

## A Platform for Functional Genomics of Pepper

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Large-scale single-pass sequencing of cDNA libraries and microarray analysis have proven to be useful tools for discovering new genes and studying gene expression. As a first step in elucidating the defense mechanisms in hot pepper plants, a total of 100,000 expressed sequence tags (ESTs) were generated and constructed as a public database. The cDNA microarray which contain 4,815 independent pepper clones is developed and gene expression analysis identified 613 hot pepper genes that were transcriptionally responsive to the non-host soybean pustule pathogen *Xanthomonas axonopodis* pv. *glycines* (*Xag*). Several functional types of genes, including those involved in cell wall modification/biosynthesis, transport, signaling pathways and divergent defense reactions, were induced at the early stage of *Xag* infiltration. In contrast, genes encoding proteins that are involved in photosynthesis, carbohydrate metabolism and the synthesis of chloroplast biogenetic proteins were down-regulated at the late stage of *Xag* infiltration. These expression profiles share common features with the expression profiles elicited by other stresses, such as fungal challenge, wounding, cold, drought and high salinity. We also identified several novel transcription factors that may be specifically involved in the defense reaction of the hot pepper. All the gene expression data were constructed as a public database and opened to research community. Strategies for functional analyses of selected candidate genes by gain-of-function (overexpression) and loss-of-function (virus-induced gene silencing) will be presented in the symposium. This is the first report of large-scale sequencing and transcriptome analysis of the pepper plant species and will serve as a platform for functional genomics of pepper plant.