Water stress induces various morphological, physiological, biochemical and molecular responses in plants. The ability of whole plant to respond and survive cellular water deficit depends on whole plant mechanism that can integrate the cellular responses. Plants have developed a number of strategies to cope with the physiological events associated with drought. These falls into three broad categories, drought escape, avoidance and tolerance (Courtois et al., 2000).

Drought can be most simply defined as a period of below normal precipitation that limits plant productivity in a natural or agricultural system (Kramer and Boyer, 1995). In the field, drought can cause a number of plant stresses including temperature, light and nutrient stresses. However, the stress component that defines drought is a decrease in the availability of soil water. This decreased water availability can be quantified as a decrease in water potential (Kramer and Boyer, 1995).

Plants over the years have evolved mechanisms broadly categorized as drought postponement and desiccation tolerance to combat water deficit. Most of the xerophytic plants adapt mechanisms underneath drought escape. Plants usually either function by avoiding tissue dehydration, by maintaining tissue water potential or by tolerating low tissue water potential. The first mechanism (drought postponement) involves traits that minimize water loss and maximize water uptake. Water loss can be minimized by stomatal closure, paraheliotropic movements to reduce heat load, increase in reflectance character by dense trichomes or waxiness of leaves in addition to minimizing cuticular transpiration,
decrease in canopy leaf area by shedding of older leaves and reduced growth (Larcher, 2000). Water uptake is maximized mainly by increasing root growth to deeper layers of soil (Jackson et al., 2000). The second mechanism, termed tolerance, involves functioning even when tissue water potential decreases. This is mainly achieved by protecting macromolecules and accumulating substances, which can further reduce water potential, powering entry of water into cell, these mechanisms operate at cellular level. Given an opportunity a plant will flourish much better by tolerating the adverse environmental conditions with a major goal of survival under stress. But the aim from agricultural point of view is not just survival of plant, but maintenances of growth and yield under stress conditions. The degree of tolerance to stress varies from species to species. Even within a plant system the susceptibility varies depending on developmental stage, tissue or organ type, with seeds being the most tolerant tissue.

**Physiological and biochemical responses of plants during drought stress**

Environmental stresses trigger a wide variety of plant responses, ranging from altered gene expression and cellular metabolism to changes in growth rates and crop yields. Among the environmental stresses, drought is one of the most adverse environmental factors for plant growth and productivity. Understanding the physiological, biochemical and molecular responses to drought is essential for a holistic perception of plant resistance mechanisms to water-limited conditions. Drought stress progressively decreases CO₂ assimilation rates due to reduced stomatal conductance and also induces reduction in the contents and activities of photosynthetic carbon reduction cycle enzymes, including the key enzyme, ribulose-1,5-bisphosphate carboxylase/oxygenase. Drought stress also causes a rapid and excessive production of reactive oxygen species (ROS). These reactive oxygen species react with nucleic acids, proteins, lipids and causing severe cellular damage (Van et al., 1995). However, with due course of evolution, plants are well adapted and have developed several mechanisms to deal with these environmental cues. These divers environmental stress conditions often active different signaling cascades and cellular pathways leading to the production of
proteins, molecular chaperons, ROS scavenging systems (antioxidative enzymes) and accumulation of compatible solutes in response to stress (Wang et al., 2003).

Relative water content (RWC)

The relative water content is one of the reliable parameters to know the water status in plants and it decreases gradually with increase in severity of drought stress. Decline of RWC as a response of stress were reported by several investigators under different stress conditions (Ramanjulu and Sudhakar, 1997; Madhusudan et al., 2002; Turkan et al., 2005; Farooq and Azam, 2006). Further, it has been suggested that the plants to retain a high RWC during stress periods are considered as tolerant ones (Ramanjulu et al., 1998). The reductions of RWC beyond 30%, in wheat plant do not survive even if they re-watered (Blum, 1996). These results clearly indicated that water stress caused significant changes in the leaf water potential and relative water content in plants. (Ramanjulu and Sudhakar, 1997; Madhusudan et al., 2002; Turkan et al., 2005; Farooq and Azam, 2006.

Cell membrane integrity

Cell membrane stability (CMS) technique was used to screen stress tolerant and stress sensitive of many crops (Blum and Ebrecon, 1981; Dexter, 1956; Martineau et al., 1979; Bewley, 1979; Tripathy et al., 2000; Farooq and Azam, 2006) and in some cases higher membrane stability could be correlated with better field performance. Among these studies, CMS exhibited a positive correlation with osmotic potential, osmotic adjustment, and/or relative water contents: the parameters that are equally affected by stress (Munns et al., 2002). However, depletion of water has usually been considered as one of the major causes of increased cell membrane permeability of plants growing under stress (Tabaei-Aghdaei et al., 2000. Farooq and Azam, 2006.

Proline

Water stress tolerance, appears to be the result of production and/or accumulation of compatible osmotic solutes. By lowering water potential the accumulation of compatible solutes involved in osmoregulation allows additional
water to be taken up from the environment. Among known compatible solutes proline is probably the most widely distributed osmolyte, and its accumulation seems to be involved in the process of adaptation to osmotic stress (Hare et al., 1998). The accumulation of osmolytes in addition to osmotic adjustments does have some roles. Novel roles for some of the osmolytes may include free radical quenching, the use of reducing power or methyl donor groups during their synthesis (Bohnert and Jensen, 1996). The genes encoding for these compatible solutes have been identified and characterized in several plant species during abiotic stresses. Proline, is catalyzed by two enzymes p5CS (pyrroline-5-carboxylate synthetase) and p5CR (pyrroline-5-carboxylate reductase). p5C-synthetase is induced by water stress, salinity and ABA, but p5C-reductase is induced by proline and rehydration (Yoshida et al., 1995). A gene encoding for proline transporter (ProT2) is induced by water deficit (Rentsch et al., 1996; Deuschle et al., 2001).

Drought stress is one of the most important environmental factors inhibiting photosynthesis due to several coordinated events such as the closure of stomata and reduction in the activity of photosynthetic enzymes (Tabacizadeh, 1998). Reduction in the leaf total chlorophyll content under drought stress has been reported in mulberry (Ramanjulu et al., 1998, Thimmannaik., 2002). Several studies demonstrated that drought stress resulted in damage to the oxygen-evolving complex of PSII (Toivonen and Vidaver, 1988). There was also a proportional reduction in the activity of various enzymes of carbon fixation pathway (Chaves et al., 2003).

Antioxidant metabolism

The effects of various environmental stresses in plants are known to be mediated, at least in part, by an enhanced generation of activated oxygen species (Foyer and Noctor 2005). This hypothesis is very plausible because chloroplasts, mitochondria and peroxisomes of plant cells are important intracellular generations of activated oxygen species. These include superoxide anion (O$_2^{•-}$), singlet oxygen (¹O$_2$), hydrogen peroxide (H$_2$O$_2$) and hydroxyl radical (OH$^•$).
which cause tissue injury (Foyer et al., 1994). AOS are highly reactive in the absence of any protective mechanism. They can seriously disrupt normal metabolism through oxidative damage to membrane lipids, proteins, pigments and nucleic acids (Foyer et al., 1994). In chloroplasts the superoxide radical (O$_2^-$) is produced by photoreduction of O$_2$ at PSI and PSII, and singlet $^1$O$_2$ is formed by energy transfer to O$_2$ from triplet excited state chlorophyll (Asada and Takahashi, 1987). H$_2$O$_2$ can originate, in turn, from the spontaneous or enzyme-catalyzed dismutation of O$_2^-$ and singlet $^1$O$_2$, mainly as consequence of electron transport and enzymic reactions (Del Rio et al., 2002). The toxicity of free radicals is extremely cytotoxic and promotes lipid peroxidation (Halliwell and Gutteridge, 1989). Lipid peroxidation is commonly taken as an indicator of oxidative stress. AOS-mediated membrane damage has been demonstrated to be a major cause of the cellular toxicity by water stress (Turkan et al., 2005) by salinity (Sudhakar et al., 2001). Under optimal conditions leaves are rich in antioxidant enzymes and metabolites and can cope with activated oxygen species, thus minimizing oxidative damage.

In plant cells, one such protective mechanism is an antioxidant system, composed of both non-enzymatic and enzymatic antioxidants (Foyer et al., 1994; Apel and Hirt 2004). The non-enzymatic antioxidants include the major cellular redox buffers, ascorbate and glutathione (GSH), as well as tocopherol, flavonoids, alkaloids, and carotenoids which remove, neutralize and scavenge the AOS. Enzymatic AOS scavenging mechanisms in plants include superoxide dismutase (SOD), ascorbate peroxidase (APX), glutathione peroxidase (GPX), and catalase (CAT). The involvement and the role of antioxidantive isozymes in protection against oxidative stress have been demonstrated using transgenic plants with enhanced levels of some antioxidant isoforms (Scandalios et al., 1997; Leonardis et al., 2000; Gomez et al., 2004; Smirnoff, 2005). Changes of expression and activities of antioxidant enzymes have been detected in many species of plants in response to adverse environmental conditions, such as water deficit and other abiotic and biotic and developmental stimuli (Smirnoff, 1993).
Superoxide dismutases (SODs)

Superoxide dismutases are ubiquitous enzymes found in nearly all aerobic organisms and they play major role in defense against oxidative stress (Touati, 1997). Within a cell, the SODs constitute the first line of defense against ROS. These are produced at locations where there is an electron transport chain present. It has been shown that phospholipid membranes are impermeable to charged molecules. Therefore, it is crucial that SODs are present in the compartments where radicals are formed (Takahashi and Asada, 1983). SOD catalyzes the conversion of $O_2^−$ to $H_2O_2$ and $O_2$ and it plays a central role in protecting cells against superoxide-derived oxidative damage (Hernández et al., 2000). Based on the metal co-factor used by the enzyme, SODs are classified into four groups: iron SOD (FeSOD), manganese SOD (MnSOD), nickel SOD (NiSOD) and copper-zink SOD (CuZn SOD) and these SODs are located in different compartments of the cell. FeSODs are located in the chloroplast, MnSOD in the mitochondrion and the peroxisome and CuZn SODs in the chloroplast, cytosol and possibly in the extracellular space (Alschlar et al., 2002). Comparison of deduced amino acid sequences from these three different types of SODs suggest that Mn and FeSODs are more ancient types of SODs, whereas CuZn SODs have no sequence similarity to Mn and FeSODs and probably have evolved separately in eukaryotes (Kanemtsu and Asada, 1990; Smith and Doolittle, 1992).

When Arabidopsis was subjected to a series of oxidative stress and changes were observed in the seven SODs; three FeSODs, three CuZn SODs and one MnSOD both at the mRNA and the protein level, Kliebenstein et al., (1998) reported increase in FeSOD2 mRNA level in response to UV irradiation and high light stress. They found that FeSOD1 is under the control of a circadian clock at the mRNA level (Kliebenstein et al., 1998). Exposure to severe salt stress results in increase in SOD activities in pea plants and in FeSOD in particular (Gomez et al., 1999; Hernandez et al., 1993, 1995), with
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corresponding decrease in CuZn SOD2, but when plants were exposed to less severe salt stress, increased activities in CuZn SOD were observed. By contrast, MnSOD was reported to respond positively to salt stress (Gomez et al., 1999; Hernandez et al., 1993, 1995), manganese toxicity (Gonzalez et al., 1998) chilling stress (Lee et al., 1999; Lee and Lee, 2000), and drought (Wu et al., 1999). When plants were kept in the dark following the treatment with methyl viologen, Mn and FeSOD transcript levels did not change, but an increase in the amount of cytosolic CuZn SOD mRNA was observed (Tsang et al., 1991). In another study, an Arabidopsis mutant that is resistant to methyl viologen and sensitive to UV-B was found to be nearly 4-fold more resistant to methyl viologen than wild type and also tolerant to freezing. Stedy state mRNA levels of plastidic CuZn SOD and stromal APX were higher than the wild type (Fujibe et al., 2004). Functional differences between the FeSOD and MnSOD enzymes of E.coli have been reported with regard to protection of DNA and proteins. (Van camp et al., 1996), reported that in plant chloroplasts, FeSOD and MnSOD have different protective properties and may be related to suborgananellar location. Thus, we can conclude that there is a definite cooperative effect between different forms of SODs in scavenging of toxic oxygen species.

The effect of SO2 on CuZn SOD enzymes activity were investigated in two pea cultivars, namely progress and Nugget to SO2 (Madamanchi et al., 1994). After the treatment, these plants with SO2, activities of both cytosolic and chloroplastic SODs increased in cv. Nugget. Chloroplastic CuZn SOD mRNA levels decreased in cv. Nugget after the treatments, whereas in cv. Progress there was a recovery in the amount of transcripts present after an initial decrease (Madamanchi et al., 1994). Over expression of a chloroplastic Cu/Zn from pea in transgenic tobacco plants resulted in increased tolerance against high light and low temperature stresses (Sen Gupta et al., 1993a, 1993b). Over expression of a CuZn SOD (a cytosolic SOD from pea) in
transgenic tobacco (Nicotiana tobacum) plants increased ozone tolerance (Picher and Zilinskas, 1996); Mn SOD-over producing plants showed improved tolerance against freezing, water deficit, winter survival (McKersie et al., 1993, 1996, 1999). In yeast, SOD2 was identified from Schizosaccharomyces pombe as Na+/H+ antiporter on the plasma membrane involved in salt tolerance (Jia et al., 1992).

Ascorbate peroxidases (APXs)

APX are class I haem peroxidases and utilizes ascorbate as its specific electron donor to reduce H$_2$O$_2$ to water, with the concomitant generation of monodehydroascorbate a univalent oxidant of ascorbate. From the database of expressed sequence tags from Arabidopsis thaliana, seven APXs have been identified, including various soluble and membrane-bound isoenzymes (Jespersen et al., 1997). For example, the presence of eight isoenzymes has been confirmed: soluble cytosolic (APX1, APX2, APX6), bound to the microsome membrane (APX3, APX4, APX5), and chloroplast sAPX and tAPX (Jespersen et al., 1997; Panchuk et al., 2002). APX4 contains the SKL motif (Ser-Lys-Lew) at the C-terminal end, which suggests targeting of this protein to peroxisome. APX has also been found in mitochondria in pea and potato (Jimenz et al., 1997; Leonardis et al., 2000).

APX in combination with enzymes of ascorbate-glutathione, pathway function to prevent the accumulation of toxic levels of H$_2$O$_2$ in photosynthetic organisms (Shigeoka et al., 2002). APX exists as a multigene family in Arabidopsis. APX 1 and 2 are both cytosolic enzymes. A membrane associated APX has been described in the peroxisome and also in the chloroplast (Mullen and Trelease, 2000). The chloroplast contains two distinct APX enzymes as well, one which is free in the stroma, and one which is associated with the thylakoids.
The cytosolic isoforms of ascorbate peroxidases are homodimers. Expression of APX2, another cytosolic isoform, is limited to bundle sheath cells in leaves exposed to excess light (Fryer et al., 2003). Peroxisomal ascorbate peroxidase plays such a role and scavenges hydrogen peroxide escaping the peroxisomal matrix by passive diffusion. The N-terminal active domain of the enzyme faces the cytosol, and its C-terminal domain is anchored (APXs are single-pass peroxisomal membrane proteins), which facilitate the protein’s functioning (Lisenbee et al., 2003).

Peroxisomal APX preferentially accumulates in spongy parenchyma, and can also be found in large amounts near the central vascular bundles (Pereira et al., 2005). In tomato, the activity of peroxisomal APX decreased markedly following inoculation of a pathogen; this may have resulted from diminution of the peroxisomal ascorbate pool in response to infection, and from inhibition by NO, generated by peroxisomal NADPH-dependent NO synthase (Kuzniak and Sklodowska, 2005).

tAPX and sAPX are both involved in the water-water cycle, where O$_2^·$ is reduced to water in a two-step reaction catalyzed by superoxide dismutase (SOD) and APX. O$_2^·$ is produced at the PS1- the Mehler reaction. Which is one of several mechanisms for dissipating excess excitation energy. The water-water cycle contributes to maintaining a proper ATP/NADPH ratio and to alleviating the over-reduction of photosystems when plants are exposed to photoinhibitory conditions (Asada, 1999).

Arabidopsis fumigated by ozone shows a large increase in the steady-state transcript level of cytosolic APX (Conklin and Last, 1995; Ovar et al., 1997). The transcript level of pea cytosolic APX also increases 4-fold in response to drought stress, but is even more dramatically enhanced (15-fold) following recovery from stress (Mittler and Zilinskas, 1994). The analysis of the protein level and activity of APX indicates that during recovery from
drought stress, cytosolic APX expression in pea is regulated at the post-transcriptional level at least in part at the level of protein synthesis.

Furthermore, many environmental factors such as high light, salt, wounding, pathogen infection, fruit ripening, and paraquat affect the steady-state transcription level of cytosolic APX (Mittler and Zilinskas, 1992; Pastori and Trippi, 1992; Schantz et al., 1995; Karpinski et al., 1997, 1999; Ovar et al., 1997; Mittler et al., 1998; Morita et al., 1999; Yoshimura et al., 2000). It is reported that heat shock induces the cytosolic APX. Pea and Arabidopsis APX1 gene expression are induced by heat stress as well as oxidative stress and both have heat shock cis elements in their promoters (Mittler and Zilinkas, 1994). At present there is no definite information on the signal transduction pathway that regulates the expression of APX although, it is clear that increased reduction state of quinone or plastoquinone in chloroplast may be essential for the cytosolic APX induction under high light intensity (Karpinski et al., 1999).

**Over view of the up-regulated genes and gene products**

Genes that are expressed under stress could be either functional (such as aquaporins or the enzymes of osmoprotectant biosynthesis) or regulatory (such as protein kinases) in nature. Most of these genes are upregulated upon stress induction (Assama et al., 2002). Microarray analysis on Arabidopsis plants using 1300 cDNAs have revealed that approximately 44 genes were up-regulated in response to dehydration, of which 30 are reported to be novel (Seki et al., 2001). Similarly several regulatory and functional genes expression has been reported during rehydration process and after dehydration (Oono et al., 2003).

Increasing evidence indicates that the genes responding to dehydration can be categorized into two classes, based on their response in terms of time-scale. Some responds immediately within seconds or minutes while others are responding later, in hours, days or even weeks. It has been speculated that the early responsive genes may provide initial protection and amplification of signals while the genes that are responding later may be involved in functional roles
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(Oono et al., 2003). The common proteins such as LEA proteins, aquaporins, lipid transfer proteins, proteinase inhibitors, proteins involved in repair etc., may protect a certain essential cellular components like photosynthetic structures, and help in acclimation (Thomashow, 1999).

Gene expression analysis

Full-length cDNA microarray is useful for analyzing the expression pattern of *Arabidopsis* genes under various stress and hormone treatments. Although a number of genes have been found to be involved in abiotic stress responses, many have not yet been characterized and identified.

Attempts were made to study the expression profile using 1300 full-length cDNA clones from *Arabidopsis*. Of the 44 drought induced genes isolated, in which nearly 30 were found to be novel drought inducible genes (Seki et al., 2001). Recently probing of 7000 full-length clones under various stress revealed that 299 were drought inducible, 54 cold inducible, 213 salinity inducible and 245 inducible by ABA were identified (Seki et al., 2004). Attempts are also in the direction of use of transgenics, over expressing stress inducible transcription factor to identify the down stream target genes. Similar attempts using DREB1A over expressing plants, lead to identification of six novel stress inducible genes (Seki et al., 2001).


Functional genes

Number of genes, with wide range of functions are upregulated by drought, these can be broadly classified as those involved in osmotic adjustment; sugars and osmolytes, chaperones or protective proteins, proteins involved in detoxification and genes down regulated under stress.
Sugars and osmolytes

The accumulation of compatible solutes may help to maintain the relatively high water content obligatory for plant growth and cellular functions. Osmotic and oxidative stress induced by drought, salinity and other abiotic stresses could be reduced by the production and accumulation of compatible solutes. Osmoprotectants and its accumulation as a key mechanism in the plants for increasing yield of crop subjected to stress conditions. The accumulation of compatible solutes is one of the mechanisms that plant species adapt to meet the challenges of environmental stresses. (Giridarakumar et al., 2003). The levels of osmoprotectants typically rise during exposure to stresses such as water deficit, salinity and low temperature (Scott et al., 1999). The frequently observed metabolites with an osmolyte function are proline, glycine betaine, soluble sugars, free amino acids and polyamines.

According to Cram, (1976) sugars contribute up to 50% of the total osmotic potential in glycophytes subject to saline conditions. The accumulation of soluble carbohydrates in plants has been widely reported as a response to drought and salinity (Popp, 1995; Dubey and Singh, 1999; Murakeozy et al., 2003). Several studies have attempted to relate the magnitude of changes in soluble carbohydrates to drought tolerance (Ashraf and Tufail, 1995). The resurrections plant Craterostigma plantagineum accumulates, an unusual 8 carbon sugars, octulose, which is rapidly converted in to sucrose during dehydration (Norwood et al., 2003). Substantial amount of trehalose was identified in Myrothamus flabellifolia and Sporobolus stapfianus, resurrection plants (Phillips et al., 2002). Other sugars (polyols, such as pinitol or ononitol) have been frequently reported in response to drought (Streeter et al., 2001).

Proline, an important amino acid, has been recognized as a potent and compatible osmoprotectant and found to be accumulated in high concentrations in glycophytes and halophytes in response to osmotic stress such as drought and high salinity. Several investigators (Delauney and Verma, 1990; Kavikishore et al., 1995; Giridarakumar et al., 2003) have demonstrated that the positive correlation between the accumulation of proline and osmoprotective role at the whole plant
level and cell cultures. Many plants and lower organisms accumulate proline in response to water deficit and salinity (Rajagopal et al., 1997; Sairam and Tyagi, 2004). Apart from these, glycine betaine is one of the important compatible solutes that accumulate in the chloroplasts of certain plants when plants are exposed to environmental stresses (Sakamoto and Murata, 2002).

**Protective proteins and chaperones**

This broad category comprises of proteins known to play role of chaperones such as LEAs and HSPs, protease and proteinase inhibitors (proteins required for protein homeostasis), water channel proteins like aquaporins and polyamines.

Late embryogenesis abundant (LEA) and heat shock protein encoding genes comprise a diverse group of stress protective proteins, which are not normally expressed in vegetative tissue under normal condition but are induced by environmental stress such as drought (Campalans et al., 2001; Ingram and Bartels, 1996). Based on the conserved structure LEA has been classified into 6 groups and are correlated with dehydration based on its response to dehydration and ABA (Dure, 1993). Although the biochemical tolerance of LEA proteins has not been proven, positive evidences of its function as protective molecules has been proposed based on over expression studies in both plants and animals. The probable function of group 1 LEA, seems to be in binding or replacement of water, group 2 or dehydrins and group 4 contribute to maintenance of protein and membrane structure where as group 3 and 5 are suggested to form dimer with coiled-coil structure capable of sequestration of ions, accumulated during water depletion (Dure, 1993; Ramanjulu and Bartels, 2002). Recently, for the first time, it was shown that LEA proteins exhibit anti-aggregation activity under water stress (Tonnacliffe et al., 2005).

Heat-shock proteins (HSPs)/chaperones are known to be expressed in plants under high-temperature stress and responsible for protein folding, assembly, translocation and degradation in many normal cellular processes, stabilize proteins
and membranes, and can assist in protein refolding under stress conditions. Major classes of HSPs are present in plants and include the small HSPs (ranging in molecular weight from 15 to 28 kD), HSP-60, HSP-70 (and a constitutively expressed HS cognate protein, HSC-70), HSP-90, and HSP100-101 (Vierling, 1991). They can play a crucial role in protecting plants against stress by re-establishing normal protein conformation and thus cellular homeostasis (Wang et al., 2004).

Increased proteolysis has been reported during drought, which is an important cellular activity to maintain protein homeostasis (de Carvalho et al., 2001). The most abundant is cysteine proteases, involved in programmed cell death, which can be prevented by proteinase inhibitors. Few of the proteinase inhibitors induced by dehydration, likely protect the proteins by inhibiting the activity of proteases (Solomon et al., 1999). Apart from these, ubiquitin conjugating enzymes are also reported to be induced by dehydration that is thought to be required for protein turnover and recycling amino acids. Of the polycationic small aliphatic amines, viz., spermidine, spermine and putrescine involved in various physiological processes, putrescine was rapidly increased by osmotic stress due to activation and transcription of arginine decarboxylase. Suggesting their role in stress response, as is correlated by expression of At ADC2 under dehydration and accumulation of putrescine (Urano et al., 2004).

Maintenance of water flux gradient is determined by water potential gradient and permeability of membrane to water. Water permeability of membrane under dehydration is increased by major intrinsic proteins namely aquaporins present on tonoplast (TIPs) and plasma membrane (PIPs). Dehydration and salt stress are reported to induce expression of aquaporin, which may trigger water permeability and facilitate water flux (Sarda et al., 1999). Some specific aquaporin gene is up regulated by dehydration and down regulated by salt stress, coinciding with behavior of plant under stress (Smith et al., 2003).
Proteins involved in detoxification

Plants exposed to various environmental stresses can lead to the generation of reactive oxygen species (ROS), such as superoxide anion radicals (O$_2^-$), hydroxyl radicals (OH$^-$), hydrogen peroxide (H$_2$O$_2$), singlet oxygen (O$_2^*$) and complex aldehydes. These ROS are highly reactive and can alter normal cellular metabolism through oxidative damage to lipids, proteins and nucleic acids (McKersie and Lesem, 1994; Imlay, 2003). Injury caused by ROS, known as oxidative stress, is one of the major damaging factors in plants exposed to environmental stresses such as drought (Price et al., 1989), desiccation (Senaratna et al., 1987), extreme temperatures (McKersie et al., 1993), high light intensity (Fryer et al., 2003). Plants have developed a wide range of enzymatic and non-enzymatic mechanisms to scavenge the reactive species.

Plants possess both enzymatic and non-enzymatic mechanisms for scavenging of ROS. Enzymatic mechanisms include superoxide dismutase (SOD), catalase (CAT), peroxidase (POD), glutathione reductase (GR), ascorbate peroxidase (APX) whereas non-enzymatic mechanism consists of low molecular weight antioxidants such as ascorbate, glutathione, carotenoids and $\alpha$-tocopherols (Harinasut et al., 2003). Plants containing high concentrations of antioxidative enzymes such as SOD, CAT, POD, APX and GR showed considerable resistance to the oxidative damage caused by the activated oxygen species (Dash and Panda, 2001; Garratt et al., 2002; Khan et al., 2002; Khan and Panda, 2003; Jungkang et al., 2004). Peroxiredoxins and thioredoxins have also been identified to be induced by drought stress; these roles have largely unexplored (Mowla et al., 2002). Like lipids, proteins are also oxidized by ROS, leading to formation of methionine sulfoxide and lose function. Recently an Arabidopsis gene At SXL3 induced by dehydration was found to play role in reduction of methionine sulfoxide, confirmed by knock down studies (Rodrigo et al., 2002).

From the literature cited above, it is clear that considerable research effort has been made towards the identification of plant genes induced by drought stress.
enumerated in several plants that are relatively sensitive to cellular dehydration, in particular *Arabidopsis thaliana* and rice. However, even with the recent addition of in-depth examination of gene expression patterns using *Arabidopsis* microarrays we have little understanding on functional aspects of the genes that respond to drought stress. Although there are few reports available in literature, concerning physiological and biochemical responses of horsegram to drought stress conditions, the molecular responses of this crop is poorly understood. To gain a better understanding of changes in stress gene expression associated with drought tolerance in horsegram, attempts have been made to clone and characterize of genes coding Superoxidedismutase (*SOD*) and Ascorbate peroxidase (*APX*) proteins from stress tolerant plant horsegram subjected to drought stress.