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Poster Abstract – D.29

TRANSCRIPTIONAL PROFILING BY MICROARRAY ANALYSIS OF NITRIC OXIDE RESPONSIVE TRANSCRIPTS IN *MEDICAGO TRUNCATULA* FOR DISSECT THE GENETIC MECHANISMS OF PLANT DEFENCE RESPONSES AND SYMBIOSIS

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Nitric oxide (NO) has been involved in the regulation of a large range of physiological processes in plants. Recent studies highlight its involvement during leaf expansion, root growth, senescence, iron homeostasis and abiotic stress. The role of NO is particularly crucial during plant-pathogen interactions, where it participates to a complex network controlling plant defence responses and resistance. Moreover, indirect indications of the possible involvement of NO during legume-rhizobia interactions have been reported. Recent transcriptomic studies evidence that the genes regulated by NO sustain a large diversity of cellular functions, in accordance with the pleiotropic role of this molecule in plant physiology. To reveal the candidate genes involved in pathogenesis and symbiosis we started a transcriptional analysis in *Medicago truncatula*, the model system for legume biology.

In this work *M. truncatula* roots from 4 week-old aeroponic-grown plants were treated with the NO donors sodium nitroprusside (SNP) and S-nitrosoglutathione (GSNO). Using a cDNA-amplified fragment lenght polymorphims (AFLP) transcript profiling approach we isolated >1000 cDNA fragments that were excised from gel, re-amplified with selective primers, cloned and sequenced. These cloned fragments were used to print a cDNA microarray that we named MtNO. To assess the functionality of MtNO microarray, we performed hybridizations with RNA extracted from plant leaves or roots after treatment with the same chemicals and time course used for cDNA-AFLP analysis. In addition, this microarray was used to perform a broader monitoring of transcriptome changes in *M. truncatula* upon infection with the soil bacterium *Sinorhizobium meliloti* 1021 and upon incompatible interaction with the fungal pathogen *Colletotrichum trifolii* race 1. This analysis led us to identify 529 genes with a modulated expression (413 induced and 116 repressed) during infection process and 455 genes (440 induced and 15 repressed) during nodule development. The analyses of a large number of *M. truncatula* genes in response to infection and interaction with a simbiotic microrganism provided a base to identify commonalities among diverse signaling pathways. By comparing gene expression profiles, we identified 73 genes induced during both *C. trifolii* race 1-infection and nodule development, and 105 genes with a significant opposite modulation.