

Profiling of pathogenesis-related genes by heterologous EST mapping*

EST-driven prediction identified 4,935 genes (16% of the total *Arabidopsis* genome) which, according to the origin of EST sets, were associated with defense responses in the reference genome. Profiles of defense-related genes, obtained by mapping of heterologous EST, represent putative *Arabidopsis* homologs of the corresponding species. Comparison of these profiles in pairs and locating common genes allowed estimating similarity between defense-related gene sets of different plant species (Fig.1). To experimentally support computer data, we arbitrarily selected a number of transcription factor genes (TF) detected by EST mapping. Their expression levels were examined by real-time polymerase chain reaction during infection with yellow strain of *Cucumber mosaic virus*, a compatible virus systemically infecting *Arabidopsis* (Fig.2). Sixty five percent of the designated TF were upregulated in accordance with the EST-generated profile (Fig.3). We thus demonstrated that heterologous EST mapping may be efficiently used to reveal genes involved in host defense responses to pathogens. Upregulated genes identified in this study substantially overlap with those previously obtained by microarrays. As a whole, two independent approaches (microarray and computer-generated gene profiling) reveal the same classes of functionally related genes with expression levels elevated as a result of defense response. These include groups of genes involved in general plant metabolism (photosynthesis, protein synthesis, mitochondrial genes) alongside with genes of host stress and defense responses.

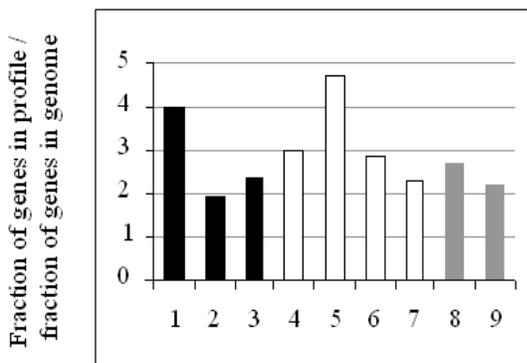


Figure 1. Involvement of different functional groups of *Arabidopsis* genes in host response against pathogens. Genes related to the general plant metabolism (black shaded columns): 1 – photosynthesis, 2 – mitochondrion, 3 – protein synthesis. Abiotic stress-responsive genes (clear columns): 4 – oxidative stress, 5 – cold, 6 – heat, 7 – water deprivation. Biotic stress-responsive genes (grey columns): 8 – fungi, 9 – bacteria. The ordinates represent a ratio between a fraction of functionally related genes in profile and a fraction of functionally related genes in the whole genome i.e. overrepresentation of the genes in the functional group as compared to the whole genome.

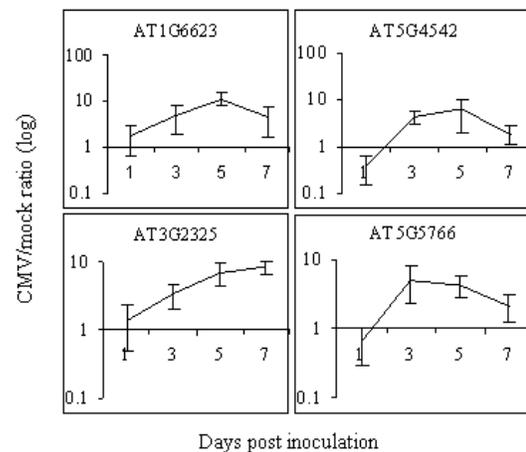


Figure 3. Activation of Arabidopsis TF genes during viral infection. The ratio between infected and control plants (CMV(Y)/mock) represents gene expression level. Maximum expression level of four TF genes was 5 to 11 times greater in infected plants as compared to healthy plants. Bars represent confidence intervals ($n=0.05$).



Figure 2. Symptoms on CMV(Y)-infected *A. thaliana* plants ecotype Col-0. A, Mock-inoculated plant. B, CMV(Y)-infected plant, 3 dpi. C, CMV(Y)-infected plant, 7 dpi.