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MECHANISM OF SALINITY STRESS TOLERANCE IN CROP PLANTS AND RECENT DEVELOPMENTS

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INTRODUCTION

The last three decades has witnessed substantial increase in productivity of cereals, pulses, oilseeds and cash crops through adoption of high yielding varieties and intensive agriculture. There has been a shift from cereals to cash crops with development of high yielding varieties and increase in irrigated acreage.

Salts are component of soil, and originate from mineral weathering, inorganic fertilizers, soil amendments (e.g., gypsum, composts and manures), and irrigation waters. But when salts are present in relatively high amounts, plant growth is adversely affected. Soil salinity is a measure of the total amount of soluble salt in soil. As salinity levels increase, plants extract water less easily from soil, aggravating water stress conditions. High soil salinity afflicts about 95 million hectares of land worldwide (Szabolcs, 1994) can also cause nutrient imbalances, result in the accumulation of elements toxic to plants, and reduce water infiltration. In India, soil salinity, spread in almost 8.5 m ha area is the factor limiting plant growth and productivity.

There are two types of salinity, dry land and irrigation salinity. The dry land salinity is classified as either primary or secondary. Primary salting occurs naturally while secondary salting is induced by human activities such as agriculture. Secondary salinity is an insidious problem that may be undetected for years until saline discharge is discovered at the soil surface. Salinity through irrigation resembles dry land salinity, except that groundwater accession is induced through irrigation water rather than rainfall alone. Irrigation salinity refers to an accumulation of salt in the plant root zone or on the soil surface, commonly as a result of saline groundwater rising within two meters of the ground surface. Classification of salt affected soil as per ICAR (ICAR 2011) are given in Table 1 and the extant of area of salt affected soil in India as identified by CSSRI, Karnal are given in Table 2.

Table 1. Classification of salt affected soil (source: Handbook of Agriculture, ICAR, 2011)

Net and Coll	USDA	Classifica	SSSA Classification		
Nature of Soil	ECe (dS m^{-1})	pH	ESP	ECe (dS m^{-1})	SAR
Normal	< 4.0	< 8.5	< 15	< 2	< 13
Saline	> 4.0	< 8.5	< 15	> 2	< 13
Sodic	Variable	> 8.5	> 15	Variable	> 13
Saline-Sodic	> 4.0	> 8.5	Variable	< 2	> 13

Table 2. Extent and distribution of salt affected soil in India (source: CSSRI, Karnal)

State	Salt affected area (× 1000 Ha)						
State	Canal Command	Outside Canal	Coastal	Total			
Andhra Pradesh	139	391	283	813			
Bihar	224	176	Nil	400			
Gujarat	540	327	302	1169			
Haryana	455	Nil	Nil	455			
Karnataka	51	267	86	404			
Kerala	NA	NA	26	26			
Madhya Pradesh	220	22	Nil	242			
Maharashtra & Goa	446	NA	88	534			
Odisha	NA	NA	400	400			
Punjab	393	127	Nil	520			
Rajasthan	138	984	Nil	1122			
Tamil Nadu	257	NA	84	341			
Uttar Pradesh	606	689	Nil	1295			
West Bengal	Nil	NA	800	800			
Total	3469	2983	2069	8521			

Soil salinity negatively affects the growth of many crop plants, and the continued salinization of arable land provides an increasing threat to global crop production, especially in irrigated systems (Munns and Tester, 2008). The soil degradation mainly salinity has resulted in 4.0-6.3% crop loss in India (Table 3). Thus, understanding the mechanism and increasing the salinity tolerance of crop plants will provide an important contribution to the maintenance of crop yields. The Na⁺ toxicity of many crops is due to over accumulation of Na⁺ in the shoot (Munns, 1993, 2002; Tester and Davenport, 2003; <u>Møller and Tester, 2007</u>). Na⁺ is taken up from the soil by the root and transported to the shoot in the transpiration stream and shoot Na⁺ accumulation is the net result of distinct Na⁺ transport processes occurring in different organs and cell types (Tester and Davenport, 2003), and each of these processes contributes to the salinity tolerance of a plant.

Table 3. Impact of soil degradation on Indian Agriculture (Source: The cost of inaction: Valuing the economy-wide cost of environmental degradation in India, World Bank)

Сгор	Percent loss
Paddy	2.7 - 4.7%
Wheat	3.9 - 6.4%
Barley	4.5 - 7.0%
Groundnut	2.8 - 4.4%
Gram	5.6-7.8%
Rapeseed & mustard	5.8 - 8.5%
Jowar	5.7 - 7.6%
Bajra	6.8 - 8.4%
Cotton	5.3 - 6.9%
Maize	3.2 - 4.9%
Sugarcane	4.5 - 7.9%
All other crops	4.0 - 6.3%
Total	4.0 - 6.3%

The knowledge of physiological and biochemical mechanism of salinity stress tolerance in crop plants is very important as understanding the basic responses of crop plants will help in identifying certain physiological, biochemical and molecular traits for screening of better genotypes tolerant against soil salinity which will help to identify genotypes suitable for cultivation in salt affected areas directly or through conventional breeding and biotechnological means. In this chapter an attempt was made to combine the existing knowledge of salinity tolerance in plants and the future prospect of research in this area.

2. BASIC RESPONSES OF PLANTS TO SALINITY STRESS

High salinity adversely affects germination, growth, physiology and productivity by causing ionic and osmotic stresses and oxidative damage (Iterbe-Ormaetxe *et al.*, 1998). Salt stress is also responsible for an increased respiration rate, ion toxicity (Sudhir and Murthy, 2004), changes in C and N metabolism (Kim *et al.*, 2004), mineral distribution, membrane instability (Marschner, 1986) and permeability (Gupta *et al.*,

2002), decreased biosynthesis of chlorophyll (Khan, 2003) and photosynthetic inefficiency (Munns, 2002), all of which ultimately leads to lowered economic productivity.

Accumulation of sugars and other compatible solutes that can serve as osmoprotectants, stabilizing biomolecules under stress conditions is a common phenomenon. Although use of ions for osmotic adjustment may be energetically more favorable, many plants accumulate organic osmolytes to tolerate osmotic stresses which include proline, betaine, polyols, sugar alcohols, and soluble sugars. Glycine betaine and trehalose act as osmoprotectants by stabilizing quaternary structures of proteins and highly ordered states of membranes. Proline serves as a sink for carbon and nitrogen and a free-radical scavenger, stabilizes sub cellular structures (membranes and proteins) and buffers cellular redox potential. A schematic diagram of the response of plant to salinity stress and possible changes and symptoms are given in Fig. 1.

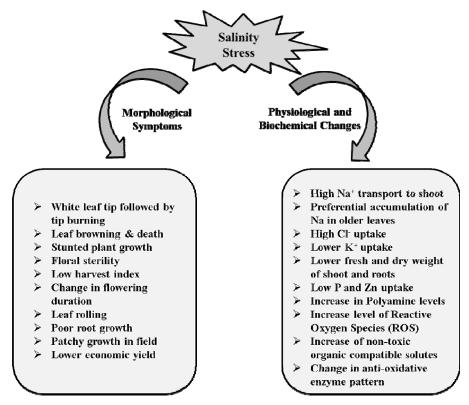


Fig. 1. Effect of soil salinity in crop plants

Salt-stress induces accumulation of reactive oxygen species (ROS), causing oxidative damage to membrane lipids, proteins, and nucleic acids. To combat oxidative stresses plants employ two strategies: i) antioxidants (e.g., ascorbate, glutathione, α -tocopherol, and carotenoids) and ii) detoxifying enzymes, viz., superoxide dismutase, catalase, and enzymes of ascorbate-glutathione cycle. The activity and expression levels of the genes encoding detoxifying enzymes are probably enhanced by ROS under abiotic stresses.

Salt stress has both osmotic (cell dehydration) and toxic (ion accumulation) effects on whole plant and leaf physiology (Flowers, 2004). Salinity reduces the supply of CO₂ to leaves, and further depresses the already low CO₂/O₂ in chloroplasts (Remorini *et al.*, 2009). The consequent accumulation of photoreducing power causes an excess of electrochemical energy in membranes (Zhu, 2001). This extra energy is canalized through the Mehler reaction, which generates ROS such as superoxide anion (O₂-) and hydrogen peroxide (H₂O₂) (Herna'ndez *et al.*, 2001), ultimately provoking oxidative-stress syndrome (Herna'ndez *et al.*, 2000; Baltruschat *et al.*, 2008).

Exposure to higher levels of NaCl affects plant water relations and creates ionic stress in the form of the cellular accumulation of Cl⁻ and in particular, Na⁺ ions. Sodium ions if accumulated in the cytoplasm are toxic to living cells because of their adverse effects on K⁺ nutrition, cytosolic enzyme activities, photosynthesis, and metabolism. Besides, salt stress also impacts heavily on the homeostasis of other ions such as Ca²⁺, Mg²⁺, and NO₃⁻ and therefore, requires insights into how transport and compartmentation of these nutrients is altered during salinity stress. Three mechanisms function cooperatively to prevent the accumulation of Na⁺ in the cytoplasm, i.e., restriction of Na⁺ influx, active Na⁺ efflux, and compartmentalization of Na⁺ in the vacuole.

Regulation of cellular ion homeostasis during salinity stress is critical for plant salt tolerance. The identification of the salt overly sensitive (SOS) pathway in *Arabidopsis* has revealed components and mechanisms involved in the plant's response to ionic stress. The DNA sequence differences of the component genes and promoters may be responsible for the variation in sensitivity of different species of *Brassica* to salt stress, as among different species of *Brassica; B. juncea* was found to be most tolerant towards salinity in terms of morphological and yield attributes followed by *B. napus* (Islam *et al.*, 2001).

3. MAJOR SYMPTOMS OF SALINITY STRESS ON CROP PLANTS

3.1. Effect of Salt Stress on Growth, Yield and Nutrient Contents

Salinity affects crop production and agricultural sustainability in many regions of the world mainly by reducing the value and productivity of the affected land (Mohammed *et al.*, 1998). Water resources in arid areas are frequently brackish and constitute the only available alternative for crop production (Botella *et al.*, 1993). Soluble salts accumulate in irrigated soils because plants absorb only a small fraction of the minerals dissolved in irrigation water and only pure water evaporates from the soil surface, causing yield reductions (Dirksen, 1985). The species Brassica napus and B. carinata are moderately salt tolerant and have a good yield potential on the marginal lands, where as B. juncea and B. compestris are salt sensitive where reduction in stem diameter, number of siliqua per plant, 1000 seed weight and other yield attributing characters is common feature (Akhtar et al. 2002).

Gupta and Yadav (1986) reported that groundnut could be grown with water having EC up to 3.0 dS m⁻¹, but our recent study shows that groundnut plant starts facing salinity stress above 2.0 dS m⁻¹ and EC above 4.5 dS m⁻¹ kills the plants, however, as enough genotypic variation exists, the salinity level in between 3-4 dS m⁻¹ during most of the cropping period was ideal for screening for salinity tolerance (Singh *et al.*, 2008). In groundnut the salinity caused accumulation of Na in leaves and to compensate that and maintain proper ratio of various nutrients there was accumulation of Ca and K content. Interestingly, the salinity tolerant cultivars showed comparatively less Na and K accumulation in their leaves than that of sensitive cultivars (Singh *et al.*, 2010a).

Some efforts have been made to study the performance of a few groundnut cultivars by recording germination and studying plant till vegetative phase in pots (Nautiyal et al., 1989; Vadez et al., 2005) and in field (Janila et al., 1999) and very few till maturity in field (Mensah et al., 2006; Nautiyal et al., 2000). Also in a recent attempt screening protocoal using rate of survival under NaCl treatment in glass house (Vadez et al., 2005) as well as in vitro regenerated shoots grown on media (Mungala et al., 2008) has been made as a measure of their tolerance to salinity. Salinity tolerance is a relative term depending mainly upon its intensity and relative performance of cultivars. The groundnut cultivars with high field emergence followed by high plant stand and low mortality under saline conditions could be considered as tolerant of salinity stress. However, data on yielding ability is more vital as increasing salinity decreases pod yield (Singh et al., 2008). Salinity caused severe reduction in plant stature and plant height with small immature pods followed by very high (56-100%) plant mortality at harvest (Singh et al., 2010a).

Assessment of the mineral nutrient status of plants facing various abiotic stresses can be done using biochemical and enzymatic methods involving marker enzymes which are based on the fact that the activity of certain enzymes in deficient tissue is lower or higher (depending on the nutrient) than in normal tissue (Lavon and Goldschmidt, 1999; Vı'llora *et al.*, 2000; Singh and Chaudhari, 1993). Catalase and peroxidase are indicators of the nutritional status of Fe in plants and are also useful as indicators of Fe and Mn deficiencies (Moreno *et al.*, 2000; Valenzuela *et al.*, 1995). Carbonic anhydrase and ribonuclease activity is a good indicator for Zn (Dwivedi and Takkar, 1974; Sharma *et al.*, 1990) and Cu deficiency increased ribonuclease activity in leaves (Agarwala *et al.*, 1985, 1995). Under salinity stress decrease in micronutrient contents are correlated with decrease in activity of related enzymes.

Salinity stress results in ionic and nutritional imbalance due to competition of salt ions with nutrients. Saline condition influences the different steps of nitrogen (N) metabolism, its uptake, reduction and protein synthesis which are responsible for the reduction in plant growth (Frechill *et al.*, 2001) and decreased dry matter production. A negative correlation between concentrations of nitrate (NO₃) and Cl⁻ was seen in the shoots and roots (Abdelgadir *et al.*, 2005). Salinity reduced potassium (K⁺), and calcium (Ca²⁺) contents, and increased Na⁺ and Cl⁻ content in leaves and stems (El-Hendawy *et al.*, 2005). Saline environment is generally deficient in nitrogen (Amonkar and Karmarkar, 1995) as a result there is reduction in NO₃⁻ uptake due to high Cl⁻ in saline condition. Addition of N to salinity, improved the growth and yield of plant, and increased salt tolerance (Dubey and Pessarakli, 1995).

The most common salinity effect is a general stunting of plant growth. As salt concentration increases above a threshold level both the growth rate and size of most plant species progressively decrease but all the plant parts are not affected equally. Shoot growth is often suppressed more that the root growth (Meiri et al., 1970). Often vegetative growth response to salinity is not so reliable guide for predicting seed or grain yield. Yield of rice (Pearson, 1959) and corn (Kaddah and Gohowail, 1964) are greatly reduced without affecting straw yield under saline condition. Growth and yield of bell pepper at different B and salinity levels and the results from the experiments and from published data for wheat, tomato and chickpea indicated an antagonistic relationship for excess B and salinity (Yermiyahu et al., 2008). Thus, toxic effects on growth and yield were less severe for combined B toxicity and salinity than what would be expected if effects of the individual factors were additive. Though the mechanism of relationships between B and salinity in plants is not clear, the possible explanations are reduced uptake of B in the presence of Cl and reduced uptake of Cl in the presence of B (Yermiyahu et al., 2008).

The crop tolerance to high B has been attributed to reduced uptake of B as a result of B efflux from roots. Salinity interacts with B toxicity by a combined effect on B and water uptake and B partitioning within the plant (Wimmer *et al.*, 2001). Salinity usually reduces shoot B concentrations. The whole tissue B concentration is a poor indicator of B tolerance, but the tissue B distribution and subcellular ion compartmentation and B and salinity interactions is important criteria in wheat (Wimmer *et al.*, 2001). Under saline conditions, the total B concentration increased in leaf tips, decreased in roots and was not affected in basal leaf parts, however, soluble B concentrations in basal leaf parts increased in the combined salt/high B treatment compared to high B treatment alone in wheat (Wimmer *et al.*, 2001). Looking to the complex relations between salinity and B toxicity the interactions of soluble B with salinity was studied on physiological response of plants in tomato plants and several

hypotheses are established by (Bastías *et al.*, 2010). The increase of aquaporin functionality due to the presence of B and Ca compared with NaCl-treated plants could be the most feasible, whereas there is currently no satisfactory explanation for the results for the cell wall amino acid composition. In addition, the elemental composition results revealed that, in addition the known interactions between B and Ca with respect to cell wall stability, Mg and Mn were also increased in NaCl+B and NaCl+Ca treatments, suggesting their possible involvement in the cell wall function necessary for plant growth (Bastías *et al.*, 2010).

3.2 Effect of Salinity on Pigment System of the Plant

Photosynthesis is the most important process affected in plants under saline conditions. Reduced photosynthesis under salinity is attributed to stomata closure leading to a reduction of intercellular CO₂ concentration and to non-stomatal factors also. There is strong evidence of salinity affecting photosynthetic enzymes, chlorophyll and carotenoid (Stepien and Klobus, 2006). Decrease in Chlorophyll and carotenoid contents of leaves in response to salt stress is a general phenomenon (Parida and Das, 2005). However, an increase in pigment content in Amaranthus sp has also been observed (Wang and Nil, 2000). The literature showed wide variations in pigment content depending on salt stress. In quite a few cases, the chlorophyll content was paralleled by changes in the Chl a/b ratio, which is an indicator of the antenna size of PS I and PS II. The core antenna contains only Chl a, whereas the outer antenna contains both Chl a and Chl b. A higher Chl a/b ratio therefore indicates a smaller antenna size and a lower ratio a larger antenna size. Chlorophyll a, b, total chlorophyll and carotenoid content decrease in response to salinity stress (Ahmad, 2009). Salt stress directly or indirectly affects the photosynthetic functions by changing the structural organization and physio-chemical properties of thylakoid membranes (Alia-Mohanti and Saradhi, 1992). Salinity stress reduces quantum yield and Fv/Fm ratio in naked oat (Zhao *et al.*, 2007).

3.3. Relative Water Content and Water Availability

Salinity and water stress have quite similar effects on the growth and cell viability (Lutts *et al.*, 2004). Salinity causes pronounced decrease in water uptake and plant growth in shoot and root (Misra and Dwivedi, 2004). High concentration of salt in the root zone (rhizosphere) reduces soil water potential and the availability of water (Llyod *et al.*, 1989), as a result reduction of the water content dehydration at cellular level and osmotic stress are obvious. The increased amount of Na⁺ and Cl⁻ in the soil-water medium affects the uptake of many indispensable nutrients through competitive interactions and by affecting the ion selectivity of membranes.

Salt stress reduces both RWC and fresh weight in *Brassica* genotypes, but with varied degree of reduction depending upon genotypes

(Siddiqui *et al.*, 2008). The ability of plants to utilize water as well as changes in plant metabolic processes was reduced due to salinity in bean (Munns, 2002). Water potential (Ψ) decreased considerably in the 100 mM sodium chloride and sodium sulphate-treated plants due to salinity induced cellular water loss in *Phaseolus vugaris* (Kaymakanova and Steova, 2008). The decrease in the fresh weight of plants after both salinity and drought-induced water stress have been reported for many species as one of the physiological symptoms of stress (Passioura and Munns, 2000; Sucre and Sua'rez, 2011).

3.4 Electrolyte Leakage and Membrane Stability

Cell-membrane stability, an indicator of the structural integrity, is affected by dehydration and salt stresses (Thomas, 1997). Under saline conditions, plasma-membrane leakage (an indicator of cell plasmamembrane integrity) increases and there is a linear relationship between external salinity and membrane-leakage rate (Orcutt and Nielsen, 2000). Cell-membrane stability using leaf discs in maize, subjected to osmotic stress, showed correlation with the salinity and drought resistance of the plant (Simond and Orcutt, 1988).

Increase in electrolyte leakage in the leaves of *B. juncea* with increasing levels of salinity has been reported by Ahmad *et al.* (2009). High salt depositions in the soil generate a low water potential zone making it increasingly difficult for the plant to acquire both water as well as nutrients (Mahajan and Tuteja, 2005). Thus, salt stress essentially results in a water deficit condition in the plant and takes the form of a physiological drought. Salt stress causes disruption of ionic equilibrium, influx of Na⁺, dissipates the membrane potential and facilitates the uptake of Cl⁻ down the chemical gradient, which is evident from the reduction of membrane stability of salt treated plants. High concentration of Na⁺ causes osmotic imbalance, membrane disorganization, , inhibition of cell division and expansion leading to reduction in growth. High Na⁺ levels also lead to reduction in photosynthesis and production of reactive oxygen species (Yeo *et al.*, 1998).

3.5 Polyamine Biosynthesis

Polyamines (PAs) are organic poly-cations of a specific group of cell growth and development regulators and are preferentially detected in actively growing tissues and under stress conditions. Plant PA metabolism is extremely sensitive to adverse environmental conditions and hence, PAs are considered as stress markers in plants (Liu *et al.*, 2007; Takahashi and Kakehi, 2010). The function of PAs is presumed to be protective, as they act as free radical scavengers, stabilize cellular membranes, and maintain cellular balance (Bors *et al.*, 1989; Besford *et al.*, 1993). However, the precise role and mode of action of PAs in plant stress have long been a matter of debate. Changes in the levels of PAs under stress cannot be predicted and may be affected by several factors, such as plant species or cultivar, duration of stress treatment, developmental stage of tissues, and stress intensity. In addition, cultivars of the same species but differing in stress sensitivity might also show different changes in the pattern of PAs under stress. In nine rice cultivars that differed in salt sensitivity, salttolerant cultivars accumulated high concentrations of Spd and Spm, while the salt-sensitive ones accumulated extensive Put and lower levels of Spd and Spm (Krishnamurthy and Bhagwat, 1989). Stress-tolerant plants generally have a large capacity to enhance PA biosynthesis in response to abiotic stresses, compared with intolerant plants (Kusano et al., 2008; Gill and Tuteja, 2010). In Lupinus luteus (a drought tolerant species), Put and Spd were accumulated in leaves in osmotic and salt-stress conditions (Legocka and Kluk, 2005). Zapata et al. (2004) studied the effect of salinity on plant growth, ethylene production, and PA level in Spinacia oleracea, Lactuca sativa, Cucumis melo, Capsicum annum, Brassica oleracea, Beta vulgaris, and Lycopersicon esculentum (Legocka and Nowicka, 2012).

4. MECHANISM OF SALINITY STRESS TOLERANCE IN CROP PLANTS

4.1 Oxidative Stress and Antioxidant Enzyme Activities

Salt stress leads to stomatal closure, reducing CO_2 availability in the leaves and carbon fixation, exposing chloroplasts to excessive excitation energy, which in turn increases the generation of reactive oxygen species (ROSs) and induce oxidative stress (Parida and Das, 2005; Parvaiz and Satyawati 2008). These ROS have potential to interact with many cellular components, causing damage to membranes and other cellular structures. However, an elaborate and highly efficient network, composed of antioxidant enzymes and antioxidants, is responsible for maintaining the levels of ROS under tight control (Gao *et al.*, 2008).

Salt induced osmotic stress as well as sodium toxicity triggers the formation of reactive oxygen species (ROS) such as superoxide (O_2^{\cdot}) , hydrogen peroxide (H_2O_2) , hydroxyl radical (OH), and singlet oxygen ($^{1}O_2$), all of these disrups cellular structures by damaging mitochondria and chloroplasts (Mittler, 2002). Plants have developed a series of enzymatic and non-enzymatic detoxification systems to counteract ROS, and protect cells from oxidative damage (Sairam and Tyagi, 2004). The Antioxidant enzymes such as superoxide dismutase (SOD), catalase (CAT), peroxidase (POX) and glutathione reductase (GR) function in detoxification of super oxide and H_2O_2 (Mittler, 2002; Kholova *et al.*, 2009).

An antioxidant enzyme dependent salinity tolerance mechanism in plants is proposed in Figure 2. The SOD constitutes the primary step of cellular defence it dismutates O_{2} . to H_2O_2 and O_2 . Further, the accumulation of H_2O_2 is restricted through the action of catalase or by the ascorbate glutathione cycle, where ascorbate peroxidase reduces it to H_2O . Finally, glutathione reductase catalyzes the NADPH dependent reduction of oxidized glutathione (GSSG) to the reduced glutathione (GSH) (Noctor *et al.*, 2002). The tolerant and susceptible wheat genotypes show differences in antioxidant activity in response to salinity stress (Sairam *et al.*, 2005). Protective roles of the antioxidant enzymes in temperature and salt stress have been reported for a number of plants species (Jaleel *et al.*, 2007). The antioxidants ascorbate and glutathione are involved in scavenging H_2O_2 in conjunction with MDAR and GR, which regenerate ascorbate (Horemans *et al.*, 2000).

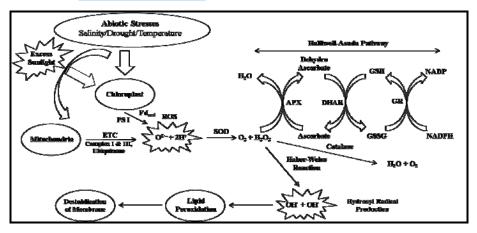


Fig. 2. Antioxidant enzyme dependent salinity tolerance mechanism in plants (modified from Mittler, 2002)

4.2 Osmotic adjustment and differential accumulation of various osmolytes

High salinity causes hyperosmotic stress and ion disequilibrium causing secondary effects (Hasegawa *et al.*, 2000; Zhu, 2001). Plants cope by either avoiding or tolerating salt stress and are either dormant during the salt episode or there is a cellular adjust to tolerate the saline environment. Tolerance mechanisms can be categorized as those that function to minimize osmotic stress or ion disequilibrium or alleviate the consequent secondary effects caused by these stresses. The chemical potential of the saline solution initially establishes a water potential imbalance between the apoplast and symplast that leads to turgor decrease, which, if severe enough, can cause growth reduction (Bohnert *et al.*, 1995). Growth cessation occurs when turgor is reduced below the yield threshold of the cell wall. Cellular dehydration begins when the water potential difference is greater than that can be compensated for by turgor loss (Taiz and Zeiger, 1998).

The cellular response to turgor reduction is osmotic adjustment which is achieved in sub-cellular compartments by accumulation of compatible osmolytes and osmoprotectants (Bohnert *et al.*, 1995; Bohnert and Jensen, 1996). However, Na⁺ and Cl⁻ are energetically efficient osmolytes for osmotic adjustment and are compartmentalized into the vacuole to minimize cytotoxicity (<u>Blumwald *et al.*</u>, 2000; <u>Niu *et al.*</u>, 1995). Since plant cell growth occurs primarily because of directional expansion mediated by an increase in vacuolar volume, compartmentalization of Na⁺ and Clfacilitates osmotic adjustment that is essential for cellular development. Filek *et al.* (2012) reported that Na⁺ may directly or indirectly exert a positive influence on the accumulation of other compounds involved in osmotic adaptation. Such an assumption could explain the greater tolerance to osmotic stress applied in wheat seedlings grown on media containing NaCl.

Salt tolerance mechanism requires osmolytes/compatible solutes accumulation in the cytosol and organelles, where these function as osmotic adjustment and osmoprotection (Rhodes and Hanson, 1993). Some compatible osmolytes are essential ions, such as K⁺, but the majority are organic solutes. Compatible solute accumulation as a response to osmotic stress is a ubiquitous process in organisms as diverse as bacteria to plants and animals. However, the solutes that accumulate vary with the organism and even between plant and genotypes. A major category of organic osmotic solutes consists of simple sugars (mainly fructose, glucose and sucrose), sugar alcohols (glycerol and methylated inositols) and complex sugars (trehalose, raffinose and fructans) (Bohnert and Jensen, 1996). Others are quaternary amino acid derivatives (proline, glycine betaine, β -alanine betaine, proline betaine), tertiary amines 1,4,5,6tetrahydro-2-mehyl-4-carboxyl pyrimidine), and sulfonium compounds (choline sulphate, dimethyl sulfonium propironate) (Nuccio et al., 1999). Many organic osmolytes presumed to be osmoprotectants, as their level of accumulation is insufficient to facilitate osmotic adjustment. Glycine betaine preserves thylakoid and plasma membrane integrity after exposure to saline solutions or to freezing or high temperatures (Rhodes and Hanson, 1993). Many of the osmoprotectants enhance stress tolerance of plants when expressed as transgene products (Bohnert and Jensen, 1996; Zhu, 2001). An adaptive biochemical function of osmo-protectants is the scavenging of ROS that are by products of hyperosmotic and ionic stresses, causing membrane dysfunction and cell death (Bohnert and Jensen, 1996).

The accumulation of proline has been observed due to salinity in several crop species in India. Salt stress stimulated the accumulation of glycine betaine (GB) and increase in levels of malondialdehyde (MDA) content in *Brassica juncea* (Ahmad, 2009). There was an abrupt rise in osmolytes accumulation in wheat cultivars under sailinity treatment (Sairam *et al.*, 2002). Tolerant genotypes of *Brassica* (CS 52 and CS 54) have inbuilt mechanism in the form of greater gene expression and activity of P5CS (pyrrolline-5-carboxylate synthetase), whose product proline provides osmotolerance in the form of retention of moisture (higher

RWC) and MSI, resulting in more yield stability (<u>Chakraborty *et al.*</u>, 2012b).

In plant kingdom the organisms ranging from bacteria to higher plants show a strong correlation between increased cellular proline levels and the capacity to survive both water deficit and salinity. The organic nitrogen may serve as the reserve that can be utilized during recovery from salinity. In *Lathyrus sativus*, a hardy grain legume, which can withstand drought, showed high proline accumulation in leaves and roots under water stress (Tyagi *et al.*, 1999). Though proline is synthesized either from glutamate or from ornithine, glutamate is the primary precursor in osmotically stressed cells. The biosynthetic pathway of proline accumulation consists of two important enzymes, viz. pyrroline carboxylic acid synthetase and pyrroline carboxylic acid reductase and transcripts corresponding to both cDNAs accumulate in response to NaCl treatment. Both these regulatory steps are keys in developing strategies for overproducing proline in selected plant species.

4.3 Expression of Osmolarity Related Genes

A common feature of compatible solutes is that these compounds can accumulate to high levels without disturbing intracellular biochemistry and have the capacity to persevere the activity of enzymes of plants growing in saline environment (Bohnert and Jensen, 1996). These compounds have minimal effect on pH or charge balance of the cytosol or luminal compartments of organelles. The synthesis of compatible osmolytes is often achieved by diversion of basic intermediary metabolites into unique biochemical reactions. Often, stress triggers this metabolic diversion. Higher plants synthesize glycine betaine from choline by two reactions that are catalyzed in sequence by choline monooxygenase (CMO) and betaine aldehyde dehydrogenase (BADH). Under salt stress expression of BADH increases (Rhodes and Hanson, 1993). Pinitol is synthesized from myo-inositol by the sequential catalysis of inositol-Omethyltransferase and ononitol epimerase (Bohnert and Jensen, 1996).

Glycine betaine accumulates in many species of the poaceae and chenopodiaceae (Flowers *et al.*, 2004) but is absent in many crop species such as rice and the model species in plant transformation, *Nicotiana tabacum*. Thus considerable work on engineering the production of glycine betaine in species that do not produce it naturally is in progress. The *E. coli* has a cluster of bet genes (betA: choline dehydrogenase, betB: betaine aldehyde dehydrogenase, bet1: a putative regulatory protein and betT: the choline transport system). Transformation of a cyanobacterium with the bet cluster resulted in glycine betaine synthesis (Nomura *et al.*, 1995).

In higher plants the pathway of glycine betaine synthesis is short and straight forward. In spinach choline monooxygenase (CMO) converts choline to betaine aldehyde and betaine aldehyde dehydrogenase (BADH) converts it to glycine betaine (Burnet *et al.*, 1995). The CMO is an ironsulphur protein which in its native form is a homodimer (Burnet et al., 1995). In sugarbeet the BADH activity increased 2 to 4-fold in leaves and roots with increase of NaCl from 0 to 500 mM and this increase in BADH activity is correlated with the level of translatable BADH mRNA. Two copies of BADH are reported in the haploid sugar beet genome and analysis of cDNA clones showed small nucleotide sequence differences consistent with the existence of two different BADH alleles (McCue and Hanson, 1992). Many species including tobacco lack both CMO and BADH. Spinach and sugarbeet cDNA sequences encoding BADH were expressed in tobacco, and even without a typical transit peptide BADH was still targeted to the chloroplast in the leaves of transgenic plants. Expressed levels and substrate affinity was comparable with the native enzyme and transgenic plants were able to synthesize glycine betaine from supplied betaine aldehyde showing a constitutive ability to transport betaine aldehyde into the chloroplast. The glycine betaine so synthesized was not metabolized further and accumulated to concentrations similar to those plants that accumulate it naturally. There is no information yet on its sub-cellular localization in transgenic plants. Betaine aldehyde is toxic when supplied exogenously in tobacco unless it was transgenic (Rathinasabapathi et al., 1994). Accumulation of BADH transcripts was a common response to osmotic stress. There was 8-fold increase in BADH mRNA levels in leaves of barley under high-salt conditions, and these levels were maintained under sustained stress, but decreased when stress was removed (Ishitani et al., 1995).

There are several other osmolytes than glycine betaine and one of them is trehalose, which play more than one role (Rhodes and Hanson, 1993; Yancey, 1994). TPS1 from *Saccharomyces cerevisiae* encodes trehalose–6-phosphate synthase, which is regarded as both a metabolic enzyme and a regulator (Serrano *et al.*, 1999). TPS1 has been reported to modulate the heat-shock response as well (Hazell *et al.*, 1995). Serrano *et al.* (1999) suggested that the products encoded by TPS1 may have a generalized role in activating stress-defence systems. Tobacco, transgenic for trehalose synthesis, was reported to have improved drought and salt tolerance (Romero *et al.*, 1997), but there was also a changed carbohydrate profile suggesting changes in basic biochemical pathways and the resultant average tissue concentration of trehalose (<0.5 mM) appeared too low to be performing a conventional osmoprotectant role. The transgenic plants for trehalose biosynthesis also showed linked severe morphological alterations including stunted growth.

Proline is another important metabolite which increases under salinity stress. The intermediates of proline biosynthesis and catabolism, such as glutamine and Δ -1-pyrroline-5-carboxylic acid could increase the expression of several osmotically regulated genes in rice (Iyer and Caplan, 1998). There is also evidence that degradation of proline in the mitochondria is directly coupled to respiratory electron transport system and ATP production. A pyrroline-5-carboxylate synthetase (P5CS) cDNA from moth-bean was introduced into rice, where expression of this P5CS transgene under the control of a stress inducible promoter led to stressinduced over-production of the P5CS enzyme and proline accumulation in transgenic rice plants. Second generation (RI) transgenic plants showed an increase in biomass under salt and water stress conditions (Zhu, 1998).

4.4 Relative Distribution of K, Ca and Na in Different Plant Parts and Na Exclusion

The fundamental basis of the adaptation of plants to salinity stress is the control of transport of salt across membranes (Hasegawa *et al.*, 2000). In glycophytes, salt exclusion is the predominant strategy of adaptation to saline substrates, i.e., tolerance to salinity depends mainly on the ability of roots to limit transport of sodium (Na⁺) to the leaves and shoot (Yahya, 1998). In sorghum (Sorghum bicolor), wheat (*Triticum aestivum*), barley (*Hordeum vulgare* L.) and corn (*Zea mays*) which are glycophytic in nature and where (Alberico and Cramer, 1993) Na⁺ exclusion mechanism is present for salt tolerance.

Also, within the plant, salt are restricted from reaching sensitive organs (Watson et al., 2001). Internal exclusion mechanisms can involve processes such as sequestering salt ions in specialized tissues by removing them from the transport stream (Blom-Zandstra et al., 1998; Jeschke, 1981) and/or by effectively compartmentalizing Na within vacuoles in the stem and leaf (Leigh and Storey, 1993). In other word, if Na⁺ ions are not strongly discriminated against at the root membrane, salinity of the xylem stream will increase under saline conditions. Some of the ions in the transpiration stream could be selectively accumulated by parenchyma cells in the xylem and then retranslocated back to the root via phloem (Orcutt and Nielsen, 2000). The K^+ content and K^+-Na^+ selectivity decreased and electrolyte leakage was increased in different cultivars of Brassica napus under salt stress. Sodium import, transport and deposition were increased by salinity stress but remobilization was decreased. The K⁺ and Mg^{2+} import, deposition, and remobilization were also decreased (Rezaei et al., 2006).

Under saline condition salt tolerance is usually related to ability to regulate Na⁺ and Cl⁻ uptake by plant root and their subsequent translocation to the shoot. In contrast, the higher concentration of essential elements (particularly K⁺ and Ca²⁺) in leaf tissues may contribute to the salt tolerance ability of plants (Ashraf and McNeilly, 1990; He and Cramer, 1993). The mechanism of selectivity of ion transport appears to confer tolerance to salt stress in Indian mustard. Higher selectivity towards K⁺ and restricted uptake of Na⁺ was observed in tolerant genotypes of Indian mustard (Kumar, 1984; Garg *et al.*, 1997).

4.5 Expression of Salt Overly Sensitive (SOS) Pathway Genes

Zhu and his co-workers identified three genetically linked *Arabidopsis* loci (SOS1, SOS2 and SOS3), which are components of a

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stress signalling pathway that control ion homeostasis and salt tolerance (Hasegawa et al,. 2000; Sanders, 2000; Zhu, 2001). Genetic analysis of Na⁺/Li⁺ sensitivity established that sos1 is epistatic to sos2 and sos3. These sos mutants also exhibit a K⁺ deficient phenotype in medium supplemented with $\mu M \, [K^+]_{ext}$ and $[Ca^{2+}]_{ext}$. Na⁺ and K⁺ deficiency of sos2 and sos3 is suppressed with mM [Ca²⁺]ext (Zhu et al., 1998). The sos1 exhibits hyperosmotic sensitivity unlike sos3 and sos2. Thus, the SOS signaling pathway regulates Na⁺ and K⁺ homeostasis and is Ca²⁺ activated. SOS3 encodes a Ca^{2+} binding protein with sequence similarity to the regulatory B subunit of calcineurin (protein phosphatase 2B) and neuronal Ca²⁺ sensors (Ishitani et al., 2000; Liu and Zhu, 1998). Interaction of SOS3 with the SOS2 kinase (Liu et al., 2000) and SOS2 activation is Ca²⁺ dependent (Halfter et al., 2000). The in planta function of SOS3 as a salt tolerance determinant is dependent on Ca^{2+} binding and N-myristoylation (Ishitani et al., 2000). After Zhu (et al., 2001) we Propose a SOS Pathway for Na⁺ homeostasis in plants as in Fig. 3.

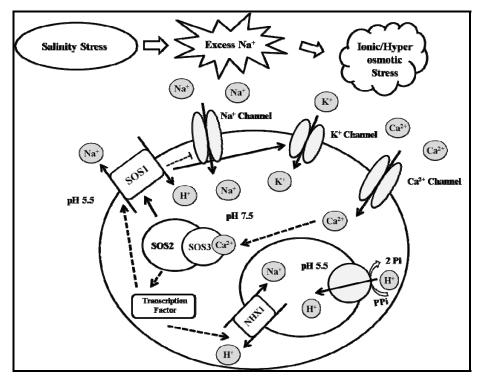


Fig. 3. Proposed Salt Overly Sensitive (SOS) Pathway for Na⁺ homeostasis in plants (Modified from Zhu *et al.*, 2001)

The SOS2 serine/threonine kinase (446 amino acids) has a 267 amino acid N-terminal catalytic domain that is similar in sequence to yeast SNF1 (sucrose non-fermenting) kinase and the mammalian AMPK (AMP-activated protein kinase) (Liu *et al.*, 2000; Zhu, 2001). The kinase activity

of SOS2 is essential for its salt tolerance determinant function (Zhu, 2001). The SOS2 C-terminal regulatory domain interacts with the kinase domain to cause autoinhibition. A 21 amino acid motif in the regulatory domain of SOS2 is the site where SOS3 interacts with the kinase and is the autoinhibitory domain of the kinase (<u>Guo et al.</u>, 2001). Binding of SOS3 to this motif blocks autoinhibition of SOS2 kinase activity. Deletion of the autoinhibitory domain results in constitutive SOS2 activation, independent of SOS3. Also, a Thr₁₆₈ to Asp mutation in the activation loop of the kinase domain constitutively activates SOS2.

Genetic and biochemical evidences indicate that components of the SOS signal pathway function in the hierarchical sequence (Hasegawa et al., 2000; Sanders, 2000; Zhu, 2001). The Ca²⁺ binds to SOS3 which leads to interaction with SOS2 and activation of the kinase. Among the SOS signal pathway outputs are transport systems that facilitate ion homeostasis. The plasma membrane sited Na+/H+ antiporter SOS1 is controlled by the SOS pathway at the transcriptional and posttranscriptional level (Guo et al., 2001; Zhu, 2001). Recently, functional disruption of AtHKT1 was shown to suppress the salt sensitive phenotype of sos3-1, indicating that the SOS pathway negatively controls this Na⁺ influx system (Rus et al., 2001). Also, the SOS pathway negatively controls expression of AtNHX family members that are implicated as determinants in the salt stress response (Yokoi et al., 2002). Chakraborty et al. (2012a) reported that mechanism governing salinity tolerance in *Brassica* could be the significantly higher induction of genes coding components of SOS pathway, viz., SOS1, SOS2, SOS3 and vacuolar antiporter NHX1, resulting in restricted uptake of toxic Na+ ,and efficient Na-exclusion and sequestration system, which was manifested in lesser reduction in tissue K⁺ content and higher K/Na ratio under salt stress, paving the way for better ion homeostasis and salinity tolerance.

The [Ca²⁺]ext enhances salt tolerance and salinity stress elicits a transient [Ca²⁺]ext increase, from either an internal or external source, implicated in adaptation (Knight et al., 1997, Läuchli, 1996). Experiments with yeast have provided insight into Ca²⁺ activation of salt stress signalling that controls ion homeostasis and tolerance (Matsumoto et al., 2001). The hyperosmotic component of high salinity induces a short duration of about 1 minute rise in [Ca²⁺]ext that is due substantially to influx across the plasma membrane through the Cch1p and Mid1p Ca²⁺ transport system. The transient increase in [Ca²⁺]ext activates the PP2B phosphatase calcineurin; a key intermediate in salt stress signalling controlling ion homeostasis, leading to the transcription of ENA1, which encodes the P-type ATPase primarily responsible for Na⁺ efflux across the plasma membrane (Nakamura et al., 1993; Mendoza et al., 1994; Matsumoto et al., 2001). The model proposes that the hyperosmoticallyinduced localized [Ca²⁺]_{ext} transient activates calmodulin that is tethered to Cch1p-Midp (Ehlers and Augustine, 1999; Sanders, 2000; Matsumoto et al.,2001). Calmodulin in turn activates signalling through the calcineurin pathway, which mediates ion homeostasis and salt tolerance (Matsumoto *et al.*, 2001).

Thus a paradigm for salt-induced Ca²⁺ signalling and the activation of the SOS pathway can be suggested. Components of the SOS pathway, either SOS3 or upstream elements, might be associated with an osmotically responsive channel through which Ca²⁺ influx could initiate signalling through the pathway. It is notable that a new elevated [Ca²⁺]_{ext} steady state is established in yeast cells, that are maintained in medium supplemented with NaCl, after the hyperosmotic induction of the short duration [Ca²⁺]ext transient (Matsumoto et al., 2001). The newly established [Ca²⁺]_{cyt} is likely to contribute to cellular capacity for growth in salinity. The vacuolar membrane H⁺/Ca²⁺ antiporter Vcx1p and endomembrane localized Ca^{2+} -ATPases are pivotal effectors that regulate the amplitude and duration of the $[Ca^{2+}]_{ext}$ transient (Miseta *et al.*, 1999). The [Ca²⁺]_{ext} steady state established in salt containing medium presumably also involves coordination of channel activation that facilitates influx from external and internal sources and energy dependent transport systems that compartmentalize the divalent cation. It is reasonable to assume that the salt induced [Ca²⁺]_{ext} transient detected in plant cells (Knight, 1997) and, perhaps, a new $[Ca^{2+}]_{ext}$ steady-state are controlled by the ECA and ACA Ca²⁺-ATPases and CAX1 and 2 transporters which are orthologs of Vcx1p (Sze *et al.*, 2000). Nevertheless, Ca^{2+} has at least two roles in salt tolerance, a pivotal signaling function in the salt stress response leading to adaptation and a direct inhibitory effect on a Na⁺ entry system.

5. SALT TOLERANT CROP PLANTS

The restriction of uptake and transport and internal tolerance mechanisms are the two important criteria which plants employ to combat high external concentrations and hence tolerance could be attributed to the lower the content and lower uptake or accumulation of these in the root and shoot and high yield in toxic soils (Singh et al., 2010b). Ameliorating high-mineral soils using soil amendments is expensive and extremely difficult. Use of tolerant crop genotypes, phytoremediation by tolerant crops, and inoculations of beneficial microorganisms are the solutions (Singh *et al.*, 2010b). The salt tolerance of a crop can best be described by plotting its relative yield as a continuous function of soil salinity (Fig 4). For most crops, this response function follows a sigmoidal relationship however, several crops may die before the seed or fruit yields decrease to zero, thus eliminating the bottom part of the sigmoidal curve (Maas and Hoffman, 1977). By plotting relative yield with increasing soil salinity level a threshold level of soil salinity is obtained for some of the crops which have its greatest value in providing general salt tolerance guidelines for crop management decisions. Farmers need to know the soil salinity levels that begin to reduce yield and how much yield will be reduced at levels above the threshold. However, more precise plant response functions would be advantageous for crop simulation modelling (van Genuchten and Hoffman, 1984). From the experimental data in general the plants were classified in four categories according to their response to salinity (Bernstein, 1962).

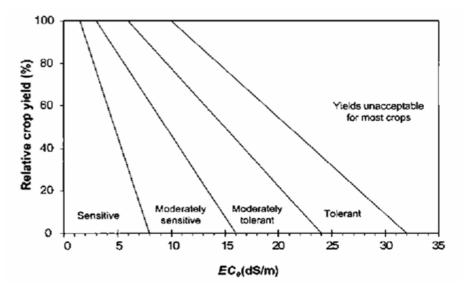


Fig. 4. Classification of the crop based on soil salinity level (source: FAO Report)

Accordingly, threshold salinity level which can cause damage, level of loss with further increase in salinity and some of the recommended crop cultivars suitable for growing in salt affected areas is listed for the important crops cultivated in India are listed in Table 4. The last column provides a qualitative salt tolerance rating that is useful in categorizing crops in general terms.

Table 4. List of field crops with their salinity tolerance level and suitable cultivars for cultivation in salt affected areas (source: FAO, ICAR, CSSRI reports)

Crop		Salinity tolerance level			Over all	
Common Name	Botanical Name	$\begin{array}{cc} Threshol & \% \ loss \\ d \ level & per \ dSm^{-1} \\ (dS \ m^{-1}) & rise \end{array}$		Tolerant Cultivars	nature of the crop*	
Rice	Oryza sativa L.	3.0	12.0	Lunishree, Sonamani, Pokkali, Nona Bokra, IR 8, Damodar, PVR 1, Basmati HBC19, Basmati 370, CSR 11 CSR 13, CSR 27, IR 28	S,	
Wheat	Triticum aestivum L.	6.0	7.1	KRL 1-4, KRL 19, Kharchia, KRL 210, KRL 213, KRL 99, KRL 35	МТ	

Indian Mustard	Brassica juncea L.			CS 52, CS 54, CS 56, Urvashi	MS
Barley	Hordeum vulgare L.	6.0	7.1	BH 924, RD 2508, Ratna, R 56	MT
Chick pea	Cicer arietinum L.			Pusa 256, Pusa 329, Pusa362, BGD 87, CSG 9651, BG 267, Karnal Chana 1, CSG 88101	$_{ m MS}$
Soybean	<i>Glycine max</i> (L.) Merrill	5.0	20.0	CoSoy 2, DS 40, PalamSoy, Pusa 16	МТ
Cotton	Gossypium hirsutum L.	7.7	5.2	Arya-Anubam, RAHS 14, Dhumad, Jayadhar, A 82-1	Т
Sesame	Sesamum indicum L.			RT 54, RT 46, RT 127	S
Oat	Avena sativa L.			JHO 815, JHO 802, JHO 816, UPO 201	Т
Groundnut	Arachis hypogaea L.	3.2	29.0	GG 4, MH 2, ICGV 86590, ICGS 44, Gangapuri, TG 37A, Kopergaon 3, VRI 4	MS
Sorghum	Sorghum bicolor (L.) Moench	6.8	16.0	JJ 1041, ICSB 707, CSV 15, S 35	MT
Sugarcane	Saccharum officinarum L.	1.7	5.9	Neeraj (Co 99006), Damodar (Co 99004), CoJ 20193	MS
Pigeon pea	<i>Cajanus cajan</i> (L.) Huth			H06-12, Pusa 991, JBP 110-B, ICPL 2037, ICPB 2039	s

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* T: Tolerant, MT: Moderately Tolerant, S: Susceptible, MS: Moderately Susceptible

6. CONCLUSION AND FUTURE RESEARCH STRATEGIES

Soil salinity adversely affects plant growth and development accompanied by an increase in uptake of Na⁺ and Cl⁻ ions and a decrease in uptake of K⁺, Ca²⁺, Mg²⁺ resulting in ionic imbalance, sodium ion injury and disturbed metabolic processes, changed concentration of biomolecules, photosynthetic activity and poor productivity. Although, the wild species are very much inferior in terms of yield and other agronomic characters but when it is to face the adverse environment, they show much more competence compared to cultivated agronomically superior genotypes. It is found that external application of potassium helps to maintain the K/Na ratio inside the plant tissue for smooth functioning of the cell. Sometimes, foliar application of certain plant growth regulators like salicylic acid, abscisic acid and polyamine viz. spermine, spermidine, putrescine, cadaverine etc. seems to ameliorate the adverse effect of salt stress in plants.

Tolerance capacity of the plants vastly depends up on its mechanism to overcome the salt stress through osmotic adjustment by accumulating compatible solutes inside the cell and thereby reducing the osmotic potential of the cell. This adaptation strategy helps the plants to still take up water from rhizosphere zone, when the water potential there goes well below normal level due to soil water salinity. Other most detrimental effect faced by the plants is sudden outburst of reactive oxygen species produced due to salinity stress, which disrupts the cellular structure and damages subcellular organelles, leading to cell death. The genotypes having better antioxidant defence capacity are more capable of combating the stress.

At molecular level, efficient operation of different signal proteins and various symporters and antiportes lying either in the plasma-membrane or tonoplast play important role in salinity tolerance. Activity of different Na⁺/H⁺ antiporters viz. SOS1 and NHX1 depends up on the activation of other signal proteins like SOS2, SOS3 and other calcium binding proteins. Apart from these, several transcription factors like *WRKY*, *DREB*, *CBF* also contribute towards salinity tolerance in plants. The physiological, biochemical and molecular biological knowledge on salinity tolerance in crop plants are important for understanding the responses and identification of the parameters for developing screening methodologies for all crop plants.

Incredible advances have been made over the last four decades to understand the response of plants towards soil and water salinity and their management, and most of the works are focused on revealing the inherent capacity of the plants to combat the ill effect of salt stress. However, only very few works has brought finished product either in the form of genetically improved varieties through biotechnological or conventional crop improvement means or in the form of some good management practices. This need consolidated effort to come out with answer to the problem of soil salinity.

Optimistically, discussing the avenues for future research strategies following approaches may be useful towards proving salinity tolerance in crop plants.

- Development of suitable methodologies for screening for salinity tolerance in all the crops and then its subsequent recommendations in saline areas.
- Exploration of all the available natural resources needs to be carried out to manage salinity in field.
- Use of known tolerant varieties/genotypes and their further improvement for yield and tolerance level.
- Mining of the differentially expressed genes from the wild relatives of the cultivated species, and subsequent transfer of those to cultivable species either through molecular or conventional plant breeding could be a possible way.

To characterise these wild genotypes for their tolerance behaviour to single or multiple stresses and search for the candidate genes responsible for the tolerance. The major setback faced by the breeders in this approach is that most of wild tolerant genotypes are often cross-incompatible with the cultivated species where there is a need to go for more precise method of gene transfer using biotechnological tools.

Search for novel salt tolerant genes or protein should be done not only in the related plant and crop species, rather sources of tolerance can also be explored in some known halophytic plants like mangroves and others which can thrive well under extremely saline environment, as nowadays it is possible to transfer target gene(s) from any organism to other. However, such type of work has been initiated by some of the reputed laboratories in India and abroad with a mission to successfully transfer the important genes imparting tolerance to soil salinity from mangrove gene pool to some of important crop plants like rice and others. Besides this, mining of the genes are also possible from wide range of microbial gene pool as well as that of *Archea*. Apart from the commonly known pathways that impart tolerance to eukaryotes including higher plants, there may be some other operating mechanism in these organisms which make them able to survive in the salty environment of sea or saline hot spring.

Few preliminary works suggest that by altering the promoter region of the genes it is possible to fetch tolerance towards various abiotic stresses. As these promoter elements work upstream to many of the genes involved in same or different pathways, so by up-regulating their function one can bring tolerance to susceptible genotypes. The proteins like dehydration-responsive element-binding proteins (DREBs), or C-repeatbinding proteins (CBFs), are among the first families of transcriptional regulators that are transcriptionally up-regulated by salinity, water deficit or low temperature stress. Also, the *WRKY* gene family has been suggested to play important roles in the regulation of transcriptional reprogramming associated with plant stress responses. Modification of the expression patterns of *WRKY* genes and/or changes in their activity contribute to the elaboration of various signalling pathways and regulatory networks.

The genotypes having superior antioxidant defence capacity in terms of either accumulation of antioxidants like ascorbic acid, glutathione, malonaldehyde etc. or higher activity of the enzymes viz. superoxide dismutase, ascorbate peroxidase, catalase, glutathione reductase, peroxidase etc. are more capable of withstanding salinity stress. Salinity stress cause osmotic and oxidative stress, hence genetic modifications in these areas could yield beneficial result in bringing salinity tolerance in crop plants. Incorporation of genes facilitating biosynthesis of compatible solutes whose accumulation will help in osmotic adjustment in the plant cell thereby maintaining better water balance inside the plant tissues when it is facing osmotic pressure from outside.

Though there is ample opportunity for research in this area, it needs multidisciplinary approaches to address all the component of the problem of salinity. Although, spectacular results leading to development of salt tolerant varieties capable enough to give comparable yield like agronomical superior varieties is unlikely. Integrated research programme soil scientists, plant breeders, agronomists, physiology and molecular biologists can yield some future product to solve the salinity problem.

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