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TRANSCRIPTOME ANALYSES OF O_3 –RESPONSIVE GENES IN LEAVES OF TWO DIFFERENTIALLY SUSCEPTIBLE POPLAR GENOTYPES

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When subjected to episodic ozone peaks, the more sensitive trees can undergo conspicuous molecular and physiological changes that frequently result in foliar lesion formation. These events involve programmed cell death and other events typical of hypersensitive responses triggered by pathogens or abiotic stressors.

By using the microarray technology, a transcriptome investigation was carried out on the leaves from two poplar clones exhibiting a contrasting susceptibility in terms of leaf injuries after an acute ozone exposure, with the aim to understand the molecular events at the base of foliar lesion formation. Unfumigated plants were used as controls. The microarray platform consisted in a collection of cDNAs extracted from different organisms subjected to abiotic (ozone and cold stress) or biotic (ceratoplatanin phytotoxic protein) stresses.

The genes modulated by ozone were compared with those of the untreated sensitive and tolerant clones. Out of the 337 genes, 119 and 41 genes were evidenced to be specifically O_3-responsive in Eridano and in I-214 poplar clones respectively. In both the genotypes (but especially in the Eridano clone), the down-regulated genes were higher in number than the up-regulated ones. Interestingly, sensitive and resistant genotypes evidenced some genes specifically up or down expressed only in one of the two clones. These genes could play a key role in determining the different behaviour displayed by the two clones when exposed to acute ozone stress and constitute an intriguing opportunity to better understand the molecular bases of ozone stress tolerance and sensitivity.

The differentially expressed genes were also compared in sensitive clones with respect to tolerant counterpart at different experimental time points (before ozone exposure, at fumigation end, and during the recovery times). The obtained results evidenced that about the 22% of all transcripts were differentially regulated overtime in the two clones: the majority of these belonged to cell metabolism (primary and secondary) and disease/defence functional categories and resulted mainly down-regulated in the sensitive clone than in the tolerant one. At 5 hrs treatments and during the subsequent recovery periods, the categories having the major number of differentially transcribed genes were those related to cell metabolism and signal transduction pathways. A significant increase in expressed genes from disease/defence and protein synthesis categories was evidenced after ozone stress.

Considering the differences displayed by the two clones in the expressed transcriptome, we suggest that a more or less efficient deployment of defence mechanisms minimizing the toxic effect of O_3 or its by-products can explain the differences in ozone sensitivity showed by the two poplar hybrids. The transcription profiles, obtained by using these cDNA microarray platforms, indicated that several genes differentially regulated by ozone in Eridano and I-214 poplar clones were the

same regulated by other abiotic or biotic stressors in different organisms, underlying the existence of a conserved and interspecific network of genes, activated during plant defence responses.