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DIFFERENTIAL GENE EXPRESSION INDUCED BY OZONE STRESS IN THE MEDITERRANEAN EVERGREEN SHRUB *PHILLYREA LATIFOLIA* L.

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In most densely-populated areas of the world, tropospheric ozone (O_3) is one of the major phytotoxic pollutants causing damage to both cultivated plants and natural vegetation. Over the last decades, forest species native of cold or continental climates have been most intensively studied, whereas the peculiar features of the Mediterranean climate, as they affect O_3 uptake and responsiveness in indigenous plant communities, have comparatively received much less consideration. In a previous study, physiological and biochemical measurements indicated *Phillyrea latifolia* L. as the most tolerant among three Mediterranean evergreen broadleaf species exposed to realistic O_3 regimes, and suggested that such tolerance might overlap with an inborn adaptability to drought. To understand the molecular basis of such tolerance, we studied differential gene expression in two-years old seedlings of *P. latifolia* exposed to either 0 or 110 nL L^{-1} for 90 days, 5 h each day, from March to May in a greenhouse. The expression profiles of the trancripts from leaves of ozonated and control plants were compared by a modified cDNA-AFLP technique. The analysis of about 300 amplification products detected 70 differentially expressed transcripts, 45 of them induced and 25 suppressed by O_3. The nucleotide and deduced amino acid sequences of 34 out of 45 O_3-induced clones, whose preferential expression in ozonated plants was verified by RT-PCR analyses, were compared with the online databases of DNA and protein sequences. On the basis of their presumed functions, 16 out of 34 O_3-induced clones were assigned to seven groups: I) energy (4 clones); II) metabolism (1); III) cell rescue/defense (3); IV) cellular organization/biogenesis (4); V) signal transduction (2); protein degradation (2). At the present preliminary stage, we can tentatively argue that, in general, the pattern of gene induction detected in phillyrea is rather logically related to the suite of known molecular responses to O_3. Eleven of the 16 isolated clones, found to match genes with known functions, have been previously recognized as O_3-responsive genes in *Arabidopsis*. The observed O_3-induced accumulation of transcripts coding for heat- and salt-inducible proteins, for a pathogenesis-related protein and for a putative mitogen-activated protein kinase, orthologous to the *Arabidopsis* AtMPK3, could lend further support to the accepted notion that O_3 behaves as an abiotic elicitor of defence responses in plants, i.e. that molecular plant- O_3 interactions might have much in common, in terms of signal perception, transduction, gene expression and defence, with the reaction cascades elicited by a variety of other biotic and abiotic environmental stressors. In contrast with previous studies from others, the transcription of genes coding for subunits of photosystem I or potentially important for the synthesis of chlorophyll was activated by the exposure to a realistically elevated O_3 level, protracted over the annual period of the most active vegetative growth in the field. This would suggest in *P. latifolia* a sort of compensative ability in coping with an accelerated turn-over of photosystems components in the presence of chronic O_3. The analysis of differential gene expression in *P. latifolia* appears as a promising approach in deciphering molecular responses to realistic O_3 dosages in natural plant communities belonging to Mediterranean ecosystems.