

MICROARRAY ANALYSIS OF GENE EXPRESSION VARIATION IN EGGPLANT ROOTS SUBJECTED TO INOCULATION WITH *FUSARIUM OXYSPORUM* AND *VERTICILLIUM DAHLIAE*

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The two fungal *Fusarium oxysporum* and *Verticillium dahliae* are the causal agents of root rot and wilt diseases in several plant species, including eggplant. Perception of these fungal diseases by model plants follows the concept of the elicitor-induced immune response, which in turn activates several defence signalling pathways. Our purpose is to compare the expression profiles of genes involved in defence response mechanisms in roots samples of an *Fusarium* resistant eggplant line after different fungal inoculations and different timings (0, 4 and 8 hours after dipping in fungal suspension). Transcriptional changes in eggplant roots induced by *Fusarium*, *Verticillium*, and mixed (*Fusarium* + *Verticillium*) inoculations were undertaken by microarray analysis, using mock-inoculated samples as control. The analysis was performed in a new CombiMatrix platform, with a 4x2K customized chip and containing 2000x4 eggplant probe sets, resulting in the hybridization of four independent samples on a single slide. The probes were selected and designed from a collection of three subtractive cDNA libraries of eggplant genes putatively involved in the plant-pathogen interaction. Changes in gene expression were examined and compared between the three different timings (T0, T4, T8), considering the different fungal inoculations and the control. Stringent control measures were applied for all steps of the experiments and for the following data analysis; thus all results obtained were within the windows of resolution of the microarray hybridization method. About 160 genes were found to be modulated in at least one condition or timing. Results show that the number of up-regulated genes was slightly higher in T8 versus T0 than in T4 versus T0. The number of down-regulated modulated genes remain comparable between T8/T0 and T4/T0. The up- and down-regulated genes were functionally assigned according to the principal GO categories (molecular function, biological process and cellular localization), and preliminary data analysis showed that most of modulated genes belong to defence response and stress induced categories. The validation of microarray data by RT-qPCR is in progress.