# MOLECULAR BIOLOGY FOR DROUGHT RESPONSE IN DIFFERENT CROP PLANTS

**Abstract**

Various crop plants in agricultural fields' natural habitats are exposed to climatic changes and environmental stresses. It is estimated that suboptimal climatic and soil conditions (abiotic factors) result in an average yield loss of 75% for field-grown crops (Trontin et al., 2011). Consequently, understanding the physiological mechanisms underlying plant stress injuries is crucial for both agriculture and the environment (Osakabe et al., 2014). Stress tolerance involves two mechanisms, adaptation and acclimation, arising from integrated events at all organizational levels, from anatomical and morphological to cellular, biochemical, and molecular levels (Zhu et al., 2013). Transcription factors (TFs) play a pivotal role in regulating gene expression through transcription, allowing plants to adapt to harsh environments and abiotic stresses like drought. Genome-wide comparative expression profiles contribute to consolidating our understanding of the molecular mechanisms plants employ in response to drought stress. Throughout evolution, plants have developed adaptation mechanisms to water stress, aiding their survival during moderate drought and adjusting their water requirements to the local climatic conditions to maintain their ecological niche. Consequently, there is potential for developing moisture stress-resistant genotypes through gene pyramiding in marker-assisted selection (MAS) breeding (Janiak et al., 2016).

**Keywords:** Water deficit; Stress response; Resistance; Adaptation; Acclimation; Abscisic acid; Molecular network; Marker assisted pyramiding

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## List of Abbreviation

ABA- Abscisic Acid
AD-Activation Domain
ADH- Alcohol Dehydrogenase1
ADP- Adenosine di-phosphate
ATP- Adenosine tri-phosphate
BC- Back Cross
CDPK- Calcium Dependent Protein Kinases
DPA- Days Post Anthesis
DREB- Drought Responsive Elementary Binding protein
FBPase- fructose-1, 6-bisphosphatase
HLH- Helix Loop Helix
HSP- Heat Shock Proteins
LEA- Late embyogenesis protein
MAPK- Mitogen Activated Protein Kinase
MAS- Marker Assisted Selection
NADP-ME- NADP-malic enzyme,
NCED- 9-c*is*-epoxy Carotenoid Dioxygenase3
PEPCase- Phosphoenol Pyruvate Carboxylase
PPDK- Pyruvate ortho phosphate dikinase
QTL- Quantitative Trait Loci
ROS- Reactive Oxygen Species
RUBISCO- 5-bisphosphate carboxylase/ oxygenase
SNAC- Stress-responsive NAC
SSR- Simple Sequence Repeat
TFs- Transcription factors
TPS-Trehalose 6- phosphates
UDP- Uridine di-phosphates
UGP- UDP-glucose pyrophosphorylase
WUE- Water Use Efficiency

 

## I. INTRODUCTION

In both natural and agricultural condition, plants are usually exposed to environmental stress such as drought, salinity, elevated temperature, water flood, nutrient deficiencies and heavy metal toxicity. It might be abiotic or biotic stress that affect on plant growth and development and ultimately that limits crop production or yield. Biotic or abiotic stress, their impact depends on their adverse force, and based on it only different biological systems will be applied in a plant. Whereas abiotic stress is arises from an excess or deficit in the physical or chemical environment conditions. Factors responsible for abiotic stress includes water logging, high temperature, too much light, excessive soil salinity, heavy metal toxicity, drought, low temperature, too little light, inadequate mineral nutrients in soil

Prosperity of Indian economy wholesome depends upon positive strides in agricultural and industrial sectors. In the new era, sustainable agriculture will be the need of the hour in the context of global and liberalization trends. Crop production encounters various biotic and abiotic stresses particularly in the arid and semiarid regions. Below Table 1. shows, the decreasing different crops productivity in India is more due to abiotic stress (Trontin *et al.,* 2011).

**Table 1: Impact of stress in different crops production**

| Crops | Average losses (Kg/hec) | | % of yield loss due to abiotic stress |
|---|---|---|---|
| | Biotic | Abiotic | |
| Corn | 1952 | 12700 | 65.8 |
| Wheat | 726 | 11900 | 82.1 |
| Soybean | 666 | 5120 | 69.3 |
| Sorghum | 1051 | 16,200 | 80.6 |
| Oat | 924 | 7960 | 75.1 |
| Barley | 765 | 8590 | 75.4 |
| Potato | 17775 | 50900 | 54.1 |
| Sugar beet | 17100 | 61300 | 50.7 |

Drought is the major environmental factor that limits crop growth and yield globally. Drought can be defined as any water content of a tissue or cell that is below the highest water content exhibited at the most hydrated state. It implies the absence of rainfall for a period of time that decrease of water potential in plant tissue and if their is long enough to cause moisture depletion in soil then it forms drought situation. . For example, as cotton is grown in India in three distinct agro-climatic regions. In the state of North Zone like Punjab, Haryana, Rajasthan, area under cotton cultivation is 2.56, 4.98 and 4.42 lakh hectares with productivity level of 598, 683 and 692 kg/ha, respectively, whereas in Central India which includes Gujarat, Madhya Pradesh and Maharashtra the area is 24.00, 5.99 and 38.06 lakh hectare with productivity level of 673, 398 and 596 kg/ha, respectively and Southern Zones states, Karnataka, Andra Pradesh and Tamilnadu comprises area 6.33, 6.66 and 1.42 lakh hectare with productivity level of 537, 613 and 599 kg/ha, respectively (Anon., 2017). The lower cotton productivity was due to its cultivation under rainfed condition more in the state of

 

Maharashtra and Karnataka. It indicates that moisture stress is now major limiting factor in reducing our country cotton productivity level. Therefore improving crop performance under water limiting conditions is an important research focus of plant scientists around the world and this chapter will gives an idea for understanding different mechanism of plant response towards abiotic stress.

## II. RESISTANCE MECHANISM OF ABIOTIC STRESS

The plant's response to drought resistance varies depending on environmental conditions and soil moisture levels. The concept of stress is closely associated with stress tolerance, signifying the plant's ability to cope with an unfavorable environment that involves a complex array of mechanisms forming a complex phenomenon. The terms stress resistance and stress tolerance are used interchangeably. If a plant's tolerance mechanism increases due to prior stress exposure, the plant is considered acclimatized (or hardened). Acclimation differs from adaptation, which refers to a genetically determined level of resistance acquired through a process of selection over many generations. Regrettably, the term adaptation is also used in the literature to describe a plant's acclimation to abiotic stress by utilizing information from biological mechanisms during prior stress exposure—a process known as acclimation or defense priming. Gene expression plays a crucial role in acclimation by making changes to biological mechanisms. Adaptation and acclimation to environmental stresses involve integrated events occurring at all levels of organization, encompassing morphological, physiological, and biochemical aspects, as well as the encoding of gene expression. Various factors, such as species, genotype, and developmental stage, contribute to resistance. Research at the genomics, proteomics, metabolomics, and physiological levels has been fundamental in advancing our current understanding of the plant's response to stress.

1. **Plant Response and Acclimation Strategies for Abiotic Tolerance:** A stress response is initiated when plant recognizes stress at cellular level through activation of signal transduction pathway that transmit information within the individual cell and the signal passes throughout the plant cell which allow changes in gene expression that may leads to modification in growth and development. This changes result in acclimation of plants under stress condition. This acclimation include first morphological change in enhanced root extension and other changes like leaf rolling, decreased leaf area, leaf abscission, wax coating on leaf. However, leaf wilting in response to water deficit serves to mitigate both water loss from the leaf and exposure to incident light, consequently reducing heat stress on leaves. At the biochemical level, plants undergo various metabolic adjustments to cope with environmental stresses, including the production of osmoregulatory compounds such as proline and glycine betaine. Cellular responses to stress encompass alterations in the cell cycle and cell division, modifications in the endo-membrane system with vacuolization of cells, and adjustments in cell wall architecture, collectively contributing to enhanced stress tolerance in cells. Molecular events that link the perception of a stress signal with the genomic response leading to abiotic tolerance depict a complex gene network. The ensuing molecular network illustrates the intricacy of the gene network responsible for regulating physiological, biochemical, and morphological mechanisms in plant responses to stress tolerance.

 

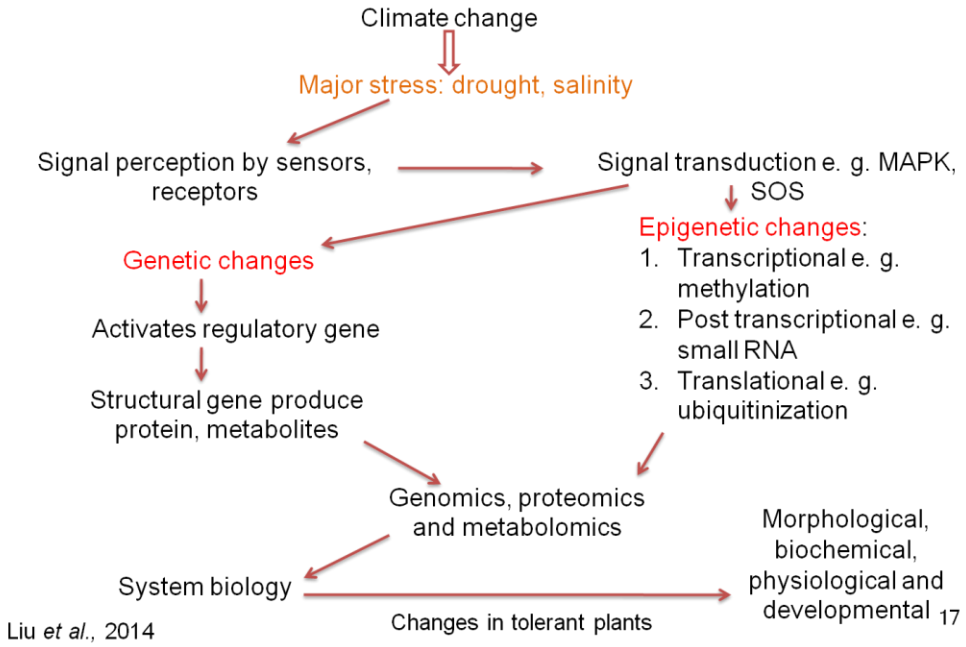


**Figure 1:** Complexness of plant response to various abiotic stresses

2. **Mechanism of Plants Response to Moisture/ Drought Stress:** Plant growth relies on photosynthesis; however, excessive exposure to light can inflict significant damage to plants. The surplus light induces photo-oxidation, leading to an increased production of highly reactive oxygen species that adversely affect various biological molecules. If the stress severity is heightened, it may result in a substantial decrease in plant productivity (Li et al., 2009). Drought stress induces a reduction in leaf water potential, causing stomatal closure, which, in turn, down-regulates genes related to photosynthesis. This reduction in the expression of photosynthesis-related genes, combined with a diminished availability of CO2, is recognized as a major factor contributing to excess light stress (Osakabe and Osakabe, 2012).

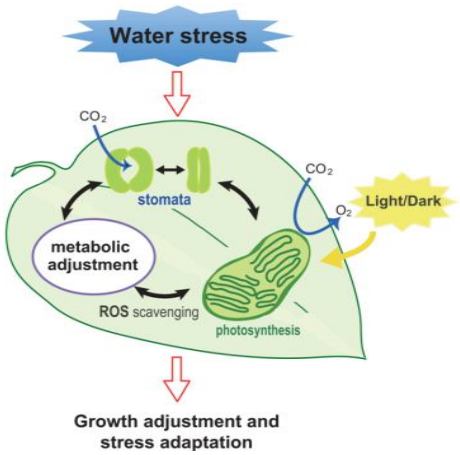


**Figure 2:** Plant response to drought

Various stress responses involve different molecular networks encoded with signal transduction pathways (Nishiyama et al., 2013; Osakabe et al., 2011, 2013b). Elucidating these networks is indispensable for improving the stress tolerance of crops. The plant's response is governed by complex regulatory pathways mediated by abscisic acid (ABA) signaling, ion transport, and the activities of transcription factors (TFs) that regulate stomata under drought conditions. All these pathways are integrated into orchestrated molecular networks, enabling plants to adapt and survive under severe drought conditions. Endogenous ABA is rapidly produced during drought, triggering a cascade of physiological responses that result in stomatal closure. In Arabidopsis, 9-cis-epoxy carotenoid dioxygenase3 (NCED3) catalyzes a key step in ABA biosynthesis, and NCED3 expression is rapidly induced by water stress in a vascular tissue-specific manner. In drought stress, accumulated ABA in the vascular tissue is transported to guard cells via passive diffusion in response to a change in pH by specific transporters. Two members of the membrane-localized ABC transporter family, ABCG25 and ABCG0, and one member from a nitrate transporter family, AIT1/NRT1.2/NPF4.6, similar to ABCG25, are expressed in yeast cells and activate transporters for drought response.

- **Closure of Stomata During Water Deficit in Response to Abscisic Acid:** Abscisic acid (ABA) binds to plant cell receptors, and this binding induces the generation of reactive oxygen species (ROS), which, in turn, activate plasma membrane Ca2+ ion channels. ABA elevates the levels of cyclic ADP-ribose and inositol tri-phosphate (IP3), subsequently activating additional calcium channels on the tonoplast. The influx of calcium triggers intracellular calcium oscillations and facilitates further calcium release from the vacuoles. The increase in intracellular calcium inhibits K+ in channels and induces the opening of channels on the plasma membrane, leading to the efflux of Cl–, causing membrane depolarization. ABA inhibits the plasma membrane proton pump, resulting in increased cytosolic calcium, a rise in intracellular pH, and further membrane depolarization. Membrane depolarization activates K+ efflux channels. Initially, K+ and anions (Cl–) released across the plasma membrane originate from vacuoles into the cytosol.

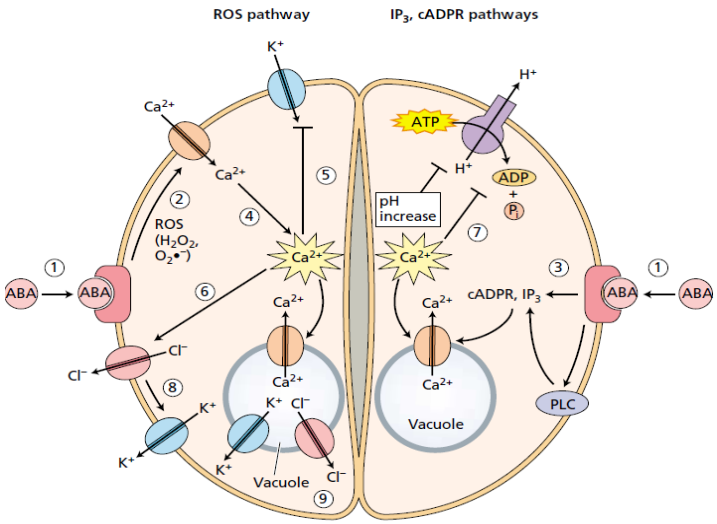


**Figure 3:** Regulation of gene expression mediated by Abscisic acid

 

ABA has been observed to regulate the expression of numerous genes across various growth stages, including seed maturation, and in response to specific stress conditions like heat shock, salinity, and extreme temperatures (Rock, 2000). In plants, the presumed role of ABA and stress-induced genes is to contribute to adaptive mechanisms for tolerance. Instances exist where ABA has been demonstrated to stimulate the transcription of several genes. Examples include late embryogenesis abundant (LEA) and chaperone genes, along with genes associated with reactive oxygen species (ROS), ion homeostasis, and signaling. Additionally, crucial transcription factors involved in regulating drought-responsive genes, such as MYB, MYC, DREB/CBF (drought-responsive cis-element binding protein/C-repeat-binding factor), ABF/AREB, NAC, and WRKY, have been identified (Nakashima et al., 2009).

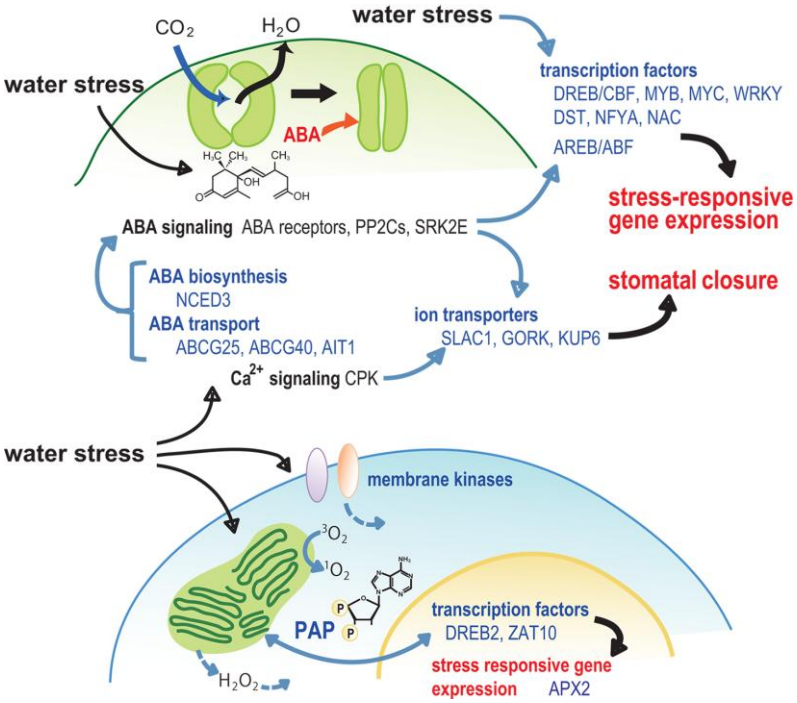


**Figure 4:** Stomatal closure in response to water stress

The activation of genes by ABA is facilitated by various transcription factors under stress conditions, where the induction of gene expression can be either ABA-dependent or independent. Additional transcription factors have been identified to specifically mediate responses to salt, cold, and drought. ABA-responsive cis-element-mediated transcription through ABF/AREB is directly regulated by an ABA receptor complex involving SnRK2, which activates ABF/AREBs through phosphorylation (Umezawa et al., 2010). In rice, SNAC1 (STRESS-RESPONSIVE NAC1) is expressed in rice guard cells, and overexpression of this gene enhances ABA sensitivity and stomatal closure in rice (Hu et al., 2006). Transcription factors AtMYB60 and AtMYB61, predominantly expressed in guard cells, play a role in regulating stomatal aperture and drought tolerance in plants (Cominelli et al., 2005).

## 3. Effect of Drought Stress on Photosynthesis :

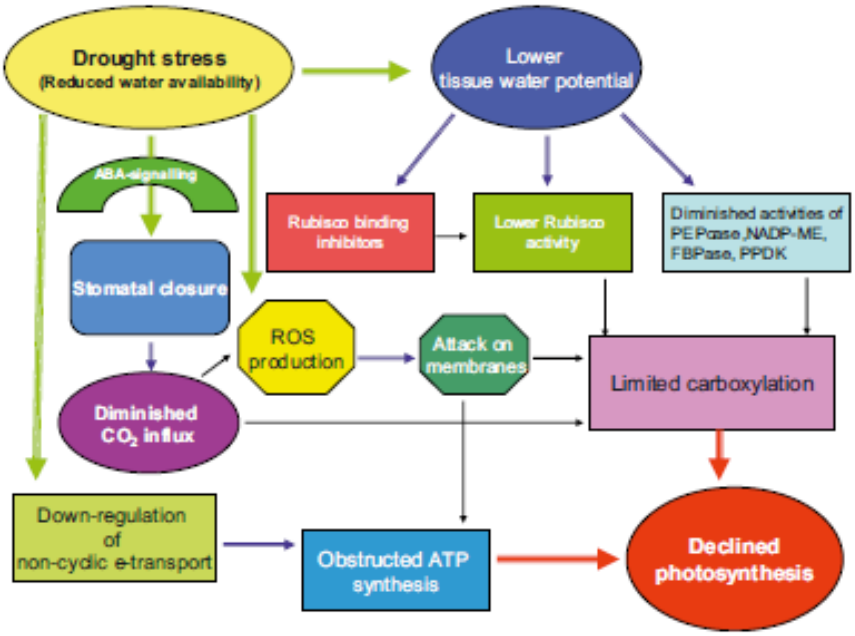


**Figure 5:** Plant response to Photosynthesis under drought

Drought stress disrupts the equilibrium between reactive oxygen species (ROS) production and antioxidant defense, leading to ROS accumulation and subsequent oxidative stress. As the available water in the soil diminishes, plants respond by closing their stomata, primarily through ABA signaling, resulting in decreased CO2 influx. The reduction in CO2 not only directly impacts carboxylation but also channels more electrons to generate ROS. Severe drought conditions adversely affect photosynthesis by diminishing the activities of key enzymes such as phosphoenol pyruvate carboxylase (PEPCase), ribulose-1, 5-bisphosphate carboxylase/oxygenase (Rubisco), NADP-malic enzyme (NADP-ME), fructose-1, 6-bisphosphatase (FBPase), and pyruvate orthophosphate dikinase (PPDK). Additionally, reduced tissue water content under drought stress enhances the activity of Rubisco binding inhibitors. Furthermore, non-cyclic electron transport is down-regulated to align with the decreased requirements for NADPH production, thereby reducing ATP synthesis. While the photosynthetic rate per unit leaf area is less responsive to mild water stress due to the lower sensitivity of photosynthesis to turgor compared to leaf expansion, mild water stress typically affects both leaf photosynthesis and stomatal conductance. This is observed in many plant species where leaf expansion is highly sensitive to water stress, leading to complete inhibition under mild stress levels that minimally impact photosynthetic rates (Taiz and Zeiger, 2010). Water stress induces reductions in both photosynthesis and assimilate accumulation in expanding leaves, indirectly diminishing the export of photosynthates from leaves. Given that phloem transport relies on turgor, decreased water potential in the phloem during stress may hinder assimilate movement. Notably, experiments have indicated that translocation remains unaffected until late in the stress period when other processes, such as photosynthesis, have already been significantly inhibited (Taiz and Zeiger, 2010).

 

4. **Osmotic Adjustment Under Drought Condition:** Osmotic adjustment refers to alterations in solute content per cell and is not contingent on volume changes resulting from water loss. The reduction in water potential is typically confined to approximately 0.2 to 0.8 MPa, unless dealing with plants adapted to extremely arid conditions. The majority of the adjustment can usually be attributed to an increase in the concentration of various common solutes, including sugars, organic acids, amino acids, and inorganic ions (especially K+). These additional solutes, termed compatible solutes (or compatible osmolytes), are organic compounds that do not disrupt enzyme function. Commonly accumulated compatible solutes include proline, sugar alcohols (e.g., sorbitol and mannitol), and a quaternary amine called glycine betaine. By replacing water molecules, glycine betaine prevents contact between solutes and biomolecules, ensuring that the structure of proline remains unchanged due to solute accumulation. This process minimizes the loss of turgor, facilitating the continuous progression of stomatal opening and growth expansion even at lower water potentials.

In cotton carbohydrates and fatty acid metabolism related gene.*(trehalose phosphate synthase-TPS)*, highly expressed at 10 dpa (44.5 fold) as compared to 5 dpa and leaf suggests a role in fibre elongation under stress. TPS geneighly expressed in *G. hirsutum* leaves in both types of genotypes, water-deficit sensitive and tolerant under water deficit condition. Sucrose synthase (*SUS*) genes was differentially expressed at various stages. For instance, *SUS3* was shown to be involved in fibre cell initiation, elongation and in the seed development (Ruan *et al.*, 2003). Up-regulation of SUS3 at 0, 5 and 20 dpa suggests its role in the crop development as well as in drought stress adaptation. UDP-Glc (UDP-D-glucose) is a central metabolite in carbohydrate metabolism and is precursor for synthesis of cell wall disaccharide, sucrose and polysaccharides such as pectin, hemicelluloses and cellulose. UDP-Glc is synthesized by UDP-glucose pyrophosphorylase (*UGP1*) from glucose-1- phosphate and by SUS from sucrose (Kim *et al.*, 2013).

## III. MOLECULAR APPROACH FOR ABIOTIC STRESS TOLERANCE MECHANISM

Since Mendel's groundbreaking discoveries in his pea garden, it has been firmly established that the growth, development, and responses of even the simplest microorganisms are determined by the programmed expression of their genes. The initial stage in gene expression is transcription, involving the synthesis of an mRNA copy from the DNA template encoding a protein. In multicellular organisms, the activation or inhibition of genes modifies a cell's array of enzymes and structural proteins, enabling cells to undergo differentiation. Various aspects of plant development are linked to the regulation of gene expression. Genes encoding proteins that directly shield plant cells against dehydration (dehydrins), heat stress (heat stress proteins, chaperones, LEA proteins), osmotic stress (osmoprotectants like glycine betaine, mannitol, sorbitol, trehalose, polyamines, and proline), freezing (antifreeze proteins), and detoxification enzymes and free-radical scavengers are involved. Additionally, genes such as calcium-dependent protein kinases (CDPKs), mitogen-activated protein kinases (MAPKs), SOS kinase, phospholipases, and transcription factors play roles in signaling cascades and transcriptional control. Genes encoding aquaporins and ion transporters participate in water and ion uptake.

 

1. **cis-acting Regulatory Sequences Control Transcription in Eukaryotes:** The minimal promoter for genes transcribed by RNA polymerase II typically spans around 100 base pairs upstream of the transcription initiation site and encompasses several sequence elements known as proximal promoter sequences. The TATA box within the promoter plays a crucial role in transcription by serving as the assembly site for the transcription initiation complex. In addition to the TATA box, the minimal promoters of eukaryotes also include two additional regulatory sequences: the CAAT box and GC box. These sequences serve as binding sites for transcription factor proteins that enhance the transcription rate by facilitating the assembly of the initiation complex. Termed cis-acting sequences, these DNA sequences are considered such because they are adjacent to the transcription units they regulate. The transcription factors binding to the cis-acting sequences are referred to as trans-acting factors since the genes encoding them are located elsewhere in the genome.

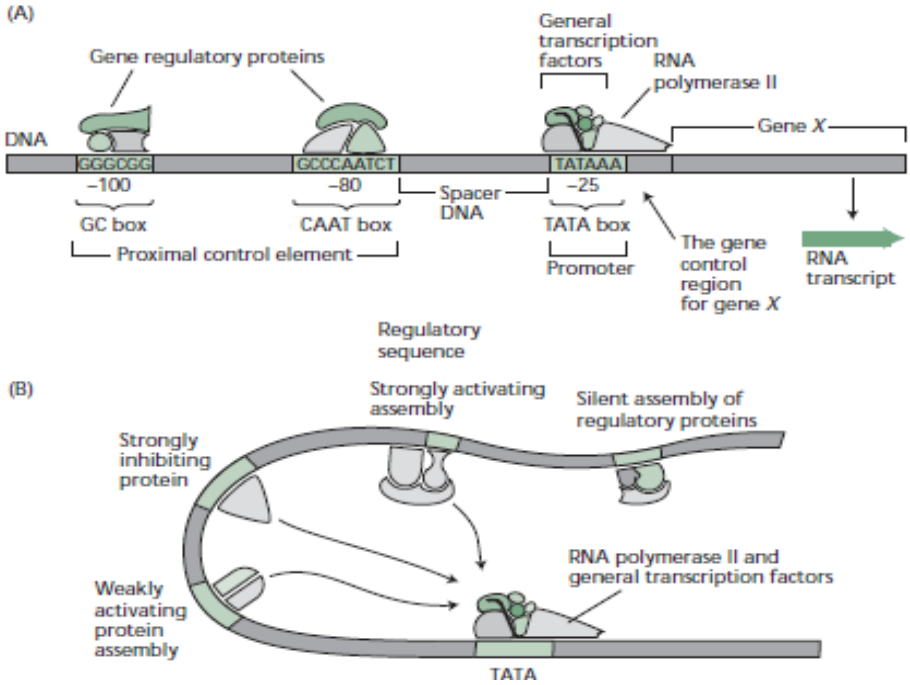


**Figure 6:** cis-acting regulatory sequence controls transcription in eukaryotes

Various cis-acting sequences situated upstream of the proximal promoter sequences can exert either positive or negative control over eukaryotic promoters. These sequences, known as distal regulatory sequences, are typically located within 1000 base pairs of the transcription initiation site. In prokaryotes, positively acting transcription factors binding to these sites are termed activators, whereas those inhibiting transcription are referred to as repressors. Gene regulation manifests as an increase in the specific mRNA quantity, enhanced translation, stabilized protein, and alterations in protein activity through transcription factors.

 

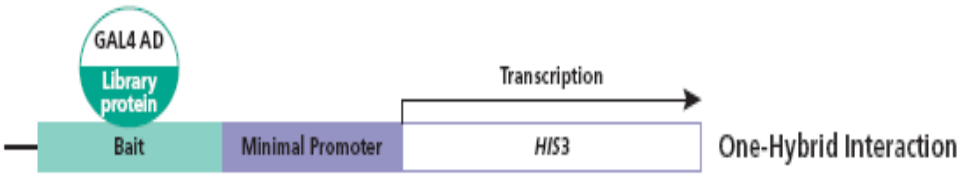


**Figure 7:** Gal4 - DNA-binding transactivator

Gal80 binds Gal4 and inhibits its transcriptional ability. Whereas in the presence of galactose, Gal 3 binds and causes a conformational change in Gal80, which then allows Gal4 to function as a transcriptional activator.

- **Types of DNA Binding Domain**

  - Zinc finger motif
  - Leucine motif
  - helix-turn-helix motif
  - helix-loop-helix (HLH)

**2. Strategy for the Isolation of cDNAs encoding DRE Binding Proteins by Selection in Yeast.**

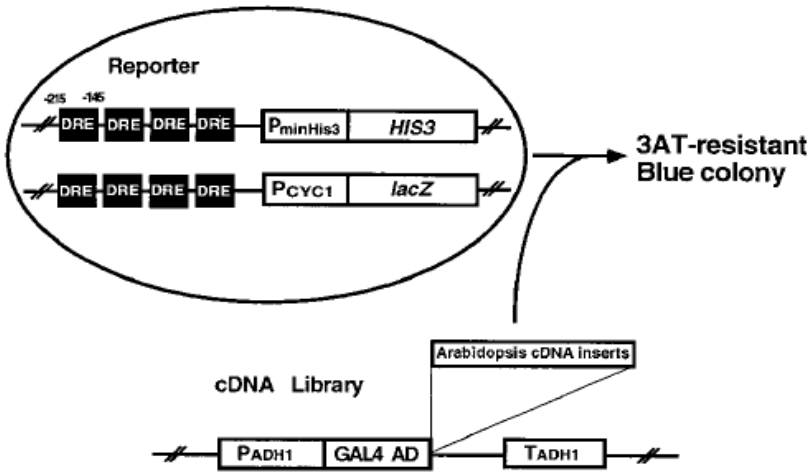


**Figure 8:** Isolation of cDNAs Encoding DRE Binding Proteins by yeast cell

An expression library containing hybrid proteins was introduced into a yeast strain harboring dual reporter genes, HIS3 and lacZ, governed by the 71-base pair promoter region of rd29A that includes the drought-responsive elements (DRE). Hybrids comprising protein coding sequences fused to the end of the GAL4 activation domain (AD) recognize the binding site, acting as transcriptional activators for the reporter genes. This activation allows cells to thrive in the presence of 3-AT, a competitive inhibitor of the HIS3 gene product, and results in the cells turning blue in the β-galactosidase assay. The designations PminHis3 and PCYC1 refer to the minimal promoter regions of the

 

HIS3 gene and yeast cyclin gene, respectively. PADH1 designates the alcohol dehydrogenase1 (ADH1) gene promoter, while TADH1 indicates the terminator of the ADH1 gene (Liu et al., 1998).

The expression of the DREB1A, DREB2A, and rd29A genes in response to dehydration, low temperature, high salt, or ABA was assessed in Arabidopsis. Each lane contained 20 mg of total RNA from 3-week-old non-bolted Arabidopsis plants subjected to dehydration (Dry), grown at 48°C (Cold), hydroponically cultivated in 250 mM NaCl after transfer from agar plates, hydroponically grown in 100 mM ABA after transfer from agar plates, or hydroponically grown in water after transfer from agar plates, as outlined in the Methods section. The number above each lane indicates the duration, in minutes or hours, following the initiation of treatment before RNA isolation. RNA was examined using RNA gel blotting, employing gene-specific probes derived from the 3' flanking sequences of DREB1A, DREB2A, and rd29A (Liu et al., 1998).

## IV. DEVELOPMENT OF DROUGHT TOLERANT CROP THROUGH MOLECULAR BREEDING PROGRAM:

To enhance plant productivity under limited water resources, a comprehensive understanding of plant mechanisms in response to water deficit stress is imperative. Two primary approaches, conventional breeding and genetic engineering, have been employed to promote sustainable and water-efficient agricultural production. Successful implementation of these approaches hinges on a profound comprehension of plant responses to drought stress. Therefore, the identification of differentially expressed genes in response to water deficit stress is a crucial step in advancing both conventional breeding and genetic engineering strategies.

1. **Molecular Markers for Drought Tolerance:** Genetic mapping using molecular markers enhances our comprehension of the intricate genetic underpinnings of drought tolerance (Ashraf, 2009). Complex traits can be deconstructed into quantitative trait loci (QTLs) to map genetic locations using DNA markers (Choudhary et al., 2008). This approach allows the identification of chromosomal regions containing genes associated with drought tolerance. An F2 population was generated through intraspecific crossing between a drought-tolerant genotype (FH-207) and a drought-susceptible genotype (FH-901) of G. hirsutum. A screening of 2365 EST-SSR primers revealed polymorphisms between the two contrasting parents, FH-207 and FH-901, resulting in 100 polymorphic primers used to score the F2 population for QTL mapping (Choudhary et al., 2008). In the QTL analysis, a total of six QTLs were identified for five different morphological and physiological traits. Biometric parameters of individual QTLs affected excised leaf water loss, relative leaf water content, cell membrane stability, stomatal size, and stomatal frequency. The linkage groups indicating the position of QTLs for different traits are depicted in the figure. Two QTLs for relative leaf water content were identified on chromosome A5, with one QTL each on chromosomes A7, A1, A6, and A13 for excised leaf water loss, cell membrane stability, stomatal size, and stomatal frequency, respectively (Amjid et al., 2015).

 

2. **Marker Assisted Pyramiding of Drought Yield QTL:** The distribution in each stage of BC1F3 development is illustrated in Fig. 1. In the initial season, 96% of the entire F1:1A population from Cross 1, 94% of the complete F1:1B population from Cross 2, and 96% of the complete F1:1C population from Cross 3 demonstrated alleles from both parents (heterozygous). This confirmed their authentic hybrid nature, as validated by employing peak simple sequence repeat (SSR) markers at each qDTY locus (RM236 for qDTY2.2, RM520 for qDTY3.1, and RM511 for qDTY12.1). In the subsequent season, Cross 4 was initiated to develop the F1(2) population, formed by crossing five confirmed F1:1A individuals with 20 confirmed F1:1B individuals. Out of 587 genotyped F1(2) individuals, only 14 displayed donor alleles at both the qDTY2.2 and qDTY3.1 loci when assessed with the peak and foreground SSR markers specific to these loci. Moreover, merely 33 BC1F2 individuals carried all three qDTYs.

Out of a comprehensive pool of 437 BC1F2 individuals exhibiting homozygosity at various qDTY loci and their combinations, a subset of 198 BC1F2 individuals was ultimately chosen due to their morphological resemblance to MR219. This selected group was subsequently progressed into the 7th season to generate 198 BC1F3 families comprising pyramided lines (PLs) (Shamsudin et al., 2016).

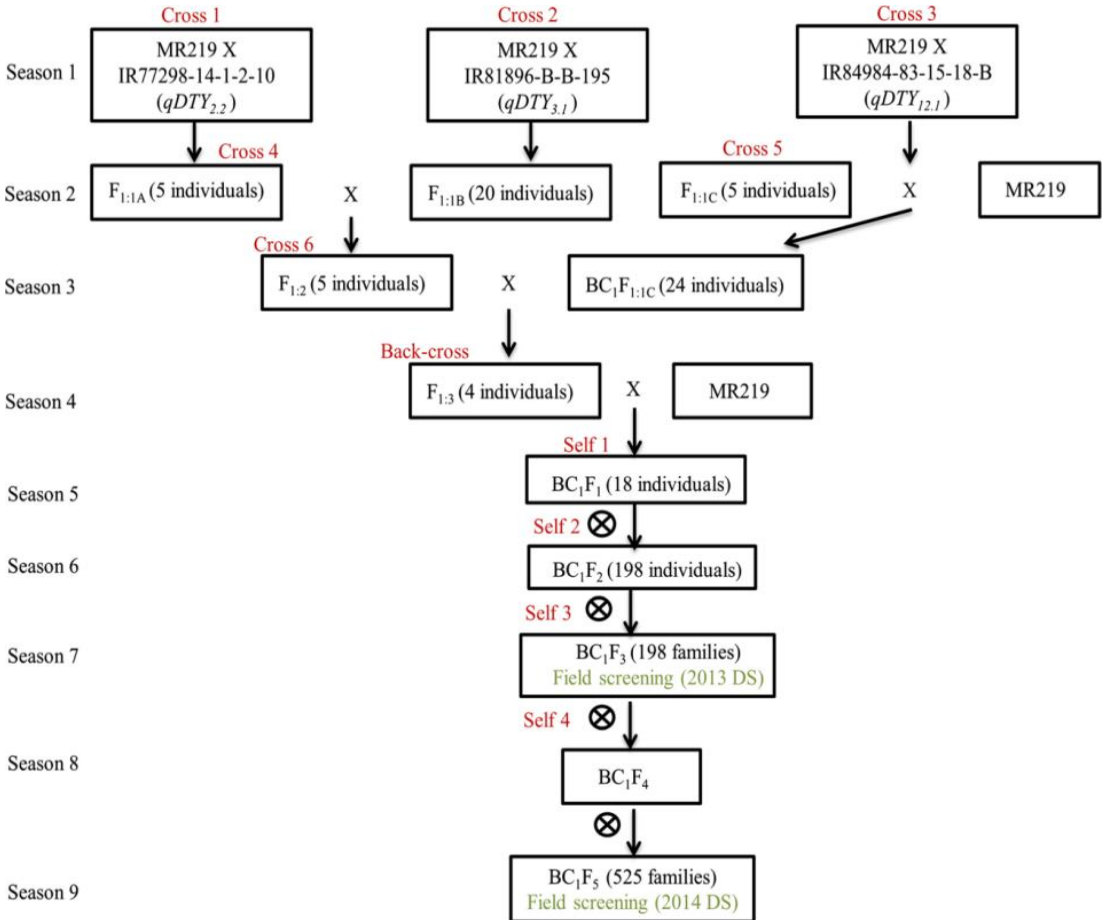


**Figure 9:** Marker assisted pyramiding of drought yield QTL

 

## V. SOME DROUGHT RESPONSIVE GENES INVOLVED FOR RESISTANCE MECHANISM

There are different classes of genes responsible for drought tolerance at molecular level that encode proteins that directly protect plant cells against dehydration such as dehydrins, heat stress proteins or chaperones, LEA proteins, osmoprotectants, antifreeze proteins, detoxification enzymes and free-radical scavengers. Genes that encode proteins that directly protect plant cells against dehydration (dehydrins), heat stress (heat stress proteins, chaperones, LEA proteins), osmotic stress (osmoprotectants such as glycine betaine, mannitol, sorbitol, trehalose, polyamines, and proline), freezing (antifreeze proteins), detoxification enzymes and free-radical scavengers. Some of the genes such as as calcium-dependent protein kinases (CDPKs), mitogen-activated protein kinases (MAPKs), SOS kinase, phospholipases and transcriptional factors are involved in signaling cascades and in transcriptional control Also, genes encoding to aquaporins and ion transporters are involved in water and ion uptake.

The genes responsible for late embryogenesis abundant proteins play a crucial role in safeguarding various cellular functions. These functions include the protection of cytosolic structures, ion sequestration, protein renaturation, transport of nuclear-targeted proteins, prevention of membrane leakage, and protein stabilization. The induction of heat shock protein (HSP) transcription is a universal response across all living organisms. In plants, these proteins are categorized into five classes based on their molecular weight: (1) Hsp100, (2) Hsp90, (3) Hsp70, (4) Hsp60, and (5) small heat-shock proteins (sHsps). Higher plants typically possess a minimum of 20 Hsps, and some plant species may have up to 40 different types of these Hsps. This diversification is thought to represent an adaptive response of plants to heat stress (Whaibi et al., 2010).

## VI. CONCLUSION

In response to water deficit stress in field, we can identify differentially expressed transcription factors (TFs). This global expression analysis generated sequence information for TFs, distribution of functional categories, and homologous genes. There is a possibility of developing moisture stress resistant genotypes by gene pyramiding through marker assisted breeding. The combination of molecular changes in gene regulation and signal transduction results in enhanced activity of ROS-related defense mechanisms and HSP driven protection machinery to provide cellular redox homeostasis and stabilization of functionally or structurally important proteins.

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