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Plant Gene Register

Nucleotide Sequence of Genomic DNA Encoding the Potato β-1,3-Glucanase[1]

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Molecular and biochemical studies of plant defense responses have identified several molecules such as salicylic acid, systemin, jasmonate, and ethylene as potential systemic signals involved in systemic acquired resistance to pathogens and pests. Among them, ethylene is known to be associated with induction of chitinase and β-1,3-glucanase, which are present in many higher plants (Boller et al., 1983). Both enzymes have been implicated in defense reactions of plants against potential pathogens (Abeles et al., 1971; Boller et al., 1983). In many plants, chitinase and β-1, 3-glucanase rapidly accumulate following pathogen attack, after elicitor treatment, and in response to the plant stress hormone ethylene (Boller, 1985). The substrates for chitinase and β-1,3-glucanase, chitin and β-1,3-glucan, respectively, are major components of the cell walls of many fungi (Wessels and Sietsma, 1981). It has been shown that chitinase and β-1,3-glucanase can degrade isolated fungal cell walls (Mauch et al., 1988). In addition, physiological concentrations of chitinase and β-1,3-glucanase effectively inhibit growth of many potentially pathogenic fungi (Schlumbaum et al., 1986; Mauch et al., 1988). As a result, chitinase and β-1,3-glucanase appear to be a part of the inducible defense response of higher plants (Mauch and Staehelin, 1989). A genomic clone for potato β-1,3-glucanase was isolated to study the regulatory expression mechanism of the plant gene. A genomic DNA library was constructed with total DNA isolated from potato (*Solanum tuberosum* L. cv Sumi) leaves. A genomic DNA clone (λGlc1) for β-1,3-glucanase was isolated by plaque hybridization of the library using a cDNA clone for tobacco β-1, 3-glucanase as a probe. Southern blot analysis showed that a genomic fragment of 1.6 kb harbored the β-1,3-glucanase gene of potato. The structure of the genomic clone was determined by nucleotide sequencing, which, together with the result of RNA mapping with nuclease S1, shows that the β-1,3-glucanase gene of potato consists of two exons and one intron, 1269 bp, and encodes 193 amino acids (Table I).

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Table I. *Characteristics of a genomic DNA encoding the potato β-1,3-glucanase*

Organism:	*Solanum tuberosum* L. cv Sumi.
Gene Product:	β-1,3-Glucanase.
Source:	Charon4A genomic library constructed from *S. tuberosum* L. cv Sumi leaves.
Clone Type:	The genomic DNA fragment, 1.6 kb, is subcloned in pGEM7Zf(+).
Techniques:	Library was screened with a cDNA clone for tobacco β-1,3-glucanase. The DNA sequence was determined by complete dideoxy sequencing of both strands using exonuclease III-generated nested deletions. The intron/exon borders were determined by RNA mapping with nuclease S1 and searching the putative intron/exon borders for characteristic features.
Features of Gene Structure:	The genomic clone consists of two exons and one intron, 1269 bp, and encodes 193 amino acids. A putative polyadenylation signal is located 125 bp 3′ to the TAA termination codon and a putative TATA box is present at 71 bp 5′ to the translation initiation site.

The GenBank accession number for the sequence reported in this article is U12781.

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