F235

Molecular Characterization of Genes Controlling the Sex Determination in a Cucumber Plant

Yoonkang Hur[C], Jeongki Cho[P], Youngsun Kwon[2], Dal Hoe Koo[1], Jeong Ran Lee[3], Jae Wook Bang[1]

[PC1]Department of biology, Chungnam National University, Daejon 305-764; [2]Kangwon National University, Chuncheon 200-701; [3]Sogang University, Seoul 100-611

Cucumbers (*Cucumis sativus* L.), one of the most important vegetable crops, have three types of sex expression. Monoecious is the most common type, and gynoecious and hermaphroditic are rare. The sex determination of the common type of cucumber is usually controlled by phytohormones, temperature and photoperiod. We have cloned and characterized genes controlling sex in a Korean cultivar (Winter Long) grown in two different photoperiods, a long day and short day conditions, which confer female and male flower development, respectively. Using DDRT and northern blot analysis, we cloned 20 female specific and 8 male specific genes. One of male specific clones has very high similarity to a GenBank enrolled clone (AF104393), but the function is not kwnown. To examine the function of this clone, we introduced the clone with antisense orientation into a cucumber plant . We will discuss further expression characteristics of clones and transgenesis results.

F236

Regulation of *trans*-Cinnamic Acid 4-Hydroxylase (C4H) Gene Expression Under Wound Stress in *Campothetica acuminata*

Dong Gwan Kim[P], Young Jin Kim[1], Sun Young Kim[2], Incheol Lee[2], Sun Hi Lee[C]

[PC1]Department of Biology, Yonsei University, Seoul 120-749; [2]Department of Biology, Daejeon University, Daejeon 300-716

Plant defense is regulated by multiple signal transduction pathways in which hydrogen peroxide, methyl jasmonate, ethylene and wounding function as signaling molecules. To study the regulation of the C4H gene expression in *Camptotheca acuminata*leaves under wound stress, we analyze the effect of hydrogen peroxide, methyl jasmonate, ethylene and wounding on the CaC4H gene expression. When exogenous methyl jasmonate and hydrogen peroxide were applied for 24 hrs, its expression was increased in detached leaves. Wounding also induced CaC4H mRNA accumulation within 2 hours after treatment. Whereas 10ppm of ethylene treatment showed no differences between control and treatment times in detached leaves. But CaC4H transcript accumulation was advanced 1 hour when treated with wounding and ethylene together in leaf disk. It suggest that ethylene is involved in wounding signal transduction pathway and it play as a signal molecule in *Camptotheca acuminata*gene expression under wound stress.

F237

Cloning of Sex-associated Genes from a Dioecious *Rumex acetosa* Plant

JiYoung Park[P], Dong Chun Jin[1], Dal-Hoe Koo[1], Jae-Wook Bang[1], Yoonkang Hur[C]

Department of Biology, Chungnam National University, Daejon 305-764

Rumex acetosa L. is a dioecious flowering plants with a well developed sex chromosome system: 2n=2X=14 (XX) in the female plants and 2n=2X=15 (XY1Y2) in the male plants. To isolate sex determination genes, we have applied three methods: RAPD and AFLP analyses, and DOP-PCR followed by chromosome dissection.As a result of RAPD analysis, one male specific band was obtained, which is about 1,5 kbp in size. One end of this DNA has high similarity (85-95%) with the Y-chromosome specific repetitive sequence of *Rumex acetosa* reported previously. As a result of Southern blot with separated fragments, one region appeared male enrich as same as the previous report, whileanother region of the clone male specific. The results were confirmed by FISH. From AFLP analysis using genomic DNA, 19 DNA fragments specific to either male or female plants were obtained. After reverse Southern blot analysis, 3 male specific AFLP cloneswere obtained. To clone markers very specific either sex chromosomes, X or Y chromosome was dissected out and performed DOP-PCR. Then, the DOP-PCR product was subjected to AFLP analysis. A total of 1,749 AFLP bands were obtained: 658 specific to X chromosome, while 1,091 specific to Y chromosome. From reverse Southern blot analysis, we identified 5 AFLP clones specific to X chromosome and 21 AFLP clones specific to Y chromosome. We are now applying molecular biology tools as well as molecular cytogenetic techniques in order to obtain more informations for above clones.

F238

Identification and Characterization of Genes Involved in Change of Sugar Content Using a Microarray

Gun Ho Lee[P], Yunmi Kim[1], Sonorous 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

Chinese cabbage plants (*Brassica rapa*) are very important vegetable in Korea and usually harvested after a heavy frost for the good taste. After the frost, the leaf sugar content increased more than 3 fold. We hypothesized that there are big changes in the expression of genes associated with sucrose biosynthesis and transport. However, it turned out that no remarkable changes occurred. To identify and characterize genes regulating sugar contents, we have carried out a microarray experiment with chinese cabbage leaf ESTs and RNA samples extracted from mature leaf and the leaf exposed to a heavy frost. Among 2,688 spotted clones, 63 and 464 clones were upregulated and down-regulated more than 4 fold, respectively. We selected and further analyzed 15 upregulated clones whose transcript levels were changed more than 6 fold. Half of the genes belong to unknown function up to date and others are related to calcium signal transduction. We also analyzed 11 clones showing over 14 fold down-regulation. These down-regulated genes are mostly photosynthesis-related ones. We further confirmed the microarray data by northern blot analysis and transformed unknown genes to *Arabidopsis*.