

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-binding 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.

Jung-A Kim and Nam-Soo Jwa.

Department of Molecular Biology, Sejong University, Seoul 143-747, Korea

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

OsEDRI for characterizing biological function.

1-38. Etiology of Rice Seedling Disease in Water-Seeded Rice.

Jung-Bo Sim¹, Young-Sook Moon¹, Hyoui-Won Choi², Se-Chul Chun¹.

¹Department of Crop Science, Konkuk University, Kwangjingu, Seoul 143-707, ²Division of Plant Pathology, National Agricultural Institute of Science and Technology, RDA, Suwon 441-707

Rice seedling disease is one of major problems in water-seeded rice. This disease is known to be caused by several pathogen such as *Pythium*, *Achlya*, and *Fusarium* species. However, seedling disease of rice in water-seeded rice in Korea is not extensively studied. *Pythium* species have been isolated from Seosan, Yeosu, Icheon areas using *Pythium* selective media and their pathogenicity was investigated. All of the *Pythium* isolates showed strong pathogenicity causing seedling emergence reduction in water-seeded rice. Seedling emergence was reduced to 0~9% at 10 days after inoculation of 23 *Pythium* isolates compared to 60% of noninoculated control in a growth chamber. However, *Fusarium* species did not cause seedling emergence reduction in water-seeded rice. In contrast, when no water added into water agar or soil, the pathogen caused seedling rot two weeks after planting. These results indicate that *Pythium* species is a cause of seedling disease in water-seeded cultivation areas in Korea.

1-39. Isolation and Characterization of Pathogen inducible Leucine Zipper containing Gene from rice (*Oryza sativa* L. cv. Dongjin)

Sang-Ryeol Park¹, Hae-Sook Song¹, Kyung-Mi Moon¹, Duk-Ju Hwang¹, Tae-Ho Kim¹, Seong-Sook Han², Seung-Joo Go¹, Myung-Ok Byun¹.

¹Molecular Physiology Division, National Institute of Agricultural Biotechnology, ²Crop Environment and Biotechnology Division, National Crop Experiment Station, RDA, Suwon 441-707, Korea

A full length cDNA, *OsLEUZIP*, encoding leucine zipper containing protein from rice EST of rice (*Oryza sativa* L. cv. Dongjin) treated *Xanthomonas oryzae* pv. *oryzae* 10331. *OsLEUZIP* contains 1,227 bp nucleotides and encodes a protein of 408 amino acid residues with predicted molecular weight of 47,229 Da. The deduced amino acid sequence of *OsLEUZIP* has consensus sequence of leucine zipper from PROSITE (PDOC00029), L-X(6)-L-X(6)-L-X(6)-L. *OsLEUZIP* gene were preferentially induced in rice during incompatible interaction with *Xanthomonas oryzae* pv. *oryzae* 10331 and *Pyracuraria grisea* KJ-301. Expression of *OsLEUZIP* gene was also induced by treatment of abiotics such as ethephon and ABA. Our data represented in this study suggesting that *OsLEUZIP* gene may play an important role in the rice defense-related. Further studies of this gene, overexpression in rice, yeast-two hybrid assay, electrophoretic mobility shift assay and northern blot analyses of transgenic plant, would be useful to elucidate the role of the *OsLEUZIP* gene in defense responses of rice.