Effects of salt stress in crop plants

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ABSTRACT: Soil salinity is a major constraint to food production because it limits crop yield and restricts use of land previously uncultivated. Water and soil management practices have facilitated agricultural production on soils marginalized by salinity but additional gain by these approaches seems problematic. Most crops are salt sensitive or hypersensitive plants (glycophytes) in contrast to halophytes, which are native flora of saline environments. Some halophytes have the capacity to accommodate extreme salinity because of very special anatomical and morphological adaptations or avoidance mechanisms. Proteins that accumulate in plants under saline conditions may provide a storage form of nitrogen that is re-utilized later and may play a role in osmotic adjustment. Under condition of stress main change will happen in lipids metabolism. Total lipids content in Canola (Brassica napus L.) with increasing NaCl levels was decreased.

Key Words: Salt stress, Lipids, Proteins, Polyols.

INTRODUCTION

Soil salinity is a major constraint to food production because it limits crop yield and restricts use of land previously uncultivated. The United Nations Environment Program estimates that approximately 20% of agricultural land and 50% of cropland in the world is salt-stressed (Flowers and Yeo, 1995). Natural boundaries imposed by soil salinity also limit the caloric and the nutritional potential of agricultural production. These constraints are most acute in areas of the world where food distribution is problematic because of insufficient infrastructure or political instability. Water and soil management practices have facilitated agricultural production on soils marginalized by salinity but additional gain by these approaches seems problematic. On the horizon are crop improvement strategies that are based on the use of molecular marker techniques and biotechnology, and can be used in conjunction with traditional breeding efforts (Ribaut and Hoisington, 1998). DNA markers should enhance the recovery rate of the isogenic recurrent genome after hybridisation and facilitate the introgression of quantitative trait loci necessary to increase stress tolerance. Molecular marker techniques were used successfully to transfer alleles of interest from wild relatives into commercial cultivars (Tanksley and McCouch, 1997). The basic resources for biotechnology are genetic determinants of salt tolerance and yield stability. Implementation of biotechnology strategies to achieve this goal requires that substantial research effort be focused on identifying salt tolerance effectors and the regulatory components that control these during the stress episode (Hasegawa et al., 2000b). Further knowledge obtained about these stress tolerance determinants will be additional resource information for the dissection of the plant response to salinity, which will reveal how plants sense salt stress, transduce signals to mediate a defensive response and define the signal pathway outputs or effectors that accomplish the processes required for stress survival and alleviation, and steady-state growth in the saline environment. Molecular genetics and plant transformation advances have made it feasible to assess biotechnological strategies based on activated signal cascades, engineered biosynthetic pathways, targeted gene or protein expression or alteration of the natural stress responsiveness of genes for development of salt tolerant crops (Hasegawa et al., 2000b; Zhu, 2001). The molecular identities of key ion transport systems that are fundamental to plant salt tolerance are now known (Hasegawa et al., 2000b). More recently, the SOS salt stress signaling pathway was determined to have a pivotal regulatory function in salt tolerance, fundamental of which is the control of ion homeostasis (Hasegawa et al., 2000b; Sanders, 2000; Zhu, 2000). This review will summarize research on plant ion homeostasis in saline environments and present a model that integrates current understanding of salt stress sensing, which leads to the activation of the SOS pathway and the regulation of ion transport systems that facilitate ion homeostasis.
**Genetic Diversity for Salt Tolerance in Plants**

The extensive genetic diversity for salt tolerance that exists in plant taxa is distributed over numerous genera (Flowers et al., 1986; Greenway and Munns, 1980). Most crops are salt sensitive or hypersensitive plants (glycophytes) in contrast to halophytes, which are native flora of saline environments. Some halophytes have the capacity to accommodate extreme salinity because of very special anatomical and morphological adaptations or avoidance mechanisms (Flowers et al., 1986). However, these are rather unique characteristics for which the genes are not likely to be introgressed easily into crop plants. Research of recent decades has established that most halophytes and glycophytes tolerate salinity by rather similar strategies often using analogous tactical processes (Hasegawa et al., 2000b). The cytotoxic ions in saline environments, typically Na+ and Cl−, are compartmentalized into the vacuole and used as osmotic solutes (Blumwald et al., 2000; Niu et al., 1995). It follows then that many of the molecular entities that mediate ion homeostasis and salt stress signaling are similar in all plants (Hasegawa et al., 2000b). In the fact, the paradigm for ion homeostasis that facilitates plant salt tolerance resembles that described for yeast (Bressan et al., 1998; Serrano et al., 1999). The fact that cellular ion homeostasis is controlled and effected by common molecular entities made it feasible to use of model genetic organismal systems for the dissection of the plant salt stress response (Bressan et al., 1998; Serrano et al., 1999; Hasegawa et al., 2000a; Sanders, 2000; Zhu, 2000; 2001). Research on the plant genetic model Arabidopsis has increased greatly our understanding of how cellular salt tolerance mechanisms are integrated and coordinated in an organismal context, and are linked to essential phenological adaptations. Since Arabidopsis is a glycophyte, a salt tolerant genetic model will be required to delineate if salt tolerance is affected.

Most by form or function of genes or more by differences in the expression of common genes due either to transcriptional or post-transcriptional control (Zhu, 2001).

**OSMOLYTES AND OSMOPROTECTANTS**

During stress conditions plants need to maintain internal water potential below that of soil and maintain turgor and water uptake for growth (Tester and Davenport 2003). This requires an increase in osmotic, either by uptake of soil solutes or by synthesis of metabolic (compatible) solutes. To accommodate the ionic balance in the vacuoles, cytoplasm accumulates low-molecular mass compounds, the compatible solutes because they do not interfere with normal biochemical reactions (Zhifang and Loescher 2003); rather, they replace water in biochemical reactions. With accumulation proportional to the change of external osmolarity within species-specific limits, protection of structures and osmotic balance supporting continued water influx (or reduced efflux) are accepted functions of osmolytes (Hasegawa et al. 2000). While some compatible osmolytes are essential elemental ions, such as K+, the majority are organic solutes (Yokoi et al. 2002). However, the solutes that accumulate vary with the organism and even between plant species and a major category of organic osmotic solutes consists of simple sugars (mainly fructose and glucose), sugar alcohols (glycerol and methylated inositols) and complex sugars (trehalose, raffinose and fructans) (Bohnert and Jensen 1996). Others include quaternary amino acid derivatives (proline, glycine betaine, β-alanine betaine, proline betaine, tertiary amines 1,4,5,6-tetrahydro-2-methyl-4-carboxyl pyrimidine), and sulfonium compounds (choline osulfate, dimethyl sulfonium propionate) (Yokoi et al. 2002).

**Polyols**

Polyols, the polyhydric alcohols, are among the compatible solutes involved in osmoregulation and are thought to play a role in plant salt tolerance (Bohnert and Shen 1999). They exist in both acyclic and cyclic forms and are widely distributed in the plant kingdom. The most common polyols in plants include acyclic forms, mannitol, glycerol, sorbitol, and cyclic (cyclitols) forms ononitol and pinitol. In general, they are thought to accumulate in the cytoplasm of some halophytes to overcome the osmotic disturbances caused by high concentrations of inorganic ions compartmentalized in vacuoles. Polyols make up a considerable percentage of all assimilated CO2 as scavengers of stress-induced oxygen radicals (Bohnert et al. 1995). Mannitol, a sugar alcohol that may serve as a compatible solute to cope with salt stress, is synthesized via the action of a mannose-6-phosphate reductase (M6PR) in celery (Zhifang and Loescher 2003) and its accumulation increases when plants are exposed to low water potential. The accumulation is regulated by inhibition of competing pathways and decreased mannitol consumption and catabolism (Stoop et al. 1996). Studies using transgenic tobacco and Arabidopsis have shown improved growth of mancholineneitol accumulating plants under stress (Thomas et al. 1995). Mannitol improves tolerance to stress through scavenging of hydroxyl radicals and stabilization of macromolecular structures. In tobacco, mannitol protects the thiol-regulated enzymes phosphoribulokinase, thioredoxin, ferredoxin and glutathione from OH (Shen et al. 1997). Abebe et al. (2003), however, state that the amount of mannitol...
accumulated in response to stress was small and its effect on osmotic adjustment was less than that of other carbohydrates. In contrast to previous approaches that used a bacterial gene to engineer mannitol biosynthesis in plants and other organisms, A. thaliana, a nonmannitol-producing, was transformed with the celery leaf M6PR gene under control of the CaMV 35S promoter. In all independent Arabidopsis M6PR transformants, mannitol accumulated in plants in amounts ranging from 0.5 to 6 μmol/g fresh weight. A novel compound, not found in either celery or Arabidopsis, 1-O-β-D-glucopyranosyl-D-mannitol, also accumulates in vegetative tissues of mature plants in amounts up to 4 μmol/g fresh weight but not in flowers and seeds. In the absence of NaCl, all transformants are phenotypically the same as the wild type; however, in the presence of NaCl, mature transgenic plants show a high level of salt tolerance and complete normal development including production of seeds on soil irrigated with 300 mmol NaCl. These results demonstrate a major role of M6PR in developing salt-tolerant plants by means of introducing mannitol biosynthesis (Zhifang and Loescher 2003).

**Proteins**

Proteins that accumulate in plants under saline conditions may provide a storage form of nitrogen that is re-utilized later (Singh et al. 1987) and may play a role in osmotic adjustment. They may be synthesized de novo in response to salt stress or may be present constitutively at low concentration (Pareek-Singla and Grover 1997). It has been concluded that a number of proteins induced by salinity are cytoplasmic which can cause alterations in cytoplasmic viscosity of the cells (Hasegawa et al. 2000). A higher content of soluble proteins has been observed in salt tolerant cultivars of barley, sunflower, finger millet, and rice (Ashraf and Harris 2004). Agastian et al. (2000) have reported that soluble protein increases at low salinity and decreases at high salinity in mulberry cultivars. Although Ashraf and Fatima (1995) found that salt tolerant and salt sensitive accessions of safflower did not differ significantly in leaf soluble proteins, there are reports of decrease in soluble protein content in response to salinity. In higher plants, osmotic stress induces several proteins in vegetative tissues, which are related to late-embryogenesis-abundant (LEA) proteins. The correlation between LEA protein accumulation in vegetative tissues and stress tolerance indicates its protective role under dehydration stress (Ingram and Bartels 1996). Engineered rice plants over expressing a barley LEA gene, HVA1, under the control of rice actin 1 promoter showed better stress tolerance than did the wild type (Xu et al. 1996).

**Pigments system**

Plant pigments content were determined in different tolerant and sensitive plant varieties at wide range of salt concentrations (Sarwat and El-Sherif, 2007). Chlorophyll a, chlorophyll b and carotenoid are main photosynthetic pigments and they play important role in photosynthesis. The changes in the amount of pigments system were evaluated as the changes in photosynthesis. Changes of pigment system contents under salt stress are used as parameter for selection of tolerant and sensitive cultivars in crop plants (Eryilmaz, 2007). Chlorophyll a, chlorophyll b, chlorophyll a/b and carotenoid contents showed increase and decrease depending on exposure time of NaCl exposure in many plants (Pinheiro et al, 2008). The reduction of chlorophyll a and chlorophyll b amounts with NaCl application was reported in many plants such as Zea mays, Carthamus tinctorius, Bean and Paulownia imperialis that this due to increasing of destructive enzymes called chlorophyllase (Rahdari et al, 2012). Pigments system reduction is attributed to a salt induced weakening of protein-pigment-lipid complex or increased chlorophyllase enzyme activity (Turam et al, 2007). Also, increase in pigment content was observed in salinity stressed plant such as Rice (Doganlar et al, 2010) and Purslane (Rahdari et al, 2012), that this increment may be due to increase in the number of chloroplast in the stressed plant leaves (Chaum and Kirdmanee, 2009). In other hand, the changes in pigment system were affected by exposure time and salt concentration (Doganlar et al, 2010).

**Lipid Content**

Lipids are among the most prominent constituents of cell membrane which play a fundamental role in cell permeability (Baybordi et al., 2010). Under condition of stress main change will happen in lipids metabolism (Kesri, 2002). Total lipids content in Canola (Brassica napus L.) with increasing NaCl levels was decreased (Baybordi et al, 2010). Increasing soil salinity levels strongly influence the essential lipids biosynthesis (Solinas and Deiana, 1996). In other hand, lipid peroxidation was synchronized with increased of the salinity level which had a relation with plants such as Wheat (Hala et al., 2005), Tomato (Neumann, 2001) and Purslane (Yazici et al, 2007; Rahdari et al, 2012) was reported. Mono galactosyl diglyceride (MGDG) is main glycerol lipid in leaf was effect of intensive stress imposing, was reduced that is express of chloroplast membrane destructions (Rahdari et al, 2012). Low
unsaturation lipids degree limited the membrane fluidity band restricted permeability to Na and Cl ions (Konova et al, 2009). Phosphatidic acid (PA) is a common phospholipids that is a major constituent of cell membranes. PA is the smallest of the phospholipids. They have long been recognized as of importance during germination and senescence, and they appear to have a role in response to stress damage and pathogen attack (Bartels and Sunkar, 2005). PA has been implicated in intracellular signaling that formed in response to salt stress has been suggested to function as a signaling molecule guiding the plants accumulation responses to salt stress. PA can bind and affect the activity of various signaling proteins, including protein kinases and phosphatases (Wang, 2005). Also, PA has been suggested to regulate the activity of vacuolar pump upon high salt treatment which may help maintain the protein gradient (Zhang et al, 2006).

RESULTS

Natural boundaries imposed by soil salinity also limit the caloric and the nutritional potential of agricultural production. These constraints are most acute in areas of the world where food distribution is problematic because of insufficient infrastructure or political instability. Water and soil management practices have facilitated agricultural production on soils marginalized by salinity but additional gain by these approaches seems problematic. On the horizon are crop improvement strategies that are based on the use of molecular marker techniques and biotechnology, and can be used in conjunction with traditional breeding efforts. However, these are rather unique characteristics for which the genes are not likely to be introgressed easily into crop plants. Research of recent decades has established that most halophytes and glycophytes tolerate salinity by rather similar strategies often using analogous tactical processes. Plant pigments content were determined in different tolerant and sensitive plant varieties at wide range of salt concentrations. Lipids are among the most prominent constituents of cell membrane which play a fundamental role in cell permeability.

REFERENCES

Rahdari P, Tavakoli S, Hosseini SM. 2012. Studying of salinity stress effect on germination, proline, sugar, protein, lipid and chlorophyll content


