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Review

Advances in genetic engineering for plants abiotic stress control

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Agricultural productivity is highly influenced by abiotic stresses, known as the most harmful factor concerning the growth and productivity of crops worldwide. Furthermore, industrial crops are nowadays highly influenced by abiotic stress; these include extremes in temperature, drought, salinity, heavy metals and radiation. Typical studies were discussed by many researchers about the control of abiotic stress in plants by the expression, over-expression or switching off abiotic stress-related genes. Despite the rapid evolution of the research, some crops are still expected to decline by 15 to 32% in the next fifty years. Consequently, engineering genes that protect and maintain the function and structure of cellular components can enhance tolerance to stress. This review presents principal methods adapted in the control of plants abiotic stresses including recent advances in using transgenes for the improvement of abiotic stress tolerance in plants. Specified analysis of recent advances in abiotic stress control could describe trehalose as a better compound in the control of plant abiotic stresses. Therefore, studies of genes-related trehalose metabolism and associated patterns could not only provide an improved plant metabolism, phenotypes and texture, but in fact, the plants become highly resistant to abiotic stress.

Key words: Abiotic stresses, crops, expression, over-expression, switching off, trehalose, genes-related.

IMPACT OF ABIOTIC STRESS IN PLANTS

Abiotic stress is known as the most harmful factor concerning the growth, productivity of crops and worldwide agricultural loss, posing a substantial challenge in the face of an ever increasing world population (Gao et al., 2007). In the recent years, many researchers have drawn their investigations in biotic and abiotic stress in plants (Boyer, 1982; Bray et al., 2000; Mittler, 2006; Brown et al., 2003). Abiotic stressors are at their most harmful stage when they occur together, in combinations of abiotic stress factors (Mittler, 2006). Although some biotic stresses can be controlled by germicide, pesticides, antibiotic treatment and/or plant metabolism, it is urgent to control abiotic stress, which can possibly affect response to biotic stress control with detrimental effect on plant growth and yields. Therefore, solving few threats such as the depletion of the ozone layer, high risk of exposure to ultra violet (UV) and infra-red radiation, environmental warming, increasing soil salinity, drinking polluted underground water, production of toxic chemicals and contaminated food materials which were not visible till 1960 is highly required. Moreover, cold weather crops like rye, oats, wheat and apples are expected to decline by about 15% in the next fifty years and strawberries will drop as much as 32% simply because of projected climate changes of a few degrees (Lane and Jarvis, 2007). Presently, industrial needs are highly influenced by abiotic stress. Improved production efficiency can be achieved by developing stress tolerant crops (Ribaut et al., 1997), which necessitates research on plant adaptation mechanisms against adverse environmental conditions. Activation of stress-response transcription factors has been found to enhance plant tolerance to various kinds of stress in transgenic plants (Kasuga et al., 1999; Vogel et al., 2005; Villalobos et al., 2004; Gu et al., 2002)

Salinity and drought are the most commonly observed

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abiotic stress; they significantly reduce yield and affect almost every aspect of the physiology and biochemistry of plants. Great efforts have been devoted to understanding the physiological aspects of response in plants to salinity and drought-tolerant genotypes (Cuartero et al., 2006). Studies on tomato cultivar Liaoyuan Duoli (*Solanum lycopersicum* L.) indicated that, soluble sugar and hexoses accumulated to higher levels and the contents of sucrose and starch were lower in mature fruit under the two stress treatments. Salt and water stresses can enhance the invertase and sucrose synthase activities of tomato fruit in a long period of time (45 to 60 days after anthesis) and elevate the expression of soluble acid invertase mRNA. Two different stresses could also regulate the soluble acid invertase activity by controlling its gene expression. The activity of sucrose synthase was linked to the changes in soluble sugar levels but not with transcript levels (Lu et al., 2009). However, little is still known about the function of other components of the plant transcription machinery during stress.

METHODS DEVELOPED AND ADVANCES IN THE CONTROL OF PLANTS ABIOTIC STRESS

Maintenance of soil biodiversity

Healthy environment (pollution free, habitat conservation, climate variability and some other changes) as well as biologically diverse soil are necessary for productivity concerns. The healthy soil community keeps pests and diseases under control. Several microorganisms have been used in the control of soil biodiversity; the fungi *Beauveria brongniartii* and *Metarhizium anisopliae* already in commercial formulas to control pests *Glomus clarum* and to grow maize and shorgumin in *Striga hermonthica* infected soils.

Resilience to abiotic stress and soil rehabilitation used some microorganisms for restoration of soil quality; for example, arbuscular mycorrhizal fungi (AMF) is used to reduce potentially toxic elements (Cd, Cr, Mn) from the soil commonly known as bioremediation. Some use mycorrhizal fungi to enable plants to cope with abiotic stress by alleviating nutrient deficiencies, improving drought tolerance, overcoming the detrimental effects of salinity ,improving the adaptation of sterile micropropagated plants to unsterile substrates and to field conditions. Although these researches have provided sufficient information in the maintenance of plants' good environment, they are still not enough to understand the impact of soil biodiversity in the control of abiotic stress and agricultural production (Barrios, 2007; Wall and Moore, 1999; Bloem et al., 2003; Swift et al., 2004).

Positive interactions between plant species

Positive interactions between plant species are widespread in natural communities and have been acknowledged as a major driver of plant community dynamics and ecosystem processes (Bruno et al., 2003). There have been no large-scale experiments designed to examine the generality of positive interactions in plant communities and their importance relative to competition. Ragan et al. (2002) found that, competition generally but not exclusively dominate interactions at lower elevations where conditions are less physically stressful. In contrast, at high elevations where abiotic stress is high the interactions among plants are predominantly positive. Furthermore, across all high and low sites, positive interactions are more important at sites with low temperatures in the early summer and competition prevails at warmer sites. Facilitative and competitive interactions are thought to be of great importance in arid and semi-arid areas (Whitford, 2002). However, only a few studies have evaluated how changes in abiotic conditions modify the relative importance of facilitation and competition in these environments (Tielborger and Kadmon, 2000; Pugnaire and Luque, 2001; Maestre et al., 2003). Furthermore, none of these studies were conducted at multiple sites across a gradient of abiotic stress. A shift from facilitation to competition under high abiotic stress conditions is likely to occur when the levels of the most limiting resource are so low that the benefits provided by the facilitator cannot overcome its own resource uptake (Fernando et al., 2004). Positive interactions between different species of plants, including cross-pollination or mutualistic actions were also studied (Maestre et al., 2007).

Conventional breeding to genetic engineering

Success in breeding for better adapted varieties to abiotic stresses depends upon the concerted efforts by various research domains including plant and cell physiology, molecular biology, genetics and breeding (Pooja et al., 2008; Muhammad and Nudrat, 2009). Common bean (*Phaseolus vulgaris* L.) because of its wide genetic variability, is one of the crops that received attention for more than 20 years in breeding program for abiotic stress control such as drought, tolerance to low soil phosphorus (P) and nitrogen (N) availability and resistance to high aluminium (Al) in acid soils (Lynch and Beebe, 1995; Thung and Rao, 1999; Rao, 2002; Beebe et al., 2008). Meanwhile, the use of modern molecular biology tools for elucidation of the control mechanisms of abiotic stress tolerance and for engineering stress tolerant crops is based on the expression of specific stress-related genes. Instead of relying on sexual recombination to thoroughly stir the parental genes, genetic engineering preserves the integrity of the parental genotype, inserting only a small additional piece of information that controls a specific trait. Genetic engineering allows the direct transfer, removing or switching off (Tables 1 and 2) a particular or just a few genes between either closely or distantly related

Table 1. Illustration of some recent genes expressed and response to abiotic stress.

Gene/molecule used and origin	Plant tested	Abiotic stress controlled	Associated pattern	Reference
Arabidopsis DREB2C	*Arabidopsis*	Heat stress	Transactivation of the DRE-dependent transcription factor HsfA3	Huan et al. (2010)
Arabidopsis ftl1-1D/ddf1	*Arabidopsis*	Enhances tolerance to cold, drought, heat and salt stresses	The induced gene encoded an AP2 transcription factor of the *CBF/DREB1* subfamily	Hong-Gyu et al. (2011)
Rice *OsABF2*	Rice	Induced by different types of abiotic stress treatments such as drought, salinity, cold, oxidative stress, and ABA.	The group A *bZIP* transcription factors play important roles in the ABA signaling pathway in *Arabidopsis*. In yeast experiments, *OsABF2* was shown to bind to ABA-responsive elements (*ABREs*) and its N-terminal region found to be necessary to transactivate a downstream reporter gene.	Md. Amir et al. (2010)
Hevea brasiliensis HbMT2	*Escherichia coli*	Strongly induced by ethephon and hydrogen peroxide (H2O2) stress. Overproduction induce more tolerance on Cu2t and Zn2t, and the recombinant *HbMT2* scavenge the reactive oxidant species (ROS) in vitro.		Jiahong et al. (2010)
Apple *cyMDH*	Apple callus and tomato	Involved in plant and cell growth as well as the tolerance to cold and salt stresses.		Yu-Xin et al. (2011)
Panax ginseng PgCat1	Panax ginseng	Different stresses, heavy metals, plant hormones, osmotic agents, high light irradiance, abiotic stresses, triggered a significant induction of PgCat1.		Munkhbaatar et al. (2010)

Table 1. Continue.

Emmer wheat (*Triticum turgidum* ssp. dicoccoides) *TdicDRF1*	Wheat; *Arabidopsis thaliana*.	Drought resistance	Analysis of the AP2/ERF DNA-binding domain of TdicDRF1 as a GST-fusion protein and its binding to DRE by electrophoretic mobility shift assay (EMSA) indicate functional differences between wheat *DREBs* and those characterized in *Arabidopsis* thaliana.	Stuart et al. (2011)
Citrus unshiu CitERF	*Citrus unshiu*	Play an important role in some biological processes during fruit ripening and in improving tolerance to drought, low temperature and salt stress.		Xiao-Yan et al. (2011)
Trichoderma harzianum hsp70	*Arabidopsis*	Enhanced tolerance to heat stress, osmotic, salt and oxidative stresses	Increased transcript levels of the Na+/H+ exchanger1 (*SOS1*) and ascorbate peroxidase1(*APX1*) genes	Marta et al. (2009) and Hervé and Ary (2010)
Rice *OsAP2LP*	Rice	Plays important roles when plants response to cold, salt and drought stresses through ABA and gibberellin pathways.		Ma et al. (2010)
Brassica juncea γ-TMT	*Arabidopsis*	Enhanced tolerance to salt, heavy 30 metal and osmotic stress		Mohd et al. (2010)
Cauliflower mosaic virus (CaMV) 35S promoter	Tobacco	Acute single dose of UVC, UVB or X-ray radiation and exposure to high temperature respe- ctively decreased and increased the transgene expression level		Alex et al. (2010)
Oryza sativa miRNAs	Rice	Control in some extend cold, dehydration, salinity and abscisic acid (ABA)		Xinyu et al. (2010)

Table 1. Continue.

L. temulentum (*eEF- 1a*，*ACT11* and *UBQ5*)	L. temulentum	Drought, UV stress, Heat stress, Wounding, Salt stress, Osmotic stress, Cold stress	*eEF-1a* and *UBQ5* were the most stable and *ACT11* was the least stable in stress Condition	James and Ruth (2009)
Maize (*Zea mays* L.) *ZmCOI6.1*	*Arabidopsis*	Cold, drought and salinity as well as the signaling molecules abscisic acid and salicylic Acid		Orlene et al. (2009
CaBI-1 from the cDNA library of heat-stressed hot pepper (Capsicum annuum)	Tobacco	High or low temperatures, drought, high salinity, flooding and heavy metal stresses, and ABA		Mohammad et al. (2009)
L. maritime *AtbZIP24* *Tamarix hispida ThbZIP1*	*Arabidopsis* tobacco	Decreased *AtbZIP24* expression activated the expression of stress-inducible genes: the Na+ transporter *AtHKT1*, the Na+/H+ antiporter *AtSOS1*, the aquaporin *AtPIP2.1*, and a glutamine synthetase. overexpression of *ThbZIP1* can enhance the activity of both peroxidase (POD) and superoxide dismutase (SOD), and increase the content of soluble sugars and soluble proteins under salt stress conditions.	Target genes of *AtbZIP24* with functions in plant growth and development were identified such as an argonaute (AGO1)-related protein and cyclophilin *AtCYP19*. The salt tolerance in transgenic plants correlated with reduced Na+ accumulation in leaves	Oksoon et al. (2009) and Yucheng et al. (2010)
Hot peppers *PepRSH*	*Escherichia coli*	*PepRSH* transcripts were highly accumulated in non-host resistance response-induced leaves and in leaves following induction with salicylic acid, methyl jasmonate, wounding, hydrogen peroxide, and ultraviolet- B. The expression of PepRSH was also influenced by abiotic stresses, such as flooding and high salinity	*PepRSH* has (p)ppGpp synthetase activity only in the (p)ppGpp synthetase domain	Tae-Ho et al. (2009)
Cypress seedlings (Cupressus simper- virens L.) cyplp009; cyplp005; cyplp006; cyplp017; cyplp010; cyplp020; cyplp012; cyplp002; cyplp007; cyplp019; cyplp003; cyplp016; cyplp008; cyplp015; cyplp021	Cypress canker	Control of cold		Luca et al. (2009)

Table 1. Continue.

Wheat TaVP1, TaVP2 and *TaVP3*	Wheat	Salinity stress	*TaVP3* transcripts were only detected in Developing seeds, and no *TaVP2* transcripts were found in germinating seeds. *TaVP2* was mainly expressed in shoot tissues and down-regulated in leaves under dehydration. Its expression was up-regulated in roots under high salinity. *TaVP1* was relatively more ubiquitously and evenly expressed than *TaVP2*	Yuezhi et al. (2009)
Wheat *TaSTRG*	Rice	Expression induced by salt, polyethylene glycol (PEG), abscisic acid (ABA), and cold. Overexpression showed higher salt and drought tolerance	Under salt stress, the transgenic rice had a lower intracellular Na+/K+ ratio Under salt and PEG treatments, these TaSTRG overexpressing rice plants had higher survival rate, fresh weight and chlorophyll content, accumulated higher proline and soluble sugar contents, and had significantly higher expression levels of putative proline synthetase and transporter genes	Wei et al. (2009)
Arabidopsis CRT/DRE binding factor 1 (*CBF1*)	Tobacco	Enhancing low temperature tolerance of plants	The photochemical efficiency of PSII(Fv/Fm) and the photo- oxidizable P700 in the transgenic lines overexpressing *CBF1*were higher .A higher NPQ and qf, lower FNF, higher activity of SOD, and lower content of MDA Higher expression levels of Nicotiana tabacum copper/zinc superoxide dismutase (*Cu/Zn SOD*) were also detected in the transgenic lines	Jia-Sen et al. (2010)
Arabidopsis AVP1	Alfalfa (*Medicago sativa*)	Enhanced salt and drought tolerance	Transgenic plants accumulate more Na+, K+ and Ca2+ in leaves and roots. Moreover, the leaves of transgenic plants retain more water during drought stress	Ai-Ke et al. (2009)
Bruguiera Gymnorhiza Bg70 and cyc02	*Arabidopsis*	Increased tolerance to NaCl		Shota and Yuichi (2009)

Table 1. Continue.

Cotton *GhTIP1;1* tonoplast intrinsic protein (TIP)	Xenopus laevis oocytes	Involved in cell freezing-tolerance;	*GhTIP1;1* facilitated water transport to the cells *GhTIP1;1* transcripts were predominantly accumulated in roots and hypocotyls.	Deng-Di et al. (2009),
Barley *HvTIP1;2, HvTIP2;1, HvTIP2;2, HvTIP2;3* and *HvTIP4;1*	Barley (Hordeum vulgare)	salt, heavy metals and nutrient deficiency), abscisic acid (ABA), gibberellic acid (GA) osmotic stress and cold.		Ayalew et al. (2011) and
Arabidopsis RAP2.6	*Arabidopsis*		Trans-activating ability tests in yeast demonstrate that *RAP2.6* could act as a transactivator. *RAP2.6* is able to bind to the *GCC* and *CE1* cis-elements	Qiang et al. (2010)
Rice (*Oryza rufip*-ogon) *OrbHLH2*	*Arabidopsis*	Increased tolerance to salt and osmotic stress	The stress-responsive genes *DREB1A/CBF3*, *RD29A*, *COR15A* and *KIN1* were up regulated in transgenic plants	Jing et al. (2009)
Brassica juncea AnnBj1	Tobacco	Significant tolerance to dehydration (mannitol), salt (NaCl), heavy metal (*CdCl2*) and oxidative stress (H2O2) at the seedling stage	Retain higher chlorophyll levels in response to the studied stresses	Sravan et al. (2008)
Cassava *CuZnSOD* and pea *APX*	Fescue	Functionally expressed under methyl viologen (MV), H2O2, heavy metals copper, cadmium, and arsenic		Sang-Hoon et al. (2007)
Maize kernel *SAT41* and *Arabidopsis MBF1a*	Maize and *Arabidopsis*	Maize clone (*SAT41*) seemed to confer elevated salt tolerance		Min-Jung et al. (2007)
Rice *OsUGE-1*	*Arabidopsis*	Tolerance to salt, drought and freezing stress	No alteration of plant morphology. Transgenic plants showed a higher level of the soluble sugar raffinose	Hui-li et al. (2007)
Rice *AtNDPK2*	Rice	*AtNDPK2* plays a regulatory role in chilling and antioxidant signaling in plants	Accumulation of transcripts of pBC442 and pBC601, is related to chilling stress. *OsAPX1*-, *OsAPX2*-, and *OsSodB*-scavenging free oxygen radicals, such as superoxide eO2_T and hydrogen peroxide (H2O2), could be induced in *AtNDPK2*-overexpressed rice plants.	Eun et al. (2007)
Pepper *CaXTH3*	*Arabidopsis*	Resistance to drought, high salinity and cold temperature	Abnormal leaf morphology	Seok et al. (2006)
Yeast *YCF1*	*Arabidopsis*	Enhanced in salt or xenobiotic chemical (1-chloro-2, 4-dinitrobenzene,CDNB) tolerance	*COR15A* and *KIN1* were less strongly induced in the transgenic plants	Eun-Ji et al. (2006)

Table 2. Illustration of advanced trahalose genes expressed in the control of abiotic stress.

Gene/molecule used and origin	Plant tested	Abiotic stress controlled	Associated pattern	References
Exogenous trehalose	*Arabidopsis*	Promotes non-structural carbohydrate accumulation; Induces chemical detoxification and stress response proteins	Increased starch and decreased ATP levels, glutamate, glutamine, hexoses and chlorophyll were unaffected. Phi glutathione S-transferase 2 (*AtGSTF2*), flavin mononucleotide-binding flavodoxin-like quinine reductase 1 (*FQR1*), cytosolic dehydroascorbate reductase 1 (*DHAR1*) and S-adenosylmethionine synthetase 2 (*SAMS2*), were involved in either detoxification or stress responses.	Hanhong et al. (2005)
Yeast trehalose-6-phosphate synthase (*TPS1*)	Tomato	Improved tolerance under drought, salt and oxidative stress	Thick shoots, rigid dark-green leaves, erected branches and an aberrant root development. Higher chlorophyll and starch content	Carolina and Francisco (2005)
Fungal entomopathogen *Beauveria bassiana* Neutral trehalase(NTH1)	*E. coli*	Crucial stress-responsive elements; NaCl and thermal stress	BbT4 is controlled by the shortest NthP4. that is, this promoter fragment is crucial to initiating high-level *BbNTH1* expression in *B. bassiana* under oxidative stress.	Qian et al. (2010)

organisms. Crop improvement can be achieved in a shorter time compared with conventional breeding. Hence, genetic engineering for developing stress tolerant plants, based on the introgression of genes that are known to be involved in stress response and putative tolerance, might prove to be a faster track towards improving crop varieties. Nevertheless, the task of generating transgenic cultivars is not only limited to the success in the transformation process, but also proper incorporation of the stress tolerance genetic material. Evaluation of the transgenic plants under stress conditions and under- standing the physiological effect of the inserted genes at the whole plant level is still the major challenges to overcome (Pooja et al., 2008). Following plant breeding for salt stress tolerance in plants, genetic engineering seems to be at the moment, the only method for efficient improvement in abiotic stress control. Some recent advances in genetic engineering for abiotic stress control in plants are represented in Table 1. Genes responsible for stress control were cloned from a wide variety of organism and studied for expression or over-expression in either model plant like *Arabidopsis*, tobacco or some other plants like rice, maize and barley as the most studied ones. Tae-Ho et al. (2009) studied the expression of *PepRSH* gene in *Escherichia coli* and provided wide information about its controlled activity due to the easy manipulation and short life cycle of *E. coli* (Tables 1 and 2) cells. Information about the abiotic stress control and interaction that may happen in the cell is important before gene trans- formation and analysis in a targeted higher plant. Meanwhile, multiple genes were successfully transformed to the control of abiotic stress in plant with substantial information on their mechanisms; this include the *Trichoderma harzianum* hsp70, L. maritime *AtbZIP24*, wheat *TaVP1*, *TaVP2* and *TaVP3, Arabidopsis CRT/DRE* binding factor 1 (CBF1), *Arabidopsis AVP1,* 1 tonoplast intrinsic protein (TIP) *GhTIP1*, rice *OrbHLH2*, rice *AtNDPK2*, pepper *CaXTH3*, *Arabidopsis DREB2C*, *Arabidopsis* ftl1-1D/ddf1, rice *OsABF2*, emmer wheat (*Triticum turgidum* ssp. dicoccoides) *TdicDRF1*, barley *HvTIP1;2, HvTIP2;1, HvTIP2;2, HvTIP2;3* and *HvTIP4;1*, *Arabidopsis RAP2.6* and yeast *YCF1* genes. The studied associated genetic patterns provides bright insight useful for the application of the gene in plant abiotic stress control and improved metabolism for a better stress-resistance leading to a large productivity. Some other genes: *Brassica juncea γ-TMT*, (CaMV) 35S promoter cauliflower mosaic virus, *Oryza sativa* miRNAs, maize (*Zea mays* L.) *ZmCOI6.1*, *CaBI-1* from the cDNA library of heat-stressed hot pepper (*Capsicum annuum*), cypress seedlings (*Cupressus simper-* virens L.) cyplp009; cyplp005; cyplp006; cyplp017; cyplp010; cyplp020; cyplp012; cyplp002; cyplp007; cyplp019; cyplp003; cyplp016; cyplp008; cyplp015; cyplp021, *Bruguiera* Bg70 and cyc02 *Gymnorhiza,* pea *APX* and cassava *CuZnSOD*, maize kernel *SAT41* and *Arabidopsis MBF1a*, *Hevea brasiliensis HbMT2*, apple *cyMDH*, *Panax ginseng* PgCat1, *Citrus unshiu CitERF*, rice *OsAP2LP* and *Tamarix hispida ThbZIP1*, were extensively studied, but still provided less information on the patterns that could affect their expression and/or overexpression. Furthermore, research on abiotic control genes overexpression is gaining an advantage on the study of expressed genes. This suggests that, over- expression of genes under the control of abiotic stress may efficiently control the stresses, although, it is still of huge interest to bring out discovery of abiotic stress-related gene expression in organisms. One specific molecule, trehalose (Kidd and Devorak, 1994; Herdeiro et al*.,* 2006) is present in a wide range of organisms and expressed under stress conditions. Some genes involve in its metabolism were studied for their overexpression and found to overproduce trehalose in the control of abiotic stress.

TREHALOSE FOR ABIOTIC STRESS CONTROL IN PLANT

All major crops are sensitive to abiotic stress and sophisticated approaches for solving crops exposed to abiotic stress are therefore needed. These will require the unraveling of additional stress-associated gene resources, from crop plants, model plant and even microorganism species that are highly stress-tolerant. Most of the recent molecular studies on plant stress tolerance have used *Arabidopsis*, rice, maize, tobacco, Cypress canker, fescue, barley, Alfalfa, etc, and the microorganism *E. coli* (in addition to a limited number of microorganism). All these wide range of organisms are viewed as a potential source of trehalose. It is one specific multifunctional molecule commercially produced and that has also been successfully applied for the control of abiotic stress in yeast, bacteria and fungi as well as in plant metabolism and is still considered to be a great challenge in the field of genetic engineering (Li et al., 2008; nez-Esparza et al., 2009; Rohan et al., 2009). Trehalose expression and activity have been successfully studied in yeast as well as many other microorganisms (Herdeiro et al., 2006; Qian et al., 2010) in the control of stress response. Despite its application in industries as active stabilizer of enzymes, proteins, biomasses, pharmaceutical preparations, organs for transplantation, agri-food and cosmetic, and because of its interesting properties (Kidd and Devorak, 1994), researchers went further to study the effect of the expression of trehalose genes in plants. otsA, otsB, *TPS, TPS1* and *TPP* from *E. coli* and yeast were transformed in tobacco, potato and rice with improved growth under stress conditions (Goddijn et al., 1997; Paul et al., 2001; Holmstrom et al., 1996; Garg et al., 2002; Goddjin and Van, 1999; Romero et al., 1997). Culture media supplemented with trehalose or sucrose presented different growth abilities; protocorm-like body (PLB) derived from Phalaenopsis and Doritaenopsis cultivars, were grown on solidified trehalose amended new phalaenopsis (NP) medium and showed higher proliferation rate than on NP medium containing sucrose. Phalaenopsis and Doritaenopsis protocorm-like-bodies proliferation rates on solidified trehalose media are almost two times higher than those on sucrose media after 8-week culture (Tsu-Hwie et al., 2006).

Recently, only few reports up till now have developed the application of trehalose in plants abiotic stress control. Exogenous trehalose functioned as an elicitor of genes involved in biotic and abiotic stress. Carbohydrate alterations produced by trehalose biosynthesis can be linked to the stress response. Carolina and Francisco (2005) found that, the yeast TPS1 gene transformed in tomato plants exhibited pleiotropic changes such as thick shoots, rigid dark-green leaves, erected branches and an aberrant root development, features commonly missed in transformed plant. Additionally, leaves of transgenic TPS1 tomato plants showed that chlorophyll and starch content were higher than the wild-type plants, which was also observed in some transgenic plants in Table 2. Under drought, salt and oxidative stress TPS1 tomato plants improved tolerance than wild type, suggesting that, carbohydrate alterations produced by trehalose biosynthesis may be linked to the stress response. The TPS1 overexpression activity emerged the feasibility of engineering tomato for increased tolerance of abiotic stress, without decreasing productivity, under both stress and non-stress conditions through trehalose biosynthesis (Table 2). Some plants were transformed with the coding sequence of a gene for trehalose-6-phosphate synthase fused to a non-constitutive plant promoter, which allows for temporal, topological or stress-induced control over the expression of the gene. This protects plants against drought, high salinity or temperature extremes and improves the storage properties of harvested plants, including green food stuffs, picked fruits and ornamental plants. Although the interaction of genes are still not well understood, trehalose control genes could even be more useful in plant tissue culture as it is not only a good carbohydrate source, but also good in regulating plant growth and metabolism during stress conditions.

THE IMPORTANT SUGAR MOLECULE ALPHA-D-GLUCOPYRANOSYL-ALPHA-D-GLUCOPYRANOSIDE

Abiotic stress is the primary cause of plant loss worldwide. Therefore, resolutions from plant biotechnology discussions aiming at overcoming severe environmental stresses need to be quickly and fully implemented, with intensive molecular assisted genetic engineering. Knowledge of how to alleviate this loss is still limited due to the complexity of both the stress condition and plant responses. A number of reports provide novel and more detailed information concerning the involvement of genes and mediated signaling in stress responses. Despite many other plant stress response factors, genes and key transcription factors involved in stress tolerance can induce the specific functions of trehalose (alpha-D-glucopyranosyl-alpha-D-glucopyranoside), its degrading enzyme trehalase and associated genes that have been studied extensively and appear to be species dependent. They are present in a wide variety of organisms, including bacteria, yeast, fungi, insects, invertebrates and plants. The fundamental role of trehalose is to protect proteins and cellular membranes from inactivation or denaturation caused by a variety of stress conditions. In addition, it also has a pivotal role in regulating sugar metabolism and signal transduction pathways involved in cell proliferation and differentiation. Trehalose increases the thermostability and thermoactivity of reverse transcriptase, proteins, biomasses, pharmaceutical preparations, organs for transplantation, agri-food, cosmetic, plant tissue culture and improving the length of cDNA synthesis. It has an *in vivo* antioxidant activity and also has a potential role as part of a therapeutic strategy for treating Alzheimer’s disease. Hopefully, Parkinson's disease, Huntington's disease and amyotrophic lateral sclerosis (ALS) (also referred to as Lou Gehrig's disease, in rats) can also have possible issue of treatment through trehalose effect investigations. Hence, genes involved in the regulation of its metabolism could be viewed as an important tool in genetic engineering for stress control on one hand and disease treatment on the other hand.

In addition, several important comestibles, cosmetics, ornamental plants and many other industrially used crops are affected by abiotic stress. The overall impact of this article is to stimulate many more researchers to utilize a genetic approach, especially with interesting and promising genes combined with a better understood connection of the four complimenting areas of physiology and biochemistry to the genetic component that controls abiotic stress. This could possibly find an answer in trehalose gene control, regulation and expression. Studies of gene-related trehalose metabolism and associated patterns did not only improve the plant metabolism, phenotypes and texture (one of the problems encountered in plants genetically transformed), but in fact, provide plants that are highly resistant to abiotic stress.

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