Literature on the modulation of various processes of plants under salt stress is reviewed here under. In general, salt stress inhibits the growth of crop plants by affecting physiological, biochemical mechanisms, water balance, ion imbalance and or a combination of these factors.

Plants are sedentary organisms and therefore can not choose suitable environment for their growth. Many of these are however, still capable of completing their life cycle in various kind of unfavorable environments which can both biotic and abiotic in nature. Moreover, plants also have the capacity of transducing the signal into a specific response through which these plants can overcome the stress.

Salinity is known to alter many aspects of plant growth and development and induce numerous changes at morphological, physiological, biochemical and molecular (genes and gene products) levels.

Effect of salt stress on growth of plants

Root growth

In general salt stress affect the growth of several crop plants by altering water content, ion homeostasis, physiological, biochemical and molecular mechanisms. Since several decades it is experienced that roots might seems to be the part of the plant, most
vulnerable as they are primary and directly exposed to salt in crop plants. The reduction in growth of roots is common phenomenon under salt stress regimes and is because of reduction in water supply there by causing turgor pressure in the expanding zone to fall below the yield threshold, so that growth stopped. It is also evident that the major effect of salinity is the shortening and thickening of roots due to a decrease in the rate of cell elongation and growth (Chen and Plant, 1999) and is resulting in reduction in the volume of soil that can be explored by roots for water and minerals. A generalized growth reduction in roots of several crop plants were reported by Silverbush and Ben-Asher, (1987) Raia and Azimov, (1988), Zhong and Lauchli, (1993) in cotton plants, Chourey et al., (2003) in Bura Rata rice seedlings, Sudhakar and Veeranjaneyulu, (1988) in horse gramme (Dolocous biflorus L.). In contrast an increased root growth was observed under mild salinity in cotton by Jafri and Ahmad, (1994), Greenway and Munns, (1980), Zhu et al., (1997), Yeo, (1998), Bohnert et al., (1999).


**Shoot growth**

From the past experiences, it is clear that the reduced growth rate is a common phenomenon under salt stress conditions in several crop species (Yeo and Flowers, 1983; Nobel and Rogers, 1992; Lutts et al., 1995; Dionisio-Sese and Tobita, 1998; Sairam et al., 2002; Meharabi et al., 2003; Azevedo et al., 2004; Sharma and Dubey, 2004). The most well known effect of salinity is to reduce growth and the effect may vary during the phase of development of the plant. It was clear that plant
growth depends on cell division; cell enlargement and cell differentiation and all are known to be affect by salt stress to a different degree based on severity and sensitivity of the process. The generalized salt stress-induced growth inhibition might also be associated with modifications of apoplast acidification (Neve-Piestun and Bernsten, 2001). Several authors have reported an inhibition in shoot growth and increase in root growth (Greenway and Munns, 1980; Zhu et al., 1997; Yeo, 1998; Bohnert et al., 1999). Ashraf, (2002) noticed the growth of cotton plants in saline medium was adversely affected at different stages of the plant life cycle.

Furthermore, several other reporters studied the decrease of shoot/root ratio under salinity; (Ackerson and Younger, 1975; Delauney et al., 1982, Dudeck et al., 1983; Weimberg et al., 1984; Munns and Termat, 1986) and the shoots are being under sensitive to salt stress than roots (Babu et al., 1987; Leidi et al., 1991; Brugnoli and Bjorkman, 1992). Similarly, Delauney et al., (1982) noticed that the decreased root growth was lesser than shoot growth under low levels of salinity in barley. In another report, Munns and Termat, (1986) stated that glycophytes exposed to salinity showed slower leaf growth rate than roots, hence there was increased root: shoot ratio.

Biomass

The tolerance to several environmental stresses including salt stress on crop plants usually represents the percent biomass production in saline condition relative to plants in non-saline conditions, after growth for an extended period of time. It is generally assumed that salinity stress alters the biomass accumulation in crop plants and this may be the alterations in root, shoot growth and leaf area. The adverse effects in biomass production under salt stress was studied by several investigators (Kuznetsov et al., 1990; Karen et al., 1996; Dionisio-Sese and Tobita, 1998; Giridarakumar et al., 2000; Sairam et al., 2002; Meharabi et al., 2003; Azivedo et al.,
2004; Sharma and Dubey, 2004; Jyothsnakumari, 2004). Greenway and Munns, (1980) heeded that a salt tolerant sugar beet showed only 20% of reduction in dry mass in 200mM NaCl, a moderately tolerant species such as cotton showed a 60% reduction, and a sensitive species such as soybean was dead. Karakas et al., (1997) reported the 44% of reduced dry mass in wild-type plants of tobacco, but was not observed such reduction in dry mass of transgenic tobacco plants.

Furthermore, Khan et al., (1995) found a marked reduction in shoot fresh weights and dry weights of 15 cotton cultivars with increasing the salt concentrations. Similarly, Allen et al., (1985) recorded a high correlation between the germination stage and biomass at the vegetative stage of alfalfa. Qadir and Shams, (1997) reported a significant decrease in leaf area, stem thickness, shoot and root dry weights of the two cotton cultivars. Foolad, (1996) studied the decrease in the dry mass production in salt treated plants for six generations.

In conflict, higher fresh and dry mass of shoots and roots was reported by Huq and Larher, (1983a, b) in NaCl stressed plants of cowpea than those of control plants up to 75mM NaCl treatments.

It is evident from the earlier reports salt stress affects shoot growth, leaf area and dry mass in several plant species.

**Accumulation of osmolytes in response to salt stress**

Osmotic adjustment, at the physiological level, is an adaptive mechanism involved in drought and salinity tolerance which permits the maintenance of turgor under conditions of water deficit as it can counteract the effect of rapid decline in plant water potentials (Hsia et al., 1973; Cutler and Rains, 1978). This can be usually achieved by the uptake of inorganic ions as well as the accumulation of compatible solutes, mainly proline and glycinebetaine (Delauney and Verma, 1993) had been.
thought to play a role in the process of the osmotic adjustment in many crops and to accumulate under conditions of environmental stress such as water stress, salinity stress etc. (Rhodes and Hanson, 1993; Heuer, 1994). Later several other investigators were also reported that osmotic adjustment in plants subjected to salt stress accompanies by the accumulation of high concentration of compatible solutes in order to lower the osmotic potentials (Karakas et al., 1997; Vidyanathan et al., 1999; Xiong and Zhu, 2002; Seeraz and Sinclair, 2002; Rontein et al., 2002; Jouve et al., 2004). The compatible solutes so called are because they don’t interfere with normal cellular biochemical reactions and act as osmoprotectants during osmotic stress. The main role is probably to insulate plant cells against the ravage of salt by preventing the osmotic balance, by stabilizing the structure of key proteins such as Rubisco, by protecting the photosynthetic apparatus and by functioning as oxygen radical scavengers (Heuer, 2003).

**Proline**

Proline is an imino acid, recognized as a potent and compatible osmoregulator which is found to be accumulated in high concentrations in glyphytes and halophytes in response to osmotic stress such as high salinity and drought. Proline synthesis can takes place from the glutamate as well as ornithine by action of two important enzymes viz., pyrroline carboxylic acid synthetase (P5CS) and pyrroline-5-carboxylic acid reductase. It has been demonstrated that plants expressing high levels of P5CS genes produced several fold more proline than the control plants (Delauney and Verma 1993; Kavikishor et al., 1995; Zhu, 2001).

Besides the biophysical effects of proline is an osmo-compatible solute (Larher et al., 1998) its biosynthesis can contribute to reduced cellular acidification allowing the regeneration of NADP\(^{+}\) needed for the maintenance of the respiratory and
photosynthetic process. Proline itself may serve also as a nitrogen and carbon source needed in stress recovery (Chiang and Dandekar, 1995; Hare and Cress, 1997; Aziz et al., 1999) and can also act as a scavenger of hydroxyl radicals avoiding cellular damage provoked by osmotic or salt-induced oxidative stress (Smirnoff and Cumbes, 1989; Polle, 1997; Borsani et al., 1999).

Several investigators have been demonstrated the osmo-protective role of proline, at the whole plant level and in cell cultures (Kandpal et al., 1981; De launey and Verm 1993; Kavikishor et al., 1995; Okuma et al., 2000; Ramanjulu and Sudhakar 2001; Giradarakumar et al., 2003; Jyothsnakumari and Sudhakar, 2003/4). Genotypic variations in proline accumulation during salt stress have been noticed in a variety of crop species (Ramanjulu and Sudhakar, 2001; Giradarakumar et al., 2003) and has been found that salt-tolerant cultivars exhibited a stronger and faster accumulation of proline than sensitive one (Igarashi et al., 1997). In contrast, there are reports indicating that the salt sensitive cultivars showed significantly higher levels of proline compared with tolerant ones (Lutts et al., 1999). Furthermore, Kavikishor et al., (1995) established a direct role to proline in transgenic tobacco plants genetically engineered to accumulate higher levels of proline and such plants are able to tolerate higher salinity.

Proline is found to be a stabilizer of sub cellular structures (Schobert and Tschescha, 1978), a sink for energy (Saradhi and Saradhi, 1991), a scavenger of free radicals (Saradhi et al., 1995) and a major constituent of cell wall structural proteins of plants in morphogenesis (Nanjo et al., 1999), protective role against UV radiation promoted peroxidative process (Saradhi et al., 1995).

Several investigators have been reported that the exogenous application of proline stimulates growth of cell (Kumar and Sharma, 1989) and plants (Fedina et al.,
1993; Hamed et al., 1994) and to improve metabolisms under stress conditions (Alia et al., 1991; Rana and Rana, 1996). However, notwithstanding negative effects were also reported (Manetas et al., 1986; Lin and Kao, 2001). According to Delauney and Verma, (1993) proline accumulation under osmotic stress is mainly a result of de novo synthesis from glutamate. Genes encoding proline biosynthesis enzymes have been cloned from higher plants (Delauney and Verma, 1990; Hu et al., 1992).

It is evident from the literature cited above, the increased levels of proline contributes significantly to the turgor maintenance of cells and proline accumulation has been considered as stress indicator in several plant species under salt stress conditions.

Glycinebetaine

Glycinebetaine is a quaternary ammonium zwitterionic compound, which is known to be effective osmoprotectant widely distributed in bacteria, marine algae and many plant families (Wyn Jones and Storey, 1981; Rhodes and Hanson, 1993, Gorham, 1996; Gage and Rathinasabapathi, 1999; Mansour, 2000).

Glycinebetaine is synthesized via a two-step oxidation of choline where in the first step choline is oxidized in to betaine aldehyde. The active enzyme involved in this step is choline monooxidase (CMO), a dimmer or trimer of identical 43kD subunits and is located in the chloroplast stroma (Burnet et al., 1995; Rathinasabapathi et al., 1997). The second step of glycinebetaine synthesis is catalyzed by betaine aldehyde dehydrogenase (BADH) a 45kD NAD-dependent dehydrogenase. However, this BADH is not unique to glycinebetaine synthesis; it is also attacks 3-dimethyl sulfoniopropinat aldehyde (DMSP-aldehyde) and seems to be identical to ω-aminoaldehyde dehydrogenase, a ubiquitous enzyme of polyamine metabolism (Trosaat et al., 1997).
Glycinebetaine accumulated in response to stress in many crops, including spinach, barley, tomato, potato, rice, carrot and sorghum and mulberry (Weimberg et al., 1984; Fallon and Phillips, 1989; Mc Cue and Hanson, 1990; Mohanty et al., 2002; Yang et al., 2003; Giridarakumar et al., 2003). Several investigators attributed the osmoprotective role of glycinebetaine in response to stress (Yancey et al., 1982; Wyn Jones, 1984; Rhodes and Hanson, 1993) and is most abundantly distributed in plants among commonly found quaternary ammonium compounds (Mansour, 2000).

Robinson and Jones (1986), Genard et al. (1991) reported that the glycinebetaine is localized in chloroplast and plays a vital role in chloroplast adjustment and protection of thylakoid membranes, thereby maintaining photosynthetic efficiency. Moreover, glycinebetaine is hypothesized to accelerate when internal turgor drops below some threshold level (Bradford and Hsiao, 1982; Hanson and Wyse, 1982), protecting cytoplasm from dehydration (Mc Cue and Hanson, 1990), protecting chloroplast from Na damage (Murata et al., 1992; Rajasekaran et al., 1997) and protecting essential K functions from Na interference (Bohnert and Jensen, 1996).

Several reporters (Wyn Jones et al., 1981; Grieve and Mass, 1984; Hanson et al., 1985; Rhodes et al., 1987) have noticed the accumulation of glycinebetaine under saline conditions and was found to be high in salt tolerant grasses than in salt sensitive grasses. Similarly, Rhodes et al., (1989) have reported low levels or no glycinebetaine in sensitive species, intermediate levels in moderately tolerant species and high levels in tolerant species of maize. Further, Giridarakumar et al., (2000, 2003) and Jyothsnakumari, (2004) were also reported a higher levels of glycinebetaine in salt tolerant cultivar of mulberry than the salt sensitive cultivar. In contrast, Varshney et al., (1988) have stated that accumulation of choline and betaine in
response to salt stress was more pronounced in salt sensitive than in salt tolerant lines of *Trifolium alexandrium*. Saneoka *et al.*, (1995) reported that glycinebetaine-containing lines of maize exhibited less shoot growth inhibition under saline conditions than glycinebetaine-deficient lines.

In addition, Weigel *et al.*, (1986) and Mc Cue and Hanson, (1990) reported that the activity of betaine aldehyde dehydrogenase, a key enzyme of glycinebetaine biosynthetic pathway was found to be more under drought and saline stress in several plant species. Transgenic rice plants expressing betaine-aldehyde dehydrogenase converted high levels of exogenously applied betaine-aldehyde to glycinebetaine than did wild type plants. The elevated level of glycinebetaine in transgenic plants conferred significant tolerance to salt, cold and heat stresses (Sairam and Tyagi, 2004).

It is evident from the literature cited above glycinebetaine significantly accumulated in several plant species and known to involve in osmotic adjustment processes.

Responses of plants to stress condition include alteration in gene expression that lead to alteration in protein synthesis. One approach to understanding the ability of plants to tolerate environmental stress is to identify stress-induced changes in the level of individual proteins with the assumption that adaptation to stress is the result of altered gene expression (Majoul *et al.*, 2000). Protein synthesis responds dramatically to environmental stress such as heat shock (Cooper and Ho 1983; Key *et al.*, 1981) and anaerobiosis (Sachas *et al.*, 1980) where the synthesis of most proteins ceases and the synthesis of a new set of proteins are induced. For other environmental stresses the response is not as dramatic; however, water stress result in an increase in the net synthesis of some proteins and a decrease in the synthesis of others, with or with out a concomitant induction of unique stress proteins.
Plants respond to salinity stress by modulating morphological, physiological and biochemical processes and these changes are brought about by altered expression of several stress responsive genes that code for specific proteins or enzymes (Bhonert et al., 1995; Ingram and Bartels 1996; Hasegawa et al., 2000; Zhu 2001). It is known that many regulatory proteins or genes are involved in stress gene expression. Several stress responsive genes have been isolated and characterized in many crop species with wide range of stress tolerance (Singh et al., 1987a; Ramagopal 1987; Ramagopal and Carr 1991), and at the transcriptional level (Thamashow 1999; Hasegawa et al., 2000; Shinozaki and Shinozaki 2000; and Zhu, 2002). The products of these stress-inducible genes have been classified into two groups: those that directly protect against environmental stress and those that regulate gene expression and signal transduction in the stress response. The first group includes proteins that probably function by protecting cells from dehydration, such as the enzymes required for the biosynthesis of various osmoprotectants, late embryogenesis abundant proteins, antifreeze proteins, chaperons and detoxifying enzymes. The second group of gene products includes transcription factors, protein kinases and the enzymes involved in phosphoinositide metabolism (Seki et al., 2003).

Protein amounts are not always correlated to mRNA levels (Gygi et al., 1999) probably due to large difference in protein turnover and post-translational modifications and therefore, only the study of proteins themselves can provide information on their real amounts and activity (Zivy and Vienne, 2000). However, several salt-induced proteins have been identified in plant species and have been classified into two distinct groups, 1) salt stress proteins, which accumulate only due to salt stress, and 2) stress associated proteins, which also accumulate in response to heat, cold, drought, water logging and high and low mineral nutrition (Hurkman et al.,
1989; Pareek et al., 1997a, b). Moreover, literature provides increasing numbers of results identifying proteins (and corresponding genes) involved in salt tolerance: proteins implied in biosynthesis and accumulation of osmoprotectors (compatible solutes like proline, glycine-betaine, etc.) (Lopez et al., 1994; La Rosa et al., 1992; Holmstrom 1996); maintenance of ion homeostasis (Niu et al., 1995); water adjustment (osmotin, mannitol, etc.) (Singh et al., 1989a; Traczynski et al., 1993; Yamada et al., 1995,) in plant defense against salt- linked oxidative stress (peroxydases, catalase, etc.), water and cation exchange channel proteins (Ballesteros et al., 1996) and antiproteases (trypsin inhibitors) (Lopez et al., 1994; Yamada et al., 1995; Ballesteros et al., 1997).

Lutts et al., (1996), Pareek et al., (1997a) were noticed a higher content of soluble proteins in salt tolerant than in salt sensitive cultivars of rice. Similar observations were made in barely (Hurkman et al., 1989), sunflower (Ashraf and Tufail, 1995), finger fimmet (Uma et al., 1995) and wheat (Mujoul et al., 2000). In contrast, Ashraf and O’Leary, (1999) reported that the increase of total proteins was more in salt sensitive cultivar (Potohar), than salt tolerant line (S24) compared with the other lines of wheat. Salt stress proteins (SSPs) which accumulate when plants subjected to saline conditions may provide a storage form of nitrogen that is reutilized when stress is over (Singh et al., 1987a) and may play a role in osmotic adjustment. Pareek et al., (1997a) attributed that these proteins synthesize de novo in response to salt stress, express constitutively and found to be up regulate when plants are exposed to salt stress.

Nitrogen is the major nutrient that plays a pivotal role in plant growth and yield. Nitrogen and nitrate are reduced to NH$_3$, which in turn are assimilated via the joint action of glutamine synthetase (GS) and glutamate synthase (GOGAT) (Lam et
al., 1996). GS is an octameric enzyme of 350 kDa which has in the form of several isoenzymes located both in the cytosol (GS1) and plastids (GS2), and has a key role in the assimilation of ammonia into amino acids, catalyze the incorporation of NH₄⁺ into glutamate to produce glutamine (Lea and Miflin, 1974). Increased accumulation of GS activity was observed with increased salinity in mulberry (Ramanjulu et al., 1994a). Similarly, elevated GS activity has been reported in the shoots of Poterium (Taylor et al., 1982), horse gram (Reddy, 1987) and cow pea (Padmavathi, 1989). In contrast, decreased Gs activity was noticed with increasing salinity in tomato and in leaves of Comavalia ensiformis (Berteli et al., 1995). Lam et al., (1996) reported the differentially regulated GS genes/gene products in different plant organs and in different physiological conditions. Further more Carvalho et al., (2003) has been showed that transformants with altered GS activity levels exhibit alterations in enzymes, transcripts and polypeptides. Sakakibara et al., (1996) reported that the alterations in enzyme activity could correlate with the protein and transcript levels in maize roots. Similarly, Ortega et al., (2001) and Jyothsna kumari et al., (2004b) noticed that the GS protein content was proportional to the levels of GS activity in alfalfa and peanut plants.

Stress induced proteins due to salt stress

Plants are able to respond and adapt to changing environments through the synthesis of specific proteins which can modify cellular metabolism. In many cases the synthesis of stress-induced proteins is a part of some tolerance mechanism. Changes in protein synthesis are attributed to changes in the gene expression induced in salt-stressed plants (Chen and Plant, 1999). Salt-responsive genes encoded proteins and
other products taking part in cellular protection, general defense (La Rosa et al., 1992), and osmoregulation (Delauney and Verma, 1993).

An important consequence under salt stress was the alteration in polypeptide profiles as shown by several workers in barley (Ramagopal, 1987; Hurkman et al., 1989), tobacco (Singh et al., 1985; Hurkman and Tanaka, 1987), Anabaena (Apte and Bhagvat, 1989), rice (Rani and Reddy, 1994), wheat (El-Shintinawy and El-Shourbegy, 2001). Plant responses to salinity and other water-deficit stress such as drought, have been investigated using proteomic/genomic based approaches (Ouerghi et al., 2000; Salekdeh et al., 2002; Wang et al., 2003).

Apte and Bhagavath (1989) reported a total of 11 SSPs with apparent molecular mass of 54, 49, 46.5, 32, 29, 28, 26.5, 21.5, 19.5, 18.5 and 17 kDa were induced with in 10 min and one more SSP with molecular weight of 79 kDa was induced after 30 min of exposure to 120 mM of NaCl stress in salt tolerant Anabaena torulosa. Similarly, Hurkman et al., (1991) have identified two polypeptides of molecular weight 26 kDa on 2D gels from salt treated barley roots and showed that these proteins are similar to germin a glycoprotein. Germin is known to possess oxalate oxidase activity, responsible for converting oxalate to H$_2$O$_2$ and CO$_2$ (Lane et al., 1993). In plants H$_2$O$_2$ plays a role in the oxidative cross-linking of cell wall polymers, and therefore, the expression of germin may result in cell-wall modification in salt-stressed plants (Olson and Varner, 1993; Schlesier et al., 2004).

Ouerghi et al., (2000) reported the increased synthesis of two polypeptides molecular mass of 16.9 and 16.3 by 2D gels in salt tolerant wheat cultivar Ben Bachir. They attributed that salt-dependent salt adapted proteins (SAP), whose terminal amino acid sequences were found to be homologous to the sequence of proline rich protein.
(Esaka and Hayakawa 1995). Further more these authors demonstrated the similarity of these polypeptides with 22 kDa (pI 5.1) protein found to increase under water-stress or salinity in *Brassica napus* leaves by Reviron *et al.*, (1992). Similarly in another study Majoul *et al.*, (2000) reported the increased amount of 26 kDa protein in wheat cultivar Chili, whose N-terminal amino acid sequence was NH2-PGLTIGDTVPNLELDSTHGK-COOH and showed the strong similarities with two proteins, 'Rab 24' identified in rice (*Oryza sativa*) and 'peroxiredixin B15C' identified in barely (*Hordeum vulgare*). Rab protein, which are responsive to abscisic acid (ABA), belonging to a family of proteins that were named LEA because of their late embryogenesis abundance. Peroxiredoxin B15C represents a family of thiol-requiring antioxidants first characterized in yeast and later identified in organisms ranging from bacteria to human (Stacy *et al.*, 1996).

Salinity stress triggers the expression of several osmoreponsive genes and proteins in rice tissues. These are includes SalT (Claes *et al.*, 1990) encodes mannose binding jacalone like lectin (Hirino *et al.*, 2000), Em gene encoding a hydrophilic late embryogenesis abundant protein (Bostock and Quatrano 1992), rMip1 and rTrip1 genes encoding the major intrinsic proteins of plasma membrane and tonoplast membranes. In addition, there is another class of genes in rice that are induced by a number of stresses like dehydration by PEG or desiccation and osmotic stress caused by ABA and also salt or both (Mundy and Chua, 1988; Skriver and Mundy, 1990; Bostock and Quatrano 1992). For instance, the rab16 gene belongs to this class of genes (Skriver and Mundy, 1990). Furthermore, Moons *et al.*, (1995, 1997a, b, c) have identified a set of salt induced proteins in the roots of rice. Prominent among these are group2 LEA, LEA dehydrins, two pathogen related proteins (PRPs), peroxidase and histidine rich proteins. They also reported that the PRP an osmotin like protein played an
important role in defense of plants against salt stress. They also showed that the group1 LEA dehydrins were involved in the protection of cellular components from osmotic stress caused by salt. Another LEA from tomato was expressed in yeast to confer tolerance to salinity and freezing (Ismail et al., 1996).

Hong et al., (1988), reported that the expression of HVA1 gene especially in aleurone layers and the embryos during late seed development, correlating with the seed desiccation stage. Moreover, it was revealed that this HVA1 gene is rapidly increased in young seedlings by ABA and by several stress conditions, including dehydration, salt and extreme temperature (Hong et al., 1992). Similarly Xu et al., (1996) found an increase in the accumulation of HVA1 (Hordeum vulgare aleuron) protein and showed positive correlation of stress tolerance in transgenic rice plants subjected to salt and water stress conditions.

Lopez et al., (1994) have reported a 22 kDa protein in response to salt stress in radish. Similarly, Rani and Reddy (1994), have found several prominent polypeptides with apparent molecular weight of 15, 23, 26 and 70 kDa under salt stress in young seedlings of rice (Oryza sativa L.). Uma et al., (1995) also have showed 54 kDa and 23 to 24 kDa proteins under salt or drought stress conditions in finger millet (Eleusine coracana Gaertn). It is evident that ABA and Jasmonets antagonistically regulate the expression of salt stress induced proteins associated with osmotic stress in the root tissues of rice seedlings (Moons et al., 1997b). Jayaprakash et al., (1998) noticed the genetic variability in differential expression of Lea genes and proteins in response to salinity stress in finger millet (Eleusine coracana) and in rice (Oryza sativa L.) seedlings. Their study demonstrates the quantitative differences in the expression of these proteins in different genotypes of finger millet and rice. They
showed a positive correlation between Lea2 and Lea3 protein levels and seedling growth and stress tolerance during stress and recovery. In another study, Cheng *et al.*, (2002) showed the expression of wheat LEA group 1 and group2 protein genes in two transgenic rice plants under salt stress. Furthermore, Wimmer *et al.*, (2003) have studied the stress induced quantitative and qualitative changes in intercellular protein composition in wheat plants under combined salt and boron stress.

Over past several years the expression of several genes/gene products has been reported to be osmotically regulated during NaCl stress (Narasimhan *et al.*, 1991, Peres-part 1992; Andrazej *et al.*, 1993). The most well characterized such protein is osmotin. Singh *et al.*, (1987b), Bressan *et al.*, (1987) named a 26 kDa protein as osmotin, accumulated in a salt adapted tobacco. Osmotin is a cationic protein with pI 8.2 and accounts for 10-12% of total proteins in NaCl and PEG adapted tobacco cells (Singh *et al.*, 1985). Singh *et al.*, 1985 extensively studied the nature and function of osmotin and found that osmotic synthesis and regulated by ABA. Further more, they reported two forms of osmotin in NaCl adapted cells: an aqueous soluble form (Osmotin-I) and a detergent soluble form (Osmotin-II) in the approximate ratio of 2:3. Osmotin-II known to be less susceptible to proteolysis than osmotin-I. Osmotin strongly resembles the sweet protein thaumatin in its molecular weight, amino acid composition, N-terminal sequence and the presence of a single peptide on the precursor protein. Osmotin found to concentrate in dense inclusion bodies with in the vacuoles and appeared to be distributed in the cytoplasm (Singh *et al.*, 1987b).

**LEA proteins**

Late embryogenesis abundant proteins (LEA) are members of a large group of hydrophilic, glycine-rich proteins originally discovered in late embryogenesis stage
of developing seeds and shown to be associated with desiccation tolerance of seeds (Dure et al., 1981). Besides plants, LEA proteins were also found in algae, fungi and bacteria; known collectively as hydrophilins that are preferentially expressed in response to dehydration or hyperosmotic stress (Soulages et al., 2003). These proteins are also accumulate in vegetative tissues exposed to exogenous abscisic acid, as well as dehydration, osmotic and low-temperatures (Close and Bray, 1993; Chandler and Robertson, 1994; Ingram and Bartles, 1996; Close, 1996; Bray, 1997; Thamashow, 1999; Nylander et al, 2001). LEA proteins have been characterized and categorized into seven different groups by virtue of similarities in their deduced amino acid sequence (Dure et al., 1989; Baker et al., 1988). The majority of the LEA proteins are highly hydrophilic and display a preponderance of certain amino acids like Ala, Gly, Glu and Thr; and lack of Trp and Cys (Dure, 1993a, 1993b, 1997) and are not compartmentalized or transported within cell but are located in the cytosol. LEA proteins also display diverse sub cellular and tissue-specific localization patterns, suggesting that different groups or group members fulfill specific functional roles (Close 1997; Nylander et al., 2001). LEA protein expression generally correlates well with desiccation tolerance in young seedlings (Reid and Walker-Simmons, 1993; Whisitt et al., 1993) as well as salt tolerance (Moons et al., 1995) and freezing tolerance (Houde et al., 1995; van Zee et al., 1995; Close, 1997; Danyluk et al., 1998).

**Group 1 LEA proteins**

Group 1 Lea proteins are distinguished from other group of LEA proteins by being very hydrophilic and highly conserved along the entire length of the protein (Dure, 1993, 1997). And also these proteins are further characterized by having an interanal 20- amino acid signature motif repeated up to four times depending on the
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species (Esperlund et al., 1992) and a high proportion of Gly, Glu and Gln residues. Soulages et al., (2002) suggested that this remarkable conservation play an important role in stress adaptation. Several investigators have reported a predicted role for group 1 LEA proteins is that of water binding property in order to provide protective aqueous environments for the cellular components under salt, water-deficit stress and ABA (Marcotte et al., 1988; Bostock and Quairano, 1992; Almoguera and Jorden, 1992).

**Group 2 LEA proteins**

Group 2 LEA proteins often referred to as dehydrins or RAB (responsive to abscisic acid) and were originally identified as the “D-11” family of Lea proteins in developing cotton (Gossypium hirsutum) embryos (Baker et al., 1988; Dure et al., 1989). These are the most commonly observed proteins induced by environmental stresses associated with dehydration or low temperature and that comprise an immunologically distinct family (Close, 1997). The term Dehydines (DHN) for these proteins was initially intended for dehydration-induced proteins and are classified as DHNs based on sequence homology rather than after expression characteristics. Dehydrins are induced typically in maturing seeds or vegetative tissues following salinity, dehydration, cold or freezing stress or abscisic acid (ABA) treatment (Close, 1996; 1997).

This group 2 LEA proteins are generally hydrophilic, lack Trp and most often Cys residues, and contain a high proportion of charged and polar amino acids and low proportion of non-polar, hydrophobic residues, which causes the solubility of this proteins at high temperatures. Dehydrins are distinguished from other LEA proteins by a highly conserved Lys-rich 15 amino acid sequence motif (Consensus=EKKGIMDKIKEKLPG) referred to as the K-segment (Close 1996;
1997), which are usually located in the ‘C’ terminus and may be reported one to 11 amino times and are predicted to form class A amphipathic α-helices (Dure, 1993, Close, 1996). In addition, the majority of group 2 LEA proteins contain another conserved sequence Y-segment (Consensus = V/TDE/QYGNP) located in N-terminus. Many dehydrins also contain Ser tract repeats (S-segment) that can undergo phosphorylation and are thought to participate in nuclear localization (Godoy et al., 1994; Godoy et al., 1994).

Numerous studies have reported a positive correlation between the accumulation of group 2 LEA transcripts or proteins and cold acclimation, chilling or freezing, drought and salinity tolerance (Houde et al., 1995; Whitsitt et al., 1997; Cellier et al., 1998; Danyluk et al., 1998; Ismail et al., 1996; Borovskii et al; 2002). Dehydrins have been found to localized to the nucleus, cytoplasm, plasmamembrane, mitochondria or vacuole of vascular tissues (Houde et al., 1995; Danyluk et al., 1998; Borovskii et al., 2002; Nylander et al., 2001). Dehydrins are known to play an important role in cellular dehydration as membrane stabilizera in freeze induced dehydration cells (Close, 1996; Danyluk et al., 1998), possess cryoprotective role (Kazuoka and Oeda, 1994; Houde et al., 1995; Wisniewski et al., 1999; Bravo et al., 2003), antifreeze activity of enzymes (Wisniewski et al., 1999; Rinne et al., 1999), to function as osmoregulators (Nylander et al., 2001) and as radical scavengers (Hara et al., 2001) under desiccation stress.

**Group 3 and group 5 LEA proteins**

The common element found in these tow groups of LEA proteins is presence of tandemly repeated 11-mer amino acid motifs, TAQAAKEKEGE, that are repeated many times with in the proteins (Dure, 1993a) and predicted to form a helix,
which is amphiphilic, having a hydrophobic surface formed by methyl groups of the DHNs repeat consensus. Unlike group 3 LEA proteins; group 5 LEA proteins are lacking a high degree of specificity at each position in 11-mer repeats (Bray, 1997). Genes encoding group 3 LEA proteins are known to be expressed in response to salt, water deficit and ABA in soybean and barley (Hong et al., 1992) and salt and ABA in roots of rice (Moons et al., 1997c). Group 5 LEA proteins are known to be involved in ion sequestration during cellular dehydration (Bray, 1997).

**Group 4 LEA proteins**

These proteins are known to contain a conserved N-terminal domain that forms a α-helix and a less conserved C-terminus, rich in glycine and amino acids containing hydroxyl groups, forming an unstructured random coil (Dure, 1993b). These proteins are known to bind water molecules and may also act as chaperons, thereby these would stabilizes the surface of membranes and possibly proteins by binding water and functioning as solvation film. Cohen et al., (1991) reported the expression of genes encoding group 4 LEA proteins in vegetative tissues in response to salinity, drought, ABA and low temperature.

**LEA D95**

This group of proteins are unusual; since there are some hydrophobic characters. LEA D95 is homologous to a pcC2745; a cDNA; where it was expressed in *Caterostigma plantagineum* in response to salt in callus tissues and in response to desiccation and ABA in both leaves and callus tissue (Piatkowiki et al., 1990). Furthermore; Galau et al., (1999) reported the accumulation of these LEA D95 proteins in cotton leaves in response to water stress.
Review of Literature

So far it is evident that stress proteins could be used as important molecular markers for improvement of salt tolerance using genetic engineering techniques. However, Ashraf and Harris, (2004) stated that using the stress proteins as salt tolerance indicators depends on the nature of cultivar. Changes in gene expression at the transcriptional and post transcriptional levels were initially demonstrated by analysis of protein profiles elicited in plants exposed to various stresses. From these studies it is evident that both qualitative and quantitative changes in the pattern of polypeptides synthesized following salt treatment (Ericson and Alfinito, 1984; Ramagopal, 1987; Singh et al., 1989; Chen and Tabaeizadeh, 1991; Moons et al., 1997b).

From the literature cited above it is clear that considerable research effort has been made towards the identification of stress tolerant plant species and genotypes of crop plants including fox-tail millet. Though a very few investigators concerned with the physiological and biochemical aspects of salt tolerance of fox-tail millet, a trace of information is available on molecular changes especially on stress induced proteins in fox-tail millet under salt stress. In the present investigation therefore; an attempt is made to understand the stress induced proteins especially salt stress induced proteins and their expression studies in an important semi arid millet crop, fox-tail millet during early seedling growth under different regimes of salinity stress.