

Plant Gene Register

ERD15, a cDNA for a Dehydration-Induced Gene from *Arabidopsis thaliana*¹

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Dehydration is one of the most common environmental stresses in higher plants, and elicits multiple physiological and metabolic changes within them. Recently, plants have been found to activate new gene sets to counteract the detrimental effects of dehydration (Skriver and Mundy, 1990; Vernon and Bohnert, 1992; Delauney and Verma, 1993).

ERD15 is a member of a set of cDNAs for dehydration-stress-induced genes in *Arabidopsis thaliana* (Kiyosue et al., 1994). The level of mRNA for ERD15 is higher in dehydrated plants within 1 h of stress onset and remains elevated for up to 24 h. The nucleic acid sequence of ERD15 contains 760 bp with an open reading frame encoding a 163-amino acid polypeptide (Table I). This deduced polypeptide is hydrophilic, with 49 charged residues out of 163, and lacks a Cys residue. The estimated mol wt of the polypeptide is 18,411. The ERD15 sequence is 61.4% homologous at the nucleotide level to the fragment of a rice cDNA expressed sequence tag from the callus (accession number of D22278).

Table I. Characterization of ERD15 cDNA

| | |
|----------------------------------|--|
| Organism: | <i>Arabidopsis thaliana</i> L. (Columbia ecotype). |
| Source: | cDNAs obtained from a cDNA library in λ ZAPII constructed from poly(A) ⁺ RNA of 1-h dehydrated rosette plants by differential screening using cDNAs of rosette plants before or after dehydration stress. |
| Technique: | Deletion subcloning and complete double-stranded cDNA sequence by dideoxy sequencing. |
| Sequence Comparison: | Comparison to GenBank/EMBL Nucleotide Sequence data base and the Swiss Prot Protein Sequence data base using FASTA computer programs. There was 61.4% identity to a rice expressed sequence tag from the callus in a 241-bp overlap. |
| Features of the cDNA: | The ERD15 cDNA contains 760 nucleotides including 5' and 3' untranslated regions (polyadenylated tail present) and an open reading frame 489 nucleotides in length. |
| (G + C) Content: | 42.24% (47.03% in the coding region). |
| Expression Characteristics: | The accumulation of the corresponding mRNAs was stimulated in whole plants by dehydration stress. |
| Features of the Deduced Protein: | 163 amino acid residues (<i>M</i> , 18,411); an isoelectric point of 4.36. |

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The GenBank/EMBL accession number for the sequence reported in this article is D30719.

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