Proceedings of the 52nd Italian Society of Agricultural Genetics Annual Congress
Padova, Italy – 14/17 September, 2008
ISBN **978-88-900622-8-5**

Poster Abstract – D.25

MICROARRAY ANALYSIS OF GENE EXPRESSION IN TOMATO PLANTS INFECTED BY DIFFERENT COMBINATIONS OF CUCUMBER MOSAIC VIRUS AND ITS SATELLITE RNAs

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tomato, Cucumber mosaic virus, defense response, microarray, Combimatrix

An analysis of transcriptional changes in tomato plants, induced by the infection of Cucumber mosaic virus (CMV), alone or in combination with satellite RNA (satRNA) variants, has been undertaken by microarray analysis. The analysis was performed a new CombiMatrix platform, on a tomato chip carrying 20200 specific probes from assembly of Tentative Consensus of the last Tomato Gene Index, release 11.0 (June 21, 2006).

Solanum lycopersicum cv. UC82 plants were infected with CMV-Fny or with CMV-Fny co-inoculated with three different satRNAs (benign: CMV-Fny/Tfn-satRNA; stunting: CMV-Fny/TTS-satRNA; necrogenic: CMV-Fny/77-satRNA). Mock-inoculated plants were used as controls. Gene expression was examined at 2 and 9 days post-inoculation. 1179 genes were modulated in at least one condition. CMV-Fny, without any satRNA, provoked wide transcriptional changes, affecting about 80% of modulated genes. Core sets of transcripts coherently modulated (either up-or down-regulated) by all infections or by the 3 CMV/satRNA combinations were identified.

To identify genes that might account for the different symptoms observed in the different CMV/satRNA co-infections, the transcriptional effect of each single CMV/satRNA combination was compared with the effect of CMV-Fny: all satellites determined a clear down-regulation of genes that are expressed in CMV-Fny-infected plants, especially at 2 days p.i., while interesting differences could be identified between gene expressions specifically associated to each CMV/satRNA infection.

Grouping of differentially expressed genes into putative functional categories revealed some peculiarities of all examined interactions, such as a very small percentage of photosynthesis-related genes and, conversely, a consistent modulation of resistance-related and signal transduction–related genes. Modulated genes related to “Lipid metabolism” and to “Nucleic acid metabolism” were also well represented. This work might serve as a basis to identify candidate genes with a functional role in susceptibility and symptom determination.