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Protective Role of Trehalose and LEA Proteins against Abiotic Stresses: Comparative Study in Transgenic Chinese Cabbage(*Brassica campestris*) Overexpressing *Calea* and *otsA*

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Trehalose, a non-reducing disaccharide of two glucose units, and LEA proteins heavily synthesized during the desiccation phases of seed development are both known to protect plants from drought stress. To compare their effectiveness on enhancing tolerance against various abiotic stresses, we generated transgenic Chinese cabbage overexpressing *E. coli* trehalose-6-phosphate synthase gene (*otsA*) and hot pepper (*Capsicum annuum*) LEA genes (*Calea*). Both of these transgenic plants exhibited altered phenotype including stunted growth and aberrant root development. However, when subjected to drought, heat or salt stress, these plants showed remarkably improved tolerance against these stresses compared with nontransformants. After dehydration treatment for 4h, leaf fresh weight of nontransformants decreased about 45% while that of trehalose-producing plants or LEA protein-producing plants decreased less than 15% or 30%, respectively. After heat-treatment at 45℃ for 4h, Fv/Fm decreased more than 80% in nontransformants while it decreased about 30% in trehalose-producing plants and less than 20% in LEA protein-producing plants. After sustained growth under the supplementation of 300 mM NaCl, both trehalose-producingplants and LEA protein-producing plants remained healthier than nontransformants showing less leaf chlorosis. Futhermore, Fv/Fm decreased much less than nontransformants. However, no significant difference was observed between these two transgenic plants.

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A Novel *Arabidopsis* Gene *AtAsT1* Decreases Arsenic Accumulation in *Saccharomyces cerevisiae*

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Arsenic (As) is a major pollutant which contaminates air, land and water. The first step toward developing As-phytoremediators and As-tolerant crops is to understand molecular mechanism of As-tolerance in plants. Arsenite-sensitive mutant yeast AsS5 was isolated from mini-Tn mutagenized pools of S. cerevisiae. To clone plant genes involved in tolerating As, AsS5 was transformed with the yeast expression library of *Arabidopsis*, and surviving transformants were selected on agar media containing inhibiting concentration of arsenite. A plasmid was isolated from the surviving transformant, and an insert was sequenced and named *AtAsT1* (458 aa). To confirm the role of *AtAsT1* it was over-expressed in AsS5 and WT (Y800). When *AtAsT1* was over-expressed in AsS5 mutant, As-tolerance increased but As accumulation decreased. However, over-expression of *AtAsT1*in WT did not alter As tolerance and accumulation. Currently we are generating transgenic plants. Taken together, it is concluded that a novel gene of *Arabidopsis*, *AtAsT1*, plays a role in decreasing As accumulation in S. cerevisiae. This gene will be applied to producing low-metal accumulating crops and metal phytoremediators using an antisense technique.

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Optimum Condition for Supension Culture of Callus from *Rhodiola sachalinensis A. Bor*

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Callus of *Rhodiola sachalinensis* were induced from leaf explants on 1/2MS solid medium combined treatments of auxin (2.4-D, NAA: 0.1-2 mg/L) and cytokinin (BA: 0.1-0.2 mg/L). The effects of various basal medium, culture conditions and phytohormones on the growth of *R. sachalinensis* callus were investigated. MS, WPM, B5 medium and each diluted/concentrated meida (1/2X, 2X, 3X) were used to investigate the growth of callus on each media. Among the madia tested, 2B5 medium was the best for the callus growth. Also, When the callus were cultured on 2B5 medium containing 0.5 mg/L NAA and 1 mg/L BA, the highest growth rate was observed. We investigated the culture condition such as pH, sucrose, light, phosphate and nitrogen concentration to increase the growth rate of callus which induced from leaf of *R. sachalinensis*. The best results of the callus culture conditions were determined for carbon source (3% of sucrose), pH (6.0), phosphate (2.16 mM of NaH_2PO_4), nitrate (49.6 mM of KNO3, 2.0 mM of $(NH_4)_2SO_4$) at 25℃ in the dark.

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Plant Telomere Binding Proteins Have Expanded DNA Binding Domain

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Telomeres are protein-DNA complexes that protect chromosome ends from being recognized and processed as DNA breaks. Plant telomeres contain long tandem arrays of double-stranded TTTAGGG repeats that are maintained by the telomerase and act as binding sites for telomere binding proteins (TBPs). The TBP families have similar architectures, defined by their sequence features. These proteins have C-terminal DNA binding motifs that are closely related to the Myb/homeodomains. We have identified three new proteins containing telomeric binding motifs in *Arabidopsis* genome. AtTBP2, AtTBP3/AtTRP1,and AtTBP4 have a single Myb telomeric DNA binding domain (SMTBD) at the C-terminus and show an extensive sequence homology with AtTBP1. The expressed C-terminal of these proteins were capable of binding sequence-specific DNA to plant duplex telomeric DNAand their binding properties were similar to each other. AtTBPs consist of five unidentified conserved domains, NLS, and SMTBD. Among those, domain E is located adjacent to the SMTBD and is highly conserved. Studies of deletion mutants of AtTBP1's domain E demonstrated the importance of domain E besides SMTBD for binding to plant telomeric DNA. These results suggest that *Arabidos*is have at least four TBPs with similar functions. Moreover, plant TBPs have expanded DNA binding domain compared with hTRF1. [Supported by grant from KRF (2002-015-DP0415)]