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**Poster Abstract – C.20**

# TOWARDS THE UNDERSTANDING OF THE OZONE-INDUCED SIGNAL TRANSDUCTION PATHWAYS IN ARABIDOPSIS

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*ROS, MAPK, signal transdunction, RLK, WRKY*

Plants are constantly exposed to a variety of biotic and abiotic stresses and react to these challenges with rapid biochemical and molecular changes that trigger physiological adaptations. Ozone ($O_3$), a component of photochemical smog, represents an oxidative stress to living organisms, damaging crops and forests and its concentration has increased dramatically during the past few decades. The plant's response to $O_3$ resembles components of the pathogen defence response, including the production of reactive oxygen species (ROS), the induction of hypersensitive response (HR) and the development of systemic acquired resistance (SAR). Along this line, the characterization of Arabidopsis transcriptional responses to ozone and pathogen treatments distinguished between shared responses of ozone and pathogen exposure and transcripts specifically regulated by ozone (reviewed in Baier et al. 2005). With the aim to study the oxidative signalling mediated by acute $O_3$ fumigation in plants, we have carried out microrray analysis to monitor the alterations in gene expression during and after $O_3$ fumigation in the in the tolerant Arabidopsis Col-0 ecotype (Tosti et al. in press). The $O_3$ –mediated transcriptional profile is complex, as new genes (i.e. reticuline oxidase) and pathways, other than those already reported as ozone-sensitive, appear to be involved. Interestingly, our microarray analysis revealed that most of the *WRKY* genes (i.e *WRKY22, 25, 33*) and some of the genes of the MAPK cascade (i.e. *AtMPK3*) induced transcriptionally by pathogens, NO or light stress were also induced by ozone. Thus, all these stresses may, at least partially, trigger the same signalling event. Yet, the W-box motifs resulted to be the only cis-element over-represented in the promoter region of up-regulated genes during $O_3$ treatment. Genes containing the W- promoter element are likely targets of *WRKY*, including *WRKY* themselves. Many W-box elements were also identified in the promoter region of most *RLK*s up-regulated during and after $O_3$ treatment. WRKYs can be substrates of MAPKs and WRKY can regulate *RLK* expression upon challenging plants with pathogens (Andreasson et al. 2005, Du and Chen, 2000). Thus, we are currently testing the hypothesis that, among the response signals induced by $0_3$ in plants, there is a MPK-dependent regulation of WRKYs and that, in turn, WRKYs are involved in the initial activation and/or maintenance of *RLK* expression during $O_3$ treatment. To this purpose, we have initiated a preliminary genetic characterization of *A.thaliana* mutant lines harbouring T-DNA insertions on key $0_3$-induced *RLK* genes, to be tested along with *wrky* and *mpk* mutant lines for their responsiveness to $O_3$. By analysing the transcriptional profiles and physical/functional interactions of candidate $O_3$ –responsive genes and proteins in single and multiple mutant lines, we expect to gain more insights into the $0_3$-mediated cascade events.

References

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