

**Review Article**DOI: <https://doi.org/10.30750/ijpbr.6.4.7>**Transgenic plant tolerant to drought**H. B. Savaliya<sup>1</sup> and T. A. Faldu<sup>2</sup><sup>1</sup>N. M. College of Agriculture, NAU, Navsari, Gujarat, India.<sup>2</sup>Collage of Agriculture, AAU, Anand, Gujarat, India.**ARTICLE INFO:****Article history:**

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Drought is the single largest abiotic stress factor leading to reduced crop yields. Approximately one-third of the Earth's land area is arid or semi-arid. The situation is aggravated by the shortage of water resources because of widespread water pollution and unpredictable climatic change. Water availability is particularly critical for agricultural crops to maintain high yields in variable growing seasons. Thus, agricultural drought, namely water deficiency, adversely affects plant and crop production by reducing leaf size, stem extension and root proliferation, disturbing plant water and nutrient relations, and inhibiting water-use efficiency. In recent years, many countries and international organizations have launched research projects on exploring the drought-tolerance and water-saving mechanisms of plants to identify key genes or tools for improving plant drought resistance.

**Introduction**

For more than two decades, scientists have conducted vast amounts of research, including studies on morphological traits, and the structural, physiological, biochemical, and molecular regulation to reveal the mechanisms of drought responses of plants. The response of plants to drought stress is a complex process involving many genes and signalling pathways. Shinozaki and Yamaguchi-Shinozaki indicated that genes involved in these responses can be grouped in two main classes: single function genes and regulatory genes based on their biological function. The single function genes encode enzymes associated with the accumulation of osmolytes, proteins, and enzymes scavenging oxygen radicals (ROS), proteins associated with the uptake and transport of water and ions (ion transporters, channels), and proteins involved in lipid biosynthesis. The regulatory genes are involved in signalling cascades and transcriptional or posttranscriptional regulation of gene expression such as transcription factors, protein kinases, protein phosphatases, and proteinases.

**The Genetic Basis of Drought Tolerance**

Expression studies have shown that drought-specific genes can be grouped into three major categories: (1) Genes involved in signal transduction pathways (STPs) and transcriptional control; (2) Genes with membrane and protein protection

functions; and (3) Genes assisting with water and ion uptake and transport.

To date, successes in genetic improvement of drought resistance have involved manipulation of a single or a few genes involved in signalling/regulatory pathways or that encode enzymes involved in these pathways (such as osmolytes/compatible solutes, antioxidants, molecular chaperones/osmoprotectants, and water and ion transporters). The disadvantage of this is that there are numerous interacting genes involved, and efforts to improve crop drought tolerance through manipulation of one or a few of them is often associated with other, often undesirable, pleiotropic and phenotypic alterations[1].

**Engineering Improved Drought Tolerance in Crops**

Most transformation studies to improve plant drought resistance have produced transformants that display a variety of both tolerance and avoidance traits. An exception was demonstrated by Rivero *et al.* (2007) who manipulated a leaf senescence gene. Leaf senescence is an avoidance strategy and is accelerated in drought-sensitive plants to decrease canopy size[2].

Transgenic plants were developed by expressing isopentenyl transferase (IPT), a key enzyme in the biosynthesis of cytokinin (a leaf senescence inhibitor) under the control of the senescence-associated receptor protein kinase promoter

(PSARK). The SARK gene, which is induced during late maturation and drought and decreased during senescence development, encodes a maturation/- senescence-dependent protein kinase.

Other drought avoidance/whole-plant traits that have been investigated include stay-green and cuticular biosynthesis. Stay-green is a variable and quantitative trait, which generally refers to delayed senescence. Cuticular biosynthesis was investigated by transgenic expression of AtMYB41 which expressed at high levels in response to drought, abscisic acid (ABA) and salt treatments, and was demonstrated to have a role in cell expansion and cuticle deposition.

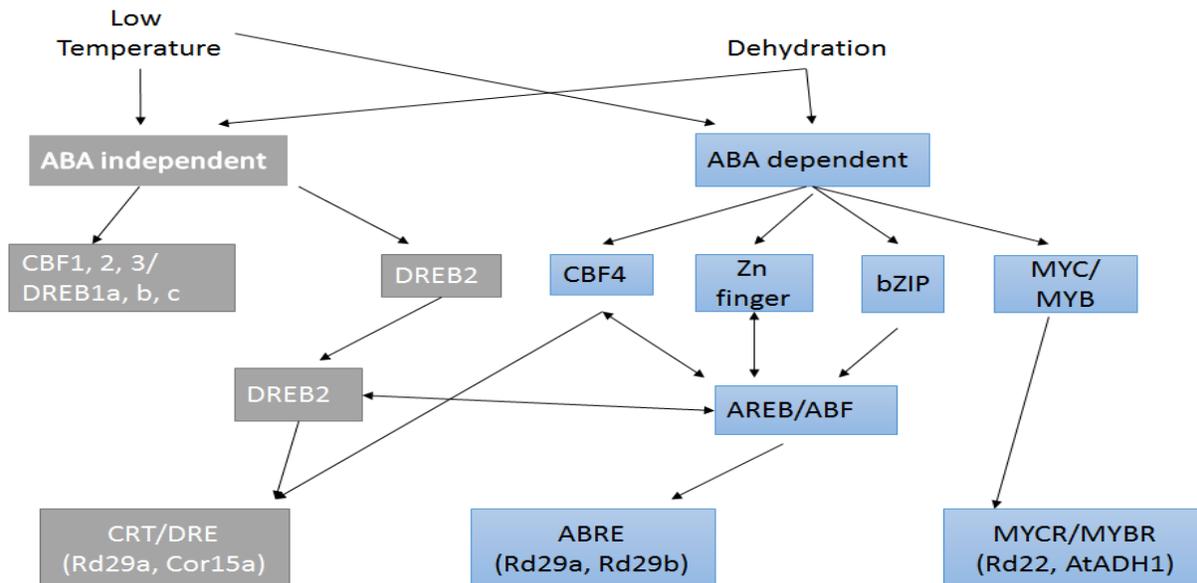
### Improving Plant Drought Tolerance Abscisic Acid and Transcriptional Regulation

The plant hormone ABA regulates the plant's adaptive response to environmental stresses such as drought, salinity, and chilling via diverse physiological and developmental

processes. Under abiotic stress, ABA induces stomatal closure, reduces water loss via transpiration, and induces gene expression [3].

Transgenic Arabidopsis plants constitutively overexpressing the zeaxanthin epoxidase gene, AtZEP, which encodes an enzyme required for an initial step in ABA synthesis from isopentyl diphosphate (IPP) and  $\beta$ -carotene (Schwartz *et al.* 2003) showed increased tolerance to drought and salinity stress[4]. Increased stress resistance was attributed to increased ABA levels in response to osmotic stress, which resulted in enhanced expression of ABA responsive stress-related genes[5]. Many of the drought stress response pathways that have been identified to date appear to be under transcriptional regulation and ABA plays a key role in this process.

Many transcriptional responses to drought stress have been well characterized and are classified as being ABA-dependent, ABA-independent, or both.



**Fig.1: Plant transcriptional processes induced by dehydration and low temperature stress**

There are two types of ABA-dependent transcription. The “direct” pathway involves cis-acting ABA-responsive elements (ABREs), which are directly activated by binding with TFs such as basic-domain leucine zipper (bZIP)-type DNA-binding proteins[6]. Alternatively, the “indirect” ABA-dependent transcription pathway involves other cis-acting elements, such as MYC and MYB. These elements are activated through binding with ABA- or drought-inducible TFs, such as basic helix-loop-helix (bHLH)-related protein AtMYC2 and an MYB-related protein, AtMYB2[7]. Some genes are induced by drought stress but are not expressed in response to exogenous ABA applications and these genes are the product of ABA-independent STPs. One such gene is rd29a (also known as lti78 and cor78). Yamaguchi-Shinozaki and Shinozaki identified a dehydration-responsive element (DRE) in the promoter region of rd29a and the DRE-binding

(DREB) protein transcription pathway has since been explored for its important roles in drought, cold, and salinity stress[8-9]. Recently, a novel drought-tolerant gene, HDG11, which encodes a protein from the homeodomain (HD)-START TF family (also known as the Class IV HD-leucine zipper TF family) was identified in Arabidopsis and was found to confer drought resistance via enhanced root growth and decreased stomatal density when constitutively over expressed in transgenic tobacco[10].

**Conflict of Interest:** None

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