Proceedings of the XLIX Italian Society of Agricultural Genetics Annual Congress
Potenza, Italy – 12/15 September, 2005
ISBN **88-900622-6-6**

Poster Abstract - D.47

DIFFERENTIAL EXPRESSION PROFILING FOR RAPID IDENTIFICATION OF DESEASE RESISTANCE GENES IN TWO TOMATO ISOGENIC LINES

L. FAINO, P. CARLI, D. CARPUTO, L. FRUSCIANTE, M. R. ERCOLANO

Department of Soil, Plant and Environmental Sciences – University of Naples "Federico II", Via Università 100, 80055 Portici, Italy

plant resistance gene, SSH, tomato, isogenic line

Comparing patterns of gene expression by PCR-select technology had important applications in a variety of biological system. We used this approach to investigate a resistance genes hot spot chromosome region difficult to analize with conventional molecular methods. In particular two tomato near isogenic lines (Momor and Monalbo) were examined for differential gene expression profile. Momor contain two resistance genes (Frl and Tm2a), located on short arm of to chromosome 9, that are absent in Monalbo. The first gene confers resistance to *Fusarium oxysporum* f. sp. *radicis-lycopersici* and the second to TMV virus. Since both lines have a common genetic background, deriving from Moneymaker cultivar, any difference between them is due to the region that contain these genes. PCR select methodology has been used to investigate mRNAs represented only in resistant variant. A suppressive subtraction hybridization (SSH) cDNA library, using Momor genotype as tester, was prepared and analyzed. A total of 200 cDNA fragments present in the library were selected following the criteria established for differential expression. Several clones coding for major pathogenesis-related proteins searching in public databases by BLAST (basic local alignment search tool) were identified. Interestingly, one clone showed sequence homology with Gpa2 gene that confers resistance to *Globodera pallida* nematode in potato. Molecular characterization of these clones is in progress to validate the their location on tomato genome.