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Poster Abstract – G.03

CHARACTERIZING THE TRANSCRIPTOME OF HcrVf12-TRANSFORMED RESISTANT APPLE IN RESPONSE TO *VENTURIA INAEQUALIS* INOCULATION

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Background: To understand the gene networks that underlie plant defense responses, it is necessary to identify and characterize the genes that respond to the pathogen infection. My research investigated the incompatible interaction between apple and the fungal pathogen *Venturia inaequalis*, causal agent of apple scab. A transcriptomic approach was used.
As plant material, scab resistent transgenic apple lines of cv Gala for the R gene *HcrVf 2* were used, in comparison to Gala *wild type* (scab susceptible). *HcVf2* codify for a putative LRR receptor-like protein, involved in the pathogen recognition, and confers resistance to apple cv. Gala.
A PCR-based suppression subtractive hybridization was used to collect ESTs (Expression Sequence Tags) that are differentially expressed in apple resistant genetically modified genotypes after infection with *V. inaequalis*.

Results: A subtractive library of 524 ESTs was constructed from infected scab-resistant apple leaves. This collection is enriched in sequences involved in the incompatible interaction between Gala GM lines and *V. inaequalis*.
A putative function was assigned to 331 ESTs (representing the 63.2% of the total collection) by BlastN and BlastX search against public database. The other clones had no homologies with known sequences or were similar to not annotated expressed or putative proteins. Genes of known functions were sorted into 12 primary functional categories. The largest set of genes was assigned to Primary metabolism (14%) and the smaller one to Cell Growth (less than 1%). Other important categories were Disease Defence, Signal Transduction, Transcription ande Cell Wall in which many putative resistance genes were classifed (40%).
Although functional assignment based only on sequence homology needs experimental verification, it nonetheless provides a measure of the diversity of the genes in the stress cDNA collection. In fact, genes from all the major functional categories are represented in the collection.