. 2019;132:817-849. DOI: 10.1007/s00122-019-03306-3

[67] Zheng J, Fu J, Gou M, Huai J, Liu Y, Jian M, Huang Q, et al. Genome-wide transcriptome analysis of two maize inbred lines under drought stress. Plant Mol. Biol. 2010;72:407-421. DOI: 10.1007/s11103-009-9579-6.

[68] Luo M, Liu J, Lee DR, Scully BT, Guo BZ. Monitoring the expression of maize genes in developing kernels under drought stress using oligo-microarray. J. Integr. Plant Biol. 2010;52:1059-1074. DOI: 10.1111/j.1744-7909.2010.01000.

[69] Rabbani MA, Maruyama K, Abe H, Khan MA, Katsura K, Ito Y, Yoshiwara K, et al. Monitoring expression profiles of rice genes under cold, drought, and high-salinity stresses and abscisic acid application using cDNA microarray and RNA Gel-Blot analyses. Plant Physiol. 2003;133:1755-1767.

[70] Wang H, Zhang H, Gao F, Li J, Li Z. Comparison of gene expression between upland and lowland rice cultivars under water stress using cDNA microarray. Theor Appl Genet. 2007;115:1109-1126.

[71] Guo P, Baum M, Grando S, Ceccarelli S, Bai G, Li R, von Korff M, et al. Differentially expressed genes between drought-tolerant and drought-sensitive barley genotypes in response to drought stress during the reproductive stage. J Exp Bot. 2009;60:3531-3544.

[72] Matsui A, Ishida J, Morosawa T, Okamoto M, Kim JM, Kurihara Y, et al. Arabidopsis Tiling Array Analysis to Identify the Stress-Responsive Genes. In: Sunkar R, editor. Plant Stress Tolerance. Methods in Molecular Biology (Methods and Protocols). 2010;639:141-155. Humana Press.

[73] Deokar AA, Kondawar V, Jain PK, Karuppayil SM, Raju NL, Vadez V, Varshney RK, Srinivasan R. Comparative analysis of expressed sequence tags (ESTs) between drought-tolerant and -susceptible genotypes of chickpea under terminal drought stress. BMC Plant Biol. 2011;11:70-90.

[74] Song Y, Wang Z, Bo W, Ren Y, Zhang Z, Zhang D. Transcriptional profiling by cDNA-AFLP analysis showed differential transcript abundance in response to water stress in Populus hopeiensis. BMC Genom. 2012;13:286-304.

[75] Miao Z, Han Z, Zhang T, Chen S, Ma C. A systems approach to spatio-temporal understanding of the drought stress response in maize.
Adapting Cereal Grain Crops to Drought Stress: 2020 and Beyond
DOI: http://dx.doi.org/10.5772/intechopen.93845

[76] Mohanta TK, Bashir T, Hashem A, Abd_Allah EF. Systems biology approach in plant abiotic stresses. Plant Physiol. Biochem. 2017;121:58-73. DOI: 10.1016/j.plaphy.2017.01.019.

[77] Kakumanu A, Ambavaram MMR, Klumas C, Krishnan A, Batlang U, Myers E, Grene R, Pereira A. Effects of drought on gene expression in maize reproductive and leaf meristem tissue revealed by RNA-seq. Plant Physiol. 2012;160:846-867.

[78] Luz HP, Juan DR. RNA-seq in kinetoplastids: A powerful tool for the understanding of the biology and host-pathogen interactions. Infect. Genet. Evol. 2017;49:273-282. DOI: 10.1016/j.meegid.2017.02.003.

[79] Shan X, Li Y, Jiang Y, Jiang Z, Hao W, Yuan Y. Transcriptome profile analysis of maize seedlings in response to high-salinity, drought and cold stresses by deep sequencing. Plant Mol. Biol. Rep. 2013;31:1485-1491. DOI: 10.1007/s11105-013-0622-z.

[80] Zenda T, Liu S, Wang X, Liu G, Jin H, Dong A, Yang Y, Duan H. Key maize drought-responsive genes and pathways revealed by comparative transcriptome and physiological analyses of contrasting inbred lines. Int J Mol Sci. 2019;20:(6):1268. DOI: 10.3390/ijms20061268.

[81] Zhang Q, Liu H, Wu X, Wang W. Identification of drought tolerant mechanisms in a drought-tolerant maize mutant based on physiological, biochemical and transcriptomic analyses. BMC Plant Biology. 2020; 20:315. DOI: 10.1186/s12870-020-02526-w

[82] Tan CT, Lim YS, Lau SE. Proteomics in commercial crops: an overview. J. Protozool. 2017;169: 176-188.
regulated differently and by different mechanisms in lichens and higher plants. Plant Biol. 2005;7:156-167.

[91] Zenda T, Liu S, Wang X, Jin H, Liu G, Duan H. Comparative proteomic and physiological analyses of two divergent maize inbred lines provide more insights into drought stress tolerance mechanisms. Int J Mol Sci. 2018;19:3225. DOI: 10.3390/ijms19103325

[92] Roitsch T. Source-sink regulation by sugar and stress. Curr. Opin. Plant Biol. 1999;2:198-206.

[93] Min H, Chen C, Wei S, Shang X, Sun M, Xia R, Liu X, et al. Identification of drought tolerant mechanisms in maize seedlings based on transcriptome analysis of recombinant inbred lines. Front Plant Sci. 2016;7:1080. DOI: 10.3389/fpls.2016.01080.

[94] Marowa P, Ding A, Kong Y. Expansins: roles in plant growth and potential applications in crop improvement. Plant Cell Rep. 2016;35:949-65. DOI: 10.1007/s00299-016-1948-4

[95] Mattionci C, Lacerenza NG, Troccoli A, Leonardis AMD, Fonzo ND. Water and salt stress-induced alterations in proline metabolism of Triticum durum seedling. Physiol Plant. 1997;101:787-92. DOI: 10.1111/j.1399-3054.1997.tb01064.x.

[96] Kumar SG, Reddy AM, Sudhakar C. NaCl effects on proline metabolism in two high yielding genotypes of mulberry (Morus alba L.) with contrasting salt tolerance. Plant Sci. 2003;165:1245-51. DOI: 10.1016/s0168-9452(03)00332-7

[97] Ghannoum, O. C4 photosynthesis and water stress. Ann. Bot. 2009;103:635-644. DOI: 10.1093/aob/mcn093.

[98] Comas LH, Becker SR, Cruz VMV, Byrne PF, Dierig DA. Root traits contributing to plant productivity under drought. Front Plant Sci. 2013;4:442. DOI: 10.3389/fpls.2013.00442.

[99] Chimungu JG, Brown KM, Lynch JP. Large root cortical cell size improves drought tolerance in maize. Plant Physiol. 2014;166:2166-78. DOI: 10.1104/pp.114.250449

[100] Liu J, Zhang F, Zhou J, Chen F, Wang B, Xie X. Phytochrome B control of total leaf area and stomatal density affects drought tolerance in rice. Plant Mol Biol. 2012;78:289-300. DOI: 10.1007/s11103-011-9860-3

[101] Xu F, Yuan S, Lin HH. Response of mitochondrial alternative oxidase (AOX) to light signals. Plant Signal. Behav. 2011;6:55-58.

[102] Yang S, Vanderbeld B, Wan J, Huang Y. Narrowing down the targets: Towards successful genetic engineering of drought-tolerant crops. Molecular Plant. 2010;3(3): 469-490

[103] Todaka D, Shinozaki K, Yamaguchi-Shinozaki K. Recent advances in the dissection of drought-stress regulatory networks and strategies for development of drought-tolerant transgenic rice plants. Front. Plant Sci. 2015;6:84. DOI: 10.3389/fpls.2015.00084

[104] Krannich CT, Maletzki L, Kurowsky C, Horn R. Network candidate genes in breeding for drought tolerant crops. Int. J. Mol. Sci. 2015;16:16378-16400. DOI: 10.3390/ijms160716378

[105] Oladosu Y, Rafii MY, Samuel C, Fatai A, Magaji U, Kareem I, Kamarudin ZS, Muhammad I, Kolapo K. Drought resistance in rice from conventional to molecular breeding: A Review. Int. J. Mol. Sci. 2019;20:3519. DOI: 10.3390/ijms20143519

[106] Nepolean T, Kaul J, Mukri G, Mittal S. Genomics-Enabled
Next-Generation Breeding Approaches for Developing System-Specific Drought Tolerant Hybrids in Maize. Front. Plant Sci. 2018;9:361. DOI: 10.3389/fpls.2018.00361

[107] Wang XL, Wang HW, Liu SX, Ferjani A, Li JS, Yan JB, Yang XH, Qin F. Genetic variation in ZmVPP1 contributes to drought tolerance in maize seedlings. Nat Genet. 2016;48:1233. DOI: 10.1038/ng.3636.

[108] Xiang Y, Shan X, Qin F, Dai M. Deletion of an endoplasmic reticulum stress response element in a ZmPP2C-A gene facilitates drought tolerance of maize seedlings. Mol Plant. 2017;10:456-69. DOI: 10.1016/j.molp.2016.10.003.

[109] Park HY, Seok HY, Park BK, Kim SH, Goh CH, Lee B-H, Lee et al. Overexpression of Arabidopsis ZEP enhances tolerance to osmotic stress. Biochem. Biophys. Res. Commun. 2008;375:80-85.

[110] Abebe T, Guenzi AC, Martin B, Cushman JC. Tolerance of mannitol-accumulating transgenic wheat to water stress and salinity. Plant Physiol. 2003;131:1748-1755

[111] Nelson DE, Repetti PP, Adams TR, Creelman RA, Wu J, Warner DC, Anstrom DC, Bensen RJ, et al. Plant nuclear factor Y (NF-Y) B subunits confer drought tolerance and lead to improved corn yields on water-limited acres. Proc. Natl Acad. Sci. U S A. 2007;104(42):16450-16455.

[112] Oh SJ, Song SI, Kim YS, Jang HJ, Kim SY, Kim M, Kim YK, Nahm BH, Kim JK. Arabidopsis CBF3/DREB1A and ABF3 in transgenic rice increased tolerance to abiotic stress without stunting growth. Plant Physiol. 2005;138:341-351. DOI:10.1104/pp.104.059147

[113] Karaba A, Dixit S, Greco R, Aharoni A, Trijatmiko KR, MarschMartinez N, Krishnan A, Nataraja KN, Udayakumar M, Pereira A. Improvement of water use efficiency in rice by expression of HARDY, an Arabidopsis drought and salt tolerance gene. Proc. Natl Acad. Sci. U S A. 2007;104:15270-15275. DOI:10.1073/pnas.0707294104

[114] Wu X, Shirotto Y, Kishitani S, Ito Y, Toriyama K. Enhanced heat and drought tolerance in transgenic rice seedlings overexpressing OsWRKY11 under the control of HSP101 promoter. Plant Cell Rep. 2009;28:21-30. DOI:10.1007/s00299-008-0614-x

[115] Xiao BZ, Chen X, Xiang CB, Tang N, Zhang QF, Xiong LZ. Evaluation of seven function-known candidate genes for their effects on improving drought resistance of transgenic rice under field conditions. Mol. Plant. 2009;2:73-83. DOI:10.1093/mp/ssn068

[116] Xu D, Duan X, Wang B, Hong B, Ho THD, Wu R. Expression of a late embryogenesis abundant protein gene, HVA1, from barley confers tolerance to water deficit and salt stress in transgenic rice. Plant Physiol. 1996;110:249-257. DOI:10.1104/pp.110.1.249

[117] Sivamani E, Bahieldin A, Wraith JM, Al-Niemi T, Dyer WE, Ho THD, Qu R. Improved biomass productivity and water use efficiency under water deficit conditions in transgenic wheat constitutively expressing the barley HVA1 gene. Plant Sci 2000;155:1-9. DOI:10.1016/S0168-9452(99)00247-2

[118] He C, Zhang CW, Gao Q, Yang A, Hu X, Zhang J. Enhancement of drought resistance and biomass by increasing the amount of glycine betaine in wheat seedlings. Euphytica 2011; 177: 16-151. DOI:10.1007/s10681-010-0263-3

[119] Shou H, Bordallo P, Wang K. Expression of the Nicotiana protein kinase (NPK1) enhanced drought
Abiotic Stress in Plants

tolerance in transgenic maize. J Exper Bot. 2004; 55:1013-1019.DOI:10.1093/jxb/erh129

[120] Hu H, Dai M, Yao J, Xiao B, Li X, Zhang Q, Xiong, L. Overexpressing a NAM, ATAF, and CUC (NAC) transcription factor enhances drought resistance and salt tolerance in rice. Proc. Natl Acad. Sci. U S A. 2006;103: 12987-12992.DOI:10.1073/pnas.0604882103

[121] Nakashima K, Tran LS, Van Nguyen D, Fujita M, Maruyama K, Todaka D, Ito Y, Hayashi N, et al. Functional analysis of a NAC-type transcription factor OsNAC6 involved in abiotic and biotic stress-responsive gene expression in rice. Plant J. 2007;51: 617-630. DOI:10.1111/j.1365-313X.2007.03168.x

[122] Li H, Han X, Liu X, Zhou M, Ren W, Zhao B, Ju C, Liu Y, Zhao J. A leucine-rich repeat-receptor-like kinase gene SbER2-1 from sorghum (Sorghum bicolor L.) confers drought tolerance in maize. . BMC Genomics. 2019; 20:737. DOI:10.1186/s12864-019-6143-x

[123] Tai FJ, Yuan ZL, Wu XL, Zhao PF, Hu XL, Wang W. Identification of membrane proteins in maize leaves, altered in expression under drought stress through polyethylene glycol treatment. Plant Omics J. 2011; 4:250-256, ISSN 1836-3644.DOI:10.1007/s11105-010-0270-5

[124] Zhao F, Zhang D, Zhao Y, Wang W, Yang H, Tai F, Li C, Hu X. The difference of physiological and proteomic changes in maize leaves adaptation to drought, heat, and combined both stresses. Front. Plant Sci. 2016; 7: 1-19. DOI:10.3389/fpls.2016.01471

[125] Murata N, Allakhverdiev SI, Nishiyama Y. The mechanism of photoinhibition in vivo: Re-evaluation of the roles of catalase, α-tocopherol, non-photochemical quenching, and electron transport. Biochim. Biophys. Acta. 2012; 1817:1127-1133. DOI:10.1016/j.bbbio.2012.02.020.

[126] Melkozernov AN, Blankenship RE. Photosynthetic functions of chlorophylls. In Grimm B, Porra R J, Rüdiger W, Scheer H. (Eds). Chlorophylls and Bacteriochlorophylls. Springer: Dordrecht. 2006; pp. 397-412.

[127] Dudhate A, Shinde H, Tsugama D, Liu S, Takano T. Transcriptomic analysis reveals the differentially expressed genes and pathways involved in drought tolerance in pearl millet [Pennisetum glaucum (L.) R. Br]. PLoS ONE. 2018; 13: e0195908. DOI:10.1371/journal.pone.0195908

[128] Shinde H, Tanaka K, Dudhate A, Tsugama D, Mine Y, Kamiya T, Gupta SK, Liu S, Takano T. Comparative de novo transcriptomic profiling of the salinity stress responsiveness in contrasting pearl millet lines. Environ. Exp. Bot. 2018; 155: 619-627. DOI:10.1016/j.envexpbot.2018.07.008

[129] Ramakrishna A, Ravishankar GA. Influence of abiotic stress signals on secondary metabolites in plants. Plant Signal Behavior. 2011;6:1720-31.

[130] Fracasso A, Trindade LM, Amaducci S. Drought stress tolerance strategies revealed by RNA-Seq in two sorghum genotypes with contrasting WUE. BMC Plant Biology. 2016; 16:115. DOI: 10.1186/s12870-016-0800-x

[131] Ma D, Sun D, Wang C, Li Y, Guo T. Expression of flavonoid biosynthesis genes and accumulation of flavonoid in wheat leaves in response to drought stress. Plant Phys Biochem. 2014;80:60-66. DOI:10.1016/j.plaphy.2014.03.024

[132] Verma V, Ravindran P, Kumar PP. Plant hormone-mediated regulation of stress responses. BMC Plant
[133] Bray EA. Plant responses to water deficit. Trends Plant Sci. 1997;2:48-54. DOI:10.1016/S1360-1385(97)82562-9

[134] Smeekens S. Sugar-induced signal transduction in plants. Ann Rev Plant Phys Plant Mol Biol. 2000;51:49-81. DOI:10.1146/annurev.arplant.51.1.49

[135] Liu T, Wu L, Gan X, Chen W, Liu B, Fedak G, Cao W, Chi D, Liu D, Zhang H, Zhang B. Mapping Quantitative Trait Loci for 1000-Grain Weight in a Double Haploid Population of Common Wheat. Int. J. Mol. Sci. 2020;21:3960.

[136] Srivastava RK, Singh RB, Pujarula VL, Bollam S, Pusuluri M, Chellapilla TS, Yadav RS, Gupta R. Genome-Wide Association Studies and Genomic Selection in Pearl Millet: Advances and Prospects. Front. Genet. 2020;10:1389. DOI:10.3389/fgene.2019.01389

[137] Pang Y, Liu C, Wang D, Amand PS, Bernardo A, Li W, He F, Li L, Wang L, Yuan X, Dong L, Su Y, et al. High-Resolution Genome-Wide Association Study Identifies Genomic Regions and Candidate Genes for Important Agronomic Traits in Wheat. Molecular Plant. 2020. DOI:10.1016/j.molp.2020.07.008

[138] Mir RR, Zaman-Allah M, Sreenivasulu N, Trethowan R, Varshney RK. Integrated genomics, physiology and breeding approaches for improving drought tolerance in crops. Theor Appl Genet. 2012; 125:625-645. DOI:10.1007/s00122-012-1904-9

[139] Messmer R, Fracheboud Y, Bänziger M, Vargas M, Stamp P, Ribaut JM. Drought stress and tropical maize: QTL-by-environment interactions and stability of QTLs across environments for yield components and secondary traits. Theor Appl Genet.

[140] Rahman H, Pekic S, Lazic-Jancic V, Quarrie SA, Shah SMA, Pervez A, Shankar MM. Molecular mapping of quantitative trait loci for drought tolerance in maize plants. Genet Mol Res. 2011;10:889-901. DOI:10.4238/vol10-2gmr1139

[141] Bernier J, Kumar A, Ramaiah V, Spaner D, Atlin G. A large effect QTL for grain yield under reproductive stage drought stress in upland rice. Crop Science. 2007;47:507-516. DOI:0.2135/cropsci2006.07.0495

[142] Kumar A, Dixit S, Ram T, Yadaw RB, Mishra KK, Mandal NP. Breeding high-yielding drought-tolerant rice: genetic variations and conventional and molecular approaches. J Exp Bot. 2014;65:6265-6278. DOI:10.1093/jxb/eru363

[143] Saint Pierre C, Crossa JL, Bonnett D, Yamaguchi-Shinozaki K, Reynolds MP. Phenotyping transgenic wheat for drought resistance. J Exp Bot. 2012;63:1799-1808. DOI:10.1093/jxb/eru385

[144] Woldesemayat AA, Van Heusden P, Ndlimba BK, Christoffels A. An integrated and comparative approach towards identification, characterization and functional annotation of candidate genes for drought tolerance in sorghum (Sorghum bicolor (L.) Moench). BMC Genet. 2017;18:119. DOI:10.1186/s12863-017-0584-5

[145] Harris-Shultz KR, Hayes CM, Knoll JE. Mapping QTLs and Identification of Genes Associated with Drought Resistance in Sorghum. Methods Mol Biol. 2019;193:11-40. DOI:10.1007/978-1-4939-9039-9_2

[146] Pham AT, Maurer A, Pillen K, Brien C, Dowling K, Berger B, Eglinton JK, March TJ. Genome-wide
association of barley plant growth under drought stress using a nested association mapping population. BMC Plant Biology. 2019;19:134. DOI:10.1186/s12870-019-1723-0

[147] Yadav RS, Sehgal D, Vadez V. Using genetic mapping and genomics approaches in understanding and improving drought tolerance in pearl millet. J Exp Bot. 2011;62:397-408. DOI:10.1093/jxb/erq265

[148] Sehgal D, Rajaram V, Armstead IP, Vadez V, Yadav YP, Hash CT et al. Integration of gene-based markers in a pearl millet genetic map for identification of candidate genes underlying drought tolerance quantitative trait loci. BMC Plant Biol. 2012;12:9. DOI:10.1186/1471-2229-12-9

[149] Großkinsky DK, Svensgaard J, Christensen S, Roitsch T. Plant phenomics and the need for physiological phenotyping across scales to narrow the genotype-to-phenotype knowledge gap. J. Exp. Bot. 2015;66:5429-5440. DOI:10.1093/jxb/erv345

[150] Passioura JB. Phenotyping for drought tolerance in grain crops: when is it useful to breeders? Functional Plant Biology. 2012;39:851-859. DOI:10.1071/FP12079

[151] Monneveux P, Jing R, Misra SC. Phenotyping wheat for adaptation to drought. Drought phenotyping in crops: from theory to practice: CGIAR Generation Challenge Program. 2011.

[152] Araus JL, Sanchez C, Edmeades GO. Phenotyping maize for adaptation to drought. In: Monneveux P, Ribaut JM, editors. Drought phenotyping in crops: from theory to practice CGIAR Generation Challenge Program; 2011. p. 263-283.

[153] Fischer KS, Fukai S, Kumar A, Leung H, Jongdee B. Phenotyping rice for adaptation to drought.

In: Monneveux P, Ribaut JM, editors. Drought phenotyping in crops: from theory to practice: CGIAR Generation Challenge Program; 2011. p. 215-243.

[154] Li L, Zhang Q, Huang D. A Review of Imaging Techniques for Plant Phenotyping. Sensors. 2014; 14: 20078-20111. DOI:10.3390/s141120078

[155] Hussain S, Mubeen M, Ahmad A, Akram W, Hammad HM, Ali M, Masood N, et al. Using GIS tools to detect the land use/land cover changes during forty years in Lodhran district of Pakistan. Environ Sci Pollut Res. 2019. https://doi.org/10.1007/s11356-019-06072-3

[156] Wang D, Fahad S, Saud S, Kamran M, Khan A, Khan MN, Hammad HM, Nasim W. Morphological acclimation to agronomic manipulation in leaf dispersion and orientation to promote “Ideotype” breeding: Evidence from 3D visual modeling of “super” rice (Oryza sativa L.). Plant Physiology and Biochemistry. 2019;(1)135:499-510.

[157] Nepolean T, Singh I, Hossain F, Pandey N, Gupta HS. Molecular characterization and assessment of genetic diversity of inbred lines showing variability for drought tolerance in maize. J. Plant Biochem. Biotechnol. 2013;22:71-79. DOI: 10.1007/s13562-012-0112-7

[158] Zaman-Allah M, Zaidi PH, Trachsel S, Cairns JE, Vinayan MT, Seetharam K. Phenotyping for abiotic stress tolerance in maize – Drought stress. A field manual. CIMMYT, Mexico. 2016.

[159] International Service for Acquisition of Agri-biotech Applications (ISAAA). Biotechnology for the development of drought tolerant crops. [Internet]. 2008. Available from: http://www.isaaa.org/resources/
Adapting Cereal Grain Crops to Drought Stress: 2020 and Beyond
DOI: http://dx.doi.org/10.5772/intechopen.93845

publications/pocketk/32/default.asp [Accessed 2020-07-07].

[160] Khan S, Anwar S, Yu S, Sun M, Yang Z, Gao ZQ. Development of Drought-Tolerant Transgenic Wheat: Achievements and Limitations. Int. J. Mol. Sci. 2019;20: 3350.

[161] Thomas WTB. Drought-resistant cereals: impact on water sustainability and nutritional quality. Conference on ‘Carbohydrates in health: friends or foes’ Symposium 1: Global challenges and solutions in cereal production. Proceedings of the Nutrition Society. 2015; 74: 191-197. DOI:10.1017/S0029665115000026

[162] Voytas DF, Gao C. Precision genome engineering and agriculture: opportunities and regulatory challenges. PLoS Biol. 2014; 12: e1001877. DOI:10.1371/journal.pbio.1001877

[163] Hilscher J, Bürstmayr H, Stoger E. Targeted modification of plant genomes for precision crop breeding. Biotechnology Journal. 2017;12:1-20. DOI:10.1002/biot.201600173

[164] Miglani GS. Genome editing in crop improvement: Present scenario and future prospects. J. Crop Improv. 2017; 31: 453-559. DOI:10.1080/15427528.2017.1333192

[165] Weeks DP, Spalding MH, Yang B. Use of designer nucleases for targeted gene and genome editing in plants. Plant Biotechnol. J. 2016;14:483-495.

[166] Razzaq A, Saleem F, Kanwal M, Mustafa G, Yousef S, Imran Arshad HM, Hameed MK, Khan MS, Joyia FA. Modern trends in plant genome editing: An inclusive review of the CRISPR/Cas9 toolbox. Int. J. Mol. Sci. 2019;20:4045. DOI: 10.3390/ijms20164045

[167] Xu R, Yang Y, Qin R, Li H, Qiu C, Li L. Rapid improvement of grain weight via highly efficient CRISPR/Cas9-mediated multiplex genome editing in rice. J. Genet. Genomics. 2016;43:529-532. DOI:10.1016/j.jgg.2016.07.003

[168] Kim D, Kim D, Alptekin B, Budak H. CRISPR/Cas9 genome editing in wheat. Funct. Integr. Genomics. 2017;18:31-41. DOI:10.1007/s10142-017-0572-x

[169] Shi J, Gao H, Wang H, Lafitte HR, Archibald RL, Yang M, Hakimi SM, Mo H, Habben JE. ARGOS8 variants generated by CRISPR-Cas9 improve maize grain yield under field drought stress conditions. Plant Biotechnol. J. 2017;15:207-216. DOI: 10.1111/pbi.12603

[170] Ahmar S, Gill RA, Jung KH, Faheem A, Qasim MU, Mubeen M, Zhou W. Conventional and Molecular Techniques from Simple Breeding to Speed Breeding in Crop Plants: Recent Advances and Future Outlook. Int. J. Mol. Sci. 2020;21:2590.

[171] Baltes NJ, Gil-Humanes J, Voytas DF. Genome Engineering and Agriculture: Opportunities and Challenges. Prog Mol Biol Transl Sci. 2017;149:1-26. DOI: 10.1016/bs.pmbts.2017 .03.011

[172] Edmeades GO. Progress in Achieving and Delivering Drought Tolerance in Maize—An Update; ISAA: Ithaca, NY , USA. 2013;pp. 1-39.

[173] Passioura JB, Angus JF. Improving productivity of crops in water-limited environments. Advances in Agronomy. 2010;106:37-75.

[174] Blum A. Mitigation of drought stress by crop management. [Internet]. 2020. Available from: https://plantstress.com/drought-mitigation/. [Accessed 2020-07-06].

[175] Hafiz MH, Wajid F, Farhat A, Fahad S, Shaqat S, Wajid N, Hafiz FB. Maize plant nitrogen uptake dynamics
at limited irrigation water and nitrogen. Environ Sci Pollut Res. 2016;24(3):2549-2557. https://doi.org/10.1007/s11356-016-8031-0

[176] Thierfelder C, Cheesman S, Rusinamhodzi L. A comparative analysis of conservation agriculture systems: benefits and challenges of rotations and intercropping in Zimbabwe. Field Crops Research. 2012;137:237-250.

[177] Fan T, Stewart BA, Payne WA, Wang Y, Song S, Luo J, Robinson CA. Supplemental irrigation and water-yield relationships for plasticulture crops in the Loess Plateau of China. Agronomy Journal. 2005;97:177-188.

[178] Alharby HF, Fahad S. Melatonin application enhances biochar efficiency for drought tolerance in maize varieties: Modifications in physio-biochemical machinery. Agronomy Journal. 2020;112(4):2826-47.

[179] Lamaoui M, Jemo M, Datla R, Bekkaoui F. Heat and Drought Stresses in Crops and Approaches for Their Mitigation. Front. Chem. 2018;6:26. DOI: 10.3389/fchem.2018.00026

[180] Zandalinasas SI, Mittlerb R, Balfagóna D, Arbonaa V, Gómez-Cadenasa A. Plant adaptations to the combination of drought and high temperatures. Physiologia Plantarum. 2018;162: 2-12. DOI:10.1111/ppl.12540

[181] Badu-Apraku B, Yallou CG. Registration of striga-resistant and drought tolerant tropical early maize populations TZ-E-W Pop DT STR C4 and TZ-E-Y Pop DT STR C4. J. Plant Regist. 2009;3:86-90. DOI: 10.3198/jpr2008.06.0356crg

[182] Qamar-uz Z, Zubair A, Muhammad Y, Muhammad ZI, Abdul K, Fahad S, Saifder B, et al. Zinc biofortification in rice: leveraging agriculture to moderate hidden hunger in developing countries. Arch Agron Soil Sci. 2017;64:147-161. https://doi.org/10.1080/03650340.2017.1338343

[183] Wu S, Ning F, Zhang Q, Wu X, Wang W. Enhancing omics research of crop responses to drought under field conditions. Front. Plant Sci. 2017;8:174. DOI: 10.3389/fpls.2017.00174.

[184] Aziz K, Daniel KYT, Fazal M, Muhammad ZA, Farooq S, FanW, Fahad S, Ruiyang Z. Nitrogen nutrition in cotton and control strategies for greenhouse gas emissions: a review. Environ Sci Pollut Res. 2017a;24:23471-23487. https://doi.org/10.1007/s11356-017-0131-y

[185] Aziz K, Daniel KYT, Muhammad ZA, Honghai L, Shahbaz AT, Mir A, Fahad S. Nitrogen fertility and abiotic stresses management in cotton crop: a review. Environ Sci Pollut Res. 2017b; 24:14551-14566. https://doi.org/10.1007/s11356-017-8920-x

[186] Ding W, Xu X, He P, Ullah S, Zhang J, Cui Z, Zhou W. Improving yield and nitrogen use efficiency through alternative fertilization options for rice in China: A meta-analysis. Field Crops Res. 2018;227:11-8.

[187] Akram R, Turan V, Hammad HM, Ahmad S, Hussain S, Hasanain A, Maqbool MM, et al. Fate of organic and inorganic pollutants in paddy soils. In: Hashmi MZ, Varma A. (Ed.). Environmental Pollution of Paddy Soils, Soil Biology. Springer International Publishing AG, Gewerbestrasse 11, CHAM, CH-6330, Switzerland. 2018a; pp. 197-214

[188] Akram R, Turan V, Wahid A, Ijaz M, Shahid MA, Kaleem S, Hafeez A, et al. Paddy land pollutants and their role in climate change. In: Hashmi MZ, Varma A. (Ed.). Environmental Pollution of Paddy Soils, Soil Biology. Springer International Publishing AG, Gewerbestrasse 11, CHAM, CH-6330, Switzerland. 2018b; pp. 113-124.
[189] Fahad S, Hussain S, Saud S, Tanveer M, Bajwa AA, Hassan S, Shah AN, et al. A biochar application protects rice pollen from high-temperature stress. Plant Physiol Biochem. 2015a;96:281-287

[190] Fahad S, Hussain S, Saud S, Hassan S, Tanveer M, Ihsan MZ, Shah AN, et al. A combined application of biochar and phosphorus alleviates heat-induced adversities on physiological, agronomical and quality attributes of rice. Plant Physiol Biochem. 2016d;103:191-198

[191] Evans JR. Improving photosynthesis. Plant Physiology. 2013;162:1780-1793. DOI:10.1104/pp.113.219006

[192] Hartman K, Tringe SG. Interactions between plants and soil shaping the root microbiome under abiotic stress. Biochemical Journal. 2019;476:2705-2724. DOI: 10.1042/BCJ20180615

[193] Adnan M, Zahir S, Fahad S, Arif M, Mukhtar A, Imtiaz AK, Ishaq AM, Abdul B, et al. Phosphate-solubilizing bacteria nullify the antagonistic effect of soil calcification on bioavailability of phosphorus in alkaline soils. Sci Rep. 2018;8:4339. https://doi.org/10.1038/s41598-018-22653-7

[194] de Vries FT, Griffiths RI, Knight CG, Nicolitch O, Williams A. Harnessing rhizosphere microbiomes for drought-resilient crop production. Science. 2020; 368:270-274.

[195] Fahad S, Hussain S, Bano A, Saud S, Hassan S, Shan D, Khan FA, Khan F, et al. Potential role of phytohormones and plant growth-promoting rhizobacteria in abiotic stresses: consequences for changing environment. Environ Sci Pollut Res. 2014a;22(7):4907–4921. https://doi.org/10.1007/s11356-014-3754-2

[196] Fahad S, Hussain S, Matloob A, Khan FA, Khaliq A, Saud S, Hassan S, Shan D, et al. Phytohormones and plant responses to salinity stress: A review. Plant Growth Regul. 2014b;75(2):391–404. https://doi.org/10.1007/s10725-014-0013-y

[197] Fahad S, Nie L, Chen Y, Wu C, Xiong D, Saud S, Hongyan L, et al. Crop plant hormones and environmental stress. Sustain Agric Rev. 2015b;15:371-400

[198] Fahad S, Hussain S, Saud S, Hassan S, Chauhan BS, Khan F, et al. Responses of rapid viscoanalyzer profile and other rice grain qualities to exogenously applied plant growth regulators under high day and high night temperatures. PLoS One. 2016a;11(7):e0159590. https://doi.org/10.1371/journal.pone.0159590

[199] Fahad S, Hussain S, Saud S, Khan F, Hassan S, Jr A, Nasim W, et al. Exogenously applied plant growth regulators affect heat-stressed rice pollens. J Agron Crop Sci. 2016b;202:139–150

[200] Fahad S, Hussain S, Saud S, Hassan S, Ihsan Z, Shah AN, Wu C, et al. Exogenously applied plant growth regulators enhance the morphophysiological growth and yield of rice under high temperature. Front Plant Sci. 2016c;7:1250. https://doi.org/10.3389/fpls.2016.01250

[201] Kamarn M, Wenwen C, Irshad A, Xiangping M, Xudong Z, Wennan S, Junzhi C, et al. Effect of paclobutrazol, a potential growth regulator on stalk mechanical strength, lignin accumulation and its relation with lodging resistance of maize. Plant Growth Regul. 2017;84:317-332. https://doi.org/10.1007/s10725-017-0342-8

[202] Fahad S, Rehman A, Shahzad B, Tanveer M, Saud S, Kamran M, Ihtisham M, et al. Rice responses and tolerance to metal/metalloid toxicity. In: Hasanuzzaman M, Fujita M, Nahar K,
Abiotic Stress in Plants

Biswa JK (Ed.). Advances in Rice Research for Abiotic Stress Tolerance. Woodhead Publ Ltd, Abington Hall Abington, Cambridge CB1 6AH, CAMBS, England. 2019a; pp. 299-312.

[203] Fahad S, Adnan M, Hassan S, Saud S, Hussain S, Wu C, Wang D, et al. Rice responses and tolerance to high temperature. In: Hasanuzzaman M, Fujita M, Nahar K, Biswas JK (Ed.). Advances in Rice Research for Abiotic Stress Tolerance. Woodhead Publ Ltd, Abington Hall Abington, Cambridge CB1 6AH, CAMBS, England. 2019b; pp.201-224.

[204] Saleem MH, Fahad S, Adnan M, Ali M, Rana MS, Kamran M, Ali Q, et al. Foliar application of gibberellic acid endorsed phytoextraction of copper and alleviates oxidative stress in jute (Corchorus capsularis L.) plant grown in highly copper-contaminated soil of China. Environmental Science and Pollution Research. 2020;1-13. [https://doi.org/10.1007/s11356-020-09764-3]

[205] Fahad S, Bano A. Effect of salicylic acid on physiological and biochemical characterization of maize grown in saline area. Pak J Bot. 2012;44:1433-1438

[206] Saud S, Li X, Chen Y, Zhang L, Fahad S, Hussain S, Sadiq A, Chen. Silicon application increases drought tolerance of Kentucky bluegrass by improving plant water relations and morph physiological functions. Sci World J. 2014; 2014:1-10. [https://doi.org/10.1155/2014/368694]

[207] Saud S, Chen Y, Fahad S, Hussain S, Na L, Xin L, Alhussien SA. Silicate application increases the photosynthesis and its associated metabolic activities in Kentucky bluegrass under drought stress and post-drought recovery. Environ Sci Pollut Res. 2016;23(17):17647–17655. [https://doi.org/10.1007/s11356-016-6957-x]

[208] Zahida Z, Hafiz FB, Zulfiqar AS, Ghulam MS, Fahad S, Muhammad RA, Hafiz MH, et al. Effect of water management and silicon on germination, growth, phosphorus and arsenic uptake in rice. Ecotoxicol Environ Saf. 2017;144:11-18