To better understand plant defense responses against pathogen attack, we identified the transcription factor-encoding genes in the hot pepper *Capsicum annuum* that show altered expression patterns during the hypersensitive response raised by challenge with bacterial pathogens. One of these genes, *Ca1244*, was characterized further. This gene encodes a plant-specific Type IIIA - zinc finger protein that contains two Cys_2His_2 zinc fingers. *Ca1244* expression is rapidly and specifically induced when pepper plants are challenged with bacterial pathogens to which they are resistant. In contrast, challenge with a pathogen to which the plants are susceptible only generates weak *Ca1244* expression. *Ca1244* expression is also strongly induced in pepper leaves by the exogenous application of ethephon, an ethylene releasing compound. Whereas, salicylic acid and methyl jasmonate had moderate effects. Pepper protoplasts expressing a Ca1244-smGFP fusion protein showed Ca1244 localizes in the nucleus. Transgenic tobacco plants overexpressing *Ca1244* driven by the CaMV 35S promoter show increased resistance to challenge with a tobacco-specific bacterial pathogen. These plants also showed constitutive upregulation of the expression of multiple defense-related genes. These observations provide the first evidence that an Type IIIA - zinc finger protein, Ca1244, plays a crucial role in the activation of the pathogen defense response in plants.

1-33. Functional analysis of genes involved in rice disease resistance

S.H. Shin, S. R. Yun, Y. C. Kim, B. H. Cho
College of Agriculture and Life Sciences, Chonnam National University, Gwangju 500-757, Korea

Several plant and microbial genes that could confer disease resistance in transgenic rice plants are being cloned and characterized. We are currently constructing transgenic rice lines that overexpress the gene products, such as a galactinol synthase, a defensin, and a bacterial ACC deaminase. Subtractive hybridization of a rice cDNA library constructed from the *Xanthomonas oryzae*-infected rice leaves resulted in isolation of many inducible cDNA clones including a elongation factor EF2, a oryzain alpha, a catalase, a aldehyde dehydrogenase, a S-adenosylmethionine synthetase, a caffeic acid O-methyltransferase, a glyceraldehyde-3-phosphate dehydrogenase, a light-regulated protein, WRKY transcription factors, and a nucleotide diphosphate kinase. Some genes among those may be useful genetic sources for construction of disease resistant transgenic rice. Full lengths of the rice *OsFIERG* and a rice oryzain genomic clones were cloned, and serial deletion fragments of the promoter regions of these genes were fused with GUS reporter gene in pCAMBIA1201, respectively. Promoter activities of these constructs will be examined upon various stresses and pathogen infections to obtain the pathogen specific inducible-promoter. This work was supported by a grant from BioGreen 21 Program, Rural Development Administration, Republic of Korea.

1-34. Hot Pepper Functional Genomics : Monitoring of Global Gene Expression Profiles During Non-Host Resistance Reactions in Hot Pepper Plant (*Capsicum annuum*).

Sanghyeob Lee, Eun-Joo Chung, Doil Choi
Plant Genomics Lab., KRIBB, Daejeon, Korea

Since hot peppers (*Capsicum annuum* L.) are getting reputation as an important source of vitamins, medicine and many other areas, consumption and cultivation is being increased in the world. In spite of this usefulness, so little attention has been given to the hot pepper plants. To date, less than 500 nucleotide sequences including redundancy has been identified in NCBI database. Therefore we started to EST sequencing project for initial characterization of the genome, because of the large genome size of hot pepper (2.7 3.3 X 109 bp), To date, a set of 10,000 non-redundant genes were identified by EST sequencing for microarray-based gene expression studies. At present, cDNA microarrays containing 4,685 unigene clones are used for hybridization labeled targets derived from pathogen infected and uninoculated leaf tissues. Monitoring of gene expression profiles of hot pepper interactions with soybean pustule pathogen (*Xag*; *Xanthomonas axonopodis* pv. *glycine*) will be presented.

1-35. Platform of Hot Pepper Stress Genomics: Identification of Stress Inducible Genes in Hot Pepper (Capsicum annuum L.) Using cDNA Microarray Analysis

Eun-Joo Chung, Sanghyeob Lee, Doil Choi
Plant Genomics Lab, KRIBB, Daejeon, Korea

Although plants have evolved to possess various defense mechanisms from local biotic and abiotic stressors, most of yield loss is caused by theses stressors. Recent studies have revealed that several different stress responsive reactions are inter-networking. Therefore, the identification and dissection of stress responsive genes is an essential and first step towards understanding of the global defense mechanism in response to various stressors. For this purpose, we applied cDNA microarray analysis, because it has powerful ability to monitor the global gene expression in a specific situation.

To date, more than 10,000 non-redundant genes were identified from seven different cDNA libraries and deposited in our EST database (http://plant.pdrs.re.kr/ks200201/pepper.html). For this study, we have built 5K cDNA microarray containing 4,685 unigene clones from three different cDNA libraries. Monitoring of gene expression profiles of hot pepper interactions with biotic stress, abiotic stresses and chemical treatments will be presented. Although this work shows expression profiling at the sub-genomic level, this could be a good starting point to understand the complexity of global defense mechanism in hot pepper.

1-36. The cloning and characterization of the small GTP-binding protein RacB in rice.

Young-Ho Jung and Nam-Soo Jaw.
Department of Molecular Biology, Sejong University, Seoul 143-747, Korea

Plants have evolved along with pathogens, and they have developed sophisticated defense systems against specific microorganisms to survive. G-protens are considered one of the upstream signaling components working as a key for the defense signal transduction pathway. For activation and inactivation of G-protein, GTP-biding proteins are involved. GTP-binding proteins are found in