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Poster Abstract – C.10

MODULATION OF GENE EXPRESSION INDUCED IN *PLATANUS ACERIFOLIA* BY CERATO-PLATANIN AND CONIDIAL SUSPENSION OF *CERATOCYSTIS PLATANI*

BACCELLI I.*, FONTANA F.**, SCALA A.**, PAZZAGLI L.***, CAPPUGI G.***, SALVINI M.****, DURANTE M.*, BERNARDI R.*

*) Department of Agricultural Plant Biology, Genetics Section, University of Pisa, Via Matteotti 1/B, I-56124 Pisa (Italy) - rbernard@agr.unipi.it
**) Department of Agricultural Biotechnology, Plant Pathology Section, University of Firenze, Piazzale delle Cascine 28, I-50144 Firenze (Italy)
***) Department of Biochemical Sciences, University of Firenze, Viale Morgagni 50, I-50142 Firenze (Italy)
****) Scuola Normale Superiore Pisa, Piazza dei Cavalieri, 56100 Pisa (Italy)

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Cerato-platanin (CP) is a small protein produced by Ascomycete *Ceratocystis platani*, the causal agent of plane canker stain. *Cep* is pathogenic to *Platanus orientalis*, *P. occidentalis* and their hybrid *P. acerifolia*. CP is located in the fungal cell walls, is early released in culture, and elicits defence-related structural and physiological responses in host and non-host plants, such as cell plasmolysis and death, phenolic compounds and phytoalexin accumulation (Pazzagli *et al.*, *J. Biol. Chem.* **274**: 24959-24964, 1999; Boddi et al., *FEMS Microbiol. Letters* **233**: 341-346, 2004; Scala *et al*., *J. Plant Pathol.* **86**: 23-29,2004; Bennici et al., *Caryologia* **59**: 291-298, 2006). Recently, it has been demonstrated the close correlation between the CP treatment of plane leaves and the subsequent growth inhibition of *C. platani* on the surface of the treated leaves together with the production of phytoalexins and the over-transcription of regulatory and defense-associated genes (Fontana *et al*., *J. Plant Pathol.* **90**: 293-304, 2008).

The aim of the present study was to provide further information on the modulation of gene expression that occurs in the plane tree by CP treatment in order to improve our understanding of the potential of CP to function as a PAMP (Pathogen-Associated Molecular Pattern) protein in the pathogenic process of the *C. platani-P. acerifolia* interaction.

In the present study we have isolated others clones from a cDNA library constructed using suppression subtractive hybridization (SSH) technique (Fontana et al., *J. Plant Pathol.* **90**: 293-304, 2008) and the putative differentially expressed genes were identified using the FASTA, BLASTN and BLASTX programs. The up-regulated clones were classified in the macro putative groups taking in account the functional categories established for *Arabidopsis* (The *Arabidopsis* Genome Initiative, *Nature* **408**: 796-815, 2000). We have analysed, moreover, some of them by relative PCR using total RNA extracted from leaves treated with CP or fungal conidia at 6, 24 and 48 hours after treatments in order to investigate possible differences in gene expression during CP/plant and fungus/plant interactions.

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