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P268

SEQUENCE ANALYSIS AND EXPRESSION OF GENES INVOLVED CYTOSKELETON AND INFECTION MECHANISMS IN THE PLANT PATHOGEN *PHYTOPHTHORA CINNAMOMI*

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Oomycetes from the genus *Phytophthora* are plant pathogens that are devastating for agriculture and natural ecosystems. The biggest productivity and yield break occurs due to the ink disease; caused by *Phytophthora cinnamomi,* which is one of the most widely distributed *Phytophthora* species, with nearly 1000 host species. The knowledge about the molecular mechanisms responsible for its pathogenicity is an important tool in order to fight diseases associated with this pathogen.

Complete open reading frames (ORFs) of *act1, act2* and *tub1,* genes that participate in cytoskeleton formation in *P. cinnamomi,* were achieved by high-efficiency thermal asymmetric interlaced (HE-TAIL) polymerase chain reaction (PCR). *act1* gene comprises a 1128 bp ORF, encoding a deduced protein of 375 amino acids (aa) and 41,972 kDa. *act2* ORF comprises 1083 bp and encodes a deduced protein of 360 aa and 40,237 kDa. *tub1* has a total length of 2263 bp and encodes a 453 aa protein with a molecular weight of 49.911 kDa.

Withthis techniquewe also identified and characterized some proteins involved in mechanisms of infection by *Phytophthora cinnamomi*: endo-1,3-beta-glucanase (complete cds), exo-glucanase (partial cds); glucanase inhibitor protein (GIP) (complete cds); necrosis-inducing Phytophthora protein 1 (NPP1) (complete cds), transglutaminase. The genes of *P. cinnamomi* revealed significant homologies with correspondent genes of species of the genus *Phytophthora*.This genes isolated from *P. cinnamomi*, were successfully expressed in *E. coli* and *P. pastoris*.

The expression of these genes was monitored during growth in different carbon sources (glucose, cellulose and sawdust) by RT-qPCR and its level of expression was evaluated at five time points. The highest expression of genes occurred in sawdust at 8 hours of induction. In vivo infection of *Castanea sativa* revealed an increase of their expression from 12 to 24 hours. After 36 hours their expression decreased suggesting that a compensatory mechanism may occur in the host plant.