Sequence analysis of a genomic clone encoding an endochitinase from Solanum tuberosum

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A genomic clone (pRU8713) encoding an endochitinase from potato (Solanum tuberosum L. cv. Russet Burbank) has been isolated and sequenced (Figure 1). A comparison of this genomic sequence to a previously isolated cDNA clone for a potato endochitinase (1) showed this gene to be intron-less. The coding region of this clone is highly homologous to the endochitinase from Phaseolus (46.7%; 2), Nicotiana (73.9%; 3), and Lycopersicon (85.6%; 4). A more detailed analysis of this clone and its expression will be published elsewhere (5).

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Figure 1. The nucleotide sequence of a genomic clone for potato endochitinase (pRU8713). The endochitinase coding region is from 2006 to 2992. The transcription start site is at 1956. A putative CAAT box (1851-1860) and TATA box (1921-1927) have been identified.

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References: