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Primary structure of an endochitinase mRNA from *Solanum tuberosum*

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A cDNA clone (pRU8604) encoding an endochitinase from potato (*Solanum tuberosum* L. *cv*. Russet Burbank) leaves has been isolated and sequenced. The predicted coding region spans 328 amino acids and establishes the complete amino acid sequence for this enzyme (Figure 1). This gene is tightly regulated by the phytohormone ethylene, showing an induction of approximately 30-fold in young leaves. It has also been demonstrated that this gene is expressed in leaves, roots, stem, and petioles of the mature potato. Although expression can also be detected in tubers, the level of induction by ethylene is greatly reduced suggesting that constitutive expression may afford greater pathogen resistance in this organ. Homology comparisons between the primary structure of potato sequence with chitinase from other Solanaceae (1) and Leguminosae (2, 3) are remarkably similar. This conservation suggests that they are orthologous genes.

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         CCAAAATTAAGAAAGAGGAGCAGGAAT ATG CGT CGA CAT AAA GAA GTT AAT TTT GTG GCT TAT TTA
TTG TTT TCC TTG TTA GTT TTG GTG TCC GCT GCC TTA GCT CAG AAC TGT GGT TCC CAG GGG GGA GGC
AAA GCT TGT GCC TCG GGA CAA TGT TGC AGC AAA TTC GGG TGG TGT GGT AAC ACC AAT GAC TAT TGT
GGT TCC GGC AAT TGT CAA AGT CAG TGT CCT GGT GGC GGC CCT GGT CCT GGT CCT GGC GGT GAT CTT
GGT TCA GCT ATT TCT AAT TCT ATG TTT GAT CAA ATG TTA AAA CAT CGT AAT GAA AAT TCT TGT CAA
GGC AAA AAT TTT TAC TCC TAC AAT GCT TTT ATT AAT GCT GCT CGT TCT TTT CCT GGT TTT GGT ACT
TCT GGT GAT ATT AAT GCT CGA AAG CGA GAA ATT GCG GCC TTT TTT GCT CAG ACA AGT CAT GAG ACC
ACT GGT GGA TGG GCT AGT GCT CCA GAT GGT CCT TAT GCT TGG GGT TAT TGT TTC CTT AGA GAA AGA
GGT AAC CCC GGT GAC TAC TGT CCA CCA AGC AGT CAA TGG CCT TGT GCA CCT GGA AGA AAA TAC TTC
GGA CGA GGC CCG ATC CAA ATA TCA CAC AAC TAC AAC TAC GGG CCA TGC GGA AGG GCC ATC GGA GTG
GAC CTC TTA AAC AAT CCT GAT TTG GTA GCC ACT GAC CCA GTC ATC TCA TTC AAA ACT GCT CTC TGG
TTT TGG ATG ACC CCC CAA TCA CCA AAG CCT TCG TGC CAC GAC GTC ATC ATT GGC AGA TGG AAC CCA
TCT TCC GCT GAC CGA GCA GCC AAT CGA CTG CCT GGA TTC GGT GTC ATC ACG AAC ATC ATT AAT GGG
GGC CTA GAA TGT GGG CGT GGT ACT GAC AAC AGA GTA CAA GAT CGC ATT GGA TTT TAC AGG AGG TAT
TGC AGC ATT TTG GGT GTT ACT CCC GGT GAT AAT CTA GAT TGT GTT AAT CAA CGT TGG TTT GGT AAT
GCT CTA TTG GTG GAC ACT TTG TAA TCCCACTCTCGTTCGTTGCTTAATAAATTCGGGGATACTCACTAAAAAAAAAA
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Figure 1. The nucleotide sequence of a cDNA for potato leaf endochitinase (pRU8604). The signal sequence (26 amino acids) begins at the first available AUG codon (position 28); the mature polypeptide starts with glutamine (Q) at base number 106 and ends at the TAA termination codon at position 1002 (underlined). The mature protein is 302 amino acids. *Solanum* endochitinase has a molecular weight of 35,400 daltons in precursor form (with signal peptide) and 32,400 daltons in the mature form (minus signal peptide). The predicted pI of the mature form is 10.55 which agrees well with measured values of other endochitinases (3). A putative polyadenylation signal is underlined at position 1036.

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