

Plant Gene Register

Tomato (*Lycopersicon esculentum*) Transcript Induced by Water Deficit and Ripening

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Tomato (*Lycopersicon esculentum*) fruit ripening is a developmental process that involves changes in color, texture, and flavor (Maunder et al., 1987). Both ethylene and ABA play a role in this process. On the other hand, ABA is known to repress expression of certain photosynthesis-related gene families during the leaf water deficit response (Bartholomew et al., 1991). We explored whether this repression was accompanied by common activation of gene expression. We report here the characterization of a cDNA (Table I) for a gene that encodes a novel chromosomal protein whose expression is activated by leaf water deficit and fruit ripening.

The reported cDNA encodes a 13-kD basic protein rich in Ala, Glu, His, and Lys (Table I). This protein was overproduced in *Escherichia coli* and was used to raise antibodies, which recognized a protein of the same size in water-stressed leaves and fruit pericarp.

Except for the N-terminal region, which is similar to short His-rich stretches of other eukaryotic proteins (Celenza and Carlson, 1986; Nagafuchi et al., 1987; Wolin et al., 1987), the protein sequence reported here exhibits no overall similarity with those of other proteins. However, this protein resembles eukaryotic nonhistone chromosomal proteins, which are abundant and basic and bind DNA (Goodbourn, 1990).

The results of subcellular fractionation experiments indicate that the protein is located primarily in the nucleus. No information concerning the function of the protein is yet available. However, biological roles for this protein are suggested based on the function of similar proteins in eukaryotes, which are involved in changes in DNA topology and in establishing or maintaining a high-order chromatin structure (Zlatanova, 1990).

Together with previous information, the results reveal similarities in both activation and repression of nuclear gene expression by water deficit and by fruit ripening, a developmental process. Overlapping in gene expression during stress and development has previously been observed for other plant genes. For instance, genes involved in pathogenesis and wounding responses are also expressed during flowering in undamaged plants (Gasser, 1991).

Table I. Characteristics of the water deficit- and ripening-specific cDNA from tomato fruit encoding a chromosomal protein

Organism:

Lycopersicon esculentum cv Ailsa Craig.

Techniques:

Tomato fruit genomic library in λ gt11 was screened by differential hybridization. Sequences were obtained by dideoxy DNA sequencing of both strands.

Characteristics of the cDNA:

cDNA of 780 nucleotides encoding an open reading frame of 116 codons with a consensus G at position 85 right after the translation initiation codon (Lütcke et al., 1987). The 5' noncoding region is 81 nucleotides long, is full-length, and contains a putative short loop from nucleotide 54 to nucleotide 72. The 3' noncoding end is 351 nucleotides long and contains a canonical polyadenylation site at nucleotide 744 as well as a poly(A) tail.

Gene Copy Number:

One per haploid genome.

Characteristics of the Deduced Amino Acid Sequence:

The open reading frame encodes a 13-kD protein rich in Ala (13%), Glu (15%), His (15%), and Lys (17%). The predicted isoelectric point for the protein is 7.9.

Homology with Other Proteins:

The N-terminal region is similar to short His-rich stretches of other eukaryotic proteins.

Expression:

Abundant transcript in ripe fruit (approximately 5% of total mRNA). Moderately abundant transcript in leaves under water deficit.

Antibodies:

Available. Raised in rabbits from protein overproduced in *E. coli*.

Subcellular Localization of the Protein:

Nuclear. Antibodies detected the protein in fruit chromatin fractions from Rheilands Rhum variety.

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The GenBank accession number for the sequence reported in this article is L08255.

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