



*Methodology*

## Identification of 18 genes encoding necrosis-inducing proteins from the plant pathogen *Phytophthora capsici* (Pythiaceae: Oomycetes)

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**ABSTRACT.** *Phytophthora capsici* is an aggressive plant pathogen that affects solanaceous and cucurbitaceous hosts. Necrosis-inducing *Phytophthora* proteins (NPPs) are a group of secreted toxins found particularly in oomycetes. Several NPPs from *Phytophthora* species trigger plant cell death and activate host defense gene expression. We isolated 18 *P. capsici* NPP genes, of which 12 were active during hypha growth from a *Phytophthora* stain isolated from pepper (*Capsicum annuum*) plants in China. The 18 predicted proteins had a sequence homology of 46.26%. The 18 *Pcnpp* sequences had a conserved GHRHDWE motif and fell into two groups. Eleven sequences in group 1 had two conserved cysteine residues, whereas the other seven sequences in group 2 lacked these two cysteine residues. A phylogenetic tree was constructed on the basis of the alignment of the predicted protein sequences of 52 selected NPP genes from oomycetes, fungi and bacteria from Genbank. The tree did not rigorously follow the taxonomic classification of the species; all the NPPs from oomycetes formed their own clusters, while fungal sequences were grouped into

two separate clades, indicating that based on NPPs, we can separate oomycetes from fungi and bacteria, and that expansion of the NPP family was a feature of *Phytophthora* evolution.

**Key words:** Oomycete; Necrosis-inducing *Phytophthora* protein; *Phytophthora capsici*; Horizontal gene transfer