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Poster Abstract - D.35

ANALYSIS OF METHYLATION PROFILE OF TOMATO GENOME FOLLOWING INFECTION BY *TOMATO YELLOW LEAF CURL SARDINIA VIRUS* (TYLCSV)

G. MASON*,**, E. PORTIS**, E. NORIS*, G.P. ACCOTTO*, A. ACQUADRO**, P. CACIAGLI*, S. LANTERI**

*) Istituto di Virologia Vegetale – CNR , Strada delle Cacce 73, 10135 Torino, Italia
**) Di.Va.PRA, Genetica Agraria, Via Leonardo da Vinci 44, 10095 Torino, Italia – sergio.lanteri@unito.it

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Activation of plant defences following recognition of pathogen attack involves a complex variety of signaling metabolic pathways and includes the transcriptional activation of an array of plant defense-related genes. This control of gene expression includes epigenetic phenomena such as DNA methylation. To date, the role of DNA methylation during viral infection in plants has been investigated to a limited extent. We analyzed the methylation profile of tomato genome during infection by *Tomato Yellow Leaf Curl Sardinia Virus* (TYLCSV). This DNA virus belongs to the *Geminiviridae* family (genus *Begomovirus*) and possesses a monopartite genome of 2.8 kb. TYLCSV is transmitted by the withefly *Bemisia tabaci* in a circulative persistent manner and causes severe crop losses in tomato, mainly in the Mediterranean basin. Geminiviruses, analogously to the animal DNA virus, have evolved the capability to interfere with host gene expression and cell cycle regulation, by reprogramming the whole host cell cycle. We assessed the methylation pattern of the tomato genome using an adaptation of the AFLP technique, called MSAP (methylation-sensitive amplified polymorphism). This technique is based on using enzymes (e.g. HpaII and MspI) sensitive to methylation of their recognition sequences.

We compared DNA profiles of infected vs uninfected tomato plants (cv 'Moneymaker'), by collecting samples at different times following whitefly inoculation (1, 7 and 14 days). Changes in MSAP profiles of genomic DNA were detected and ten polymorphic fragments were excised from gels and sequenced. Sequences were compared with the ones available from the Solanaceae Genomics Network (SGN) website or GenBank database (NCBI). Some of the differentially methylated genes appeared to be involved in the plant defence mechanism, i.e. *cysteine protease*, *methionine adenosyltransferase*, while others showed similarity with leucine-rich repeat (LRR) proteins. This confirms the efficiency of MSAP in identifying gene sequences potentially involved in the defence of tomato plant to TYLCSV infection.

The expression level of these genes is currently being evaluated with Reverse Trascription-Real Time PCR.