Abstracts

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Identification of a *Phytophthora cinnamomi* glucanase inhibitor protein: A molecular factor asso ciated to infection mechanism

S12 P23

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The oomycete *P. cinnamomi*, the causal agent of *Castanea sativa* ink disease, is one of the most destructive species of *Phytophthora* genus, and has been associated with the decline of several forest, ornamental and fruit trees and shrubs, causing enormous economic losses worldwide.
Phytophthora cell walls are composed of glucans and have no chitin. Production of glucanase inhibitor proteins (GIPs) by *Phytophthora* species are thought to provide them a counter-defense against plant hosts β-1,3-glucanases (Rose *et al.*, 2002), that otherwise would degrade these pathogen cell walls. GIPs belongs to the chymotrypsin family of serine proteases but are catalytically nonfunctional because one or more residues of the essential catalytic triad are absent.
We report the identification of the gene encoding the first known *P. cinnamomi* GIP, presumably involved in the pathogen infection mechanism.
Total genomic DNA was obtained from strain *P. cinnamomi* Pr120 and polymerase chain reaction was used to amplify a 308bp fragment of the GIP gene, using degenerate oligonucleotide primers, which were designed based on homology of previous published sequences of *Phytophthora sp.* GIP□s from EMBL databases. Full gene sequence length (1171bp) was obtained by flanking the known sequence with asymmetric PCR.
P. cinnamomi GIP gene encodes a 269 amino acids protein with 28,818.2Da and a calculated global iso-electric point value of 8.54. It shares great identity and similarity with already described GIPs of *P. sojae* and *P. infestans* (E-values from $3.4e^{-49}$ to $2.6e^{-38}$), showing the importance of these proteins as effectors in plant-pathogen infection process.
The UniProtKB/TrEMBL accession number for the sequence reported in this paper is B0B0H5_PHYCI.

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