

Mapping of apple genes found to be expressed during the *Erwinia amylovora:Malus* interaction

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The necrogenic enterobacterium, *Erwinia amylovora* (Ea) is the causal agent of the fire blight (FB) disease of many Rosaceae species, including apple and pear. During the infection process, the bacteria induce an oxidative stress response with kinetics similar to those induced in an incompatible bacteria-plant interaction. In order to understand the mechanisms that distinguish resistant and susceptible responses in FB resistant and susceptible apple genotypes after inoculation with Ea, differentially expressed genes were identified by cDNA-AFLP analysis. cDNA was isolated from M.26 (susceptible) and G.41 (resistant) apple tissues collected 2 and 48h after challenge with a virulent Ea strain or mock (buffer) inoculated. To identify differentially expressed transcripts, electrophoretic banding patterns obtained from cDNAs treated with the Licor cDNA-AFLP kit. In the AFLP experiments, using both kits, M.26 and G.41 showed different patterns of expression, including genes specifically induced, not induced, or repressed by Ea. In total, 190 EST's differentially expressed between M.26 and G.41 were identified using 42 pairs of AFLP primers. cDNA-AFLP analysis of global EST expression in a resistant and in a susceptible apple genotype identified three major classes of genes. Sequencing data for the EST's showed that genes linked to resistance, encoding proteins involved in perception, signaling, defense and apoptosis, were modulated by Ea in its host plant. The time course of expression of some of these EST's selected via a bioinformatic analysis has been determined. Some of these EST's have been also mapped

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