**Plant Gene Register**

**Deduced Amino Acid Sequence of a Plant cDNA Containing a Leucine Zipper Motif**

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We screened a tomato (*Lycopersicon esculentum* L.) cDNA library (1.3 × 10⁶ plaque-forming units [7]) with a polymerase chain reaction fragment that was thought to be a specific probe for a shikimate dehydrogenase, and we isolated 11 independent clones (Table 1). The cDNA inserts were subcloned into pSK+ (Stratagene) and sequenced from the 3' end. All 11 clones contained the same sequence, and the clone with the largest insert (called sgut1) was sequenced completely (Fig. 1). The cDNA without the polyadenylation tail has a length of 2096 bp and contains an open reading frame from its 5' end to bp position 1902. The first ATG triplet at position 10 is situated in this open reading frame, and the sequence around it (TATCCATGGCT) shows homology to the consensus sequence around plant initiation codons (TAACAATGGCT [3]), which suggests that the cDNA is a full-length clone encoding a polypeptide of 631 amino acids. The function of this protein is unknown, and a sequence comparison to the EMBL data base revealed no similarity to known proteins. Searching for protein motifs using the University of Wisconsin Genetics Computer Group program package (Motifs, version 7.0) led to the identification of a potential leucine zipper. A certain class of DNA-binding protein contains leucine zippers that are responsible for dimerization of transcription factors by the formation of coiled-coil structures (2, 4). The DNA-binding domain of these proteins is normally a basic domain that is in close proximity to the leucine zipper (1). However, no such basic domain could be identified in the deduced sgut1 sequence. It contains a very acidic region of six glutamic acid residues followed by one valine and seven aspartic acid residues (Fig. 1; amino acid position 157–170), which for no function is known. The sgut1 peptide contains an unusually high amount of charged residues (Asp + Glu = 16%; His + Lys + Arg = 15%).

**Table 1. Characteristics of cDNA sgut1 from Tomato**

Organism: *Lycopersicon esculentum* L., cv UC82b.

Techniques:
- cDNA library screening (5), restriction fragment subcloning (5), complete dideoxy sequencing of both strands (6).

Sequence Comparison:
- Comparison to EMBL data base by use of the University of Wisconsin Genetics Computer Groups programs.

No sequence homology observed. Putative leucine zipper identified.

Features of cDNA Structure:
- Potential translational start site at nucleotide 10 and stop site at nucleotide 1903. Polyadenylation signal (AATACT) at nucleotide 2038.

Structural Features of Deduced Amino Acid Sequence:
- Coding region codes for a polypeptide of 631 amino acids with a calculated mol wt of 71,792 and a predicted isoelectric point of 5.2. The sequence has no homology to known sequences. It contains a leucine zipper motif between amino acids 109 and 130 and a very acidic region of six Glu and seven Asp separated by a single Val (position 157–170).

EMBL Accession No.:
Z12127.

**LITERATURE CITED**


Plant Physiol. (1992) 100, 1609–1610

Received for publication June 3, 1992

Accepted July 10, 1992
Figure 1. Nucleotide sequence and deduced amino acid sequence of sgut1. The putative leucine zipper is underlined.