

Review Article

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A Review: Advances in Draught Stress Tolerance in Wheat (*Triticum aestivum* L.)

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ABSTRACT

The major threat of the agricultural crop is the climate change, which grown globally in the subtropical and the tropical regions. Negative impact on the plant growth, development and the economic yield regarding climate change due to consequences of the draught stress. For the prediction of the climate change and occurrence of the draught many simulation models were recorded, it's very necessary to improve the crop against the draught stress which ultimately limits the production and the productivity of the crop. Wheat crop is widely used crop because of their social and the economic values. Many country around the world which depends on the wheat crop for food as well as feed and mainly wheat are the vulnerable against the draught stress. It's very challenging task to improve the draught stress of many researchers. The advances in the technology which ultimately gives understanding and the improvement in draught tolerance including the main three research areas viz., breeding, physiology and the genetics. When plants exposed to the draught stress the biochemical and the physiological pathways activated, the physiology focused on that research. In wheat, making the crosses through the breeding program which give the some high degree of the draught tolerance genotypes and also the many genes responsible for the draught tolerance which is identified by using the advanced biotechnological tools like QTL mapping, association mapping and GWAS technology for particular trait. In the past studies recorded, the draught tolerance shows the polygenic trait and its genetic constitution will helpful for the dissecting the gene network for controlling the draught tolerance. The presented review gives the recent advances in the main three research field for improvement of the draught tolerance in wheat.

Keywords

Water deficit,
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Introduction

The many crops grown all over world but the most important cereal crop is wheat (*Triticum aestivum* L.) and which grown in the rain fed area in which the draught causes prime role for the yield reduction (Rana *et al.*, 2013). The occurrence of the draught stress is not only regionally but also globally widespread, which grows experimental formula encountered by the wheat plant and due to the so long time of water deficit stress lead to several minimize the overall production (Nezhadahmadi *et al.*, 2013). Mainly the three factors like intensity, duration and the incidence time which determined draught stress. Due to variable conditions of the nature under draught stress is very complex for the breeder point of view for the improvement of the plant trait first to enhance the plant production (Mujtaba and Alam, 2002).

During the water stress given to plant at all stages of the plant growth affects the total grain yield but it has taken place in the critical stages of the growth which ultimately decreased grain yield sharply (Hanif *et al.*, 2013, Zamurrad *et al.*, 2013, Subhani *et al.*, 2012). During reproductive stage, the crop yield reduced by the 70-80% due to draught stress reported (Kulkarni *et al.*, 2008). Therefore, now a day it has important to develop the new better yield performing varieties, tolerant to the several climate condition to peculiar draught (Mahmood *et al.*, 2013).

In the past decades, most of the researchers have reported draught tolerance in wheat and barley but unable to improvement of the crops against the draught tolerance limited for many reasons recorded. First, draught cause changes in the many physiological parameters of the plant in which needed measured and more understood. Second, genotype x environment

interaction (GE) affects the selection procedure. Third, draught is very complex trait which is controlled by the many genes, which most makes the minor genetic contribution. Finally these are the important to improve genetically draught tolerance. Other factors also related to the complexity and the structure of wheat genome. Through the different technique draught stress studied to physiological, morphological, gene expression, breeding and genetic studies.

Some recently developed advance technique which related with the crop responses against biotic and abiotic stresses mainly water deficit stress is obtaining the significant impact, as globally fluctuation in the environmental conditions (Ullah *et al.*, 2010). For better knowledge regarding draught stress tolerance with relation to physiological and morphological parameters helps in the characterization of germplasm for evaluation of genotypes against draught stress. One of the main superior aims of the plant breeders is the making of the wheat genotypes which suitable for the draught stress finally ensures the increases grain yield.

The field of the genomics results for whole-genome sequencing for the each and every genotypes possible. Researchers mostly and widely used technique is genotyping by sequencing, finally generates the single nucleotide polymorphism (SNP) marker that ultimately covers the whole genome of the wheat and barley (Hussain *et al.*, 2017; Thabet *et al.*, 2018). The reference genomes are available of wheat and barley. For identifying the correct position and location of the genes on the chromosome against the reference genome by using the SNP marker generated through genotype by sequencing technique. For the controlling the target traits by identifying the genes by using the genome wide association study (GWAS) and the Quantitative trait loci (QTL) through the

implanting of the more number of SNPs used in the draught tolerance case. For measuring the traits depends on the number of genes identified which are associated with draught tolerance, proximity and magnitude of the gene. The many traits lead for the identification of the many genes controlling draught tolerance (Ovenden *et al.*, 2017, Qaseem *et al.*, 2018).

For draught gene such as Dreb and Fehw3 gene for specific molecular markers in draught stress (Rasheed *et al.*, 2016). These two genes presence or absence can be tested for many germplasm, Draught tolerance, controlled by using the GWAS or QTL mapping through identifying the new genes (Zeng *et al.*, 2014, Sukumaran *et al.*, 2018). New era has been started by using the gene editing and genomic selection can be used to improve draught tolerance in the barley and wheat (Singh *et al.*, 2015).

For mixing of the three broad research area including breeding, genetics and physiology with directly helps for identifying the draught tolerant genotypes which having the more number of genes control the draught tolerance in many conditions. This presented reviews gives the more explores the recently developed technique including the breeding, physiology and genetic research for enhancing the draught tolerance and the possible fates to identify the most promising draught tolerance plants for the further improvement of the trait.

Draught and plant growth

Draught is the most widespread environmental condition, severely diminish to the plant growth habit and crop production which are more than other environmental stresses (Edema *et al.*, 2014, Rauf *et al.*, 2007, Noorka *et al.*, 2009, Shao *et al.*, 2009). Draught stress often accumulates very slowly

over the considerable time period which differs from the abiotic stress. Due to these characteristics of draught termed as “Creeping phenomena”. As compared to the other natural stresses, its spread over very big geographical area relation to the greater damage. The situation is more serious regarding the climate change and draught worldwide spread problem eventually decreases the world crop production (Pan *et al.*, 2002). Out of all worlds agricultural land 25% land affected as the higher level of water stress (Jajarmi *et al.*, 2002). Out of total wheat production 50% affects the draught stress (Pfeiffer *et al.*, 2005). During grain filling stage in wheat crops shows draught in arid and semiarid regions. At the time of grain shriveling due to draught that time reduces yield. For the critical constraint to primary productivity in the arid climates, water limitation provides the critical role during the stages of the wheat production (Fischer *et al.*, 2001). In arid areas draught supremacist is expected any plant growth critical stages (Hanif *et al.*, 2013, Zamurrad *et al.*, 2013, Subhani *et al.*, 2012). Due to water shortage at the seedling and tillering ultimately poor crop growth and abnormal germination (Hasan *et al.*, 2013, Noorka *et al.*, 2007). At anthesis stage of growth which causes the maximum reduction yield in wheat crop (Akram *et al.*, 2007).

Physiological and biochemical responses

In the past decades, many physiological and biochemical responses characterized in responses to the draught stress. Many physiological traits that show the effect of draught stress regarding growth and development of the wheat and barley plants. Many genes involved in the physiological changes governed by the plant are very prime role for the breeders and the field researchers, they used these genetic material for improve draught tolerance by breeding program.

Gaseous exchange and photosynthesis

Photosynthesis is the primary role in the plant growth, development and economic grain yield. But for understanding the crop physiological responses during the draught is very critical at the water stress condition the photosynthesis determines by the use of photosynthetic pigment contents are the key factors which indicates the rate growth and development. In the cereals, during the draught which decreases the photosynthetic rates (Dawood *et al.*, 2019). Improper imbalance between the light capture and utilization because of the metabolic photosynthetic activity distortion (Foyer *et al.*, 2000), due to decrease in the Rubisco activity in the plant which ultimately loss of chloroplast membrane (Amirjani *et al.*, 2013), chloroplast structure degradation and photosynthetic material, biosynthesis of chloroplast inhibition, chlorophyll substrate destruction, photo oxidation of chlorophyll and chlorophyllase activity increases (Kabiri *et al.*, 2014). Stomatal limitations are much easier than the metabolic distortions which happened through the reduced form of the synthesis of the photosynthetic pigments (Rama *et al.*, 2014). The responses of the draught decreases by the mesophyll and stomatal conductance to the CO₂ (Centritto *et al.*, 2009). For the conserve water status during the draught stress the stomatal closure which minimizes the transpirational water loss from the plant. Due to stomata closure decreases CO₂ for photosynthetic metabolism, CO₂ assimilation decreases which ultimately prohibits the dry matter accumulation of plant ability (A. *et al.*, 2003). Draught stress affect the chlorophyll pigment which deferentially depends on the genotype or species studied. Chlorophyll content affected by the genetic variation. Under the water stress conditions high chlorophyll contents gives the more seed yield (Alaei *et al.*, 2011). Chlorophyll content, number of grains per spike and grain

filling period are positively correlated with the grain yield in wheat were recorded (Kilic *et al.*, 2010).

Water relation

The plant water relation are influenced by the some prime characteristics like water loss rate, relative water content, water content, succulence index, residual transpiration rate and excised leaf water retention. Plant water status is measured by Relative Water Content (RWC), tissue reflects the metabolic activity and this index noted for the dehydration tolerance. Due to the draught stress noted many varieties of plants decreases their relative water content (Allahverdiyev *et al.*, 2015). Under the draught stress the leaf water potential was negatively correlated with the grain yield of barley (Samarah *et al.*, 2009). In draught stress grain yield and water content are significantly positive correlation at the time of reproductive stages in the barley and wheat. Therefore, improvement of draught tolerance through breeding programs in the high yield combination with the use of relative water content and leaf rolling (Tahara *et al.*, 1990, Teulat *et al.*, 1997).

Nutrient relation

Soil water content decreases, also decrease in the radius of the water filled pores, increases tortuosity and the decreases in the mobility of the P (Faye *et al.*, 2006). P uptake reduces due to the decline availability of the P and foliar content of the P reduces consequently (Sardans *et al.*, 2004). Cations like K⁺, Ca²⁺, Mg²⁺ (membrane permeability and the active transport) reduces during draught stress, and finally absorption of the cations through roots decreased (Farooq *et al.*, 2012). On the above ground biomass the Ca²⁺ concentration decreases in the draught stress and this resulting the gradually transpiration flux reduction (Sardans *et al.*, 2008). In wheat

plant during the water stress in the root and shoot the level of phosphorus, calcium and potassium reduced and this result recorded by the (Noman *et al.*, 2018). In the draught stress some micronutrients viz., Mo, Mn and Fe can be induced (Hu *et al.*, 2005). In the well water conditions micronutrients are more available because of their soluble and reduced uptake form (Havlin *et al.*, 1999).

Hormonal effect

Abscisic acid production affect during draught stress adaptation by avoidance of dehydration and the tolerance dehydration (Thomposon *et al.*, 2007). Many hormones regulating the tolerance mainly ABA against abiotic stresses like heat, cold, wounding and draught (Lata *et al.*, 2011). ABA has been identified as a stress signal from root to shoot (Schachtman *et al.*, 2018), contains the leaf expansion inhibition and the responses in the short term as a stomatal closure. ABA gives the systemic responses against the abiotic stress, before its detectable changes in terms of the nutrient status and the leaf water (Suzuki *et al.*, 2013). Moreover, the ABA reported as enhancer for the root growth and development in the wheat and significantly correlated with the grain yield under the draught stress (Xu *et al.*, 2013).

Breeding approaches against draught stress

Now a day, new technique developed after the DNA sequencing which provides the high density marker technology by using the single nucleotide polymorphism (SNP) markers (Eltaher *et al.*, 2018). Genotyping by sequencing is one of the most prime sequencing methods and it gives the number of SNPs that coverage total genome of wheat and barley. In targeting the essential genes which controlling the draught stress tolerance in the wheat and barley by using the

combination of the traditional breeding and advanced DNA sequencing technology (Hussain *et al.*, 2017; Sukumaran *et al.*, 2018; Reinert *et al.*, 2016; Mwadzingeni *et al.*, 2017).

Genetic variation at different growth stages

Germination stage

The series of events is happened during the seed germination and it's usually starts with the water imbibition in the seeds, further its convert to emerge radical from the seed coat (Srivastava *et al.*, 2003). It's very sensitive stages during draught stress, reduces the seed germination percentage and the emergence of the seedlings in the wheat and barley crop. For example many farmers in the India and Pakistan, the rainfed area totally depend on the coming monsoon (Kerr *et al.*, 2019). For induction of the draught stress there are so many various concentration of PEG solution, due to responses gives at different concentration that why it's essential to for testing the different rage of concentration (Kido *et al.*, 2016). Due to the high weight of PEG (6000 or 8000 KDa) which inhibits the cell wall from penetrating the water. Due to that reason PEG mostly used for controlling the water potential at the germination stage (Khazayi *et al.*, 2008).

Seedling stage

At the seedling stage, seedling stage comes after the seed germination stage, when the plants developed the cannabis leaves traditionally. Seedling stage is also been the critical stage when the moisture stress are present surroundings. For evaluating the draught tolerance during the seedling stage is primary role and which ultimately affects the upcoming stages and finally total grain yield (Gallagher *et al.*, 1976). After experienced in the genetic variation at seedling stage, which

eventually increases the possibility of the draught tolerant varieties during the breeding selection program (Hameed *et al.*, 2010).

Improvement of draught tolerance in wheat by high throughput phenotyping

Using the newly developed technology that is High Throughput Phenotyping (HPP) which rapidly screen the thousands of genotypes for many desired trait of interest. The high automated facility is needed for this technology in the growth chamber or the greenhouses with controlled environmental condition, with accurate sensing technology is essential and also robotics (Araus *et al.*, 2014) or phenocarts in the field. By using HPP regarding the particular trait of interest through the screening of the thousands of the genotypes which improves the breeding process more precisely because its evaluate the previously unavailable and useful data in the draught stress viz., plant water status, leaf temperature and predicted level of yield (Winterhalter *et al.*, 2013). For the estimation of the plant parameters and the different vegetation indices by using these platform mainly including passive and spectral sensors (Erdle *et al.*, 2011, Hackl *et al.*, 2012).

Draught tolerance improvement by using nanotechnology

In recent decades, many plant researchers shows their interest in the nanotechnology related to the agriculture, which by applying the nanoparticles (NP) and some beneficial effects were recorded by many researchers in relation to the enhancing the agricultural production and tolerance against the biotic and abiotic stresses (Jsarotia *et al.*, 2018). Many advantages of nanotechnology regarding agriculture were recorded out of them cheap, low phytotoxicity and cheap (Taran *et al.*, 2017) and nanoparticles work as a positive or negative biological effects on the

basis of their concentration (Olkhovych *et al.*, 2016). For improving the yield components by the application of SiO₂ under the draught stress, TiO₂ at some concentration gives decreased seed yield (Ghorbanian *et al.*, 2019).

Genetic basis of draught tolerance in wheat

By using the molecular markers and genome sequencing in the wheat and barley which provides genetic analysis studies of the draught tolerance. Such genetic analysis containing the many approaches like association mapping QTL mapping genome wide analyses and transcriptome expression analysis goals to characterize and detection of particular gene to draught stress adaptation (Hu *et al.*, 2014).

QTL for draught tolerance

So many prime genomic regions have been recorded by many researchers through the QTL mapping tool. These researches are helped to identify the regions underlying the difference of the draught tolerance traits and the genetic factor of the mixed trait in the wheat and barley. For the evaluation of the genotypic performance commonly used multi environmental conditions are necessary (Mathews *et al.*, 2008, Von *et al.*, 2008) using various type of population like recombinant inbred line (RIL) population (Mathews *et al.*, 2008, Von *et al.*, 2008, Maccaferri *et al.*, 2008, McIntyre *et al.*, 2010) specially bi parental population, doubled haploid (DH) population (Quarrie *et al.*, 1994, Obsa *et al.*, 2016) and advanced backcross (Kalladan *et al.*, 2013). For identifying the QTL and population genotyping various molecular markers like Restriction Fragment Length Polymorphism (RFLP), Simple Sequence Repeats (SSR), Amplified Fragment Length Polymorphism (AFLP) (Maccaferri *et al.*, 2008, Quarrie *et al.*, 1994) and Single

Nucleotide Polymorphism (SNP) (Kalladan *et al.*, 2013). Now a day's population genotyping through the genetic SNP with the high density marker were carried out (Obsa *et al.*, 2016).

Analysis of draught tolerance through the genomics

By using the huge number of SNPs that ultimately generates the high density linkage map through the GWAS approaches and to identify the gene on the whole chromosome can also be detected whereas GWAS study used both diverse population as well as the bi-parental population. The biggest strength of the GWAS to detect the novel regions and regions for the draught stress tolerance in wheat and barley. For example, GWAS recorded QTLs regarding the yield components in the 208 varieties of durum wheat with the use of 6211 SNPs (Sukumaran *et al.*, 2018), by using the 16383 DArTs 93 bread wheat genotypes (Mwadzingeni *et al.*, 2017), 123 wheat cultivar through 90 k SNP array (Ain *et al.*, 2015). Diverse collection and the marker type which detect the genomic regions associated with the grain yield and related traits significantly (Mobasser *et al.*, 2017, Faye *et al.*, 2006, Sardans *et al.*, 2004). Candidate gene and the genetic architecture of the draught stress tolerance and related traits mainly root, yield and leaf were predicted by the use of 108 bread wheat and 9646 SNPs (Qaseem *et al.*, 2018) and 20881 SNPs using the 200 bread wheat genotypes (Beyer *et al.*, 2019).

In conclusion, water stress is so important to detect the genomic responses. Firstly, transcriptional reaction prepares the more information of the plants to draught stress. Secondly, during the stress environment it's possible to understand the genes and their functions. Thirdly, more important to differ the promoter's reacts during the stress and

their related cis elements, which are both very primitive studies in the crop engineering (Zhou *et al.*, 2007). For fast improvement against the draught resistance by using the manipulation of genes responsible for the antioxidants, proteins, transcriptional factors and plant growth regulators (Gupta *et al.*, 1999). Molecular mapping and the QTL mapping are also most efficient methods for detecting the qualitative and quantitative characters mainly in the resistance against the stress. But also the some limitation of this methods that is inconsistent repeatability, interaction between the environment and the genotypes QTL detection for the instance, numerous genes that's regulating the yield and wrong mapping population used. Other limitation of the QTL like improper interaction epistasis, to extract the substance to carry the alleles influences its difficult (Collins *et al.*, 2008, Podlich *et al.*, 2004). Moreover, in the many circumstances, the QTL does not show marked impact; even stop in various ground work, even also the same growth conditions (Collins *et al.*, 2008, Cho *et al.*, 2006). Due to this high changeable in the nature of the water stress and the less information of the complexness have caused, and eventually it's hard to identify the particular physiological traits necessary for improved the crop performance.

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