

# Chapter 9

## Osmoprotectants: Potential for Crop Improvement Under Adverse Conditions

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### Abbreviations

|             |   |
|-------------|---|
| ROS         | Reactive oxygen species                                   |
| M6PI        | Mannose-6-phosphate isomerase                             |
| M6PR        | Mannose-6-phosphate reductase                             |
| M1PP        | Mannose-1-phosphate phosphatase                           |
| MtlD        | Mannitol-1-phosphate dehydrogenase                        |
| NAD         | Nicotinamide adenine dinucleotide                         |
| GFOR        | Glucose-fructose oxidoreductase                           |
| S6PDH       | Sorbitol-6-phosphate dehydrogenase                        |
| NADP        | Nicotinamide adenine dinucleotide phosphate               |
| S6PP        | Sorbitol-6-phosphate phosphatase                          |
| <i>Stp1</i> | Gene encoding sorbitol-6-phosphate dehydrogenase          |
| MIPS        | <i>myo</i> -Inositol-1-phosphate synthase                 |
| IMP         | Inositol monophosphatase                                  |
| ABA         | Abscisic acid   |
| PINO1       | <i>Porteresia coarctata</i> inositol-1-phosphate synthase |
| TPS         | Trehalose-6-phosphate synthase                            |
| TPP         | Trehalose-6-phosphate phosphatase                         |
| <i>OtsA</i> | <i>E. coli</i> gene encoding TPS                          |
| <i>OtsB</i> | <i>E. coli</i> gene encoding TPP                          |
| P5CS        | L- $\Delta^1$ -pyrroline-5-carboxylate synthetase         |
| P5CR        | L- $\Delta^1$ -pyrroline-5-carboxylate reductase          |
| ProDH       | Proline dehydrogenase                                     |
| P5C         | L- $\Delta^1$ -pyrroline-5-carboxylate                    |

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|             |  |
|-------------|--|
| Put         | Putrescine                                   |
| Spd         | Spermidine                                   |
| Spm         | Spermine                                     |
| ODC         | Ornithine decarboxylase                      |
| ADC         | Arginine decarboxylase                       |
| CPA         | <i>N</i> -carbamoylputrescine amidohydrolase |
| SPDS        | Spermidine synthases                         |
| SPMS        | Spermine synthases                           |
| SAMDC       | <i>S</i> -adenosylmethionine decarboxylase   |
| SMCs        | Small molecule chaperones                    |
| DABA        | L-2,4-diaminobutyrate                        |
| EctB        | L-2,4-diaminobutyric acid transaminase       |
| EctA        | L-2,4-diaminobutyric acid acetyltransferase  |
| EctC        | Ectoine synthase                             |
| CMO         | Choline monoxygenase                         |
| BADH        | Betaine aldehyde dehydrogenase               |
| <i>codA</i> | Gene encoding choline oxidase                |

## 1 Introduction

The world human population is constantly rising and is expected to reach eight billion by 2025 and 8.9 billion by 2050. Hence, there is an urgent need to double the world food production to feed eight billion people by 2025 (FAO 2008). This is even more challenging to meet such huge demand in the current context of climate variability, particularly extreme temperature and unusual rainfall. It has been estimated that approximately 70 % of yield reduction is direct result of abiotic stresses alone (Acquaah 2007; Lobell and Field 2007).

One approach to increase crop production is to develop stress tolerant crops by transferring gene(s) for the adaptive traits from the tolerant species to the crops. However, through conventional breeding, this process has only been partially successful, partly because of poorly described traits and transfer of unavoidable genes during crossing (Yeo and Flowers 1989). Furthermore, complexity of stress tolerance trait, low genetic variance of yield component under stress and lack of efficient selection techniques make it more difficult to produce such stress resistant germ-plasms (Ribaut et al. 1996, 1997; Frova et al. 1999).

In contrast to traditional breeding, genetic engineering appears to be an attractive alternative with respect to the possibility of direct introduction of single or multiple genes into crops for betterment (Holmberg and Bülow 1998; Smirnov 1998). Among various abiotic stresses, drought, salinity, and temperature (low and high) are the major factors that primarily limit plant growth and productivity and the common effect that all these factors impose on plant is osmotic stress.

In response to such stress, certain plants, marine algae, bacteria, and few other organisms synthesize and accumulate various low molecular weight organic

compounds known as osmoprotectants or osmolytes or compatible solutes (Johnson et al. 1968; Yancey et al. 1982; Serraj and Sinclair 2002). Though, many crops lack the ability to synthesize some specific osmoprotectants found in stress tolerant organisms, ectopic expression of osmoprotectants is reported to be functional in several crop plants.

These osmoprotectants have been one of the favorite targets for genetic engineering for many years. Many crops are engineered using osmoprotectants like mannitol, glycine betaine, and trehalose, though the level of tolerance exhibited by these engineered crops varies greatly (Sheveleva et al. 1997; Huang et al. 2000). In this chapter, we elaborate the role of these osmoprotectants in stress tolerance including constraints and prospects of their use in metabolic engineering.

## 2 Osmoprotectants

Osmoprotectants are low molecular weight organic compounds primarily accumulated in response to osmotic stresses in diverse taxa including plants (Yancey et al. 1982). These are highly soluble compounds carrying no net charge at physiological pH and are nontoxic even at high concentrations. These molecules increase the osmotic pressure in the cytoplasm, thereby maintaining driving gradient for both water uptake and turgor pressure. Apart from osmotic adjustment, these compounds are reported to function as scavengers of reactive oxygen species (ROS), having chaperone-like activity and help in metabolic detoxification (Serraj and Sinclair 2002). In addition, osmoprotectants play an essential role in stabilizing proteins and membranes during oxidative damage by stress-induced ROS outburst (Yancey 1994; Bohnert and Jensen 1996).

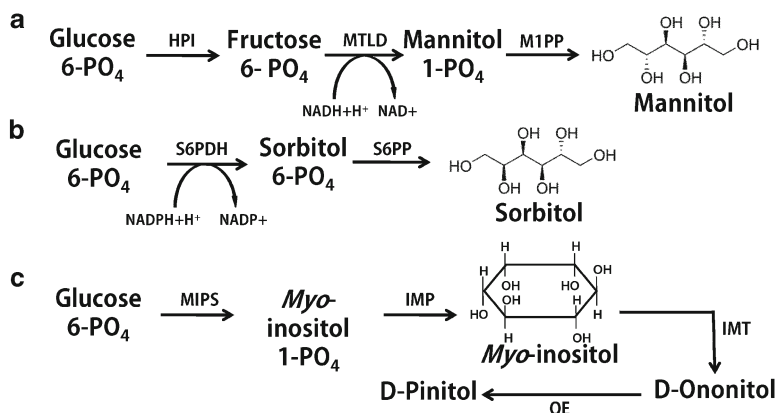
Chemically they fall into three major groups viz. amino acids (e.g., Proline), quaternary ammonium compounds (e.g., glycine betaine), polyols and sugars (mannitol, D-ononitol, trehalose, fructans) (Yancey 1994). Among these osmoprotectants, proline, glycine betaine, and mannitol are commonly found in plants. In plant cells, osmoprotectants are primarily accumulated in cytosol and chloroplast but are also reported to be distributed in few other organelles.

### 2.1 Polyols

Polyols such as glycerol, mannitol, and sorbitol are straight chain metabolites and cyclic polyols like inositols, pinitol have been shown to accumulate in evolutionary diverse organisms in response to dehydration, salinity, and osmotic stress.

#### 2.1.1 Mannitol and Sorbitol

Mannitol is a hexitol sugar alcohol and widely distributed in nature including more than 100 species of vascular plants. Mannitol is known to serve as a major carbon source in many organisms (Stoop et al. 1996). The mannitol biosynthetic pathway



**Fig. 9.1** Polyol biosynthetic pathways. [a] Mannitol biosynthesis: *HPI* hexose phosphate isomerase; *MTLD* mannitol-1-phosphate dehydrogenase; *M1PP* mannitol-1-phosphate phosphatase. [b] Sorbitol biosynthesis: *S6PDH* sorbitol-6-phosphate dehydrogenase; *S6PP* sorbitol-6-phosphate phosphatase. [c] *Myo*-Inositol biosynthesis: *MIPS* *myo*-inositol-1-phosphate synthase; *IMP* inositol monophosphatase; *IMT* inositol methyltransferase; *OE* ononitol epimerase

in higher plants starts with the isomerization of fructose-6-phosphate to mannose-6-phosphate by mannose-6-phosphate isomerase (M6PI, EC 5.3.1.8) which is then converted to mannitol-1-phosphate by mannose-6-phosphate reductase (M6PR, EC 1.1.1.224) (Loescher et al. 1992). In the final step, mannitol-1-phosphate is acted upon by mannose-1-phosphate phosphatase (M1PP, EC 3.1.3.22) to release free mannitol (Fig. 9.1a). In *E. coli*, mannitol is catabolized by the enzyme mannitol-1-phosphate dehydrogenase (MtlD, EC 1.1.1.17) in a reversible reaction whereas when expressed in transgenic tobacco it functions anabolically and synthesizes mannitol (Tarczynski et al. 1993).

Initially Tarczynski et al. (1993) demonstrated transgenic plants engineered for *MtlD* from *E. coli* in tobacco and *Arabidopsis* result in salinity tolerant phenotype. Targeted mannitol biosynthesis in chloroplasts with the help of an amino terminal transit peptide in tobacco resulted in increased tolerance to methyl viologen-induced oxidative stress and a better photosynthetic efficiency in transgenics, which was attributed to their increased ROS scavenging capacity (Shen et al. 1997b). The gene *MtlD* has also been engineered in economically important plants with substantial results, e.g., Sorghum transgenics overexpressing this gene were found to perform better under salt stress and demonstrated an overall better growth in comparison to control (Maheswari et al. 2010).

Another report of mannitol engineering in potato (*Solanum tuberosum* L.) revealed enhanced NaCl tolerance in both *in vitro* and in hydroponic culture, where transgenic plants were shown to retain more fresh weight than wild-type plants during salt stress (Rahnama et al. 2011). In addition to these, a series of experiments demonstrate transgenic eggplants expressing *mtlD* gene to be tolerant not only towards abiotic stress but biotic stress as well since they demonstrated increased

resistance towards three fungal wilts caused by *Fusarium oxysporum*, *Verticillium dahlia* and *Rhizoctonia solani* under both *in vitro* and *in vivo* conditions (Prabhavathi et al. 2002; Prabhavathi and Rajam 2007).

Sorbitol is a sugar alcohol accumulated in higher plants especially in Rosaceae (Bielecki 1982). In microorganisms (*Zymomonas mobilis*), sorbitol biosynthesis requires a one step reaction catalyzed by the enzyme glucose-fructose oxidoreductase (GFOR, EC 1.1.99.28) from glucose and fructose. While in higher plants, NADP-dependent sorbitol-6-phosphate dehydrogenase (S6PDH, EC 1.1.1.200) catalyzes the key step conversion of glucose-6-phosphate to sorbitol-6-phosphate, which is later converted into sorbitol by sorbitol-6-phosphate phosphatase (S6PP, EC 3.1.3.50) (Fig. 9.1b). Many plants use it as a major photosynthetic product which is translocated from mature leaves to growing tissues such as fruits and young leaves (Webb and Burley 1962; Bielecki and Redgwell 1985). Studies show that transgenic tobacco plants over expressing *Stpd1* gene coding for S6PDH from apple accumulate higher amounts of sorbitol and were found to be phenotypically altered with necrotic lesions on the leaves. This was explained on the basis of higher concentration of sorbitol interfering with inositol biosynthesis and leading to osmotic imbalance (Sheveleva et al. 1998).

### 2.1.2 Inositol and Derivatives

Inositols and their derivatives are a functionally important class of compounds required for normal growth of cells. These inositols are cyclohexane hexitols and exist in nine isomeric forms, out of which *myo*-inositol is the most favored form in nature. The two step inositol biosynthetic pathway is the only *de novo* pathway for inositol synthesis and an out branch of the central glycolytic pathway. This inositol biosynthetic pathway is highly conserved throughout the biological kingdom where the rate limiting enzyme *myo*-inositol-1-phosphate synthase (MIPS, EC 5.5.1.4) catalyzes the conversion of glucose-6-phosphate to *myo*-inositol-1-phosphate and subsequently *myo*-inositol-1-phosphate is converted to free *myo*-inositol by the enzyme *myo*-inositol mono phosphatase (IMP, EC 3.1.3.25) (Fig. 9.1c). Free inositol can be further channelized to other physiologically significant pathways and produce various inositol derivatives (Loewus and Murthy 2000; Stevenson et al. 2000).

These inositols are required for normal growth and development, membrane biogenesis along with the roles of their phosphorylated derivatives as phosphorus store and as a secondary messenger in signal transduction pathways (Loewus and Murthy 2000). In addition to this, inositol and its derivatives such as pinitol, galactinol and other raffinose series oligosaccharides have been found to act as osmoprotectants and provide protection against abiotic stresses like salt and osmotic stress (Taji et al. 2002). Inositol is also utilized by the cell for the synthesis of molecules like stachyose and verbose which are carbohydrate stores for the cells and are stress induced in some species (Bohnert et al. 1995).

The very first plant gene for MIPS was isolated from *Spirodela polyrrhiza* and was shown to be spatially upregulated during ABA-induced morphogenic responses

(Smart and Fleming 1993). The gene was further overexpressed in *Arabidopsis* and the plants were shown to contain fourfold increase in *myo*-inositol content (Smart and Flores 1997). Paul and Cockburn (1989) demonstrated that *Mesembryanthemum crystallinum* (Ice plant) could tolerate upto 400 mM NaCl by accumulating an inositol derivative pinitol which accounts for around two third of the soluble carbohydrate content. The osmotic adjustment of this particular plant under such stress was thus attributed to its high level of pinitol. Further, coordinated induction of *myo*-inositol-1-phosphate synthase with inositol methyl transferase (*IMTI*) in ice plant was shown, resulting in tenfold accumulation of free inositol during salt stress condition. However, no such response was observed in *Arabidopsis thaliana* during similar stresses, which indicates a remarkable difference in the regulation of gene expression between halophytes and glycophytes (Ishitani et al. 1996). Tobacco plants expressing *McIMTI* gene accumulated increased amounts of D-ononitol and were shown to be less inhibited in growth and photosynthetic carbon fixation than wild-type plants in salt and drought stress condition (Sheveleva et al. 1997).

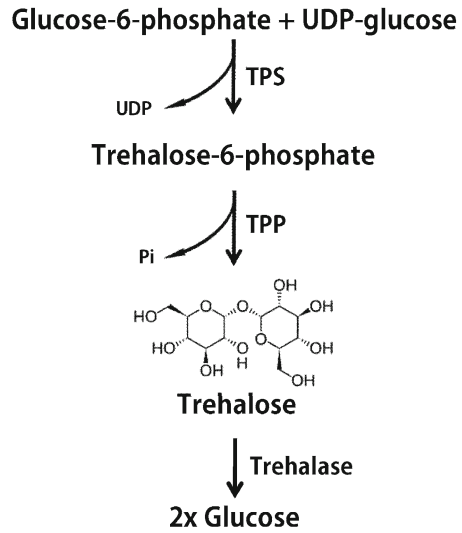
A novel salt tolerant MIPS (*PINO1*) from *Porteresia coarctata* has been reported and it's over expression in tobacco plant results in better growth and photosynthetic efficiency than control plants under high salinity stress (Majee et al. 2004). In a follow up study, it was shown that functional over expression of this gene could confer salt tolerance to a wide variety of organisms from bacteria to crop plants (Das Chatterjee et al. 2006). Later on, it has also been shown that co expression of *PINO1* and *McIMTI* allowed the transgenic tobacco plants to perform better under salt stress in comparison to expression of *PINO1* or *McIMTI* alone (Patra et al. 2010).

Recently, two divergent genes (*CaMIPS1* and *CaMIPS2*) encoding MIPS have been reported in chickpea and *CaMIPS2* has been shown to be highly induced under dehydration stress and provides better stress tolerance to transformed yeast under high salt and temperature stress (Kaur et al. 2008).

## 2.2 Trehalose

Trehalose is a nonreducing disaccharide (1,1  $\alpha$ -D glucopyranosyl,  $\alpha$ -D-glucopyranoside) found in various organisms including bacteria, algae, fungi, yeast, insects, and some plants (Miranda et al. 2007; Elbein et al. 2003). Besides being a carbohydrate reserve, trehalose protects organisms against several physical and chemical stresses (Van Laere 1989; Wiemken 1990; Eleutherio et al. 1993). Trehalose is synthesized in a two step process in bacteria and yeast, first reaction catalyzed by trehalose-6-phosphate synthase (TPS, EC 2.4.1.15) forming trehalose-6-phosphate from UDP-glucose and glucose-6-phosphate; in second reaction trehalose-6-phosphate phosphatase (TPP, EC 3.1.1.12) converts trehalose-6-phosphate to trehalose (Goddijn and Van Dun 1999) (Fig. 9.2). In *E. coli*, these TPS and TPP enzymes have been shown to be encoded by genes *OtsA* and *OtsB*, where as *Saccharomyces cerevisiae* have evolved a trehalose synthase complex which includes a TPS (*Tps1*) and a TPP (*Tps2*) along with a regulatory subunit TSL (*Tps3*). In *Arabidopsis thaliana*,

**Fig. 9.2** Trehalose biosynthetic pathway in plants. *TPS* trehalose-6-phosphate synthase; *TPP* trehalose-6-phosphate phosphatase



a family of TPS genes with 11 members including trehalose-6-phosphate synthase exists with a subfamily of TPPs (Leyman et al. 2001).

Trehalose is having a unique water absorption capacity which protects the macromolecules from desiccation-induced damage (Rontein et al. 2002). During dehydration, trehalose has been thought to replace water molecules and thereby prevent protein denaturation and membrane fusion (Clegg 1985). It has been shown that trehalose along with other compounds like glycine betaine, proline, and mannitol is active in scavenging ROS (both hydrogen peroxide and superoxide anion) in a concentration-dependent manner (Zhu 2001; Luo et al. 2008). A significant amount of trehalose has been found in two resurrection plants *Myrothamnus flabellifolia* and *Sporobolus stapfianus* (Phillips et al. 2002) where trehalose is thought to prevent intracellular structural damage due to anhydrobiosis (Lunn 2007).

Trehalose metabolism and its engineering in plants for stress tolerance has been an area of immense interest. But studies in tobacco and potato plants (Holmström et al. 1996; Romero et al. 1997; Goddijn et al. 1997; Goddijn and Van Dun 1999; Paul et al. 2001) with a constitutive over expression of yeast or bacterial TPS and TPP genes have shown undesirable effects like stunted growth and abnormal metabolism. Later on, transgenic rice plants were generated using a fusion construct of coding regions of *OtsA* and *OtsB* (with TPS and TPP activity respectively) with either stress inducible (ABA) or tissue specific (rice rbcS) promoter. The phenotypically normal and fertile transgenic rice was achieved with an increased amount of trehalose with increased tolerance to a variety of stresses like salt, drought and low temperature. Transgenic plants also showed increased photosynthetic capacity (Garg et al. 2002). The over expression of trehalose-6 phosphate synthase (*AtTps1*) using 35S promoter in *Arabidopsis* led to significant dehydration tolerance without affecting its morphological traits (Avonce et al. 2004). The level of tolerance

provided by these transgenic plants did not correlate well with amount of trehalose accumulated, signifying the other roles of trehalose apart from osmoprotection (Iordachescu and Imai 2008).

### 2.3 Proline

Proline, an imino acid, is one of the most common compatible osmolyte with high water solubility and stable conformation. It is an essential component of cellular and metabolic events and also responsible for osmotic adjustment in cell (Yancey 2005). Apart from plants, the accumulation of proline has been observed in bacteria, protozoa, algae, and marine invertebrates (McCue and Hanson 1990; Delauney and Verma 1993).

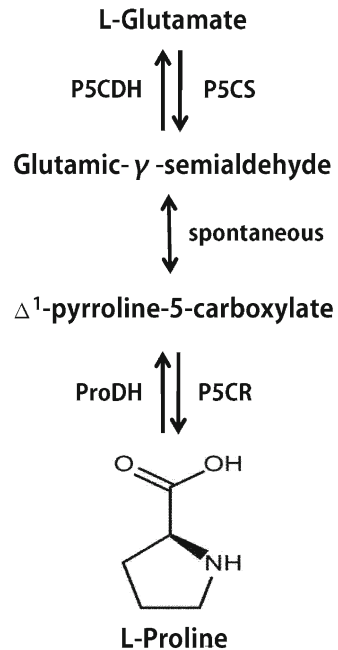
In plants, the biosynthesis of proline can occur via glutamate or ornithine pathway. Glutamate is the primary precursor for proline synthesis in osmotically stressed out and nitrogen deficient cells, while at higher levels of available nitrogen, the ornithine pathway is followed (Delauney et al. 1993). Biosynthetic pathway from glutamate to proline involves two important enzymes L- $\Delta^1$ -pyrroline-5-carboxylate synthetase (P5CS, EC 2.7.2.11) and L- $\Delta^1$ -pyrroline-5-carboxylate reductase (P5CR, EC 1.5.1.2). First glutamate is converted to glutamic- $\gamma$ -semialdehyde (GSA) and L- $\Delta^1$ -pyrroline-5-carboxylate (P5C) by the action of P5CS, and then P5CR catalyzes the conversion of P5C to L-proline (Fig. 9.3). The level of proline in plants is controlled by degradation or metabolism of proline, where ProDH (proline dehydrogenase, EC 1.5.1.12) oxidizes proline to P5C in plant mitochondria and finally P5C dehydrogenase (P5CD, EC 1.5.1.12) converts P5C to L-glutamate (Boggess and Koeppel 1978; Elthon and Stewart 1981). In normal conditions, this oxidation pathway is followed whereas, under salt and water stress such proline degradation pathway is inhibited, as a result proline level increases (Delauney and Verma 1993; Peng et al. 1996).

Increased cellular proline content is reported to stabilize protein structure and protect cellular functions possibly by scavenging ROS under osmotic stress. Proline may also serve as a source of organic nitrogen, carbon, and energy during recovery from stress (Tyagi and Sairam 2004). This molecule is also involved in maintaining osmotic balance in the cell under dehydration conditions (Singh et al. 1972; Wyn Jones and Storeys 1978). During stress, higher proline content helps in maintaining the NADP<sup>+</sup>/NADPH ratio in the cell (Hare and Cress 1997). In *E. coli*, proline has been shown to be a potent osmoprotectant as proline over-producing mutant of *E. coli* was found to possess increased osmotolerance and enhanced stability of proteins and membranes in low water and high temperature conditions (Csonka et al. 1988).

Transgenic plants or mutants raised in several studies demonstrate metabolism and accumulation of proline and its importance for development and survival of plants in various adverse environmental conditions (Hong et al. 2000; Mattioli et al. 2008; Szekely et al. 2008). Over expression of moth bean P5CS in rice, wheat and in carrot cell lines conferred enhanced tolerance to salt stress (Zhu et al. 1998; Sawahel and



**Fig. 9.3** Glutamate pathway for the biosynthesis and metabolism of proline in plants. *P5CS*  $\Delta^1$ pyrroline-5-carboxylate synthetase; *ProDH* proline dehydrogenase; *P5CDH* P5C dehydrogenase; *P5CR* P5C reductase



Hassan 2002; Han and Hwang 2003). Various studies revealed upregulation of *P5CS* in *Oryza sativa* and *Arabidopsis thaliana* exposed to salt, dehydration, and ABA (Yoshiba et al. 1995; Igarashi et al. 1997). Tolerance to freezing and high salinity was established in antisense transgenic *Arabidopsis* plants carrying *AtProDH* encoding proline dehydrogenase, resulting in higher proline accumulation (Nanjo et al. 1999).

Studies have shown that *P5CS* is feedback inhibited by proline (Hu et al. 1992). A correlation between induction of *P5CS* gene and accumulation of proline has been found in *Arabidopsis thaliana* under abiotic stress (Savouré et al. 1995), but this feedback regulation of *P5CS* is relieved in plants under stress conditions, so as to accumulate more proline for combating disturbance in osmotic balance. In a study of transgenic tobacco plants, over expressing wild-type *P5CS* from *Vigna aconitifolia* and *P5CSF1298* (a mutated *P5CS*, where feedback inhibition was removed through site directed mutagenesis) were used to compare proline level. Tobacco plant over expressing mutated *P5CS* accumulated almost twofold more proline than that of transgenic plants expressing wild-type *P5CS* (Kishor et al. 1995; Verma 1999).

## 2.4 Polyamines

Polyamines are small organic compounds with two or more primary amino groups, found in all eukaryotic cells. Putrescine (Put, a diamine), spermidine (Spd, a triamine), and spermine (Spm, a tetramine) are the major polyamines found in plants involved

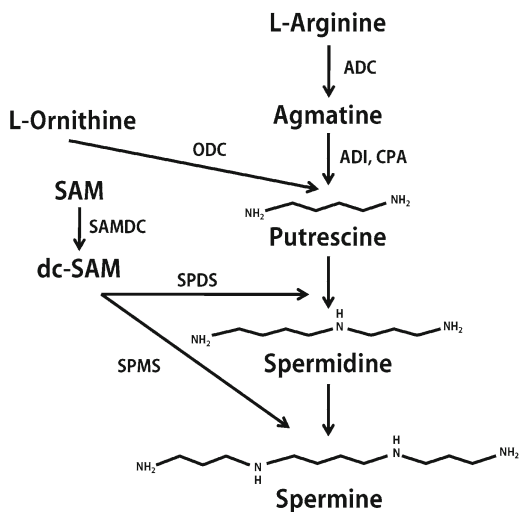
in various processes such as cell proliferation, growth, morphogenesis, differentiation, and programmed cell death (Yamaguchi et al. 2007; Alcázar et al. 2010a). In addition, several uncommon polyamines such as homospermidine, 1,3-diaminopropane, cadaverine, and canavalamine have been reported across the kingdoms of life (Minguet et al. 2008). Polyamines occur in free or conjugated forms either with phenolic compounds or macromolecules such as proteins and nucleic acids. Polycationic nature of polyamines at physiological pH is attributed for their biological activity (Gill and Tuteja 2010).

Polyamines play an important role in several plant developmental processes such as cell division, embryogenesis (Bastola and Minocha 1995), fruit ripening (Mehta et al. 1997, 2002), root growth (Watson et al. 1998), tuber development (Kumar et al. 1996; Rafart-Pedros et al. 1999), floral initiation, floral development, and stem elongation (Gerats et al. 1988; Masgrau et al. 1997; Hanzawa et al. 2000; Panicot et al. 2002).

Putrescine, spermidine, spermine, and cadaverine accumulation is well studied under abiotic stress conditions and has been reported in many plant species (Evans and Malmberg 1989; Alcázar et al. 2006, 2010b). Putrescine in plants is either directly synthesized from ornithine by ornithine decarboxylase (ODC, EC 4.1.1.17) or from arginine via *N*-carbamoylputrescine and agmatine. Arginine conversion requires the enzymes arginine decarboxylase (ADC, EC 4.1.1.19), *N*-carbamoylputrescine amidohydrolase (CPA, EC 3.5.1.53) and agmatine deiminase (ADI, EC 3.5.3.12) (Urano et al. 2003). Putrescine is further converted into spermidine and consequently to spermine by spermidine or spermine synthases (SPDS, EC 2.5.1.16; SPMS, EC 2.5.1.22) by the addition of an aminopropyl moiety from decarboxylated *S*-adenosylmethionine generated by *S*-adenosylmethionine decarboxylase (SAMDC, EC 4.1.1.50) (Fig. 9.4). *S*-adenosylmethionine is also the precursor of an important source of ethylene, aminocyclopropane carboxylic acid, thus metabolism of polyamine and ethylene is coupled together, which has significance in stress response (Zapata et al. 2004).

The less common polyamine cadaverine is the product of direct decarboxylation of lysine (Bakhanashvili et al. 1985). In *Arabidopsis*, genes involved in polyamine synthesis were identified as ADC, SAMDC, SPDS, SPMS (Urano et al. 2003), CPA (Piotrowski et al. 2003) and ADI (Janowitz et al. 2003). Beside their possible effects on the osmotic adjustment, polyamines are also involved in stomata closure by regulating voltage-dependent inward K<sup>+</sup> channels in the plasma membrane of guard cells (Liu et al. 2000). In addition polyamines are known to be components of the cellular antioxidant system and are usually regarded as scavengers of hydroxyl radicals. Cadaverine via hydroxyl radical-generating system inhibits DNA oxidative degradation in vitro (Kuznetsov et al. 2007). Putrescine, spermidine, and spermine act as hydroxyl radical scavengers in a dose-dependent manner. In addition spermine or spermidine was shown to quench singlet oxygen at higher concentrations (Das and Misra 2004). Transgenic approaches helped to generate plants expressing polyamine biosynthetic enzymes such as ADC, ODC, SAMDC, SPDS, ACC (1-amino cyclopropane-1-carboxylic acid) synthase and ACC oxidase, with enhanced environmental stress tolerance (Gill and Tuteja 2010; Rubén et al. 2010).

**Fig. 9.4** Polyamine biosynthetic pathway in plants. *ADC* arginine decarboxylase; *ADI* agmatine deiminase; *CPA* *N*-carbamoylputrescine amidohydrolase; *ODC* ornithine decarboxylase; *SAMDC* *S*-adenosylmethionine decarboxylase; *SPDS* spermidine synthase; *SPMS* spermine synthase

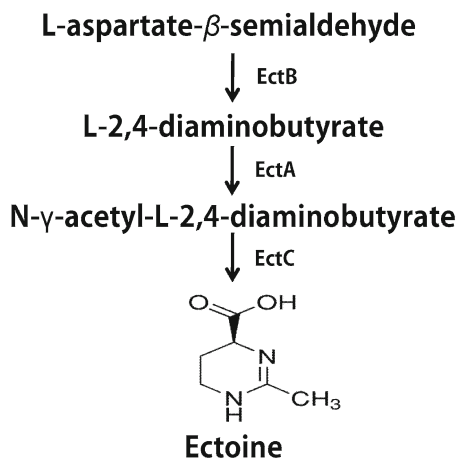


## 2.5 Ectoine

Ectoine (1,4,5,6-tetrahydro-2-methyl-4-pyrimidine carboxylic acid), a common solute of aerobic heterotrophic bacteria (Kempf and Bremer 1998; Galinski 1995; Severin et al. 1992; Kalyuzhnaya et al. 2001), was first discovered as an osmoprotectant in the halophilic bacterium *Ectothiorhodospira halochloris* (Galinski et al. 1985). Ectoines constitute a class of small molecule chaperones (SMCs), which accumulate to high intracellular concentrations without affecting the cellular functions and prevent the misfolding of proteins and other labile macromolecules from environmental stresses (Marina et al. 2008). This organic solute can either be synthesized *de novo* or taken up from the environment when available (Galinski and Trüper 1994; Kempf and Bremer 1998). The exact mechanisms of protein stabilization by ectoines are poorly understood, but they are believed to aid in hydration of proteins with solvent molecules (Kanapathipillai et al. 2005). Ectoine is synthesized from aspartate semialdehyde which is converted to L-2,4-diaminobutyrate (DABA) by L-2,4-diaminobutyric acid transaminase (EctB, EC 2.6.1.76). After that, DABA is acetylated to form  $N\gamma$ -acetyl-L-2,4-diaminobutyrate ( $N\gamma$ -acetyl-DABA) by L-2,4-diaminobutyric acid acetyltransferase (EctA, EC 2.3.1.178) (Fig. 9.5). The final step is the cyclization of  $N\gamma$ -acetyl-DABA to form ectoine by the action of ectoine synthase (EctC, EC 4.2.1.108) (Reshetnikov et al. 2011).

The *ectABC* gene cluster involved in the biosynthesis of ectoine has been isolated from *Chromohalobacter salexigens* (Cánovas et al. 1997), *Marinococcus halophilus* (Louis and Galinski 1997), and *Halomonas elongata* (Göller et al. 1998). Functional expression of *Marinococcus halophilus* ectoine biosynthetic pathway genes in *E. coli* resulted in enhanced tolerance to salt (Louis and Galinski 1997).

**Fig. 9.5** Ectoine biosynthetic pathway in bacteria. *EctB* diaminobutyric acid (DABA) aminotransferase; *EctA* DABA acetyltransferase; *EctC* ectoine synthase



Plants transformed with ectoine biosynthesis genes from *Halomonas elongata* demonstrated enhanced tolerance to mannitol and NaCl (Nakayama et al. 2000; Moghaieb et al. 2006, 2011).

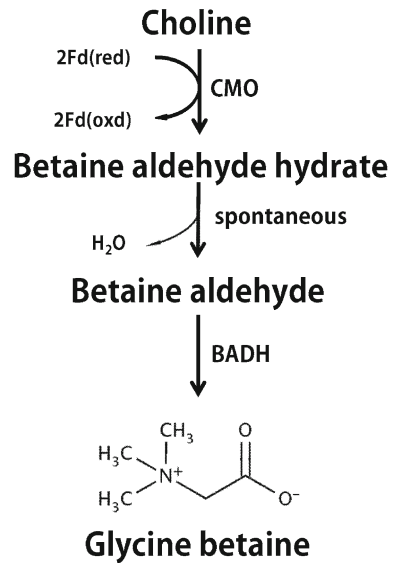
## 2.6 Glycine Betaine

Glycine betaine, a quaternary ammonium compound is widely distributed in microorganisms, higher plants and animals and one of the most common betaines found in plants (Rhodes and Hanson 1993). In many halotolerant plants, glycine betaine is reported to accumulate in plastids (Allard et al. 1998) and higher levels of glycine betaine correlates with higher level of stress tolerance (McNeil et al. 1999). Glycine betaine has diverse functions in plant cell such as stabilization of the quaternary structure of enzyme, proteins, and maintenance of membrane integrity under salt, cold, and heat stress (Sakamoto and Murata 2000).

The biosynthetic pathway in most plants follows the conversion of choline to glycine betaine in two oxidation steps via the intermediate betaine aldehyde. The first reaction is catalyzed by choline monooxygenase (CMO, EC 1.14.15.7) that converts choline to betaine aldehyde hydrate thus spontaneously forming betaine aldehyde which is acted upon by betaine aldehyde dehydrogenase (BADH, EC 1.2.1.8) to form glycine betaine, whereas in *Arthrobacter spp.* only one enzyme, choline oxidase (CO, EC 1.1.3.17) is required (Ikuta et al. 1977) (Fig. 9.6).

In higher plants, both these enzymes are localized in stroma of chloroplast (Lerma et al. 1988; Rathinasabapathi et al. 1997). Glycine betaine, when engineered in plants or exogenously applied provides sufficient tolerance to a variety of abiotic stresses (Sakamoto and Murata 2001, 2002). Transgenics generated in rice and tomato using choline oxidase (*codA*) targeting both chloroplast and cytosol have shown that the accumulation of glycine betaine in chloroplast is more efficient in providing stress

**Fig. 9.6** Pathway for the biosynthesis of glycine betaine in plants. *CMO* choline monoxygenase; *BADH* betaine aldehyde dehydrogenase; *Fd(red)* and *Fd(ox)* ferredoxin in reduced and oxidized forms, respectively



tolerance than accumulation of glycine betaine in cytosol (Sakamoto et al. 1998; Chen and Murata 2002; Park et al. 2004, 2007). The photosynthetic machinery was found to be protected against salt and cold stresses in transgenic rice expressing *codA* with no negative effects on growth and development (Alia et al. 1998; Sakamoto et al. 1998). Interestingly, the *codA* over expressing *Arabidopsis* produced more flowers, siliques, and seeds than wild-type plant when grown under normal conditions (Park et al. 2004). Most of the plants are vulnerable to abiotic stress in their reproductive stage and it has been observed that accumulation of glycine betaine in reproductive organs can effectively protect the various organs from the damaging effect of stress and increase the crop yield (Park et al. 2004; Quan et al. 2004). Microarray studies in *Arabidopsis* reveals that exogenous application of glycine betaine also enhances the expression of other genes that are directly or indirectly involved in stress tolerance such as genes for ROS scavenging enzymes, transcription factors, ferric reductase, and membrane trafficking components (Einset et al. 2007).

### 3 Mechanism of Stress Tolerance

Osmoprotectants generally localize in cytoplasm following osmotic stress, though the mechanism by which these molecules provide tolerance under stress is not clearly understood (Ramanjulu and Bartels 2002). These osmoprotectants are thought to counteract osmotic imbalance by reducing cell's osmotic potential and thereby maintaining turgor pressure under conditions of low water potential and high ionic strength (Pathan et al. 2004). They also function to protect or replace the water shell around proteins (Yancey et al. 1982; Stoop et al. 1996) and stabilize

**Table 9.1** Osmoprotectants and their role in stress tolerance

| Osmoprotectant                                | Role in stress tolerance   | Reference   |
|---|--|---|
| Mannitol                                      | Protects cellular structures from hydroxyl radical by reducing it  | Shen et al. (1997a, b)  |
| Glycine betaine                               | Salt and cold tolerance by protecting photosynthetic protein complex and reducing lipid peroxidation. Also works as chaperon in refolding of enzymes | Holmström et al. (2000), Chen et al. (2000), Sakamoto and Murata (2001) |
| Proline                                       | Adjustment of cellular redox state   | Shen et al. (1999), Kuznetso and Shevyakova (1999)                      |
| Ectoine, trehalose, fructan                   | Mainly stabilize the membranes from oxidative damage   | Romero et al. (1997), Nakayama et al. (2000)                            |
| Polyols (myo-inositol, D-ononitol, D-pinitol) | Dual functions—osmotic adjustment and supporting redox control   | Shen et al. (1999)  |
| Polyamines                                    | Scavengers of hydroxyl radicals and stomata closure  | Liu et al. (2000), Kuznetsov et al. (2007)                              |

protein complexes and membranes (Murata et al. 1992; Papageorgiou and Murata 1995). The accumulation of these osmolytes in overexpressing transgenic plants is too low to provide protection by the way of osmotic mass action alone (Sheveleva et al. 1997; Sakamoto et al. 1998; Huang et al. 2000). Apart from this, investigators have also revealed some alternative modes of stress protection offered by these osmoprotectants like scavenging of ROS and chaperon like activities that protect protein structure (Shen et al. 1997b; Serraj and Sinclair 2002). Table 9.1 summarizes the specific functions of some common osmoprotectants under abiotic stress.

## 4 Metabolic Engineering for Osmoprotectant Synthesis

Genetic transformation technology enables us to achieve gene transfer in precise and predictable manner. Hence genetic engineering approaches would be useful to manipulate these osmoprotectants biosynthetic pathways for accumulating such molecules that act by scavenging ROS, reducing lipid peroxidation, maintaining protein structure and functions (Hare et al. 1998; McNeil et al. 1999; Diamant et al. 2001; Yamada et al. 2005). The physiological and agricultural implications of metabolic engineering of plants for osmoprotectant biosynthesis have been thoroughly reviewed and analyzed (Jain and Selvaraj 1997; Nelson et al. 1998; Bohnert and Sheveleva 1998; Yeo 1998). Table 9.2 summarizes different transgenics developed using genes involved in osmoprotectant biosynthesis for abiotic stress tolerance.

**Table 9.2** List of transgenic plants engineered for stress tolerance using osmoprotectant genes

| Osmolyte        | Gene  | Gene source             | Plant species engineered | Stress tolerance  | Reference                   |
|-----------------|---|-------------------------|--------------------------|---|-----------------------------|
| <i>Mannitol</i> |   |                         |                          |   |                             |
| Mannitol        | <i>mtlD</i> , Mannitol-1-phosphate dehydrogenase  | <i>E. coli</i>          | Tobacco                  | No contribution to sustain growth under salinity and drought stress                           | Tarczynski et al. (1993)    |
| Mannitol        | <i>mtlD</i> , Mannitol-1-phosphate dehydrogenase  | <i>E. coli</i>          | <i>Arabidopsis</i>       | Increased germination under salinity stress   | Thomas et al. (1995)        |
| Mannitol        | <i>mtlD</i> , Mannitol-1-phosphate dehydrogenase  | <i>E. coli</i>          | Wheat                    | Drought and salinity tolerance of calli and plants  | Abebe et al. (2003)         |
| Mannitol        | <i>M6PR</i> , Mannose-6-phosphate reductase   | <i>Apium graveolens</i> | <i>Arabidopsis</i>       | Mannitol accumulation under salt stress leading to salt tolerance                             | Zhifang and Loescher (2003) |
| Mannitol        | <i>mtlD</i> and <i>GutD</i> , Mannitol-1-phosphate dehydrogenase and glucitol-6-phosphate dehydrogenase | <i>E. coli</i>          | Loblolly pine            | High salt tolerance due to mannitol and glucitol accumulation                                 | Tang et al. (2005)          |
| Mannitol        | <i>mtlD</i> , Mannitol-1-phosphate dehydrogenase  | <i>E. coli</i>          | <i>Petunia</i>           | Chilling tolerance  | Chiang et al. (2005)        |
| Mannitol        | <i>mtlD</i> , Mannitol-1-phosphate dehydrogenase  | <i>E. coli</i>          | Tobacco                  | Increased plant height and fresh weight under salinity stress                                 | Hu et al. (2005)            |
| Mannitol        | <i>M6PR</i> , Mannose-6-phosphate reductase   | <i>A. graveolens</i>    | <i>Arabidopsis</i>       | Mannitol accumulation led to higher yield as well as chloroplast protection under salt stress | Sickler et al. (2007)       |

(continued)

Table 9.2 (continued)

| Osmolyte             | Gene  | Gene source                             | Plant species engineered | Stress tolerance   | Reference   |
|----------------------|---|---|--------------------------|--|---|
| Sugars               | <i>AtGolS2</i> , Galactinol and Raffinose accumulation  | <i>Arabidopsis</i>                      | <i>Arabidopsis</i>       | Tolerance to cold, salinity, and drought stresses  | Taji et al. (2002)                                |
| <i>Sorbitol</i>      |   |   |                          |  |   |
| Sorbitol             | <i>Sip1I</i> , Sorbitol-6-phosphate dehydrogenase   | Apple                                   | Tobacco                  | Not much stress tolerant; phenotypic alterations with necrotic lesions on leaves             | Sheveleva et al. (1998)                           |
| <i>Inositols</i>     |   |   |                          |  |   |
| Ononitol             | <i>IMT1</i> , <i>Myo</i> -inositol- <i>o</i> -methyltransferase                               | Ice plant                               | Tobacco                  | Higher photosynthetic rate under salinity stress. Better recovery after drought stress       | Sheveleva et al. (1997)                           |
| <i>Myo</i> -Inositol | <i>ING1</i> , <i>Myo</i> -inositol-1-phosphate synthase                                       | <i>Porteresia coarctata</i> (wild rice) | Tobacco                  | Higher photosynthetic efficiency and better growth under salt stress                         | Majee et al. (2004)                               |
| <i>Trehalose</i>     |   |   |                          |  |   |
| Trehalose            | <i>TPS</i> , Trehalose-6-phosphate synthase   | Yeast                                   | Tobacco                  | Drought tolerance but decreased growth rate  | Holmström et al. (1996)                           |
| Trehalose            | <i>otsA</i> , <i>otsB</i> , Trehalose-6-phosphate synthase, Trehalose-6-phosphate phosphatase | <i>E. coli</i>                          | Tobacco                  | Improved growth under stress conditions, morphological alterations                           | Goddijn et al. (1997), Goddijn and Van Dun (1999) |
| Trehalose            | <i>TPS1</i> , Trehalose-6-phosphate synthase  | Yeast                                   | Tobacco                  | Stunted growth, lance shaped leaves, reduced sucrose content, and improved drought tolerance | Romero et al. (1997)                              |
| Trehalose            | <i>otsA</i> , <i>otsB</i> , Trehalose-6-phosphate synthase, Trehalose-6-phosphate phosphatase | <i>E. coli</i>                          | Tobacco                  | Increased leaf dry weight and photosynthetic activity under drought                          | Pilon-Smits et al. (1998)                         |



|           |   |                          |                    |  |                               |
|-----------|---|--------------------------|--------------------|--|-------------------------------|
| Trehalose | <i>TPS</i> , Trehalose-6-phosphate synthase   | <i>E. coli</i>           | Potato             | Trehalose level was not increased  | Goddijn et al. (1999)         |
| Trehalose | <i>TPS</i> , <i>TPP</i> , Trehalose-6-phosphate synthase, Trehalose-6-phosphate phosphatase     | <i>E. coli</i> and Yeast | Tobacco            | Enhanced rate of photosynthesis ( <i>TPS</i> ), Reduced rate of photosynthesis ( <i>TPP</i> )                            | Paul et al. (2001)            |
| Trehalose | <i>otsA</i> , <i>otsB</i> , Trehalose-6-phosphate synthase, Trehalose-6-phosphate phosphatase   | <i>E. coli</i>           | Rice               | Sustained plant growth, less photo oxidative damage, Increased stress tolerance  | Garg et al. (2002)            |
| Trehalose | <i>TPSP</i> (Fusion protein), Trehalose-6-phosphate synthase, Trehalose-6-phosphate phosphatase | <i>E. coli</i>           | Rice               | Drought, salt and cold tolerance   | Jang et al. (2003)            |
| Trehalose | <i>TPS1</i> , Trehalose-6-phosphate synthase  | Yeast                    | Tomato             | Apart from improved tolerance to drought, salinity, & oxidative stresses, transgenics had pleiotropic anatomical changes | Carolina and Francisco (2005) |
| Trehalose | <i>TPS1-TPS2</i> , Trehalose-6-phosphate synthase, Trehalose-6-phosphate phosphatase            | Yeast                    | <i>Arabidopsis</i> | Improved drought, freezing, salt, and heat tolerance   | Miranda et al. (2007)         |
| Trehalose | <i>TPS1</i> , Trehalose-6-phosphate synthase  | <i>Arabidopsis</i>       | Tobacco            | Drought resistance and sustained photosynthesis  | Almeida et al. (2007)         |
| Trehalose | <i>TPS1-TPS2</i> , Trehalose-6-phosphate synthase, Trehalose-6-phosphate phosphatase            | Yeast                    | Tobacco            | Maintenance of water status under drought stress   | Karim et al. (2007)           |

(continued)

Table 9.2 (continued)

| Osmolyte       | Gene   | Gene source               | Plant species engineered | Stress tolerance  | Reference                 |
|----------------|--|---------------------------|--------------------------|---|---------------------------|
| <i>Proline</i> |  |                           |                          |   |                           |
| Proline        | <i>P5CR</i> , Pyrroline-5-carboxylate reductase  | <i>Vigna aconitifolia</i> | Tobacco                  | Enhanced P5CR activity in transgenics did not yield significant increase in proline level                               | LaRosa et al. (1991)      |
| Proline        | <i>P5CS</i> , Pyrroline-5-carboxylate synthetase | <i>V. aconitifolia</i>    | Tobacco                  | Increased biomass production and enhanced flower and seed development under salinity stress                             | Kishor et al. (1995)      |
| Proline        | <i>P5CS</i> , Pyrroline-5-carboxylate synthetase | <i>V. aconitifolia</i>    | Rice                     | Increased biomass production under drought and salinity stress  | Zhu et al. (1998)         |
| Proline        | <i>P5CS</i> , Pyrroline-5-carboxylate synthetase | <i>V. aconitifolia</i>    | <i>Arabidopsis</i>       | Antisense plants showed hypersensitivity to osmotic stress and showed morphological changes during non-stress condition | Nanjo et al. (1999b)      |
| Proline        | <i>ProDH</i> , Proline dehydrogenase             | <i>V. aconitifolia</i>    | <i>Arabidopsis</i>       | Altered levels of proline dehydrogenase conferred salt and freezing tolerance   | Nanjo et al. (1999b)      |
| Proline        | <i>P5CS</i> , Pyrroline-5-carboxylate synthetase | <i>V. aconitifolia</i>    | Rice                     | Elevated proline and reduced free radical levels  | Hong et al. (2000)        |
| Proline        | <i>P5CR</i> , Pyrroline-5-carboxylate reductase  | <i>V. aconitifolia</i>    | Soybean                  | Antisense plants failed to survive after 6 days of drought stress   | De Ronde et al. (2000)    |
| Proline        | <i>P5CS</i> , Pyrroline-5-carboxylate synthetase | <i>V. aconitifolia</i>    | Wheat                    | Wheat transgenic plants showed enhanced proline levels and conferred salt tolerance                                     | Sawabel and Hassan (2002) |

|         |  |                        |                    |  |                        |
|---------|--|------------------------|--------------------|--|------------------------|
| Proline | <i>ProDH</i> , Proline dehydrogenase             | <i>V. aconitifolia</i> | <i>Arabidopsis</i> | Antisense plants showed hypersensitivity to exogenous proline  | Mani et al. (2002)     |
| Proline | <i>OAT</i> , Ornithine-D-aminotransferase        | <i>Arabidopsis</i>     | Tobacco            | Overexpression increased proline biosynthesis and osmotolerance  | Roosens et al. (2002)  |
| Proline | <i>P5CS</i> , Pyrroline-5-carboxylate synthetase | <i>V. aconitifolia</i> | Rice               | Transgenic rice plants showed better root growth and biomass development during NaCl treatment                                     | Anoop and Gupta (2003) |
| Proline | <i>OAT</i> , Ornithine-D-aminotransferase        | <i>Arabidopsis</i>     | Rice               | Overexpression led to increase in proline levels during osmotic stress and transgenic plants showed improved yield under stress    | Wu et al. (2003)       |
| Proline | <i>P5CS</i> , Pyrroline-5-carboxylate synthetase | <i>V. aconitifolia</i> | Carrot             | Tolerance to salt stress   | Han and Hwang (2003)   |
| Proline | <i>P5CR</i> , Pyrroline-5-carboxylate reductase  | Tomato                 | Soybean            | Enhanced heat and drought stress tolerance   | De Ronde et al. (2004) |
| Proline | <i>ProDH</i> , Proline dehydrogenase             | <i>V. aconitifolia</i> | Tobacco            | Antisense plants showed increased proline content and cytoplasmic osmotic pressure   | Kochetov et al. (2004) |
| Proline | <i>P5CS</i> , Pyrroline-5-carboxylate synthetase | <i>V. aconitifolia</i> | Rice               | Stress inducible expression of <i>P5CS</i> gene in rice seedlings showed significantly higher tolerance to drought and salt stress | Su and Wu (2004)       |

(continued)

Table 9.2 (continued)

| Osmolyte             | Gene   | Gene source            | Plant species engineered   | Stress tolerance  | Reference                  |
|----------------------|--|------------------------|----------------------------|---|----------------------------|
| Proline              | <i>OsP5CS2</i> , Pyrroline-5-carboxylate synthetase  | Rice                   | Rice                       | Enhanced salt and cold stress tolerance                 | Hur et al. (2004)          |
| Proline              | <i>P5CSF129</i> , Pyrroline-5-carboxylate synthetase   | Tomato                 | Citrus                     | Drought tolerance                                       | Molinari et al. (2004)     |
| Proline              | <i>P5CR</i> , Pyrroline-5-carboxylate reductase  | <i>Arabidopsis</i>     | Potato                     | Salinity tolerance                                      | Hmida-Sayari et al. (2005) |
| Proline              | <i>P5CS</i> , Pyrroline-5-carboxylate synthetase   | Tomato                 | Sugarcane                  | Protection from drought stress and higher biomass yield | Molinari et al. (2007)     |
| Proline              | <i>P5CS</i> , Pyrroline-5-carboxylate synthetase   | <i>V. aconitifolia</i> | <i>Medicago truncatula</i> | Enhanced tolerance to osmotic stress                    | Verdoy et al. (2006)       |
| <i>Polyamines</i>    |  |                        |                            |   |                            |
| Putrescine           | <i>ADC</i> , Arginine decarboxylase  | Oat                    | Rice                       | Salt tolerance  | Roy and Wu (2001)          |
| Putrescine           | <i>ODC</i> , Ornithine decarboxylase   | Mouse                  | Tobacco                    | Salt tolerance  | Kumria and Rajam (2002)    |
| Spermidine, spermine | <i>SAMDC</i> , S-Adenosylmethionine decarboxylase  | <i>Triticordeum</i>    | Rice                       | Salt tolerance  | Roy and Wu (2002)          |
| Spermidine           | <i>ACC</i> (1-amino cyclopropane-1-carboxylic acid) synthase, <i>ACC</i> oxidase, Arginine decarboxylase | Carnation              | Tobacco                    | Tolerance to many stresses                              | Wi and Park (2002)         |
| Spermidine, spermine | <i>SAMDC</i> , S-Adenosylmethionine decarboxylase  | Human                  | Tobacco                    | Tolerance to osmotic stress                             | Waite and Rajam (2003)     |

|                |   |                           |                    |  |                         |
|----------------|---|---------------------------|--------------------|--|-------------------------|
| Putrescine     | <i>ADC</i> , Arginine decarboxylase   | <i>Datura stramonium</i>  | Rice               | Drought tolerance  | Capell et al. (2004)    |
| Spermidine     | <i>SPE</i> , Spermidine synthase  | Yeast                     | <i>Arabidopsis</i> | Tolerance to chilling, freezing, salinity, drought, hyperosmosis | Kasukabe et al. (2004)  |
| Spermidine     | <i>SAMDC</i> , S-Adenosylmethionine decarboxylase   | Carnation                 | Tobacco            | Broad spectrum stress tolerance                                  | Wi et al. (2006)        |
| Putrescine     | <i>ADC1</i> , Arginine decarboxylase  | <i>Arabidopsis</i>        | <i>Arabidopsis</i> | Freezing tolerance   | Altabella et al. (2009) |
| Spermidine     | <i>SAMDC</i> , S-Adenosylmethionine decarboxylase   | Yeast                     | Tomato             | Heat tolerance   | Cheng et al. (2009)     |
| Spermidine     | <i>SPDS</i> , Spermidine synthase   | Apple                     | Pear               | Aluminum stress tolerance  | Wen et al. (2009)       |
| Putrescine     | <i>ADC2</i> , Arginine decarboxylase  | <i>Arabidopsis</i>        | <i>Arabidopsis</i> | Drought tolerance  | Alcázar et al. (2010b)  |
| <i>Ectoine</i> |   |                           |                    |  |                         |
| Ectoine        | <i>ectABC</i> , L-2,4-diaminobutyric acid acetyltransferase   | <i>Halomonas elongata</i> | Tobacco cell lines | Tolerance hyperosmotic stress                                    | Hideki et al. (2000)    |
|                | L-2,4-diaminobutyric acid transaminase  |                           |                    |  |                         |
|                | Ectoine synthase  |                           |                    |  |                         |
| Ectoine        | <i>ectABC</i> , L-2,4-diaminobutyric acid acetyltransferase, L-2,4-diaminobutyric acid transaminase, Ectoine synthase | <i>H. elongata</i>        | Tobacco            | Tolerance to salt and osmotic stress                             | Moghaieb et al. (2006)  |

(continued)

Table 9.2 (continued)

| Osmolyte               | Gene   | Gene source                     | Plant species engineered     | Stress tolerance   | Reference                                 |
|------------------------|--|---------------------------------|------------------------------|--|---|
| Ectoine                | <i>ectABC</i><br>L-2,4-diaminobutyric acid acetyltransferase<br>L-2,4-diaminobutyric acid transaminase<br>Ectoine synthase | <i>H. elongata</i>              | Tomato                       | Salt tolerance   | Moghaieb et al. (2011)                    |
| <i>Glycine betaine</i> |  |                                 |                              |  |   |
| Betaine                | <i>betA</i> , Choline dehydrogenase  | <i>E. coli</i>                  | Tobacco                      | Increased tolerance to salinity stress                                     | Lilius et al. (1996)                      |
| Betaine                | <i>codA</i> , Choline oxidase  | <i>Arthrobacter globiformis</i> | <i>Arabidopsis</i>           | Seedlings tolerant to salinity stress and increased germination under cold | Hayashi et al. (1997), Alia et al. (1998) |
| Betaine                | <i>codA</i> , Choline oxidase  | <i>A. globiformis</i>           | Rice                         | Increased tolerance to salinity and cold                                   | Sakamoto et al. (1998)                    |
| Betaine                | <i>GS2</i> , Chloroplastic glutamine synthetase  | Rice                            | Rice                         | Increased salinity resistance and chilling tolerance                       | Hoshida et al. (2000)                     |
| Betaine                | <i>codA</i> , Choline oxidase  | <i>A. globiformis</i>           | <i>Arabidopsis</i> , Tobacco | Increased stress tolerance to salt and cold                                | Huang et al. (2000)                       |
| Betaine                | <i>BADH1</i> , Betaine aldehyde dehydrogenase  | Sorghum                         | Tomato                       | Maintenance of osmotic potential   | Moghaieb et al. (2000)                    |
| Betaine                | <i>CMO</i> , Choline monoxygenase  | <i>Atriplex hortensis</i>       | Tobacco                      | Better in vitro growth under salinity and osmotic stress                   | Yi-Guo et al. (2002)                      |
| Betaine                | <i>codA</i> , Choline oxidase  | <i>A. globiformis</i>           | Rice                         | Recovery from a week long salt stress                                      | Mohanty et al. (2003)                     |
| Betaine                | <i>codA</i> , Choline oxidase  | <i>A. globiformis</i>           | <i>Arabidopsis</i>           | Salt tolerance in terms of flowering                                       | Ronan et al. (2003)                       |

|         |   |                             |                        |   |                           |
|---------|---|-----------------------------|------------------------|---|---------------------------|
| Betaine | <i>BADH1</i> , Betaine aldehyde dehydrogenase | Carrot                      | Carrot                 | Salinity tolerance  | Kumar et al. (2004)       |
| Betaine | <i>betA</i> , Choline dehydrogenase           | <i>E. coli</i>              | Maize                  | Drought resistance at seedling stage and high yield after drought condition | Ruidiang et al. (2004)    |
| Betaine | <i>codA</i> , Choline oxidase                 | <i>A. globiformis</i>       | <i>Brassica juncea</i> | Tolerance to stress-induced photoinhibition                                 | Prasad and Saradhi (2004) |
| Betaine | <i>BADH1</i> , Betaine aldehyde dehydrogenase | <i>Atriplex hortensis</i>   | Tobacco                | Heat tolerance and increased photosynthetic efficiency                      | Yang et al. (2005)        |
| Betaine | <i>COX</i> , Choline oxidase                  | <i>Arthrobacter pascens</i> | Rice                   | Salt stress tolerance   | Su et al. (2006)          |

## 5 Constraints in Path of Metabolic Engineering

It has been observed that out of many transgenics developed for higher osmoprotectant accumulation, only a few succeeded due to metabolic constraints, a few are enlisted here:

1. Transgenes used for transforming a plant were of non-plant origin, mainly bacterial, while plants have their own genes for osmoprotectant synthesis. Use of plant origin genes can aid in overcoming this hurdle (Hanson et al. 1994).
2. Two major factors that generally limit the accumulation of osmoprotectants in transgenic plants are the availability of endogenous substrate and transport of osmolytes across the membranes (Nuccio et al. 1998, 2000; McNeil et al. 2000; Huang et al. 2000).
3. Some of the metabolic pathways are very rigid from flux point of view; they oppose the flux redistribution which arises due to over expression of transgene for metabolite biosynthesis (Stephanopoulos and Vallino 1991; Fernie et al. 2002).
4. Metabolic flux of the transgenics developed using constitutive promoter remains diverted all the time and there by affects plant's growth and development. Employing tissue specific and stress inducible promoters may support in balancing metabolic flux (Nelson et al. 1998; Russell et al. 1998; Garg et al. 2002).
5. Over expression of transgene may lead to diversion of metabolic flux from primary metabolism and therefore this can give rise to undesirable consequences (Sheveleva et al. 1998; Bohmert et al. 2000; Roessner et al. 2001; Garg et al. 2002) or it may lead to feedback effects on engineered pathway (Fernie et al. 2002; Regierer et al. 2002).
6. Cells may recognize the over expressed metabolite as non-self and may degrade it using endogenous machinery (Goddijn et al. 1997) or the host may lack regulatory control upon the over expressing enzyme (Trethewey 2004).
7. Over accumulation of various compatible solutes (mannitol, sorbitol, and trehalose) in transgenic plants have shown some harmful side effects (Karakas et al. 1997; Sheveleva et al. 1998; Yeo et al. 2000).
8. Studies show that osmolytes have minor impact on cellular water retention or osmotic adjustment in comparison to stabilization and protection of cellular components (Blum et al. 1996; Konstantinova et al. 2002; Turner et al. 2007).
9. Transgenic plants engineered for over expression of osmoprotectant synthesis gene could not be assessed rigorously for their stress tolerance potential (Bhatnagar-Mathur et al. 2008).

## 6 Conclusion

The avenues and possibilities of plants engineered for osmoprotectants has been an area of consistent research for plant scientists and have been reviewed extensively in Bohnert et al. 1995; Nuccio et al. 1999; Rathinasabapathi 2000; Chen and Murata



2002. Although the mode of action of these diverse categories of osmoprotectants might be overlapping, it is still a mystery as to what triggers the accumulation of different osmolytes under different stress conditions. Additionally, the protection offered by these molecules is still under speculation as whether it is a result of a better osmotic adjustment of the cell under stressful situations or they have some deeper impacts on the cellular system coping with stress. Among many attempts made at installing genes for osmoprotectant biosynthesis in plants, only a moderate level of stress tolerance has been achieved in controlled stress conditions and no significant performance has been reported from the field trials if any.

The past has nevertheless shown us that the way forward now is to first understand the comprehensive roles of these molecules in relieving stress in the cellular system along with the implications of over expressing these genes in terms of energy efficiency and channelization of metabolic flux away from physiologically important pathways.

## 7 Future Prospects

Considering the multigenicity of stress tolerance trait, transgenics developed through single gene insertions are inefficient in providing sustainable stress tolerance to crop plants. Therefore, it is important to carefully identify regulatory factors, which affect expression of key genes following any abiotic stress. Use of these regulatory factors like stress inducible transcription factor in transforming any crop plant may lead to regulation of many genes involved in stress response and thereby impart tolerance to multiple stresses. The overall functional analysis of transgenics made for different osmoprotectants may help us to select key regulatory genes for developing multiple stress tolerant crop varieties. So far, attempts for developing stress tolerant transgenics are restricted mostly to model plants, therefore focus on crop plants is the need of the hour.

Though in some cases, it has been reported that modification of compatible solute machinery could lead to no benefit in terms of yield under stress, therefore further research is necessary in order to genetically manipulate tissue specific and stress inducible osmoprotection in crop plants as these transgenics will be more efficient in abiotic stress tolerance without much affecting the metabolic flux. Broad stress tolerant genotypes may be generated by combining different strategies involved in enhancing stress tolerance, like stress-related genes, and their regulatory transcription factors.

Defining the exact mechanism of action of osmolyte and the specific macromolecules being targeted will lead to further improvement in metabolic engineering of osmoprotectants. Identification and characterization of novel osmoprotectants from stress tolerant crop varieties will also aid in achieving this objective.

Therefore, after analyzing these prospects it can be safely concluded that there exists a lot of scope in crop improvement using osmoprotectants but further developments will demand extensive evaluation of stress tolerance potential of these transgenic crops as there is much difference between controlled lab and field conditions.

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