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CERATO-PLATANIN AND CERATO-POPULIN INDUCE DIFFERENTIAL GENE EXPRESSION IN *PLATANUS ACERIFOLIA*

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Cerato-platanin (CP) and cerato-populin (Pop1) are small non-catalytic proteins produced by the ascomycetes *Ceratocystis platani* and *C. populicola. C. platani* is responsible for the canker stain disease of plane trees, and *C. populicola* for the black canker of poplar trees. CP and Pop1 are PAMPs (pathogen-associated molecular patterns) inducing typical defense responses in various host and non-host plants. CP and Pop1 have an identity of about 63% and the conservative substitution of approximately 12% of amino acids, and both belong to the "cerato-platanin family" (Pfam PF07249).

The aim of the present research was to analyse the gene expression induced in *Platanus acerifolia* leaves after treatments with CP and Pop1 using cDNA microarrays containing sequences isolated from suppressive subtractive libraries (SSH) from *P. acerifolia* after treatment with CP, and from *Populus* after cold or ozone treatment.

There are many reports on cross-tolerance induction by abiotic stresses against other biotic stresses and vice versa and on the existence of a network of regulatory signalling occurring in plants during the interaction with biotic and abiotic stresses.

PCR amplified sequences of the clones isolated from the cDNA libraries were spotted on microarray glass slides by CRIBI (Padoa, Italy). For the cDNA microarray analysis, mRNA was reverse transcribed in the presence of Cy3-dUTP or Cy5-dUTP. RNAs were extracted from leaves treated with sterile distilled water droplets containing CP or Pop1, or sterile distilled water as a control.

Out of the 318 genes, 131 and 50 genes resulted to be modulated in CP- and Pop1-treated leaves, respectively. Moreover, several transcripts were differentially regulated. In both treatments the up-regulated genes were more than the down-regulated ones. Inducible expression of some candidate genes selected from the microarray results was confirmed by using semi-quantitative RT-PCRs.

These results show that several differentially regulated genes induced by the PAMPs CP and Pop1 in *P. acerifolia* are in common with those induced in response to ozone and cold stresses in *Populus*, underlying the existence of a conserved network of genes activated by different stresses during plant defence responses.

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