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Plant Gene Register

Tomato (*Lycopersicon esculentum*) Genomic Clone Homologous to a Gene Encoding an Abscisic Acid-Induced Protein

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The plant hormone ABA is involved in a number of important physiological and developmental processes including the response of vegetative tissues to osmotic stress and fruit ripening (Davies and Mansfield, 1983). We report here the main structural features of a gene termed *Asr2* (Table I), homologous to *Asr1* (standing for ABA, stress, and ripening), whose cDNA has been previously characterized (Iusem et al., 1993). *Asr1* is induced by ABA, water deficit, and ripening as demonstrated by independent hybridization with RNA from water-deficit and ABA-induced plants as well as RNA from immature, mature, and ripe fruit (our unpublished results). The genomic sequence reported here contains 935 nucleotides, starting 131 nucleotides upstream of the translation initiation codon. Two exons were identified: one comprising nucleotides 132 to 290 and another between nucleotides 402 and 551; these were separated by an intervening sequence. The coding region shows 73% homology with the *Asr1* cDNA sequence, resulting in an overall homology of 85% at the protein level. This probably indicates that *Asr1* and *Asr2* are different members of a gene family.

This gene family enlarges the list of the known ABA-responsive genes (Skriver and Mundy, 1990). Further sequencing of upstream regions from *Asr2* will enable us to identify 5′ regulatory elements involved in ABA-mediated responses in tomato. In monocots, *cis*-regulatory elements have been demonstrated to be functional in ABA-responsive genes from wheat (Marcotte et al., 1989), rice (Mundy et al., 1990), and maize (Vilardell et al., 1991). In some cases, those elements helped characterize specific nuclear DNA-binding proteins that mediate responses to ABA (Guiltinan et al., 1990; Mundy et al., 1990; Pla et al., 1993). It is interesting that the product of *Asr1* itself is a nuclear basic protein that binds DNA (P.A. Scolnik, unpublished results from south-western and filter-binding experiments done with the protein overexpressed in *Escherichia coli*) and therefore might, in turn, modulate gene expression.

Confirming the universality of suggested consensus motifs involved in ABA responses such as CCACGTGG (Pla et al., 1993), as well as the finding of new genomic regulatory elements, will allow a deeper understanding of the molecular mechanisms by which ABA transcriptionally regulates gene expression in plants.

Table I. *Characteristics of Asr2*

Organism:
Lycopersicon esculentum cv Ailsa Craig.
Gene Designation:
Asr2.
Source:
Obtained from a tomato genomic library constructed in EMBL3 by Clontech (Palo Alto, CA) using *Asr1* cDNA (Iusem et al., 1993) as a probe.
Techniques:
Sequences were obtained by dideoxy-DNA sequencing of both strands.
Method of Identification:
Sequence comparison with *Asr1* cDNA (73% nucleotide homology to coding region of genomic clone; 85% homology at the amino acid level).
Features of Gene Structure:
Genomic sequence containing exon 1 from nucleotides 132 to 290 and exon 2 from nucleotides 402 to 551. A 111-bp intron between nucleotides 291 and 401 conforming to the GT-AG rule was identified.
Gene Copy Number:
One per haploid genome.
Location on Chromosome:
Unknown.
(G + C) Content:
Overall, 34.2%; within coding regions, 45.6%.
Expression and Characteristics of the Encoded Protein:
See Iusem et al. (1993).

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The GenBank accession number for the sequence reported in this article is L20756.

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