

A Review on Molecular Mechanisms of Wheat (*Triticum aestivum* L.) and Rice (*Oryza sativa* L.) against Abiotic Stresses with Special Reference to Drought and Heat

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ABSTRACT

Plants face to different changes in environmental conditions that keep on challenging its normal growth and acclimatization. Cereal crops play a key role in supplying food and energy to growing population and these crops are bare to substantial environmental changes causing inferior growth and performance. To overcome the abiotic stresses experienced by plants, several differential molecular and physiological responses were evolved that make the plants to mitigate climatic aberrations. Latest technological developments in genetic engineering as well as molecular breeding register a significant role in developing crop varieties and hybrids those are tolerant to environmental aberrations. Several Transgenes and their Quantitative Trait Locus (QTL) were invented and incorporated into crops for superior performances against abiotic factors in cereals like wheat and rice.

HIGHLIGHTS

- Growth and productivity of cereals are hampered due to abiotic stresses and under the present context of climate change there is the need for adoption of suitable measures.
- Understanding molecular mechanisms are important for development of suitable varieties/ hybrids of cereals combatting ill effects of abiotic stresses.

Keywords: Wheat, Rice, Abiotic stress, Drought stress, Heat stress

Agricultural production and productivity are severely affecting due to the rapidly changing climate across the globe. Due to growing human population, increasing demand of food is the major challenge of the present and future agriculture (Maitra *et al.* 2018). For human consumption as well as livestock feed, cereals are the vital source throughout the world for food material and nutritional components. Abiotic stresses due to water, salinity, cold and high temperatures represent the main constraint for agriculture and if affecting during the reproductive stage, cause significant loss in terms of productivity and quality. Abiotic stress is defined as the damaging

effect on living organisms by non-living factors in a specific environment. Abiotic stresses usually cause abnormal functioning of protein. The strategy is to obtain superior performance of crop species under abiotic stress conditions by identifying and modifying the molecular mechanisms that take place under environmental extremities. Drought and high-temperature stresses are predominant challenges to sustainable agriculture. Drought

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tolerance is the lenience of crops under the shortage of moisture in the cytoplasm when the water content constitutes ~23% or ~0.3 g of the fresh and dry tissue, respectively (Sahebi *et al.* 2018). Drought tolerance mechanisms, including physiological adaptations, morphological acclimation, and cellular adjustments, are regulated by genetic factors (Hossain *et al.* 2021). During the monsoon period, Eastern India faces shortage in precipitation that adversely impacts on crop production. Efficacious establishment, survival and yield of a crop mainly rely on the adaptation of the crop to abiotic conditions in which the crop grows. Further, the farmers' realization as well as national productions and food security are negatively influenced by the abiotic stresses. According to Kreps *et al.* (2002), up to 50% of agricultural production is lost due to different abiotic abnormalities, however, about 10 to 20% of crop damage is caused by biotic factors. By affecting sink potency and source capacity, stress due to high temperature influences the grain production and quality of wheat. Considering the above, more widespread approaches that comprise quantitative and qualitative studies of gene expression products are essential at the transcriptome, proteome, and metabolome stages. The specific proteins are developed under distinct abiotic stresses and therefore, precise importance will be given for stresses due to high temperature and soil moisture shortage by proteomics approaches. For enhancing stress tolerance QTL identification plays an important role (Fig. 1).

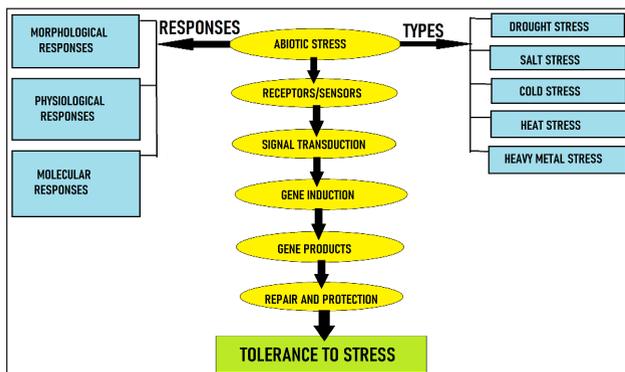


Fig. 1: Abiotic stresses and mechanism of plant molecular responses to environmental stresses for tolerance

To understand the process of plant growth in stress conditions, different functional genomic technologies make it feasible, for instance, metabolomics, proteomics, transcriptomics, and

next-generation sequencing. It is feasible to attain an exhaustive and comprehensive analysis by gathering all this information on the mechanism of plant protection against abiotic stresses. There are many genes control drought and these are complex traits, however, the most of these genes make a minor genetic impacts, but for genetically improved plants tolerant to drought these genes are of greater importance. According to Nezhadhamadi *et al.* (2013), by the year 2025, close to 65% of the world's population will live in a drought situation with 1.8 billion people facing complete water shortage.

Response of Wheat to Drought

Universally, drought is a major problem affecting quality and grain yield in wheat. Drought is caused due to shortage and uneven distribution of rain, soil moisture shortage and higher evapo-transpiration (ET) than soil moisture absorption by the plants. Water deficit signals in the roots during drought and convey the message to the leaves through multiple signalling pathways. The important signalling is caused by abscisic acid (ABA). Drought undesirably influenced the root traits and cell size of the piliferous layer (Adda *et al.* 2005) and severe drought stress significantly reduced root traits.

Proline

Proline accumulation occurs in wheat during drought stress and can be formed from pyrroline-5-carboxylate synthetase or P5CR (Gowda *et al.* 2011). According to Shao *et al.* (2008), there is a close relationship of proline content with soil moisture deficit threshold and wheat anti-drought. In transgenic wheat, stress-induced synthesis of proline helps to develop lenience mechanism to water deficit. According to Vendruscolo *et al.* (2007), the lenience to water shortage noted was mainly due to defence mechanisms against oxidative stress and not caused due to osmotic adjustment, more precisely in transgenic plants. Proline degradation is catalysed in the mitochondria by proline dehydrogenase (PDH) then P5C dehydrogenase (P5CDH) by sequential reactions, both of which are induced by gathering of proline in the cells. Thus, genes related to synthesis and degradation of proline are up-regulated where proline is accumulated.

According to Saddique *et al.* (2020) the speed of rice germplasm screening against water stress can be

expanded by utilizing the osmotic pressure initiated change in proline substances, Total Antioxidant Capacity (TAC) and the expression of OsP5CS in the rice seedlings as indicator attribute of drought tolerance. Synchronized heat and drought stresses are considered as more hazardous as compared to independently applied heat or water stress. In such cases, external application of proline (30 mM) stimulates the performance of the enzymes like SOD, POD, CAT, TSP and glycine betaine which helps in improvement of photosynthetic pigments and ultimately increases yield of the rice (Hanif, 2021).

Abiotic Stress Gene

According to Zhang *et al.* (2007), based on the functioning of methyltransferase and the SAM-binding motif, to transduce stress signals the SAM-binding motif of gene W89 was supposed to be related with other proteins or transcription factors and in an early stage of drought, it finally controls the expression of stress-responsive genes.

Heat Stress

In wheat, heat stress affects growth and productivity, predominantly at the grain development stage. Schapendonk *et al.* (2007) showed that the effects of the pre- and post-treatment growing temperature were more than the impact of a 3-day heat shock on yield. HSPs produced to deal with the high-temperature stress in different organisms are known to provide tolerance and repairing of the cellular damage caused by high temperature. Additional carbon assimilates and nitrogen inputs are needed for the inclusion of terminal heat tolerance into high-yielding cultivars (Mitra and Bhatia, 2008).

Molecular Responses of Drought Tolerance in Wheat

Some genes are manipulated by drought and produced different proteins related to drought stress and enzymes including dehydrins, late embryo abundant (LEA) protein, vacuole acid invertase, and glutathione S-transferase (GST) (Anderson and Davis, 2004), expression of ABA genes and synthesis of proteins like RAB, rubisco, helicase, proline (Fig. 2). Expression of ABA genes and carbohydrate are the molecular basis of drought tolerance. In stressful environments, plants respond

by modifying their gene expressions and protein productions. The available details on drought-responsive genes are still limited as their functions have not been completely determined. The junction stage is susceptible to drought because this phase is the linkage point in the vegetative and flowering growth phase and it is significant for growth and reproduction (Shi *et al.* 2010).

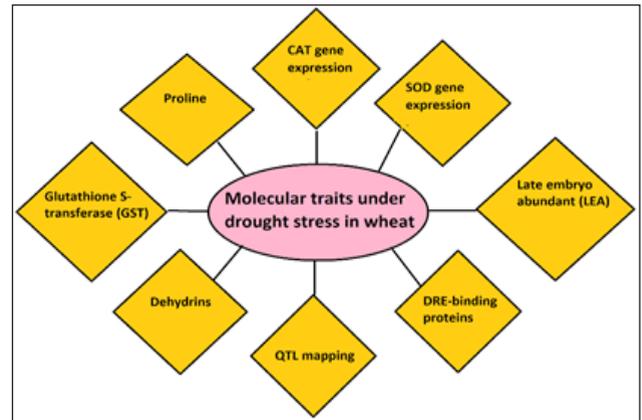


Fig. 2: Molecular traits under drought stress in wheat

According to Sivamani *et al.* (2000), the HVA1 gene promotes the enhancement of wheat growth under water stress conditions. A protein is formed by the HVA1 gene that is in group 3 LEA and has 11 amino acids. Proline is an essential protein that has the vital function in drought stress tolerance. Hong-Bo *et al.* (2006) narrated that the proline plays a vital role against drought under water stress conditions. In drought stress, gathering of late embryogenesis abundant (LEA) proteins are inclined and these proteins have been recognized through the amino acid sequence and help other proteins to recover after denaturation during drought stress. Protein constituent of groups one, two, and three of LEA were noticed in wheat. V-PPase genes in wheat, TaVP1, TaVP3, and TaVP2, were identified by Wang *et al.* (2009). Kam *et al.* (2007) also noticed the genes which are responsible in wheat for drought stress. In wheat, the Em gene encoded LEA protein the first group has also been reported. Ali-Benali *et al.* (2005) reported that group two (dehydrins) proteins and group four of LEA proteins in durum wheat. Transcripts of the Td27e, Td29b, and Td16 genes were saved late in embryogenesis and throughout the development of the seed. In embryo and endosperm, TaRZF74 and TaRZF59 were articulated and TaRZF38 and TaRZF70 were uttered in the



wheat root at the utmost level. A sequence of putative DREB labelled DREB3A (TaDREB3A, Gene bank ID: AY781349) from wheat to seclude a DREB from wild wheat and for recognition of its function in higher drought resistance (Lucas *et al.* 2011).

Molecular Responses for Drought Tolerance in Rice

Rice being the most important staple crop of the world (Ashkani *et al.* 2015) is grown under various levels of input conditions and provides up to 80% calories daily to individuals (Khush, 2005). Serraj *et al.* (2011) reported that nearly 23 million hectares of rain-fed rice face drought stress. By developing drought-tolerant varieties, in the future, it is possible to counteract drought stress in rice. Various abiotic stresses such as drought, salinity, high and cold temperature, etc. affect its yield depending on the environmental situations. Apparently, due to its petite root system, swift stomatal closure and thin cuticular wax rice is considered one of the most drought-susceptible plants. Genes responsible for abiotic tolerance in rice have been revealed that causes genetic variation in it by the characterization and screening of rice germplasm at a different molecular and genetic level under abiotic stress.

For drought tolerance, a wide range of genes are responsible that can be identified through significant advances in model plant species. In this regard, the genome sequencing has been done in various model crops inclusive of major plant species (Feuillet *et al.* 2011). A number of studies were carried out in this regard such as genome annotation, functional genomics and molecular physiology to find out candidate genes for drought tolerance in several models and major crops. Drought associated candidate genes express various proteins that perform magnificant roles in: (I) cellular protection by osmotic adjustment, structural adaptation, repair, degradation, and detoxification and (II) positive interactions with other proteins and transcription factors, namely, protein kinases and Bzip, MYB, and DREB associated in drought responses by modifying other responsive genes involved in protection of cell to fight with water stress in plants. Candidate genes should be established via approaches, such as qRT-PCR, expression analysis, linkage mapping, incorporation into QTL maps, TILLING, and allele mining, and applications of these approaches have

been reviewed previously (Varshney *et al.* 2005). One common approach for isolating the candidate genes responsible for drought stress in drought-resistant genotypes is the generation of expressed sequence tags from cDNA libraries of tissues collected under water stress. Another approach to identifying candidate genes is transcriptional profiling that includes the various gene expression analysis in plant tissues after the onset of drought stress, as well as between drought-tolerant genotypes and drought-susceptible genotypes (Hampton *et al.* 2010).

Management Options

To survive against abiotic stresses, numerous cultural practices has been long practiced. However, the utilization of the genetic/hereditary tools for this reason is latest inclusion. Previously Plant breeders gave major focus on development of high yielding genotypes which performed better under non stressful condition but at present due to fluctuating climatic conditions plants are more susceptible to different abiotic stresses. In recent studies, researchers have given more focus on developing stress tolerance varieties by practicing conventional and molecular breeding approaches (Farooq *et al.* 2009).

Conventional Approach

The choice of appropriate breeding programme for the development of tolerant cultivars to a distinct environmental stress depends on variety of factors such as screening techniques, sources and tolerance mechanisms, approaches of geneaction and heritability, and their association to agronomical traits. Conventional breeding techniques are used to develop drought tolerance lines in many cereals and leguminous crops like wheat, barley, maize, safflower, chickpea, common beans and soybean (Meena *et al.* 2017). One of the major challenges to apply this methodology is recognizing phenotypes that relate well with abiotic stress tolerance. Considerable work has been done in wheat to produce stress tolerance genotypes. A diploid wild species of bread wheat (*Aegilops tauschii*) was crossed with a tetraploid (*Triticum turgidum*) at CIMMYT (Valkoun, 2001). IRRI, Philippines is also working on developing drought tolerant rice cultivars using this typical old technique in plant



breeding. Similar research has been going on at ICARDA and ICRISAT to introduce the drought tolerant genotypes of major cereal crops (Ashraf, 2010).

Modern Breeding Approach

Conventional breeding approaches has been effectively utilized to develop abiotic stress tolerance varieties with high production but this practice has many limitations to develop multiple stress tolerant varieties. Marker assisted breeding has opened up opportunity to transfer genetic material from one species to another to identify abiotic stress tolerance traits. This reproducing technique used both sub-atomic and ordinary ways to deal with consolidate various characteristics followed by rigid choice during every age. This advanced breeding strategy uses both traditional and molecular approaches to integrate multiple traits and strict selection during respective generation. Marker assisted selection has played a very crucial role in development of rice genotypes with two or more genes/QTLs in short time (Pradhan *et al.* 2015). Dixit *et al.* (2020) developed seven introgression lines (ILs) using MAS breeding method and claimed that these ILs are performing better than their respective recurrent parents in terms of quality and overall agronomic performances. Dixit *et al.* (2017) developed drought tolerance NILs of a rice variety sabitri using marker-assisted backcross breeding in combination with phenotypic selection. Reynolds *et al.* (2012) studied several physiological trait based variations to fight against drought and heat stress at different growth phases of the wheat. Sinha *et al.* (2018) reported that expression analysis of the underlying candidate gene AK248593.1 in meta-QTL26 region discovered two times higher expression in the NILs carrying the co-localized SSR markers and claimed that the linked markers of the several meta-QTL regions linked with different traits can be used for effective transfer of the QTLs through marker assisted selection in wheat breeding.

Transgenic Approach

To fulfill the increasing need for food and to distinguish the detrimental impacts of abiotic stress on plants, it is crucial to produce transgenic lines that have further developed protection from a wide range of abiotic stresses (Noman *et al.* 2017). Ali and

Kim (2020) while studying on transgenic breeding approaches for improving abiotic stress predicted that application of CRISPR/Cas9 technology in various plant species could reform second green revolution in agriculture, which could be possible solution to fulfil the increasing demand of food and food security for the growing populations. Since last decade, a bunch of abiotic stress-related genes has effectively been relocated into rice to work on its obstruction against abiotic stresses. Numerous transgenic rice plants with improved abiotic stress-resilience have been identified (Zhao and Zhang, 2007). Huang *et al.* (2005) claimed that two transgenic varieties namely GM Xianyou 63 and GM-II-Youming 86 required minimal amount of pesticides (20%) and shown 6% increase in the production when compared with wild type rice. Introduction of such transgenic plants diminish the danger of wellbeing risks brought by pesticides, are harmless to the ecosystem and assist with expanding the overall gain for the farmer. In case of transgenic wheat, several genes have been recognized which deliberate drought tolerance and help to survival and plant growth development. Notwithstanding, less examination has been led for the improvement of transgenic wheat when contrasted with other cereal crops which might be due to the complex hereditary attributes of wheat (Araus *et al.* 2019).

Molecular Breeding for Drought Tolerance

In cereals, the genetic upgradation against drought greatly hinges on some factors such as the genetic resources availability, the complexity of the marked production system, selection strategies and the ability for implementing the cost-effective breeding process. Currently, the important focus is on detection and the genetic mapping of major QTLs performing under drought stress, and thus, development of drought resistant genotype marker assisted breeding programs will provide accurate phenotyping and integration of marker (Kumar *et al.* 2009). The selection of single secondary trait is not desired to be effective for improvement towards drought tolerance (Zhao *et al.* 2008). Before using marker-assisted selection the identified QTLs for grain yield, morphophysiological traits should carefully confirm. According to Chen *et al.* (2011), QTL detection with minimum inputs and could also create valuable materials for breeding with wide genetic variability for tolerating drought.

**Table 1:** Abiotic stress-responsive proteins in wheat and rice cultivars

Sl. No.	Species	Functions	Accession no.	Gene Name
1	<i>Triticum aestivum</i>	Heat shock protein 16.9 H	Q42417_WHEAT	hsp16.9- 17LC3
2	<i>Triticum turgidum subsp. durum</i>	Alpha-tubulin H	gi 82174009	atu3
3	<i>Triticum aestivum</i>	Aquaporin D,S,C	gi 161897630	PIP1-8
4	<i>Triticum monococcum</i>	Beta-amylase 1 H	gi 148529650	BAMY1
5	<i>Oryza sativa subsp. Japonica</i>	Calcineurin B-like protein 10 H,S	CNBLA_ORYSJ	CBL10
6	<i>Triticum aestivum</i>	Catalase I H	CATA2_WHEAT	CATA
7	<i>Triticum aestivum</i>	Cyclin dependent protein kinase D	gi 86438780	cdc2-1A
8	<i>Oryza sativa subsp. Indica</i>	Cyclin-B2-2 D	CCB22_ORYSI	CYCB2 -2
9	<i>Triticum aestivum</i>	Cyclophilin D,C	gi82547214	CYP23- d
10	<i>Oryza sativa</i>	Drought-induced S-likelibonuclease D	Q69JX7_ORYSA	P0569E
11	<i>Oryza sativa subsp. japonica</i>	Heat stress transcription factor C-1b H	HFC1B_ORYSJ	HSFC1 B
12	<i>Triticum turgidum subsp. durum</i>	Lipid transfer protein precursor D	Q9FEK9_TRITU	ltp7.1
13	<i>Triticum aestivum</i>	Small heat shock protein, chloroplastic H	HS21C_WHEAT	HSP21

D: Drought stress; H: Heat stress; S: Salt Stress; C: Cold Stress (Sources: Abu *et al.* 2010).

The molecular instruments in drought-tolerant plants are inclusive of (i) transcriptional activation and regulation leading to the activation of signal transduction cascade, (ii) proteins such as LEA proteins and chaperones HSPs (heat shock proteins), (iii) biosynthesis of proline, betaine, glycine, mannitol and trehalose, (iv) accelerated synthesis of chemical antioxidants, such as glutathione and ABA, (v) reactive oxygen species (ROS) toxicity reduced by glutathione S-transferase and superoxide dismutase (Aprile *et al.* 2009).

CONCLUSION

With the increasing population, demand for food and other commodities are also increasing significantly, however, the productivity of these crops is in risk with ever enhancing abiotic stresses that negatively impacting on the food security. Under such challenging circumstances, the selection of the crop varieties tolerant to these types of stresses is considered as achievable alternative to maintain the productivity of the crops in many regions. The role of molecular mechanisms is also widely discussed for each abiotic stress factor. Researchers have focused on mechanism of tolerance to abiotic stresses. Many innovative techniques have been developed to screen and identify the genotype for the tolerance to abiotic factors. Genotype with developed tolerance mechanism to different abiotic stresses may help to produce sustainable yield under stress affected conditions. The cumulative

effect of various abiotic stresses has become more complex, and that require new strategies to fight the stress factors for increased crop production. New advanced techniques in sequencing, marker development and genomic analysis have provided the opportunity to review the method of generating populations suitable for analysis.

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