Nucleotide Sequence of an Abscisic Acid-Responsive, Embryo-Specific Maize Gene

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We report here the nucleotide sequence of an ABA-responsive, embryo-specific gene from Zea mays L (Table I). This gene, referred to as Emb5, was obtained from a maize embryo cDNA library using differential hybridization, with radiolabeled mRNA from seedlings and from embryos as probes. The sequence of 431 nucleotides contains an open reading frame of 110 codons (Fig. 1). The predicted amino acid sequence of Emb5 is very hydrophilic, is rich in glycine and glutamate, and contains no cysteine, tryptophan, or asparagine. The predicted amino acid sequence of Emb5 was found to share significant similarity with mid- to late-embryogenesis genes from maize (6), wheat (2), cotton (1), radish (3), and carrot (5), exhibiting amino acid identity ranging from 54 to 76%. A distinct feature of the Emb5 protein is a tandem duplication of a 20-amino acid segment that is absent in the five homologs.

LITERATURE CITED


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Figure 1. Nucleotide sequence of Emb5. The DNA and predicted amino acid sequence are numbered from the first nucleotide in the clone and the first methionine, respectively. The asterisks indicate the termination codon. Both strands were sequenced by the method of Sanger et al. (4). Arrows indicate imperfect tandem repeats.
Table I. Characteristics of Emb5, a cDNA from Maize Embryos

Organism:
Zea mays.

Method of Identification:
Hybridization with radiolabelled seedling mRNA and embryo mRNA as probes (1).

Techniques:
Isolation of cDNA clone from pBR322 library; dideoxy sequencing (6) of both strands using double-stranded pBR322 templates and single-stranded templates isolated from BlueScript (Stratagene) subclones.

Location of Gene:
Nuclear.

Expression Characteristics:
A 0.8-kb transcript was first detected in 10-mg embryos, reached maximum steady-state concentration in 20- to 30-mg embryos, and then declined gradually during maturation. Emb5 transcript is not detected in vegetative tissues (northern analysis).

Regulation:
Precociously accumulated in embryos treated with ABA.

Codon Usage:
Codon third position = 92.6% G + C; open reading frame = 69.7% G + C.

Structural Features of Protein:
An open reading frame encodes a 110 amino acid protein with a predicted molecular mass of 11941 Da and a predicted pl 5.51.
Imperfect tandem repeats: Gln^{44}-Gly^{63}, Gln^{44}-Gly^{83}

GenBank Accession Number:
M90554.