Poster Abstract – C.13

BIOINFORMATIC ANALYSIS OF cDNA-AFLP DERIVED SEQUENCES DIFFERENTIALLY EXPRESSED IN A COMPATIBLE INTERACTION TOMATO - PYRENOCHAETA LYCOPERSICI

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Pyrenochaeta lycopersici is the causal agent of tomato corky root. In a previous cDNA-AFLP study aimed at fungus gene identification, several differentially expressed Transcript-Derived Fragments (TDFs) were obtained, in the compatible interaction between the tomato cultivar 'Corbarino' and the fungus. The present work was aimed to investigate the response of tomato to *Pyrenochaeta lycopersici*, by sequencing a set of differentially expressed fragments, and by bioinformatic analyses.

Previously sequenced, up-regulated TDFs (derived from infected roots) have been analyzed by BLAST homology searches against NCBI, Tomato Gene Indices and Potato Gene Indices available from Dana Faber Cancer Institute, and SOL Genomics Network (SGN) databases. The sequences with highest similarities to plant genes were further characterized. Gene Ontology was derived from Gene Indices, UniProt and SGN databases. Down-regulated TDFs (derived from control plants) that had not been analyzed so far were sequenced and subjected to the same homology and gene ontology search procedures as for the up-regulated TDFs. About 100 upregulated and about 150 down-regulated tomato genes have been identified and their classification as far as Biological Process Gene Ontology is concerned was performed.

Differentially expressed genes were then categorized into functional categories based on annotations, to get molecular and physiological insights into the response of tomato plants to the pathogen.