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Isolation and Characterization of Jasmonic Acid Carboxyl Methyltransferase Gene from *Capsicum annuum* L.

Min Sik Song[P], Sun Hi Lee[C]

Department of Biology, Yonsei University, Seoul 120-749

Methyl jasmonate, the methyl ester of jasmonic acid, is a plant volatile hormone that acts as an important cellular regulator mediating diverse developmental process and defense responses. Methyl jasmonate is synthesized from methylation of jasmonic acid. Jasmonic acid carboxyl methyltrasferase (JMT) catalyzes the methylation of jasmonate to form methyl jasmonate. It has been reported that the JMT cDNA was isolated from *Arabidopsis thaliana* only. We isolated the JMT cDNA from *Capsicum annuum* L. leaves by PCR. The 389 amino acid sequence deduced from JMT gene showed 92% identity to *Arabidopsis thaliana*. Southern blot analysis showed that JMT gene is present in genome as a few copies. Nothern blot analysis showed that the JMT transcript was not detectable. We performed RT-PCR, and the productswere analyzed by using a JMT gene-specific probe because JMT transcript quantity was very few. Southern blot analysis showed that JMT transcript levels increased by wounding in leaves. 40M methyl jsamonate induced JMT gene expression in leaves. The transcript level of JMT started to increase 10 minutes after wound and maintained 1 to 4 hour

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Identification and Characterization of Genes Responding to Temperature Stresses in Chinese Cabbage Using cDNA Microarray

Hayoung Song[P], Yunmi Kim[1], Sooryun Choi[1], Yong-Pyo Lim[1], Kwan-Sam Choi[1], Sangdun Choi[2], Yoonkang Hur[C]

[PC1]Genome Research Center, Chungnam National University, Daejon 305-764; [2]California Institute of Technology, Pasadena, CA 91125, USA

To identify and characterize genes responding to temperature stresses, we have carried out a microarray experiment with chinese cabbage leaf ESTs. The temperature stresses, chilling and heat-shock, were treated by the exposure to 100 mol photons m-2s-1 at 5? and 32?for 1-12 h, respectively. In the case of light-chilling experiment, 1,545 clones among 2,688 clones on a chip show the clean signal and 227 clones were changed more than 8-fold in terms of transcript levels. The latter clones consist of 115 up-regulated and 112 down-regulated ones. Up-regulated genes included chilling or drought stress resistant genes, auxin-repressed protein gene, and genes associated with membrane lipid fluidity. Down-regulated genes are composed of Rubico activase and geneswhose functions are unknown up to date. From heat-shock experiment, we obtained 90 clones showing more than 4-fold changes in expression. Sixty up-regulated clones include heat-shock protein genes, genes associated with defense and stress resistance, and 21 putative protein genes. Thirty down-regulated genes were related to signal transduction, cell growth and metabolism, and unknown function (11 clones). We further confirmed the microarray data by the northern blot analysis.

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Study on the Expression Pattern of Genes Associated with Flowering in Chinese Cabbage Plants

Hyunseung Jang[P], Yong-Pyo Lim[1], Yoonkang Hur[C]

Genome Research Center, Chungnam National University, Daejon 305-764

To understand the flowering mechanism in chinese cabbage plants, 35 flowering-related genes were cloned by using degenerated primers and RT-PCR, and their expression patterns were examined by a dot blot analysis. Allfloral genes were spotted on a membrane and hybridized with probes generated by reverse transcription. During the photoperiod, the big changes in the expression were observed from circadian rhythm related genes, such as *CO* (increased in the dark period) and *LHY* (induced in the dark period). Vernalization affects a gene *NAP* expression only in A line, which is the first observation in this study. However, most genes tested in this experiment did not show the detectable signal, implying either that those genes are expressed at very low level or that they are not expressed in the tested tissues. During flower development, flower identity-associated genes, such *API*, *AP2* and *PI*, were remarkably induced. We are examining the expression pattern of the floral genes under various conditions and tissues, and trying to clone a full-length *NAP* cDNA for further study.

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Identification, Genomic Organization and Expression Characteristics of *hsp* Gene Family in *Brassica rapa*

Yunmi Kim[P], Dal-Hoe Koo[1], Yong-Pyo Lim[1], Jae-Wook Bang[1], Yoonkang Hur[C]

Genome Research Center, Chungnam National University, Daejon 305-764

Heat-shock proteins confer to protect organisms from external stresses as well as to buffer against internal signals. The 90-kDa heat-shock protein (Hsp90) family includes members and is essential molecular chaperone that plays a role in the folding and activation of proteins involved in signal transduction and control of cell cycle. Chinese cabbage (*Brassica rapa*), the very important vegetable in Korea, is hardly cultivated during the summer season when temperature is very high. To examine the heat-shock associated genes, we have carried out a microarray experiment with the chinese cabbage leaf ESTs and RNA samples extracted from heat-shock treated leaf discs. We obtained 9 different *hsp90* genes from the study and among them three genes showed very high homology, but rest has very low sequence similarity. However, all 9 genes were upregulated upon the heat-shock stress and levels of transcripts increased more than 4 fold. We further confirmed the microarray data by a northern blot analysis. We will also present the FISH (florescent in situ hybridization) results on 10 chromosomes of the plant and expression characteristics of the genes.