1-17. Hypersensitive and Apoptotic Responses of Pepper Fruit Against *Xanthomonas axonopodis* pv. *glycines* Infection

Sung Pae Chang and Young Ho Kim
Graduate School of Agricultural Biotechnology and Center for Plant Molecular Genetics & Breeding Research, Seoul National University, Suwon 441-744, Korea

Generally, plants defend themselves against pathogens by structural and biochemical reactions. Defense structures act as physical barriers and inhibit the pathogen from gaining entrance and spreading through the plant. *Xanthomonas axonopodis* pv. *glycines,* the causal pathogen of bacterial pustule of soybean, causes hypersensitive response (HR). When pepper fruits were inoculated with *X. axonopodis* pv. *glycines*, *in situ*, time-series defense-related structural changes occurred in the inoculated sites. Early responses were programmed cell death (PCD), characterized by condensation and vacuolization of the cytoplasm, condensation of nuclear materials, and fragmentation of the nuclear DNA, which were observed by transmission electron microscopy. Nuclear fragmentation was proven by TUNEL method under confocal laser scanning microscopy and DNA laddering through eletrophoresis. At later stages, plant responses were cell elongation and cell division, forming a periderm-like boundary layer that demarcated healthy tissues from the inoculation sites. Using several stains such as toluidine blue, sudan Ⅳ, annexin V, and phloroglucinol-HCl, defense-related materials and structural changes were also examined.

1-18. Identification of differentially displayed genes from a soybean (*Glycine max*) cultivar resistant to a strain of *Pseudomonas aeroginosa*

Hyeon Wook Cha[1], Sang-Gu Kang[2], Moo Ung Chang[1,2] and **Euiho Park**[1,3]
[1]Institute of Biotechnology, [2]Department of Biology, [3]Department of Agronomy, Yeungnam University, Gyeongsan 712-749, Korea

We found a soybean (*Glycine max*) cultivar 561 that was strongly resistant to a virulent bacterial strain of a *Pseudomonas spp.* Further identification revealed that the *Pseudomonas spp.* was a strain of *Pseudomonas aeruginosa.* Furthermore we identified specific genes involved in the resistance of soybean 561 and analyzed the pattern of gene expression against the *Pseudomonas* infection using differential-display reverse transcription PCR (DDRT-PCR). More than 126 cDNA fragments representing mRNAs were induced within 48 hours of bacteria inoculation. Among them, 28 cDNA fragments were cloned and sequenced. Twelve differentially displayed clones with open reading frames had unknown functions. Sixteen selected cDNA clones were homologous to known genes in the other organisms. Some of the identified cDNAs were pathogenesis-related genes (PR genes) and PR-like genes. These cDNAs included a putative calmodulin-binding protein, an endo-1,3-1,4-b-D-glucanase, a b-1,3-endoglucanase, a b-1,3-exoglucanase, a phytochelatin synthetase-like gene, a thiol protease, a cycloartenol synthase, and a putative receptor-like serine/threonine protein kinase. Among them, we found that four genes were putative pathogenesis-related genes (PR) induced significantly by the *P. aeruginosa* infection. These included a calmodulin-binding protein gene, a b-1,3-endoglucanase gene, a receptor-like serine/threonine

protein kinase gene, and pS321 (unknown function). These results suggest that the differentially expressed genes may mediate the strong resistance of soybean 561 to *Pseudomonas aeruoginosa*.

1-19. CGMMV Resistant Watermelon Stock

Sung Jegal[1], Bo Young Jeon[1], Nam Han Her[1], Jang Ha Lee[1], Min Jung[1], Ki Hyun Ryu[2], Sang Lyul Han[1], Yoon Sup Shin[1], Seung Gyun Yang[1] and Chee Hark Harn[1].
[1]Biotechnology Center, Nong Woo Bio Co., Ltd., Jeongdan, Ganam, Yeoju, Kyonggi, Korea;
[2]Dept. of Horticultural Science, Seoul Womans University, Seoul, Korea

In order to cultivate watermelon on farm, grafting of the watermelon seedling to the watermelon stock is necessary because the watermelon root is less viable than the root of watermelon stock. Recently, commercially important watermelon varieties further require a resistant stock against especially CGMMV to control the heavy loss of the total yield of watermelon by CGMMV infection. Therefore, we have set out a project to develop a CGMMV-resistant watermelon stock. We have successfully transformed dozens of watermelon stocks (gongdae) during last two years especially using a cDNA encoding the coat protein of CGMMV (cucumber green mottle mosaic virus). Recently we have tested levels of resistance of those watermelon stocks against CGMMV infection. For CGMMV inoculation, the leaves of one month old gongdae (T1) were rubbed by carborundum mixed with the CGMMV. A total of 140 plants (T1) were exposed to the CGMMV and we found that ten plants were completely resistant to virus infection. This is the first report that by genetic engineering a cucubitaceae crop resistant to CGMMV infection is ever developed. Further information will be provided in the poster.

1-20. Association of Aster Yellow Phytoplasma with Witches' Broom Disease of Ash (*Fraxinus rhynchophylla* Hence) in Korea

Sangsub Han[1], Tae Heon Lim[2], and Byeongjin Cha[1]
[1]Dept. of Agricultural Biology, Chungbuk National University, Cheongju 361-763, Korea,
[2]Technology Innovation Center, Sangju National University, Sangju 742-711, Korea

Typical whiches broom symptoms caused by phytoplasma were observed in Ash (*Fraxinus rhynchophylla* Hence) in Korea. The symptoms were showing abnormally small leaves, short internodes, and proliferation of shoots. Fluorescence and electron microscopy of leaf midribs revealed phytoplasma positive DAPI fluorescence and numerous phytoplasma bodies localized in the phloem sieve tubes. Phytoplasma DNA of 1.8 Kb was detected consistently from all symptomatic samples by the amplification of phytoplasma DNA with the phytoplasma specific primer pair P1/P7. But no phytoplasma DNA was detected in healthy ash seedlings. Based on sequence analyses of an amplified region, this phytoplasma is closely related to Eqilodium phyllody, Mulberry dwarf, and Aster yellows phytoplasmas with the homology of 99.95 %, 99.79 % and 99.78 %, respectively, This phylogenetic analyses indicate that ash witches broom phytoplasma but is evidently distinct from the ash yellows group 16SrVII and should be classified into the Aster yellows group 16SrVI.