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RESEARCH ARTICLE

GENETIC ENGINEERING FOR OSMOLYTE OVERPRODUCTION FOR ABIOTIC STRESS TOLERANCE IN PLANTS

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ABSTRACT

Many plants accumulate organic osmolytes in response to the imposition of environmental stresses that cause cellular dehydration. Even though an adaptive involvement of these compounds in regulating osmotic adjustment and preventing subcellular structure from adverse conditions has vital role in stress physiology, the proof in favour of this proposition is largely correlative. Transgenic plants engineered to accumulate proline, mannitol, fructans, trehalose, glycine betaine or ononitol exhibit marginal enhancement in salt and/or drought tolerance. There is significant causative relationships which connects both osmolyte levels and stress tolerance, the complete osmolyte concentrations in these plants are improbable to mediate osmotic adjustment. Metabolic benefits of osmolyte accumulation may supplement the classically proved the roles of these compounds. In re-assessing the functional significance of compatible solute accumulation, it is suggested that proline and glycine betaine synthesis may buffer cellular redox potential. Instability in hexose sensing in transgenic plants which modify to produce trehalose, fructans or mannitol may be an important causative factor to the stress-tolerant phenotypes observed. Osmolyte transport between compartments of subcellular organs or different organs correspond to a bottleneck that confines stress tolerance at the whole-plant level is presently imprecise. None the less, if osmolyte metabolism interrupt on hexose or redox signalling, then it may be important in long-range signal transmission throughout the plant.

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INTRODUCTION

Abiotic stresses are one of the major causes for crop losses throughout the world. Abiotic stresses such as drought, salinity, extreme temperature and ion imbalance are key limitations for growth and productivity of crop plants. Certain plants, marine algae, bacteria and other organism have developed a number of adaptations in responses to such abiotic stresses. Different approaches have been proposed for overcome from these adverse conditions. As abiotic stress is influenced by many factors, conventional breeding have resulted less success in getting stress tolerant plant. One such metabolic adaptation that is omnipresent in plants is the accumulation of certain organic solutes of low molecular weight that are collectively known as compatible solutes (known as osmoprotectants) (Bohnert *et al* 1995). Osmoprotectants or compatible solutes are small molecules that act as osmolytes and accumulate at high intracellular levels to help organisms to survive under extreme adverse conditions (Lang *et al* 2000). Osmolytes are naturally accumulated organic compounds, which represent different chemical classes including betaines (fully N - methylated amino acid derivatives) and related compounds such as dimethylsulfoniopropionate (DMSP) and choline-O-sulfate;

certain amino acids like proline and ectoine; and polyols and nonreducing sugars such as trehalose. These compounds are non toxic even if accumulate in high concentrations they do not inhibit the activity of enzymes and increase the ability of cells to maintain osmotic balance under stress conditions. Some of osmolytes can also stabilize protein and membranes against deleterious effects of high salt concentrations such as Na⁺ and Cl⁻ and others (especially polyols) protect against reactive oxygen species.

The osmoprotectants are commonly present in plants and differ in their taxonomic distribution. Glycine betaine is widespread among both angiosperms and algae, whereas DMSP is common in algae and lacking in higher plants, while ectoine is occur only in bacteria. Certain crop plants such as rice, soybeans, and potatoes are deficient in considerable amounts of betaines or any other osmoprotectant. This deficiency is the basis for metabolic engineering technology to establish the osmolyte synthesis pathways in such crops for improving their tolerance to drought, salinity, and other stresses.

Biosynthetic Pathways

Ectoine

Ectoine occurs in halophilic bacteria mostly in *Halomonas elongate*, and it synthesized from aspartate semialdehyde in

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three steps (Ono *et al.*, 1999). There are three *H. elongata* genes namely, ectA, ectB, and ectC which encodes enzymes responsible for ectoine synthesis were each placed and regulated by constitutive CaMV 35S promoter in a single gene construct, which was transformed into cultured tobacco cells (Nakayama *et al.*, 2000). Tobacco transformed cell lines produced small amount of ectoine and showed a low level of resistance against osmotic stress under certain level of mannitol (Nakayama *et al.*, 2000).

Glycine Betaine

Quaternary ammonium compounds such as glycine betaine, proline betaine, b-alanine betaine, choline O-sulphate and the tertiary sulphonium compound dimethylsulphoniopropionate are efficient osmoprotectants showed wide taxonomic distribution in various organism, marine algae, bacteria and many plants (Rhodes and Hanson, 1993; Gorham, 1995; Gage and Rathinasabapathi, 1999). Glycine betaine synthesis is a two-step oxidation reaction of choline via betaine aldehyde but different enzymes are involved. Choline is the precursor for phosphatidylcholine, a main constituent of cell membrane phospholipids in eukaryotes. In the enteric bacterium, *Escherichia coli*, the aldehyde, which in turn is oxidized to glycine betaine by a soluble, NAD-linked betaine aldehyde dehydrogenase (Andersen *et al.*, 1988). In the plant pathway, choline oxidation via betaine aldehyde two different enzymes are involved. Choline oxidation to betaine aldehyde is catalysed by ferredoxin dependent choline monooxygenase (CMO), an iron-sulphur enzyme (Burnet *et al.*, 1995; Rathinasabapathi *et al.*, 1997). Betaine aldehyde oxidation to glycine betaine is catalysed by betaine aldehyde dehydrogenase (BADH). (Trossat *et al.*, 1997; Vojtechova *et al.*, 1997). Both these enzymes are chloroplastic stress-inducible enzymes (McCue and Hanson, 1992; Russell *et al.*, 1998). All these enzymes have been used to transform plants that lacks Gly Bet synthesis pathways by introducing these genes under the control of CaMV 35S promoter to enhance stress tolerance.

Polyols Biosynthesis

Polyols such as glycerol, mannitol, sorbitol and sucrose are osmoprotectants occur in certain halophytic plants, algae and insects exposed to extreme low temperature (Yancey *et al.*, 1982). Glucose-6-phosphate serves as a precursor to a number of metabolites for synthesis of Myo-inositol, which are related to membrane biogenesis, cell signalling and protection against several stresses (Loewus and Murthy, 1999). Mannitol synthesis is catalyzed by the action of NADPH-dependent mannitol 1-phosphate dehydrogenase from fructose 6-phosphate. When tobacco and *Arabidopsis* is transformed by a gene encoding mannitol 1-phosphate dehydrogenase (mtlD) from *Escherichia coli* causes mannitol production and a resistance against salinity stress (Tarczynskiet *al.*, 1993; Thomas *et al.*, 1995).

Trehalose

Trehalose is a non-reducing disaccharide of glucose that accumulate as a osmoprotectant and play a vital role in the stabilization of biological structures under abiotic stress in

bacteria, fungi, and few extremely desiccation tolerant lower plants (resurrection plants including the fern *Selaginella lepidophylla*, which tolerate complete dessication and upon rehydration spring back to life) (Goddijn and van Dun, 1999; Iturriaga *et al.*, 2000). It is very rare compound, all members of the plant kingdom do not seem to accumulate trehalose. Therefore trehalose accumulation is one of the significant area of scientific research. The rationale for this is the ability of trehalose is to stabilize enzymes, proteins, and cell membranes during dehydration. However, homologous genes for biosynthesis of trehalose have been recently identified in several prokaryotes and eukaryotes (Goddijn and van Dun, 1999, Zentella *et al* 1999) which proved to be excellent candidates for genetic engineering for trehalose accumulation in plants not only to enhance stress resistance but also to produce trehalose at low cost for use as a stabilizing agent for pharmaceuticals and other products. Trehalose is synthesized by two steps reaction initiating from glucose-6-phosphate and uridine diphosphoglucose, via trehalose-6-phosphate. The first step is catalyzed by trehalose-6-phosphate synthase (TPS), and the second by trehalose-6-phosphate phosphatase (TPP).

Trehalose-6-phosphate synthase is a important enzyme for trehalose biosynthesis in *Saccharomyces cerevisiae*, encoded by the gene TPS1. The gene from yeast was expressed in transgenic potato plants (Yeo *et al* 2000). The transformants showed various morphological phenotypic alterations in vitro - from normal to severely anomalous growth and shapes. But after acclimatize in soil mixture, the plants improved to normal phenotype. The TPS1 transgenic potato plants showed significantly improved stress tolerance. The TPS1 gene was expressed in tobacco plants also (Romero *et al* 1997) and accumulated trehalose at very low levels in the transformants. They exhibited various morphological phenotypes, including less sucrose content and enhanced drought tolerance. These results showed that trehalose accumulation causes alteration of sugar metabolism, plant development and significantly improved stress tolerance, inspite of providing an osmoprotectant effect. Significantly, abiotic stress tolerance was showed in rice by overexpression of *Escherichia coli* trehalose biosynthetic genes (otsA and otsB) under the control of either tissue specific or stress inducible promoter resulted in high content of trehalose in comparison to control plants (Garg *et al* 2002). Compared with control rice plants, transgenic lines exhibited increased tolerance to salt, drought, and low-temperature stress conditions.

Increased trehalose accumulation directly related to the enhanced photosynthetic activity and with higher soluble carbohydrate levels. Recently trehalose synthase (TSase) gene from the edible wood fungi *Grifola frondosa* was transformed in tobacco (Zhang *et al* 2005). The transformants showed a increased trehalose accumulation ascompared to other transgenics plants. Various phenotypic alterations were reported, like dark coloured leaves, but growth is not inhibited. Trehalose accumulation in 35S-35S:TSase plants showed improved tolerance to dessication and salt stress. These results proposed that expression TSase gene in transgenic plants can cause higher accumulation of trehalose and have increased tolerance to drought and salt stresses.

Osmolytes	Gene source	Gene	Plant species engineered	Reference
Glycine betaine	<i>E.coli</i>	<i>CDH</i>	Tobacco	Lilius <i>et al.</i> , 1996
	<i>E.coli</i>	<i>CDH+BADH</i>	Tobacco	Holmstrom <i>et al.</i> , 2000
	<i>Arthrobacter</i>	<i>codA</i>	<i>Arabidopsis</i>	Sakamoto and Murata 2000
	<i>Arthrobacter</i>	<i>codA</i>	Rice	Su <i>et al.</i> , 2006
	<i>Arthrobacter</i>	<i>COX</i>	Canola	Huang <i>et al.</i> , 2000
	<i>Arthrobacter</i>	<i>codA</i>	Tobacco	
	<i>A.halophytica</i>	<i>GSMT+DMT</i>	Tomato	Park <i>et al.</i> , 2007
	<i>Beta vulgaris</i>	<i>BvCMO</i>	<i>Arabidopsis</i>	Waditee <i>et al.</i> , 2005
	<i>Spinacia oleracea</i>	<i>BADH</i>	Tobacco	Zhang <i>et al.</i> , 2008
		<i>betaine aldehyde dehydrogenase.</i>	Tobacco	Yang <i>et al.</i> , 2008
	<i>Arthrobacter</i>	<i>codA</i>	Medicago sativa	G.B.; Zhang <i>et al.</i> , 2011
	<i>Arthrobacter</i>	<i>codA</i>	Eucalyptus globules	Yu, X. <i>et al.</i> , 2009
			<i>Brassica chinensis</i>	Wang, Q.B <i>et al.</i> , 2010
	<i>Spinacia oleracea</i>	<i>BADH</i>	potato	Zhang, N <i>et al.</i> , 2011
		<i>codA</i>	Rice	Kathuria, H <i>et al.</i> , 2009
	<i>Spinacia oleracea</i>	<i>BADH</i>	<i>Ipomoea batatas</i>	Fan, W <i>et al.</i> , 2012
	<i>Oryza sativa</i>	<i>BADH</i>	Tobacco	Hashtanasombut, S. <i>et al.</i> , 2010
	<i>Arthrobacter</i>	<i>codA</i>	Tomato	Bansal, K.C <i>et al.</i> , 2011
Proline	<i>Mothbean</i>	<i>P5CS</i>	Tobacco	Kishor <i>et al.</i> , 1995;
				Hong <i>et al.</i> , 2000
	<i>Brassica juncea</i>	<i>BjDREB1B</i>	Tobacco	Cong <i>et al.</i> , 2008
	<i>Arabidopsis</i> , Rice	<i>P5CS</i>	Petunia	Yamada <i>et al.</i> , 2005
	<i>Arabidopsis</i>	<i>P5CS1</i>	<i>Arabidopsis</i>	Mattioli <i>et al.</i> , 2008
	Barley	<i>hva1</i>	Mulberry	Lal <i>et al.</i> , 2008
	<i>Arabidopsis</i>	<i>SOS</i>	<i>Populus trichocarpa</i>	Zhou J; 2014
Ectoine	<i>Halomonas</i>	<i>ectA+ectB+ectC</i>	Tobacco cells	Nakayama <i>et al.</i> , 2000
	<i>Halomonas</i>	<i>ect. ABC</i>	Tobacco	Moghaieb <i>et al.</i> , 2006
Mannitol	<i>Elongate</i>			
	<i>Escherichia coli</i>	<i>mtlD</i>	<i>Populus tomentosa</i>	Hu <i>et al.</i> , 2005
	<i>E.coli</i>	<i>MtlD</i>	Tobacco	Tarczynski <i>et al.</i> , 1992; Thomas <i>et al.</i> , 1995
			<i>Arabidopsis</i>	
	<i>E.coli</i>	<i>MtlD</i>	Wheat	Abebe <i>et al.</i> , 2003
Sorbitol	Apple	<i>Stpd 1</i>	Tobacco	Tao <i>et al.</i> , 1995
				Sheveleva <i>et al.</i> , 1998
		<i>PmSDH1</i>	<i>Plantago major</i>	Pommerrenig <i>et al.</i> , 2007
Polyamines	<i>D.stramonium</i>	<i>ADC</i>	Rice	Capell <i>et al.</i> , 2004
	Yeast	<i>ySAMdc</i>	Tomato	Mattoo <i>et al.</i> , 2007
	Apple	<i>MdSPDS1</i>	Pear	Wen <i>et al.</i> , 2008
Trehalose	Yeast	<i>TPS1</i>	Potato	Stiller <i>et al.</i> , 2008
	Yeast	<i>TPS1-TPS2</i>	<i>Arabidopsis</i>	Miranda <i>et al.</i> , 2007
	Yeast	<i>TPP</i>	Tobacco	Karim <i>et al.</i> , 2007
	<i>Arabidopsis thaliana</i>	<i>TPS</i>	Tobacco	Almeida <i>et al.</i> , 2007
	<i>E.coli</i>	<i>TPS or TPS+TPP</i>	Tobacco	Goddijn <i>et al.</i> , 1997
			Potato tuber	Pilon Smits <i>et al.</i> , 1998
	Yeast	<i>TPS 1</i>	Tobacco	Holmstrom <i>et al.</i> , 1996, Romero <i>et al.</i> , 1997
	<i>E.coli</i>	<i>TPSP</i> (<i>otsA + otsB</i>)	Rice	Garg <i>et al.</i> , 2002.
	<i>S.cerevisiae</i>	<i>TPS 1</i>	Tomato	Cortina <i>et al.</i> , 2005
	<i>Grifola frondosa</i>	TSase	Tobacco	Shu-Zhen Zhang <i>et al.</i> , 2005
	<i>Grifola frondosa</i>	TSase	Sugarcane	Shu-Zhen Zhang 2006

Conclusion

There can be some uncertainty that transgenic plants will be important in assessing the role that osmolytes play in the functional network that involved in stress tolerance. Although biosynthetic pathways reactions causing osmolyte accumulation in bacteria, yeasts and plants have been characterized at the molecular level, the exact role of participants which are involved in the multifaceted regulation of osmolyte accumulation in plants remains to be identified. This will necessitate not only improved knowledge of the degradation and transport of compatible solutes, but also

explanation of the molecular events involved in stress perception and stress-related signal transduction. Basic research leading to the recognition of strongly regulated stress-inducible promoters that are also responsive to suitable tissue-specific expression and endogenous developmental regulation is likely to be significant in increasing the overall physiological and metabolism performance of transgenic crops.

The up-and-coming view that the functional significance of osmolyte accumulation may not yet have been fully acceptable is mainly because of the known complexity of stress tolerance, which is a multifactorial product of the coordinated interplay of

various levels of cellular control, including hormonal regulation, nutrient status and redox potential as well as inter- and intracellular signalling and transport capacity. Irrespective of whether the definitive target of alleviating stress effects will be realized by efforts to increase osmolyte accumulation, there can be little misgiving that continued work in this area will not only be possible for the identification of rational approaches to improve crop productivity, but also enable appreciation of how plants coordinate growth and development in a constantly changing environment.

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