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Plant Gene Register

Nucleotide Sequence of a cDNA Encoding a Pathogenesis-Related Protein, P1-p14, from Tomato (*Lycopersicon esculentum*)

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We report the sequence of a cDNA clone, pTE 28.1, corresponding to a tomato (*Lycopersicon esculentum*) pathogenesis-related protein mRNA. It was selected from an ethylene-treated tomato leaf cDNA λZAP II library screened by differential hybridization with single-stranded cDNA probes prepared from untreated and ethylene-treated leaf poly(A$^+$) RNA. The pTE 28.1 cDNA clone is 711 bp long. The open reading frame encodes a precursor protein of 159 amino acids, and the molecular mass of the deduced protein is similar to that predicted by in vitro translation-immunoprecipitation experiments (Vera et al., 1989). The first 24 amino acids represent a signal peptide that is processed to render the mature protein as previously described (Vera et al., 1989). The deduced protein sequence from the pTE 28.1 cDNA contains five additional amino acid residues (Trp-Arg-Asn-Ser-Val) positioned between amino acid 97 and 98 of the published sequence of p14 obtained by direct protein sequencing (Lucas et al., 1985). Three potential polyadenylation signals, AAAATA, AAATA, and TAATATGAATAA are found in the 3′ noncoding region. A search for homologies in data banks revealed coincidence with a cDNA clone (P6) isolated from fungi-infected tomato leaves (EMBL:M69248, J.A. Van Kan, unpublished data), but the pTE 28.1 clone we have obtained extends 25 more nucleotides in the 5′ end. pTE 28.1 clone also shows similarities with counterpart pathogenesis-related genes from tobacco (Cornelissen et al., 1986).

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The GenBank accession number for the sequence reported in this article is X68738.

Table I. *Characteristics of pTE 28.1 clone*

Organism:
Lycopersicon esculentum Mill, cv Rutgers.
Function:
Unknown.
Clone Type, Designation:
cDNA, full length, pTE 28.1.
Source:
cDNA library in λZAP II vector constructed from the poly(A$^+$) RNA fraction isolated from ethylene-treated tomato leaves.
Method of Isolation:
Differential hybridization with single-stranded cDNA probes prepared from untreated or ethylene-treated tomato leaf poly(A$^+$) RNA.
Sequencing Strategy
Complete dideoxy sequencing of both strands.
Structural Features of the Protein:
The open reading frame is 159 amino acids. From comparison with information from the sequence of the protein, positions 1 to 24 encode a signal peptide that is proteolytically removed during translocation of the polypeptide to the ER (Vera et al., 1989). Additionally, the deduced protein sequence contains five more amino acids (positions 98–103) not detected when the protein was directly sequenced (Lucas et al., 1985).
Antibodies:
Polyclonal antibodies raised in rabbits against the purified protein.
Subcellular Localization:
Intercellular space and vacuole (Vera et al., 1989).

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LITERATURE CITED

Cornelissen BJC, Hooft van Huijsduijnen RAM, Van Loon LC, Bol JF (1986) Molecular characterization of messenger RNAs for "pathogenesis-related" proteins 1a, 1b and 1c, induced by TMV infection of tobacco. EMBO J **5:** 37–40

Lucas I, Camacho Henriquez A, Lottspeich F, Henschenz A, Sänger HL (1985) Amino acid sequence of the "pathogenesis-related" leaf protein p14 from viroid-infected tomato reveals a new type of structurally unfamiliar protein. EMBO J **11:** 2745–2749

Vera P, Hernández-Yago J, Conejero V (1989) "Pathogenesis-related" P1(p14) protein. Vacuolar and apoplastic localization in leaf tissue from tomato plants infected with citrus exocortis viroid: in vitro synthesis and processing. J Gen Virol **70:** 1933–1942