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Drought stress tolerance in Wheat: Recent QTL mapping advances

Laxmidas Verma[1], Anand Kumar[2] and Anamika Yadav[3]

[1]*Department of Genetics and Plant Breeding, Acharya Narendra Dev University of Agricultutre and Technology, Kumarganj, 224229 Ayodhya, India*
[2]*Faculty of Agricultural Sciences, GLA University, Mathura, 281406 Uttar Pradesh, India*
[3]*Indian Institute of Technology, Guwahati - 781039, Assam, India*

ABSTRACT

In the last decade, the increasing of global warming has bad impact on crop plants. Climate change is a major threat for plants in several locations including tropical and subtropical areas. Global warming has negative effects on plants including drought resistance. Drought stress is a major concern that reduces the crop yield of plants.. Drought stress is a global challenge that significantly impacts crop productivity. It adversely affects plants at morphological, physiological, and molecular levels. However, plants can adapt to drought stress through mechanisms that can be modified using breeding techniques, such as drought avoidance, drought tolerance, drought escape, and hardening. Wheat plants, for instance, can survive under drought stress by altering their internal mechanisms or activating specific signaling pathways. In response to drought stress, wheat plants exhibit a variety of morphological, physiological, and biochemical adaptations. In addition, molecular breeding is a very good step to reduce the effect of drought stress on wheat plants. In molecular breeding, several drought-resistance quantitative trait loci (QTLs) have been identified. In this review paper, we included some major drought-stress QTLs for wheat.

Keywords: *drought stress, morphological responses, physiological responses, molecular responses, wheat and quantitative trait loci.*

1. INTRODUCTION

Drought stress is an evil condition, in which survival rate of plant is very low, if plants survive under drought conditions gives low yield. Drought stress is a major challenge in agriculture for the production of crop, and also a major challenge for agriculture and researchers who is working on drought stress (Deribe, 2024). In a changing climatic condition, some regions of cultivated land are expected to give a normal performance, but some regions is not good for the production of crop (Cui and Zhong, 2024). Therefore, for good production, need of the development of good cultivar that can tolerate drought conditions, these cultivars will ensure to fight for food shortage and starvation (Liaqat*et al*., 2024).

Wheat is one of the most important cereal crops globally, ranking second in production worldwide. It is cultivated extensively for both food and feed. With the Earth's population increasing at an alarming rate, boosting wheat production is essential to ensure food security (Kumar and Singh, 2020; Pickson et al., 2024). Wheat is known for its adaptability to diverse climatic conditions, including drought-prone areas, enabling better yields under challenging environments. The high degree of genetic variability in wheat is crucial for selection and further crop improvement efforts (Zewdu et al., 2024). But some major challenges for growing the wheat has been faced by plant breeders, therefor breeder is developing drought resistant variety of wheat (Paudel*et al*., 2024). Even though, crop productivity in semi-arid and arid places will be enhanced by the utilization of genetic resources for a sustainable future under climate change (Nadeem*et al*., 2024). For understanding the plant responses under drought stress are very important for plant breeder, in which, plant breeder can develop drought drought-resistant variety of wheat under drought stress condition(Paudel *et al*., 2024; Saeed*et al*., 2024).

In addition, many factors influence the plant acclimatization under drought stress conditions such as the ambient temperature of the environment, plant genotype, the growth stage of plants, and physiological growth of plants and molecular response of plants (Alsamadany*et al*., 2024). Contribution of molecular breeding method has enormous distribution for wheat gives the good idea to breeder (Rafiei*et al*., 2024). However, the little contribution of marker assisted breeding for drought tolerance has advantage over conventional breeding (kumar*et al*., 2024). Due to the environmental effect QTL X QTL interaction and low heritability characteristics, molecular breeding does not have an enormous contribution for drought tolerance (Poggi*et al*., 2023). However, several other approaches have been facilitated to dissect the quantitative trait loci on genomic regions by researchers (Mulugeta*et al*., 2023).

Diversity in wild germplasm plays a significant role in contributing favorable genes that enhance agronomic traits in wheat, such as spike length and days to heading, which are critical for yield improvement (Visioni et al., 2023). Yield is a complex trait influenced by multiple factors, and quantitative trait loci (QTLs) associated with yield traits have been identified under drought conditions through QTL mapping (Mulugeta et al., 2024; Manjunath et al., 2024).

Corresponding Author: **Laxmidas Verma*

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2. RESPONSE OF PLANTS UNDER DROUGHT STRESS

Drought stress suppresses the growth, development and yields of plants. Secondary metabolic activities may enhance drought tolerance by the accumulation of some kind of natural hormones under drought stress. In addition, priming induces the tolerant verities by defense seed priming (Tabassum*et al*., 2018). Several factors affect the plant's growth under drought stress including morphological, physiological, and molecular responses.

2.1 Morphological responses under drought stress

Adverse impact of drought is seen on wheat during morphological including burn like appearance in leaves (Zulkiffal,*et al*., 2021). Adopting the challenges of plants under drought stress is a major concern. Several methods have been included such as drought tolerance, drought avoidance, escaping, etc. In which, two methods are very popular such as avoidance and drought tolerance (Fang and Xiong, 2015). Drought tolerance is the ability of plant survival under drought stress by osmotic adjustments through osmoprotectants (Basu*et al*., 2016). On another hand, drought avoidance, the ability of plant to with stand by changing the physiological process involving root system and stomata closure (Pirasteh-Anoshehe*t al*., 2016). And, drought escaping, in this, plants adjust their life cycle by changing the time as earliness and lateness (Shavrukov*et al*., 2017). Drought resistance is the activity of plants, in that, plant lose the yield under drought stress tolerance (Salehi-Lisar and Bakhshayeshan, 2016).

2.1.1. Leaf structure and shape

Reduction of transpiration under drought stress conditions by dropping the leaves that reduce the transpiration is a major strategy of plants (Seleiman*et al*., 2021). Under drought stress, plants would be exhibit various negative features including yellow leaves, wilt, development of deep root system, and effect on shoot growth resulting losses in productivity(Lipiec*et al*., 2013). Reduction of transpiration in plants is decreased by use of waxy and thick cuticle layer on leaves. Moreover, changes in xeromorphic characters by the changing structure of large number of trichomes, thiny and many leaves, smaller and less number of stomata and develop vascular tissue (Wickens and Wickens, 1998).

2.1.2.Root structure

As we know, deep root absorbs enough water than shallow root therefore; survival rate of plants under drought stress is good by changing the root system (Kalra*et al*., 2024). In drought stress, wheat plants, survive to alter the morphology of root such as deeper root system and intense root system (Li*et al*., 2023). Plants maintain to themselves under water scarcity condition by altering the morphology such as deeper root when water in deeper or not available on surface (Comas*et al*., 2013). Dense root system absorbs more water than the thinner root system because of dense room system hold water than the thinner root (Zhang*et al*., 2023).

2.2. Physiological activity under drought stress

Plants can survive under drought stress by altering physiological activity such as stomata closure, photosynthetic activity, etc.

Stomata

Under drought stress, plants leave reduce the transpiration by closing stomata. Even though, opposite relation between drought tolerance and stomata conductance are disclosed that closing of stomata and reduce transpiration. Direct relationship of stomata is with photosynthetic, because regulation of photosynthesis is occurred by stomata (Khan, 2023). The relationship between photosynthesis and stomata has a direct impact on plant functioning, as stomatal closure reduces the photosynthetic rate (Wall et al., 2023). Stomatal opening facilitates photosynthesis by allowing the uptake of CO2. Under drought stress, changes in stomatal behavior are a key physiological response. The number of stomata decreases under severe drought conditions, while moderate drought can have an additive effect on stomatal activity. Additionally, small and thick stomata help reduce the transpiration rate, thereby enhancing drought tolerance in wheat (Ahmed et al., 2024).

2.3 Molecular responses

Plants exhibit molecular responses under drought condition by the production of some special kind of protein and gene expression. Plants have numerous functions including, enzyme activation (peroxidase), ascorbate (ASC), and accumulation of solutes (like sugar and protein) for adaption to drought stress (Celi*et al*., 2023). And, drought stress affect the production of some endogenous level of hormones including, abscisic acid (ABA), Ethylene, Gibberelic acid (GA), Salicyclic acid (SA), Cytokinins (CK), Auxins (Ax), these hormones are responsible for drought stress (Agarwal and Ray, 2023). These phytohormones are responses during water stress conditions. During stress, these phytohormones give numerous signal pathways and enhance antioxidant enzyme production, heat shock proteins and secondary metabolism (Ahmad*et al*., 2023). However, increases drought stress, and several phytohormones is required for study/ dissection for phytohormones is needed.

2.3.1 Abscisic acid

Abscisic acid is one of the most important phenomena for plant survival under drought stress. It regulates the differential processes such as physiological and developmental stage plant developmental, seed dormancy, stomata opening and synthesis of lipids and proteins. When osmotic stress occurred, then phytohormone responses to plants (Kambona*et al*., 2023). ABA controls the different morph-physiological process that helps plant to adopt to abiotic stress. ABA level of plants increases under drought stress. Under drought conditions, ABA increase and consequently it activates the drought response signaling pathway in plants (Ahmad*et al*., 2023). It triggers the various drought stress genes that are leading to stomata closing and improve root architecture under drought stress. Accumulation of ABA in plants leads to help in stomata closing.

Auxin

In addition, Auxin is another important drought stress hormones that control the growth and development and responds in unfavorable conditions such as drought. Biosynthesis of auxin takes place in leaf primordial, juvenile leaves and developing seed (Naikwade,2023).

Reactive oxygen species

Incomplete reduction of atmospheric oxygen leads to reactive oxygen species and, it is also known as active oxygen species (AOS) and reactive oxygen intermediate (ROI).

There are four types of ROS namely Hydroxyl radical (HO), hydrogen peroxicide (H2o2), Singlet oxygen (102) and superoxide anion radical (o2-) (Reddy*et al*., 2023). Plants activate diverse signaling pathways to regulate stress-responsive genes, leading to the production of various proteins, including enzymes, protein kinases, transcription factors, and other functional proteins. These molecules drive multiple metabolic and physiological responses, ultimately enhancing drought stress tolerance (Ma et al., 2024).Under drought conditions, imbalance of ROS level lead to intolerance of plants. Two important sources of reactive oxygen species i.e. metabolic and signaling ROS (Panda*et al*., 2024).

CYTOKINENIN

Cytokinenin is another important plant hormone, it promotes the cell division, development of root nodule, delay leaf senesces, allocation of regulate nutrient, plant interaction with pathogen and leads drought stress responses. Several mechanisms of cytokinenin that enhance drought tolerance include the protection of photosynthetic apparatus, an increase of antioxidant substances, regulation of water balance, and control of plant growth (Chieb and Gachomo, 2023). In addition, plants regulate the cytokinenin during drought stress which regulates the genes which is involved in electron transportation rate, chlorophyll level, increase photosynthetic rate and CO2 assimilation rate (Talaat, 2023).

Mapping of QTLs for drought tolerance

Conventional plant breeding was an efficient tool to detect the drought tolerance plant by morphology. But it takes more time for the detection of drought stress genotypes.

Moreover, molecular plant breeding has a good tool to detect the plant that can survive under drought stress.

The best method to detect the quantitative trait loci is QTLs mapping. This technique is mostly utilized by plant breeder nowadays. In this, first linkage is prepared to detect the location of genes where is located (Sood and Chauhan, 2023). Several important genomic regions have been detected by using the QTL mapping approach. This research facilitates the detection of QTLs associated with drought stress tolerance genes for complex traits in wheat. Both single-environment and multi-environment approaches are used for QTL detection, with multi-environment trials being more commonly employed to evaluate genotype performance. Detecting QTLs requires a mapping population, which can include both mortal and immortal populations, such as recombinant inbred lines (RILs), near-isogenic lines (NILs), backcross inbred lines (BILs), doubled haploids (DHs), and advanced backcross lines (ABLs) (Majhi et al., 2024).

Markers used for QTL mapping include restriction fragment length polymorphism (RFLP), amplified fragment length polymorphism (AFLP), simple sequence repeats (SSR), and single nucleotide polymorphisms (SNPs) (Rani et al., 2023).

Understand the mechanism of drought tolerance, a statistical power tool is needed, that include phenotypic and genotypic variation. Several approaches such as simple interval mapping (SIM), composite interval mapping (CIM), and multi-environment QTL mixed with a regression model have been used to dissect the drought stress traits (Sallam*et al*., 2024)

Several studies reveal about that these QTLs which mapped by breeders are stable with drought tolerance or not other any other stages. In addition, drought has an irreversible impact on seed germination, and seedling development stage, several studied have been identified drought impact on early vegetative growth by using QTLs mapping population in wheat (Hashmi*et al*., 2023).

TRAIT NAME	QTL NAME	MARKER NAME	MAPPING POPULATION	CHROMOSOME NUMBER	LOD	PVE (%)	ADDITIVE EFFECT	REFERENCES
DH(Days to Heading)	QDH.C.IM.wwc	SSR	84 DH	2D	7.69	34.8	2.88	Fatima *et al.* 2018
	QDH.C.IM.wwc			2D	3.89	21.4	-2.4	
	QDH.C.IM.wwc			6A	1.91	37.1	2.99	
	QDH.C.IM.wwc			6A	2	44.6	-3.41	
DPM(Days to Physiological Maturity)	QDPM.C.IM.wwc			1B	3.06	80.4	-5.98	
G/S(Grain per Spike)	QG/S.C.IM.wwc			6A	2.31	13.9	-4.81	
	QG/S.C.IM.wwc			7B	2.43	13.1	-4.55	
TGW(Thousand Grain Weight)	QTGW.S.IM.wwc			5A	2.14	59.5	7.97	
Sp-L(Spike length)	QSp.L.C.IM.wwc			6A	2.02	14	-0.68	
DH(Days to Heading)	QDH.C.MQ.wwc			2D	6.93	35.7	2.91	
	QDH.S.MQ.wwc			2D	3.14	72.1	-9.7	
DPM(Days to Physiological Maturity)	QDPM.C.MQ.wwc			2D	9.39	79.4	5.94	
Sp-L(Spike length)	QSp.L.C.MQ.wwc			4A	3.45	17.7	0.76	
	QSp.L.S.MQ.wwc			7A	4.93	31.9	-1.86	
TGW(Thousand Grain Weight)	QTGW.S.MQ.wwc			5A	2.03	10.8	-2.94	
G/S(Grain per Spike)	QG/S.C.MQ.wwc			6A	3.98	28.8	-6.75	
	QG/S.S.MQ.wwc			1B	2.41	27.2	-5.99	

FLA (flag leaf area)	qFLAWD	SSR	206 RIL	2D	5.7	12.7	-1.9	Chopra *et al.* 2019
	qFLAWD			2D	3.9	10.8	-1.9	
FLL(flag leaf length)	qFLLWD			2D	4.6	11.4	-1.3	
	qFLLWD			4B	3.9	10.3	-0.53	
FLW(lag leaf width)	qFLWWD			2D	3.6	10.1	-1.1	
	qFLWWD			5A	6.7	11.8	-1.9	
CMS(cell membrane stability)	qCMSWD			2D	3.9	10.8	-1.9	
	qCMSWD			3B	4.3	15.2	-2.59	
	qCMSWD			3B	6.8	13.8	-2.09	
Yld(grain yield)	QYld	869 Dart and 107 SSR	186 RIL	1A	6	19.7	0.4	Zandipour *et al.* 2019
	QYld			1B	4.4	9.1	0.28	
	Qyld			2D	5.8	8	0.54	
Byld (biological yield)	QByld			1B	5.1	9.8	0.34	
Sl(spike length)	QSl			7A	6.8	12.1	0.75	
	QSl			1B	5.8	11.8	0.75	
Spn(grain number per spike)	QSpn			4A	5.7	10.5	1.39	
Stw(stem weight)	QStw			1B	5.6	14.2	0.21	
	QStw			3B	3.8	9.9	0.18	
Ht(Plant height)	QHt			1B	3.4	8.3	−4.58	
Nn	QNn			2B	4.9	11.2	−0.10	
	QNn			3B	3.2	10.2	−0.10	
	QNn			2D	4.7	8	−0.9	
Yld(grain yield)	QYld			1B	4.4	9.1	0.28	
Byld (biological yield)	QByld			1B	5.1	9.8	0.28	
Sl(spike length)	QSl			1B	5.8	11.8	0.75	
Stw(stem weight)	QStw			1B	5.6	14.2	0.21	
Ht(Plant height)	QHt			1B	3.4	8.3	−4.58	
Leaf rolling	Qlr.nhv	3589 SNP and 72 SSR	92 RIL	1B	5.32	15.35	– 0.26	Verma *et al.* 2020
	Qlr.nhv			2A	10.85	12.03	– 0.32	
	Qlr.nhv			2A	5.64	12.13	– 0.27	
	Qlr.nhv			2D.2	4.21	15.8	– 0.31	
	Qlr.nhv			4A.1	14.18	15.26	0.36	
	Qlr.nhv			4A.2	5.13	13.43	0.24	
	Qlr.nhv			4A.2	5.06	11.38	0.26	
	Qlr.nhv			5D.1	11.47	14.01	0.35	
	Qlr.nhv			5D.2	17.19	20.1	– 0.41	
	Qlr.nhv			5D.2	5.84	16.08	– 0.26	
	Qlr.nhv			5D.2	6.45	14.25	– 0.29	

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