Proceedings of the XLIX Italian Society of Agricultural Genetics Annual Congress
Potenza, Italy – 12/15 September, 2005
ISBN **88-900622-6-6**

Oral Communication Abstract - 1.02

GENE INDUCTION IN *PLATANUS ACERIFOLIA* AFTER TREATMENTS WITH CERATO-PLATANIN AND CONIDIA OF *CERATOCYSTIS FIMBRIATA* SP. *PLATANI*

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plant disease, defence genes, Platanus acerifolia, stress tolerance

Cerato-platanin (CP) is a 120 amino acids-long protein purified from the culture filtrate of *Ceratocystis fimbriata* (Ell. and Halst.) Davidson f. sp. *platani* Walter (*Cfp*), the causative agent of the canker stain of the plane trees (Pazzagli *et al.*, 1999). CP contains 4 cysteines forming two S-S bridges, Cys20-57 and Cys60-115, and has a high percentage (40%) of hydrophobic residues. It is the founder member of the cerato- platanin family, and its N-terminal region is very similar to cerato-ulmin, a class II hydrophobin involved in the pathogenesis of Dutch elm disease (Del Sorbo *et al.*, 2002). CP is located in the *Cfp* cell walls, and is early-detected in *Cfp* culture filtrates. In *in vitro* experimental conditions CP self-assembles, and interacts with the host plane leaves by eliciting phytoalexin synthesis, extended cell plasmolysis and crushing, and abundant starch accumulation in the chloroplasts (Bennici *et al.*, 2005; Boddi *et al.*, 2004; Pazzagli *et al.*, 2005; Scala *et al.*, 2004).

cDNA libraries were constructed from RNA extracted from leaves treated with CP (treated) and with water (control) for 48 hours using the Suppressive Subtractive Hybridisation (SSH) method, a powerful technique that enables to compare two population of mRNA and to obtain clones of genes that are expressed in one population of mRNA but not in the other.

The positive clones were sequenced and the sequences were analysed using the FASTA, BLAST, ProDom, BLOCK software for their identification in GenBank, EMBL. Many clones from the forward library contain sequences involved: i) in synthesis, processing and translation of proteins, i.e., the DEAD box ATPase/RNA helicase protein, the oligouridylate binding protein, an unknown protein with the RIBOSOMAL S8E domain, the elongation factor 1 alpha, the translation factor erF3, the ribosomal protein PRPL5; ii) in signal transfer in the cell, i.e. the Pto-like serine-threonine kinase; iii) in transcription control, i.e. the histone deacetilase, the DEAD-box helicase; iv) in photosynthesis, i.e. the PSI-D subunit, the ferredoxin, the chlorophyll a/b binding protein. Someone else interesting are: the TUBBY-like protein (TULP); the Fatty Acid Elongase (FAE), in particular, a keto-acyl CoA synthase; the Inosine 5'-phosphate-dehydrogenase; the PEP-carboxyl-kinase; the alanine-amino-transferase; the selenium binding protein; the RAR1; a protein with a DUF597 domain; the thaumatin protein. Moreover, many clones were analysed by Real Time RT-PCR and/or relative PCR in order to study their regulation

after treatments with CP or with conidia of Cfp wild strain. Analysis of forward clones showed that many genes are positively regulated.

The knowledge of the gene expression after treatments could open the possibility of inducing resistance to *Cfp* in plane trees.

Acknowledgments: This work was supported by grants from PRIN 2003.