

Analysis of Hot Pepper Promoters and Gene Expression Regulation

PAEK Kyung-Hee

College of Life Sciences, Korea University, Seoul, Korea

Basically the useful promoters are valuable tools for effective control of gene expression related to various developmental and environmental condition. In practical terms, the promoter itself is a very valuable asset as a patent and can be used for development of pathogen and harsh environment resistant crop plants and/or increasing the crop yield in a favorable environmental manner. And moreover, useful promoters from hot pepper can be directly used for other *Solanaceae* family crop plants. So far it usually required long time and a lot of efforts to isolate useful promoters. Genome Walker PCR experiment for isolation of promoters of mainly already characterized genes in the lab and northern blot analysis for characterization of new genes were paralleled to obtain the ambitious quantitative result. For the functional analysis of promoters, promoter deletion study with GUS reporter system was carried out for dissection of useful domain search. In addition, *in vivo* functional study was done by introducing these promoters into model plant, tobacco plant. Proteomic approach combined with important domain binding method was also launched to analyze specific factors including transcription factors which can bind to a specific domain. Finally the thorough functional analysis of the useful promoters will eventually contribute to analysis of hot pepper genome and development of useful crops.

Expression Profiles of Hot Pepper Genes Following Pathogen Infection

LEE Sanghyeob, KIM Soo-Yong, CHUNG Eun-Joo, JOUNG Young-Hee, PARK Jeong Mee, HUR Cheol-Goo, PAI Hyun-Sook and CHOI Doil

Korea Research Institute of Bioscience and Biotechnology, Daejeon, Korea

Large-scale single-pass sequencing of cDNA libraries and microarray analysis have proven to be useful tools for discovering new genes and understanding biological processes. As a first step to understand the mechanism of plant defense in hot pepper, a total of 8,525 expressed sequence tags (ESTs) of which were generated and analyzed *in silico*. Clustering analysis revealed that 4,685 ESTs (55%) were unique and 323 (7%) ESTs were tentatively identified as being unique to hot pepper. Functional classification of the ESTs derived from pathogen-infected pepper leaves indicated that about 25 Xag) infiltration, the cDNA microarray analysis was carried using 4,685 unigen array. The genes coding metabolism-related functions were either dynamically up- or down-regulated during the defense reaction. The expression levels of defense, signal transduction component, transcription regulator, and transport facilitator-related genes were increased during the defense reaction. However, transcription of photosynthesis, carbohydrate metabolism and chloroplast biogenesis-related genes was suppressed during the defense reaction. Overall, our study represents the first analysis of sequence data and non-host defense related genes from the hot pepper plant species.