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

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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.

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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

all organisms. Small GTP-binding proteins, having masses of 21 to 30kD, belong to a superfamily, often named the Ras superfamily because the founding members are encoded by human Ras genes initially discovered as cellular homologs of the viral ras oncogene. Members of this superfamily share several common structural features, including several guanine nucleotide binding domains and an effector binding domain. However, exhibiting a remarkable diversity in both structure and function. They are important molecular switches that cycle between the GDP-bound inactive form into the GTP-bound active form through GDP/GTP replacement. In addition, most GTP-binding proteins cycle between membrane-bound and cytosolic forms. such as the RAC family are cytosolic signal transduction proteins that often are involved in processing of extracellular stimuli. Plant RAC proteins are implicated in regulation of plant cell architecture secondary wall formation, meristem signaling, and defense against pathogens. But their molecular mechanisms and functions are not well known. We isolated a *RacB* homolog from rice to study its role of defense against pathogens. We introduced the constitutively active and the dominant negative forms of the GTP-binging protein *OsRacB* into the wild type rice. The dominant negative forms are using two forms (full-sequence and specific RNA interference with RacB). Employing southern, and protein analysis, we examine to different things between the wild type and the transformed plant. And analyzing biolistic bombardment of onion epidermal cell with GFP-RacB fusion protein revealed association with the nucle.

1-37. Molecular characterization of a novel rice(*Oryza sativa* L.) MAP kinase, *OsEDR1*, its role in defense signaling pathway.

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Plants have evolved differently from animals having mobile activities. Thus, plants should have developed unique defense mechanisms against biotic/abiotic stresses to which plants are differently exposed, according to seasons. Most organisms have an conserved signaling network using mitogen-activated protein kinase (MAPK) cascade(s). The phenomenon implied that they are functionally very important in all organisms. In fact, they constitute one of the major components of signaling pathways involved in regulating a wide range of cellular activities from growth and development to cell death. Recently, complete MAPK cascade was first characterized in Arabidopsis from the receptor kinase (FLS2) through following MEKK1-MKK4/MKK5-MPK3/MPK6-WRKY22 /WRKY29 pathway. Whereas, MAPK cascade signaling pathway in monocot plant including rice (*Oryza sativa*. L.), the most important of all food crops and an established monocot plant research model, MAPKinase kinase kinases (MAPKKK) of rice are the first upstream component of the MAPK cascade, but MAPKKK has been first identified and characterized in our lab and designated as, *OsEDR1* based on its homology with the Arabidopsis *EDR1*. The Arabidopsis *EDR1* was regarded as a negative regulator of defense response and the role of rice OsEDR1 was analyzed. Transcriptional regulation of *OsEDR1* was detected under various stresses and immunoblotting analysis is going on to detect the level of OsEDR1 protein in the mutants showing unique phenotype. We also introduced the constitutively active and the dominant negative forms of the