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Functional analysis of galactinol synthase in *Arabidopsis* in stress response

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Raffinose family oligosaccharides (RFO) is thought to function as an osmoprotectant when plants are exposed to drought, high salinity and cold stresses. Galactinol synthase catalyzes the first committed step in the biosynthesis of RFO and plays a key regulatory role in the carbon partitioning between sucrose and RFO in developing seeds.

To analyze the role of RFO in stress tolerance, we cloned six cDNAs encoding galactinol synthase of *Arabidopsis* and named them *AtGalS1* to *6*. Northern blot analysis was performed to investigate stress (dry, cold, NaCl, sorbitol)-responsive and tissue-specific gene expression. *AtGalS1* and *AtGalS2* were induced by these stresses within 1h. A strongly hybridizing band was detected in seed for *AtGalS1* and *AtGalS2*. Sugar analysis showed that drought or high salinity treated plants contain a very large amount of raffinose, which is barely detectable in non-stressed plant. Also, sugar analysis of mature seeds showed that they contained large amounts of stachyose rather than like other plant species.

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The DREB family of genes in Rice, *Oryza sativa*

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The DREB family of transcription factors bind specifically to a *cis*-acting element (DRE/CRT) in *A. thaliana*. They have been shown to play key roles in orchestrating the plant's response to stress factors such as cold, drought and salinity. Cloning of similar genes in rice may be a prerequisite for the development of superior transgenic cultivars that can withstand or thrive in adverse environments. Here we report the characteristics of the corresponding DREB homologues in rice, Os (*Oryza sativa*) DREB1A, 1B and OsDREB2 cDNA from rice.

OsDREB1A was isolated from cDNA libraries constructed from cold- and salt-stressed 3-week-old rice plants whereas OsDREB1B was obtained as an EST clone from the Rice Genome Project. Both genes show extensive similarity to *Arabidopsis* DREB1A (AtDREB1A), especially in a portion of their N-terminal regions and in their ERF/AP2 domains. OsDREB1A, like AtDREB1A, is upregulated in plants exposed to cold. OsDREB2 was obtained from a cDNA library constructed from drought-stressed, 3-week-old rice seedlings. The putative amino acid sequences of *Arabidopsis* DREB2A (AtDREB2A) and OsDREB2 also show extensive similarity especially in a portion of their N-terminal regions and in their ERF/AP2 domains. Similar to AtDREB2A, OsDREB2 is induced by drought and salinity but not by cold exposure. The extensive conservation of protein sequence and stress-response characteristics of these DREB proteins indicate their fundamental function in plant stress physiology. The OsDREB genes in this report may play an important role in the production of superior transgenic rice plants that are resistant to multiple stress environments.

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MONITORING GENE EXPRESSION PATTERN UNDER DEHYDRATION AND COLD STRESS USING ARABIDOPSIS FULL-LENGTH cDNA MICROARRAY

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We prepared a *Arabidopsis* full-length cDNA microarray using ca. 1300 full-length cDNAs including drought-inducible genes. The cDNA microarray was used to identify drought- and cold- inducible genes, and target genes of DREB1A, a transcription factor that controls stress-inducible gene expression. The *rd29A, cor15a, kin1, kin2, rd17, and erd10* genes were also identified as DREB1A target genes using the cDNA microarray, which confirmed the previous report. Also, several genes, such as a homolog of wheat putative cold acclimation protein, were identified as novel drought- and cold- inducible genes, and DREB1A target genes. These results show that our full-length cDNA microarray is a useful material to analyze expression pattern of *Arabidopsis* genes under dehydration and cold stress and to identify target genes of stress-related transcription factors.

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ANALYSIS OF TISSUE SPECIFICITY OF ICE PLANT *MCMIPA* PROMOTER

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A number of genes for a plasma membrane-localized water channel (PIP-aquaporin) have been found in higher plants. Some of them were found to be different in tissue specificity and/or responses to environmental condition changes. We wished to compare tissue- and cell-specific expression of *McMipA*, an abundantly expressed PIP from the common ice plant (*Mesembryanthemum crystallinum*), to that of the previously characterized *McMipB*.

A 2.2kb DNA fragment containing the promoter region of *McMipA* in a fusion with the GUS coding region was studied in transgenic tobacco. The *McMipA* promoter was active in pericycle and cortex cells in roots and in phloem-associated cells and cells surrounding the pericycle in shoots. In green leaves, mesophyll cells and the minor veins showed GUS activity, however the major veins did not. In floral tissues, GUS activity was observed in pistils and anthers of immature buds and tips of mature pistils and pollens. No GUS activity was observed in apical meristems and root tips. The differences in tissue specificity between the *McMipA* and *McMipB* promoters indicated that the two PIPs, MC-MIPA and MC-MIPB, serve different functions in plants.