RESEARCH PAPER

Verification of the resistance of a *LEA* gene from *Tamarix* expression in *Sac-charomyces cerevisiae* to abiotic stresses

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Abstract: The role of late embryogenesis abundant (LEA) proteins in stress tolerance was examined by using a yeast expression system. LEA protein tolerance to the abotic stresses in plants involved in salt, drought and freezing stresses and additional tolerance to heat, Na-HCO₃ (salt-alkali) and ultraviolet radiation was also investigated. The transgenic yeast harboring the *Tamarix LEA* gene (DQ663481) was generated under the control of inducible GAL promoter (pYES2 vector), yeast cells transformed with pYES2 empty vector were also generated as a control. Stress tolerance tests showed that *LEA* yeast transformants exhibited a higher survival rates than the control transformants under high temperature, NaHCO₃, ultraviolet radiation, salt (NaCl), drought and freezing, indicating that the *LEA* gene is tolerant to these abiotic stresses. These results suggest that the *LEA* gene is resistant to a wider repertoire of stresses and may play a common role in plant acclimation to the examined stress conditions.

Keywords: LEA gene; abiotic stress; transgenic yeast; stress tolerance

Introduction

Late embryogenesis abundant proteins (LEA) accumulate during the late stage(s) of embryogenesis and they are found in a wide range of plant species. These proteins are highly hydrophilic and are proposed to play a role in desiccation tolerance based on their accumulation and physicochemical properties. Many *LEA* genes were cloned from plants, including *Physcomitrella patens* (Liang et al. 2004), *Pisum sativum* (Grelet et al. 2005), *Glycine max* (Shih et al. 2005), *Capsicum annuum* (Kim et al. 2005), *Oryza sativa* (Moons et al. 1997), *Gossypium hirsutum* (Galau et al. 1993) and *Raphanus sativus* (Raynal et al. 1990). The abiotic stress tolerance of *LEA* proteins has been investigated extensively, and the resistance to stresses of freezing (Shimamura et al. 2006), drought or osmosis (Manfre et al. 2006; Goyal et al. 2005a), and salt (Chourey et al. 2003) has been also confirmed.

The yeast, Saccharomyces cerevisiae, is widely used to pro-

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duce heterologous proteins (Hasegawa et al. 2000), and it is an excellent model organism for studying the mechanisms underlying stress tolerance (Han et al. 1999; Posas et al. 2000; Serrano and Rodriguez-Navarro, 2001; Jeong et al. 2000). As the glyceraldehyde-3-phosphate dehydrogenase gene was transferred into yeast cells, and yeast transformants exhibited significantly higher resistance to cold, salt, heat, and drought stresses than controls. In addition, Mahalakshmi et al. (2006) reported that expression of the serine-rich protein gene from Porteresia coarctata conferred increasing NaCl tolerance in yeast. Wang et al. (2005) cloned the novel Ca2+-permeable channel gene, TaTPC1, from wheat and expression of TaTPC1 in a yeast mutant lacking CCH1 recovered its growth under lithium stress. Overexpression of the sugar beet *eIF1A* gene also increased the sodium and lithium salt tolerance of yeast (Rausell et al. 2003). These results illustrate that the yeast expression system is a desirable tool for studying stress tolerance gene. In the present study, we utilized yeast expression system to study the stress tolerance of the Tamarix LEA gene.

Materials and methods

Construction of the yeast expression vector and yeast transformation

Yeast strain, *S. cerevisiae* INVSc1 (His-, Leu-, Trp-, Ura-), from Invitrogen, was used for all transformation. The yeast plasmid, pYES2 (Invitrogen), with the inducible GAL1 promoter was used as an expression vector. Primers for amplifying the *LEA* gene were designed according to the sequence of the *LEA* gene (<u>DQ663481</u>) from *Tamarix*: LEA1, 5'CTAGA<u>GGTACC</u>A- TGGCTCGCTGCTCTTACTCTAAT3', (KpnI site underlined) and LEA2, 5'TCTAGCTCGAGTCAGTGAGAGGATCGATT-GAACTTG3' (XhoI site underlined). The LEA gene was amplified by PCR method using a cDNA library plasmid (pBluescript; Stratagene) containing the Tamarix LEA gene. The amplified product was digested with KpnI plus XhoI and ligated to KpnI/XhoI -digested pYES2 to construct the expression vector, pYES2-LEA. pYES2-LEA was transferred into Escherichia coli for amplification. To confirm whether the LEA gene was correctly inserted into the pYES2 vector, the plasmid was extracted from E. coli cells transformed with pYES2-LEA, and digested with KpnI and XhoI. The pYES2-LEA and control plasmid, pYES2 (empty vector), were transformed into S. cerevisiae INVSc1 using a lithium acetate method, as described in the manufacturer's protocol (pYES2, Invitrogen). The selected yeast clones were grown at 30°C in SC-ura medium (containing 2% glucose) without uracil. The transformant of empty pYES2 was used as a control.

Level of *LEA* gene expression in *S. cerevisiae* at different inducing time

Northern blot analysis was performed to determine the expression level of LEA gene at different inducing time in yeast. Yeast transformants were cultured under different conditions as follows: yeast transformants harboring LEA gene were cultured in the induction medium (SC-ura medium supplied with 2% galactose) for 3, 12, 24, 36, 48 and 60 h at 30°C and harvested for RNA isolation. The empty pYES2 transformants were cultured in the induction medium for 24 h at 30°C, then harvested as a control. Total RNA was extracted from each samples using Trizol reagent (Invitrogen) according to the manufacturer's protocol. RNA (20 µg) was dissolved in denaturing buffer (formamide: formaldehyde [37% solution]: 10 x Mops buffer, 500:162:100 [v/v/v]), heated (65°C, 15 min), fractionated on formaldehyde agarose gels, blotted on Hybond $N^{\scriptscriptstyle +}$ membranes, and fixed by UV cross-linked (254 nm, 8 min). Probe was labeled with digoxigenin (Roche) using PCR method. After prehybridization at 65°C for 2 h, the membrane was hybridized with probe for 18 h at 65°C. The washing and detection procedures were performed following the manual's instruction (Dig Northern starter kit instruction manual, Roche).

Characterizing the stress resistance of LEA gene

Yeast transformants harboring pYES2-*LEA*, or a control vector, were cultured in SC-ura liquid medium containing 2% glucose, and incubated for 24 h at 30°C. The cell densities were measured at OD600, adjusted to OD600 of 0.4 in 5 mL of induction medium (SC-ura medium supplied with 2% galactose), and incubated for 24 h at 30°C to promote further expression of the *LEA* gene. After incubation, cell densities were recalculated at OD600, and the culture samples (cells transformed with the *LEA* gene or the control) were adjusted to an equal cell number (about 1 x 10^7 cells) for the stress experiments.

To measure responses to NaCl stress, the yeast cells were in-

cubated in a 5 mol/L NaCl solution, placed at 4°C for 24 h, and diluted 100- and 1000-fold for spread plates. To measure responses to NaHCO3 stress, yeast cells were added to an 8% or 10% NaHCO₃ solution and mixed before being placed at 30°C for 8 h, and diluted 100-fold for spread plates. To calculate responses to drought stress, yeast cells were vacuumed for 8 h, treated with an 8 mol/L sorbitol solution for 24 h, and diluted 1000-fold for spread plates. To quantitate responses to high temperature stress, yeast cells were incubated for 2 or 3 h at 53°C and for measuring freezing stress, yeast cells were placed in an ethanol bath at -20°C for 24 h, and then diluted 100- and 1000-fold for spread plates. Following the above treatments, the stressed cells (100 µl) was spread on SC-Ura solid medium (supplying with 2% glucose) and incubated for 48-52 h at 30°C. To measure ultraviolet radiation stress, yeast cells were spread on SC-Ura solid medium and exposed to ultraviolet radiation at a wave length of 254 nm (100 μ J/ cm²) for 12 s or 36 s; then the plates were incubated for 48 h at 30°C. The plates were scanned and the survival rates of two samples (LEA transformed yeast cells and the control) were compared for the assay of LEA gene stress tolerance.

Results

LEA gene reached a high expression level at the induction time of 12 h to 24 h

Yeast transformants harboring the *LEA* gene were induced by galactose at different times (3, 12, 24, 36, 48 and 60 h), and analyzed by northern blot to demonstrate the presence of the RNA transcript during expression of the *LEA* gene. Northern blot results showed that the *LEA* gene was transcribed in yeast cells, with transcription reaching a high level at the induction time of 12 h to 24 h (Fig. 1).



Fig. 1 Analysis of *Tamarix LEA* gene expression in yeast cells by northern blot.

Yeast transformants harboring *Tamarix LEA* gene were induced by galactose for 3, 12, 24, 36, 48 or 60 h; CK, yeast cells transformed with empty pYES2.

Stress tolerance analysis of the *LEA* gene in transgenic yeast cells

The stress tolerance of *LEA* gene, or control transformant yeast cells was tested by treating them with a variety of stress inducers. The cells were then spread on plates, incubated for 48 h at 30°C, and the survival rates of *LEA* transformant and control cells were compared. The results showed that there was no difference in survival rate between the transgenic and nontransgenic yeast under non-stress conditions (Figs. 2–7), indicating that the transgenic and nontransgenic and nontransgenic wate. While the survival rate of the transgenic and nontransgenic \mathcal{L} Springer

yeasts varied significantly when treated with different stress.

Resistance to NaCl stress

There was no difference in survival rate between the transgenic and nontransgenic yeast under non-stress conditions. Following exposure to 5 mol/L NaCl at 4°C for 24 h, the survival rate of yeast cells transformed with the *LEA* gene was about 6-fold higher than that of the control transformants (Fig. 2), indicating that the expression of *LEA* gene enhances the salt tolerance of yeast cells.



Fig. 2 NaCl tolerance of yeast cells

Yeast cells were incubated in a 5 mol/L NaCl solution, placed for 24 h at 4°C, diluted 100- and 1000-fold, and plated on SC-Ura medium. LEA+, *LEA* transformed yeast cells; LEA-, yeast transformed with the empty pYES2; Con, untreated yeast cells; 100 x, 1000 x, cells were diluted 100-, 1000-fold and plated.

Resistance to NaHCO3 stress

Yeast cells were treated with an 8% or 10% NaHCO₃ solution and incubated at 30°C for 8 h. No difference in survival rate between the transgenic and nontransgenic yeast were found under non-stress conditions. The survival rate of *LEA* yeast transformants was significantly higher than the control transformants, especially after exposure to 10% NaHCO₃ solution (Fig. 3).



Fig. 3 NaHCO₃ tolerance of yeast cells

Yeast cells were added to an 8% or 10% NaHCO₃ solution, incubated at 30°C for 8 h, and plated on SC-Ura medium. LEA+, *LEA* transformed yeast cells; LEA-, yeast transformed with the empty pYES2; Con, untreated yeast cells.

At 8% NaHCO₃ stress the survival rate of *LEA* yeast transformants was more than 2-fold higher than that of control cells. At 10% NaHCO₃ stress, the survival rate of the *LEA* gene transformants was about 5-fold that of the control cells. The results show that the *LEA* gene has significant salt-alkali stress tolerance.

Resistance to Sorbitol stress

The vacuum-treated yeast cells were incubated in 8 mol/L sorbitol solution for 24 h at 4°C. The transgenic and nontransgenic yeast were shown as Fig. 4. The cells were then diluted 1000-fold and plated on medium. The survival rate of the *LEA* transformed yeast cells was about 2.4-fold that of control cells, showing that expression of *LEA* gene enhances the drought tolerance of yeast cells.

Fig. 4 Drought resistance of yeast cells

Yeast cells were treated with 8 mol/L sorbitol solution for 24 h and plated on SC-Ura medium. LEA+, *LEA* transformed yeast cells; LEA-, yeast transformed with the empty pYES2; Con: untreated yeast cells; 1000X: cells were diluted 1000 fold and plated.



Ultraviolet radiation stress resistance

The yeast cells were treated with ultraviolet radiation (100 μ J/cm²⁾ for 12 s or 36 s. Although *LEA* transformed and control yeast cells all suffered serious injury, the survival rate of *LEA* transgenic cells was about 2-fold greater than that of the control cells when exposed to ultraviolet radiation for 12 s. After exposed to ultraviolet radiation 36 s, there were 9 colonies of *LEA* transformants in plate, while only 1 colony of control was found (Fig. 5). These results suggest that the *LEA* gene also has ultraviolet radiation stress resistance.



Fig. 5 Ultraviolet radiation resistance of yeast cells.

Yeast cells were spread on SC-Ura solid medium and exposed to ultraviolet radiation (254 nm, 100 μ J/ cm²) for 12 s or 36 s, incubated for 48 h at 30°C. LEA+, *LEA* transformed yeast cells; LEA-, yeast transformed with the empty pYES2; Con, untreated yeast cells.

High temperature (53 °C) stress resistance

Yeast cells were incubated at a 53°C water batch for 2 h and 3 h, and plated on culture medium. No differences between *LEA* transformed and control cells were found under non-stress condition. However, after 2 h and 3 h, the *LEA* transformed cells exhibited significantly higher survival rates than the control cells (Fig. 6). After the 3-h incubation, the survival rate of *LEA* transgenic cells was more than 10-fold greater than that of the control cells. The results clearly indicate that the *LEA* gene induces high tolerance to heat.



Fig. 6 High temperature resistance of yeast cells

Yeast cells were incubated at 53°C for 2 or 3 h and plated on medium. LEA+, *LEA* transformed yeast cells; LEA-, yeast transformed with the empty pYES2; Con, untreated yeast cells

Freezing stress resistance

After incubation in a -20°C alcohol bath for 24 h, the yeast cells were diluted 100- and 1000-fold and plated on SC-Ura culture medium. The survival rate of *LEA* transgenic cells was about 3-fold greater than that of the control cells, indicating that the *LEA* gene enhances the freezing tolerance of yeast cells (Fig. 7).



Fig. 7 Freezing tolerance of yeast cells

Yeast cells were placed in an ethanol bath for 24 h at -20°C and diluted 100or 1000-fold for spread plates. LEA+, *LEA* transformed yeast; LEA-, yeast transformed with the empty pYES2; Con, untreated yeast cells; 100 X, 1000 X, cells were diluted 100-, 1000 fold and plated.

Discussion

The precise role of LEA proteins is not fully defined (Goyal et al. 2005a), although their various functions have been proposed. It is thought that LEA proteins confer stress resistance by stabilizing membranes and protein structures (Serrano and Montesinos 2003; Danyluk et al. 1998; Grelet et al. 2005; Babu et al. 2004); preferentially hydrating at moderate desiccation and replacing water at extreme desiccation (Serrano and Montesinos 2003). LEA proteins can also adopt certain structures by interacting with macromolecules from other plants, thus promoting protection from stress-induced damage (Soulages et al. 2002). Goyal et al. (2005b) found that LEA proteins can act as molecular chaperones or shields that might prevent irreversible protein aggregation. Goyal et al. (2005a) further illustrated that LEA proteins can prevent aggregation by binding to non-native proteins, and maintaining them in a folding competent state. In addition, LEA proteins are shown to sequester ions, protecting enzymes from desiccation, and replacing water (Grelet et al. 2005) when the plant is under stress-inducing conditions. These studies primarily focus on LEA protein tolerance to the abotic stresses of salt, drought and freezing in plants. We confirm that the Tamarix LEA gene is tolerant to these stresses and illustrate that it has additional tolerance to heat, NaHCO3 (salt-alkali) and ultraviolet radiation.

Our study shows that expression of the *Tamarix LEA* gene confers heat tolerance and enhances the survival of yeast cells. *Tamarix* can endure a high temperature in desert, implying that they have developed an efficient heat resistance system. Through this study, we suggest that the *LEA* gene may contribute to heat stress resistance in *Tamarix*. High temperature stress affects plant growth and development and is a common environmental stress to plants in summer season. The finding and study of heat tolerance gene will be helpful for us to enhance the heat stress tolerance of plants by genetic methods.

Our study also shows that the *LEA* protein has NaHCO₃ tolerance. Expression of the *LEA* gene in yeast cells significantly enhanced their survival rate in response to NaHCO₃ stress. Thus, it appears to be an attractive candidate gene in improving plant salt-alkali tolerance by genetic engineering. The ability to make transgenic plants with tolerance to salt-alkali stress has important implications. According to incomplete statistics of UNESCO and FAO, 950 million ha (6.4%) of the world's land area has saline-alkali soil (Zhang et al. 2006). In saline-alkali soil, plants endure concomitant saline and alkali stress; consequently it is difficult to grow in the saline-alkali soil. The *Tamarix LEA* gene has high saline-alkali resistance, and may be used to genetically engineer plants that will survive these soil conditions.

The studies confirmed that the *LEA* gene was tolerant to many kinds of environmental stress, suggesting that the *LEA* gene may contribute to the ability of adapting to stressful environments of plants. This study improves our understanding of how the *LEA* gene functions during stress, and has implications for the genetic engineering of plants with enhanced stress tolerance.



References

- Babu RC, Zhang JX, Blum A, Ho THD, Wu R, Nguyen HT. 2004. HVA1, a *LEA* gene from barley confers dehydration tolerance in transgenic rice (*Oryza sativa* L.) via cell membrane protection. *Plant Sci*, **166**(4): 855–862.
- Chourey K, Ramani S, Apte SK. 2003. Accumulation of LEA proteins in salt (NaCl) stressed young seedlings of rice (*Oryza sativa* L.) cultivar Bura Rata and their degradation during recovery from salinity stress. *J Plant Physiol*, 160(10): 1165–1174.
- Danyluk J, Perron A, Houde M, Limin AE, Fowler DB, Benhamou N, Sarhan F. 1998. Accumulation of an acidic dehydrin in the vicinity of the plasma membrane during cold acclimation of wheat. *Plant Cell*, **10**(4): 623–638.
- Galau GA, Wang HY, Hughes DW. 1993. Cotton Lea5 and Lea14 encode atypical late embryogenesis-abundant proteins. *Plant Physiol*, 101(2): 695–696.
- Grelet J, Benamar A, Teyssier E, Avelange-Macherel MH, Grunwald D, Macherel D. 2005. Identification in pea seed mitochondria of a late-embryogenesis abundant protein able to protect enzymes from drying. *Plant Physiol*, **137**(1): 157–167.
- Goyal K, Walton LJ, Tunnacliffe A. 2005a. LEA proteins prevent protein aggregation due to water stress. *Biochem J*, 388, 151–157.
- Goyal K, Walton LJ, Browne JA, Burnell AM, Tunnacliffe A. 2005b. Molecular anhydrobiology: identifying molecules implicated in invertebrate Anhydrobiosis. *Integr Comp Biol*, 45(5): 702–709.
- Han Y, Wilson DB, Lei XG. 1999. Expression of an aspergillus niger phytase gene (phyA) in *Saccharomyces cerevisiae*. Appl Environ Microbial, 65(5): 1915–1918.
- Hasegawa PM, Bressan RA, Zhu JK, Bohnert HJ. 2000. Plant cellular and molecular responses to high salinity. *Annu Rev Plant Physiol Plant Mol Biol*, 51: 46–499.
- Jeong MJ, Park SC, Kwon HB, Byun MO. 2000. Isolation and characterization of the gene encoding Glyceraldehyde-3-Phosphate Dehydrogenase. *Biochem Biophys Res Commun*, 278(1): 192–196.
- Kim HS, Lee JH, Kim JJ, Kim CH, Jun SS, Hong YN. 2005. Molecular and functional characterization of *CaLEA6*, the gene for a hydrophobic LEA protein from *Capsicum annuum*. *Gene*, **344**: 115–123.
- Liang CY, Xi Y, Shu J, Li J, Yang JL, Che KP, Jin DM, Liu XL, Weng ML, He YK, Wang B. 2004. Construction of a BAC library of *Physcomitrella patens* and isolation of a *LEA* gene. *Plant Sci*, **167**(3): 491–498.

Mahalakshmi S, Christopher GS, Reddy TP, Rao KV, Reddy VD. 2006. Isola-

tion of a cDNA clone (PcSrp) encoding serine-rich-protein from *Porteresia coarctata* T. and its expression in yeast and finger millet (*Eleusine cora-cana* L.) affording salt tolerance. *Planta*, **224**(2): 347–359.

- Manfre AJ, Lanni LM, Marcotte Jr, WR. 2006. The Arabidopsis group 1 LATE EMBRYOGENESIS ABUNDANT protein ATEM6 is required for normal seed development. *Plant Physiol*, **140**(1): 140–149.
- Moons A, De KA, Van MM. 1997. A group 3 LEA cDNA of rice, responsive to abscisic acid, but not to jasmonic acid, shows variety-specific differences in salt stress response. *Gene*, **191**: 197–204.
- Posas F, Chambers JR, Heyman JA, Hoeffler JP, de Nadal E Arino J. 2000. The transcriptional response of yeast to saline stress. *J Biol Chem*, 275(23): 17249–17255.
- Rausell A, Kanhonou R, Yenush L, Serrano R, Ros R. 2003. The translation initiation factor eIF1A is an important determinant in the tolerance to NaCl stress in yeast and plants. *Plant J*, 34(3): 257–267.
- Raynal M, Gaubier P, Grellet F, Delseny M. 1990. Nucleotide sequence of a radish cDNA clone coding for a late embryogenesis abundant (LEA) protein. *Nucleic Acids Res*, 18(20): 6132.
- Serrano R, Montesinos C. 2003. Molecular Bases of Desiccation Tolerance in plant cells and potential applications in food dehydration. *Food Sci Technol Int*, 9(3): 157–161.
- Serrano R, Rodriguez-Navarro A. 2001. Ion homeostasis during salt stress in plants. *Curr Opin Cell Biol*, **13**: 399–404.
- Shao HB, Liang ZS, Shao MA. 2005. LEA proteins in higher plants: Structure, function, gene expression and regulation. *Colloids Surf B Biointerfaces*, 45(3-4): 131–135.
- Shih MD, Lin SC, Hsieh JS, Tsou CH, Chow TY, Lin TP, Hsing YI. 2004. Gene cloning and characterization of a soybean (*Glycine max* L.) LEA protein GmPM16. *Plant Mol Bio*, 56: 689–703.
- Shimamura C, Ohno R, Nakamura C, Takumi S. 2006. Improvement of freezing tolerance in tobacco plants expressing a cold-responsive and chloroplast-targeting protein WCOR15 of wheat. J Plant Physiol, 163: 213–219.
- Soulages JL, Kim K, Walters C, Cushman JC. 2002. Temperature-Induced extended Helix/Random coil transitions in a group 1 late embryogenesis-abundant protein from Soybean. *Plant Physiol*, **128**(3): 822–832.
- Wang YJ, Yu JN, Chen T, Zhang Z, Hao Y, Zhang J, Chen S. 2005. Functional analysis of a putative Ca²⁺ channel gene TaTPC1 from wheat. *J Exp Bot*, **56**(422): 3051–3060.
- Zhang XX, Takano T, Liu SK. 2006. Identification of a mitochondrial ATP synthase small subunit gene (*RMtATP6*) expressed in response to salts and osmotic stresses in rice (*Oryza sativa* L.). J Exp Bot, 57(1): 193–200.