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Poster Abstract - D.30

TRANSCRIPTIONAL PROFILING OF TOMATO PLANTS INFECTED WITH THE TOMATO YELLOW LEAF CURL SARDINIA VIRUS BY LONG SERIAL ANALYSIS OF GENE EXPRESSION

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The geminivirus Tomato Yellow Leaf Curl Sardinia Virus (TYLCSV) is one of the agents of the tomato yellow leaf curl disease, which causes dramatic crop losses in the Mediterranean and sub-tropical regions. The viral genome is a 2,7 kb single stranded circular DNA; two proteins are encoded by the viral strand and four by the complementary one. Although a huge amount of molecular data exist on TYLCSV, little is known about its interaction with the host plant. In order to gain insight into TYLCSV-tomato interactions at molecular level, we decide to analyse the transcriptional profile of TYLCSV infected tomato plants. To do this, Long-Serial Analysis of Gene Expression (Long SAGE) was used; this technique, based on the identification of 20 nt long sequences (TAGs), allows the quantitative analyses of transcripts without the need for any prior knowledge of their sequences.

Tomato plants were infected with TYLCSV in three independent experiments and leaf samples were collected from five plants in each experiment at four weeks post-inoculation; parallel sampling was performed on control healthy plants. Total RNAs were extracted and pooled resulting in two final samples, the infected and the control ones, which were used to construct two Long SAGE libraries.

About 41.000 TAGs were produced for each library, representing a total of 9.433 genes; among these, 5809 differed in their expression at least two-fold. A preliminary analysis was performed on TAGs whose expression differs at least seven-fold between the two samples. 62 and 50 TAGs were respectively up- and down-regulated by TYLCSV infection. In the up-regulated group, beside viral transcripts, 39 TAGs matched tomato unigenes and 15 were not found in the SGN data bank, representing possible novel genes. In the down-regulated group only 20 TAGs matched tomato unigenes. It is noteworthy that only 37 out of 59 unigenes identified were represented on the TOM1 cDNA chip. Moreover, 10 out of 59 TAGs matching tomato unigenes were in antisense orientation; further analysis will be done to understand the biological relevance of this observation. Regarding the functions of up- and down-regulated genes, TYLCSV infection stimulates expression of genes involved in defense and stress responses, signal transduction and protein metabolism, while it reduces expression of genes implicated in photosynthesis.

These preliminary data suggest that transcriptome analysis by Long SAGE is a powerful tool to study virus-host interactions.