Plant Physiol. (1993) 101: 703–704

Plant Gene Register

Nucleotide and Deduced Amino Acid Sequence of the 22-Kilodalton Cathepsin D Inhibitor Protein of Potato (*Solanum tuberosum* L.)[1]

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Several storage proteins of potato (*Solanum tuberosum* L.) tubers have been identified, including several proteinase inhibitors such as proteinase inhibitor I and II and the 22-kD protein group (Melville and Ryan, 1972; Bryant et al., 1976; Suh et al., 1990). The 22-kD cathepsin D inhibitor protein of potatoes (PDI) has been purified and characterized (Mares et al., 1989). This glycosylated protein inhibits cathepsin D and trypsin activity and is homologous with the soybean trypsin inhibitor family (Mares et al., 1989). Recent studies showed that PDI transcripts accumulate in potato tubers, stems, roots, and leaves depending on genotype and stage of development (Hannapel, 1991). Accumulation of potato cathepsin D inhibitor mRNA is wound inducible in leaves and occurs both locally and systemically (Suh et al., 1991). The PDI cDNA clone p749 was isolated from a tuber cDNA library using differential screening (Table I). The DNA sequence data and the deduced amino acid sequence are shown in Figure 1. The triangle indicates the site of cleavage for the signal peptide, and the first asterisk at Arg^{99} marks the trypsin-binding reactive site. The second asterisk marks the TAG stop codon, and the polyadenylation signals are underlined. The deduced amino acid sequence has 92 and 87% homology, respectively, to a purified PDI (Mares et al., 1989) and another novel inhibitor of cathepsin D (Ritonja et al., 1990). The nucleotide sequence of p749 has 94% homology to an aspartic proteinase inhibitor homolog from potato tubers (Strukelj et al., 1990).

[1] This work was supported by the Iowa State University Biotechnology Council. Journal Paper No. J-14950 of the Iowa Agriculture and Home Economics Experiment Station, Ames, IA. Project No. 3056.

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Table I. *Characteristics of a cDNA encoding the cathepsin D inhibitor protein of potato*

Organism:
Potato (*Solanum tuberosum* L. cv Superior).
Location in Genome:
Nuclear genome.
Gene, Function, Pathway:
p749; inhibitor of aspartic proteinases.
Techniques:
cDNA library screening; double-stranded plasmid sequencing of both strands; subcloning of cDNA fragments.
Method of Identification:
Amino acid sequence comparison with a cathepsin D inhibitor from potato.
Expression Characteristics:
Transcript of about 1100 nucleotides. Transcripts accumulate in leaves in response to wounding and high levels of sucrose; transcripts abundant in potato tubers.
Features of cDNA structure:
Contains an open reading frame of 663 bp.
(G + C) Content:
37.7%.
Structural Features of the Protein:
An open reading frame of 221 amino acids; M_r 28,430; signal peptide cleavage site at Glu^{33}; trypsin-binding reactive site at Arg^{99}; protein is most abundant in tubers but accumulates in leaves in response to wounding.

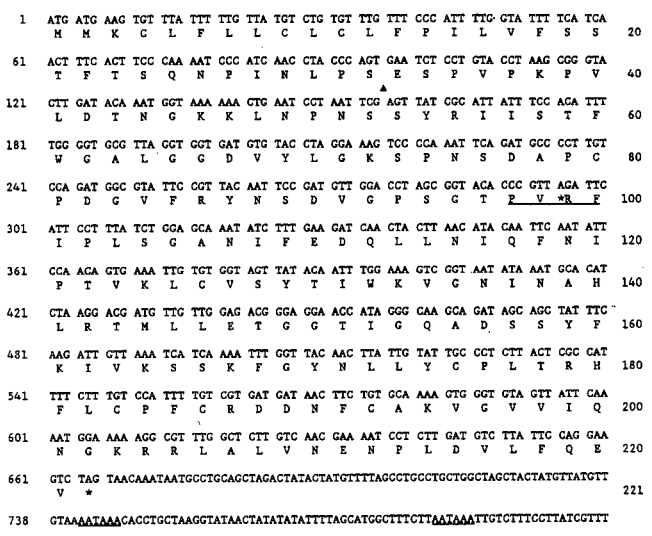

Figure 1. Primary nucleotide sequence of the 22-kD cathepsin D inhibitor of potato. The deduced amino acid sequence is indicated under the nucleotide sequence. The triangle indicates the cleavage site for the signal peptide, and the first asterisk, at Arg^{99}, marks the trypsin-binding reactive site. The second asterisk, at nucleotides 664 to 666, marks the stop codon, and putative polyadenylation signals are underlined.

Received July 13, 1992; accepted September 23, 1992.
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The GenBank accession number for the nucleotide sequence reported in this article is M96257.

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