진균병학(생리, 저항성)

B-01. Sensitivity of *Magnaporthe grisea* to Edifenphos and Iprobenfos in Korea. Yun Sung Kim and Ki Deok Kim. Department of Agricultural Biology, Korea University, Seoul 136-701, Korea.

Sensitivity of *Magnaporthe grisea*, the causal agent of rice blast, to edifenphos and iprobenfos was assessed on fungicide-amended potato dextrose agar. In 1997 and 1998, 1,080 isolates of *M. grisea* were obtained from 11 locations (Chonju, Chunchon, Donghae, Gwangju, Haman, Ichon, Kangnung, Kimhae, Kwangju, Taejon, and Yangyang) represented a wide geographic distribution in Korea. With seven sensitive isolates of *M. grisea* from various locations, minimum inhibitory concentrations (MIC) of edifenphos and iprobenfos were determined at concentrations of less than 5% relative mycelial growth. The MIC's of edifenphos and iprobenfos were determined to be 20$\mu\ell$ a.i./ml and 55$\mu\ell$ a.i./ml, respectively. About 57 and 84% of the fungal populations sampled were resistant to edifenphos and iprobenfos, respectively. Sensitivity of *M. grisea* isolates to edifenphos also significantly (r=0.545, P=0.0001) correlated to that of iprobenfos. In addition, isolates from Chonju and Kwangju showed the greatest mycelial growth on edifenphos-amended media while isolates from Kwangju did on iprobenfos-amended media. The differences in the fungal sensitivity to the fungicides and among locations suggest that different sensitivity among *M. grisea* populations to edifenphos and iprobenfos exists in and across Korea.

B-02. Expression of Defense-Related Genes in Host and Non-Host Resistant Responses of Tobacco Against Pathogens. Sang-Keun Oh[1], Young-Chul Kim[1], Jong-Joo Cheong[1], Ingyu Hwang[2] and Doil Choi[1]. [1]Plant Cell Biotechnology Lab., KRIBB, P.O. Box 115, Yusung, Taejeon, 305-600, [2]Department of Applied Biology and Chemistry, SNU, Suwon 441-744, Korea

Plants respond to pathogen in various ways which include diseased symptoms, hypersensitive responses (HR), or no phenotypic change upon inoculation. In this study, we are using tobacco as a model plant to investigate the molecular responses of plants during host- and non-host-pathogen interactions. Following inoculation with five different pathogens, TMV (host and HR) and *Pseudomonas syringae* pv. *tabaci* 11528 (host and disease), *P. s.* pv. *syringae* 61 (non-host and HR) and *P. s.* pv. *phaseolicola* NPS3121 (non-host and HR), and *Xanthomonas campestris* pv. *glycines* 8ra (non-host and no HR), expression of twelve different defense-related genes was monitored in *Nicotiana tabacum* cv. Xanthi nc. When tobacco plants were inoculated with these pathogens, three different phenotypes, susceptible, HR, or null response were observed. Northern blot analyses revealed that the expression of twelve defense-related genes was almost identical among different responses regardless of interaction of tobacco as a host or non-host to the pathogens. Expression of pathogenesis-related genes in different types of interactions were temporarily coincided with the time of plant cell death after pathogen invading. Expression of secondary metabolite-associated genes were also similarly observed among three different reactions. Enhanced level transcripts of three HR-related genes, *hin*1, *hsr*203J and *Ng-CDM*1, were detected in tobacco by HR-inducing pathogens than inoculated with *X. c.* pv. glycines 8ra. However, no induction of *Ng-CDM*1 transcript by *X. c.* pv. *glycines* 8ra was observed. These results imply that there may present common defense signalling pathways in host- and non-host-pathogen interactions leading to expression of defense-related genes following early specific recognition between host (or non-host) plant and pathogen.

B-03. Molecular Characterization of Non-Host Resistance in Plant: Isolation of Non-Host Resistance-Related Genes of Hot Pepper Using DDRT-PCR Following Inoculation with a Soybean Pustule Pathogen(*Xanthomonas campestris* pv. *glycines*). So-Young Yi[1,2], Sang-Keun Oh[1], Seung-Hun Yu[2] and Doil Choi[1], [1]Plant Cell Biotechnology Lab. KRIBB, P.O. Box 115, 305-600, Korea. [2]Department of Agricultural Biology, CNU, Taejeon 305-764, Korea

The establishment of a plant-pathogen interaction involves changes in gene expressions in both organisms. For understanding the molecular mechanisms involved in non-host resistance in plant, we are using bean pathogen (*Xanthomonas campestris* pv. *glycines, Xcg*) and hot pepper plant (*Capsicum annuum* L.) as a model system. Wild type *Xcg*-8ra induce HR cell death on pepper within 12 hr of inoculation but a *hrpF*$^-$ mutant *Xcg* (8-13) did not. Eighty-two differentially expressed cDNA fragments (CaNR; *Capsicum annum* Non-host Resistance) were isolated by comparative DDRT-PCR following inoculation of *Xcg*-8ra and *Xcg*-8-13. Partial cDNA sequencing and data base analyses of all 82 clones revealed that 41 were known and 41 were unknown genes. From reverse Northern blot analysis, 46 clones were selected for further study. Northern blot analyses of these genes revealed that *Xcg*-induced changes in mRNA accumulation occurred rapidly, within 4 hr of inoculation, for the most of the CaNR clones. Enhanced level transcripts of CaNR 36, CaNR 40, CaNR 42, CaNR 51, CaNR 77a were detected in HR tissues of hot pepper inoculated with *Xcg*-8ra. Isolation and characterization of hot pepper genes whose expression is up-regulated by inoculation with bean pathogen *Xcg* will be presented.

B-04. In Situ Hybridization Study of Organ- and Pathogen-dependent Expression of a Novel Thionin Gene in Pepper Plant. Sung Chul Lee, Yeon Kyeong Lee, Ki Deok Kim and Byung Kook Hwang. Department of Agricultural Biology, Korea University, Seoul 136-701, Korea

Expression of a gene encoding the antifungal protein thionin by plant pathogens was investigated in pepper plants. Northern and *in situ* hybridization were performed to examine the temporal and spatial expression pattern of thionin mRNA in leaf and fruit tissues infected by anthracnose pathogens. Transcripts of *CATHION1* gene were more rapidly induced in pepper leaves at 4-leaf stage than at 8-leaf stage by *Colletotrichum coccodes* infection. Typical fungal anthracnose symptoms were observed on green pepper fruits inoculated with *Colletotrichum gloeosporioides*, but not on red pepper fruits. The transcript accumulation was more pronounced in green fruits than in red fruits upon *C. gloeosporioides* infection. The *CATHION1* transcripts were detected in the cells of phloems infected by anthracnose pathogens. In healthy, untreated plants, transcripts of *CATHION1* gene were induced in organ-specific manner, as revealed by RNA blot analysis and *in situ* hybridization. Low levels of the transcripts were detected in stems and roots, particularly in endodermis and phloem cells. However, high transcript levels were observed in all the cells of flowers.

B-05. Epidemiological Studies on *Phytophthora* Blight of Red Pepper. Park, Young Chul. Lee, Soon Gu. Hwang, Eui Hong. Department of Agricultural Biology, Andong National University

The experiment field that was located in Andong National University has continuously occured *Phytophthora* Blight of Red Pepper over the duration of period of 4 years. So The research tried to construct the estimate model to express the relationship between the meteorological factors and *Phytophthora* Blight of Red Pepper of the duration of period of 2 years (1997, 1998). The estimate model was selected variable of 2 kinds with the effective period and the effective condition of the disease outbreak. First, the effective period of the disease outbreak was selected from 1 to 40 day before the outbreak. Second, the effective condition of the disease outbreak was choosen with 4 factors, the mean of soil temperature, the mean of soil moisture, the cumulative hours of relative humidity = 100 % and the cumulative hours of rainfall.

B-06. A Plant Esterase Induces Disease Resistance in Plants. Moon Kyung Ko, Kwang Sang Kim, Young Soon Kim, Igor Kostenyuk, Hye Kyung Kee, Jaemo Yang & Boung-Jun Oh. Kumho Life and Environmental Science Laboratory, Korea Kumho Petrochemical Co., Ltd., 1Oryong-Dong, Puk-Ku, Kwangju 500-712, Korea

Carboxylesterases are enzymes that catalyze the hydrolysis of compounds containing an ester bond. In plant-microbe interactions, an esterase gene from the hypersensitive reaction and a lipase gene that is an essential component of R gene-mediated disease resistance have been recently isolated. However, physiological role of the enzymes in plant defense mechanisms is still unclear. In addition, many of phytopathogenic fungi secrete cutinases as esterases that break the ester linkages between cutin molecules of plant cuticles to invade plant. Another role of the cutinases is hypothesized to induce disease resistance in plant by generating cutin monomers from plant cuticles. We report here the cloning and characterization of an esterase gene of pepper (*Capsicum annuum*) that is accumulated to high levels only in the incompatible interaction with anthracnose fungus *Colletotrichum gloeosporioides*, but not in the compatible interaction. Exogenous applications of the pepper esterase inhibit appressorium formation that is prerequisite of the fungus to infect the host during infection process, and elicit H2O2 that is parameter for plant defense as well as a defense-related gene. Here we show that a pepper esterase induces disease resistance to protect pepper against fungal infection.

B-07. Degradation Products of Pepper Cuticles by Pepper Esterases Protect Plant Against Fungal Infection. Moon Kyung Ko, Jaemo Yang, Kwang Sang Kim, Young Soon Kim and Boung-Jun Oh. Kumho Life and Environmental Science Laboratory, Korea Kumho Petrochemical Co., Ltd., 1Oryong-Dong, Puk-Ku, Kwangju 500-712, Korea.

We cloned an esterase gene (*PepEST*) of pepper (*Capsicum annuum*) that is accumulated to high levels only in the incompatible interaction with anthracnose fungus *Colletotrichum gloeosporioides*, but not in the compatible interaction. The *PepEST* gene was expressed in *Escherichia coli*, and the enzyme showed esterase activity. Fungal cutinases as esterases break the ester linkages between cutin molecules of plant cuticles and release cutin monomers as well as oligomers. These cutin monomers have been hypothesized as signals for inducing disease resistance in plants. Thus, to examine whether PepEST generates cutin monomers by degrading pepper cuticles, and these cutin monomers protect pepper against *C. gloeosporioides* infection, cuticle layers were isolated from pepper fruits and digested by PepEST enzyme. Exogenous applications of degradation products from pepper cuticles by PepEST protect unripe-susceptible fruit against fungal infection. These results suggest that PepEST induces disease resistance to protect pepper against fungal infection by generating cutin monomers as fungal cutinase do. In addition, we have cloned two *Arabidopsis* esterase genes, *AtEST*-1 and *AtEST-2*. AtEST-1 has higher enzymatic activity than AtEST-2. Currently, we are characterizing expression of two *Arabidopsis* esterases and examining whether *Arabidopsis* esterases protect susceptible *Arabidopsis* ecotype against fungal infection as the pepper esterase does.

B-08. Induction of Defense-related Genes Via Different Signal Transduction Pathways During Pre-and Post-ripening Stages of Pepper Fruit Against *Colletotrichum gloeosporioides*. Jung-Yoon Park, Kwang Sang Kim, Moon Kyung Ko and Boung-Jun Oh. Kumho Life and Environmental Science Laboratory, Kumho Petrochemical Co., Ltd. ,1Oryong-Dong, Puk-Ku, Kwangju 500-712, Korea

We previously identified that *C. gloeosporioides* showed compatible interactions with unripe-mature-green pepper fruits, but not with ripe-red fruits. The differential responses have been used as a model pathosystem to study plant-pathogen interactions during pre- and post-ripening stages of fruit. To investigate molecular mechanisms involved in the incompatible interaction, we isolated several defense-related genes that highly induced in the incompatible interaction against fungal infection by using differential display and cDNA library screening. Expression of those genes was examined with both unripe and ripe fruits by fungal infection and exogenous applications of salicylic acid (SA) or jasmonic acid (JA), respectively. It is reported that JA as a chemical elicitor induces defense-related genes for disease resistance as well as other wound inducible genes. In addition, SA also induces pathogenicity-related protein genes. RNA gel blot analyses showed that some genes induced only in the unripe fruit by SA, but others only in the ripe fruit by JA. To characterize these phenomena, we examined whether exogenous applications of SA or JA are able to protect unripe or ripe fruits against fungal infection by induction of disease resistance, respectively. As a preliminary result, SA applications protected unripe fruits against fungal infection, but JA didnt. These results suggest that the induction of the genes for disease resistance is regulated via different signal transduction pathways during pre- and post-ripening stages of pepper fruit against fungal infection. To confirm these phenomena, we have measured amount of SA and JA induced in both fruits after fungal infection by GC analysis.

B-09. A Pepper MADS-box Gene Controls Disease Resistance in Transgenic *Arabidopsis thaliana* Against Phytopathogenic Fungi. Kwang Sang Kim, Moon Kyung Ko, Hyun Hwa Lee and Boung-Jun Oh. Kumho Life and Environmental Science Laboratory, Korea Kumho Petrochemical Co., Ltd., 1Oryong-Dong, Puk-Ku, Kwangju 500-712, Korea.

Colletotrichum gloeosporioides causes anthracnose diseases on fruit crops such as pepper (*Capsicum annuum)*. In our previous study, it interacts incompatibly with ripe fruits of pepper and compatibly with unripe-mature fruits. To investigate molecular mechanisms involved in the incompatible interaction, we have cloned genes that specifically involved in the incompatible interaction by using differential display. A full length of pepper MADS-box gene (*PepMADS*) was isolated through 3rd round cDNA library screening. MADS genes are transcription factor in plants and have been reported mainly as homeotic genes that involved in flower development. However, its gene expression was confirmed in the incompatible interaction, but not in flower by RNA gel blot analysis. By amino acid sequence analysis, the protein encoded by *PepMADS* contains a MADS-box DNA-binding domain and shows significant homology to floral homeotic genes. These data suggest that *PepMADS* is a MADS gene that involved in the incompatible interaction. To reveal whether *PepMADS* is involved in plant defense mechanism, we have made transgenic *Arabidopsis* containing 35S viral promoter and *PepMADS*. T2 generation transgenics infected with phytopathogenic fungi have been evaluated for enhanced disease resistance. As a preliminary result, four lines among transgenics tested showed disease resistance to *Alternaria brassisicola* and *Fusarium oxysporum* f.sp. *matthiolae*. This result suggests that PepMADS gene plays a critical role in the defense mechanism of ripe fruit against fungal infection. Currently, to further characterize whether *PepMADS* controls disease resistance as a transcription factor, we are generating transgenic *Arabidopsis* containing 35S viral promoter + PepMADS + rat glucocorticoid receptor.

B-10. Identification of Anaerobic Pathway During Interaction Between Pepper (*Capsicum annuum*) Fruits and Anthracnose Fungus *Colletotrichum gloeosporioides*. Hye kyung Kee, Young Soon Kim, Moon Kyung Ko and Boung-Jun Oh. Kumho Life and Environmental Science Laboratory, Korea Kumho Petrochemical Co., Ltd., 1 Oryong-Dong, Puk-Ku, Kwangju 500-712, Korea.

Pepper fruits show differential responses against fungal infection during pre- and post- ripening stages. Only ripe fruits show incompatible interaction with the anthracnose fungus, *Colletotrichum gloeosporioides*. To clarify the developmental stage dependent incompatibility in the ripe fruit, several genes were cloned from the incompatible interaction using mRNA differential display. One of them was acetaldehyde dehydrogenase (ALDH) gene that is involved in so called anaerobic pathway. The *PepALDH* gene was developmentally regulated during fruit ripening, organ-specifically regulated, and highly induced from the incompatible interaction. The *PepALDH* gene is inducible in both unripe and ripe fruits by fungus, wound, and salicylic acid, but only in ripe fruit by jasmonic acid. To examine whether anaerobic pathway is involved in plant defense mechanism, we measured the endogenous level of acetaldehyde (AA), ethanol and various sugars during plant/pathogen interaction. AA and ethanol were basically accumulated in the ripe fruit where fungal invasion was suppressed. After fungal infection, the production of AA and ethanol was highly induced while the sugar contents were decreased. These results suggest that an anaerobic pathway in pepper is involved in defense mechanism of the ripe fruit against fungal infection.

B-11. Effect of Environmental Factors on Population Structure of *Pyricularia grisea*.. Seong-Sook Han[1], Sang-Won Ahn[2] and Seong-Ho Choi[1]. [1]Plant Pathology Div., National Institute of Agricultural Science and Technology, RDA, Suwon 441-707, Korea. [2]INGER, IRRI, PO.BOX 933, Manila, Philippines

Population of rice blast fungus *Pyricularia grisea* in blast nursery comprising 50 different rice cultivars or lines was analyzed at three different locations, Icheon, Iksan and Milyang in 1996. *P. grisea* isolates were randomly collected from the nursery plots. There was no significant correlation between the average disease severity of all the tested rice lines or an individual line and environmental factors such as nitrogen content of soil, temperature and precipitation at the three locations during the experiment period. Among the 43, 49 and 41 strains collected from Icheon, Iksan, and Milyang, respectively, KJ201 race was the predominant in Icheon and Iksan, while KI409 was the predominant in Milyang. When tested only those strains collected from three susceptible cultivars Chucheongbyeo, Ilpumbyeo and Nagdongbyeo, distribution rate of pathotype at each location was also similar to that of the whole collection. Thirty-five strains from the three susceptible cultviars were classified into two groups, which were further divided into two sub-groups, respectively, when analyzed by genome RFLP. Nine strains isolated from two rice cultivars Chucheong and Ilpum at Milyang formed a single lineage, while 14 strains collected from the same rice cultivars at Icheon or Iksan were groupd into different lineages. Similar phenomenon were found from the strains collected at Icheon and Iksan, indicating that geographic factors significantly affected population structure of *P. grisea*. Effect of the three susceptible rice cultivars on genetic lineages of *P. grisea* was not distinct in this study. Similar results were obtained from the 53 *P. grisea* strains isolated from foreign rice genotypes, International Rice Blast Nursery (IRBN) rice lines.

B-12. Effects of Environmental Factors on the Occurrence of Chestnut Cankers in Chestnut Foreststands. Sang-Hyun Lee[1], Jong Kyu Lee[2], Myoung-Soo Hwang[3] and Byung-Ju Moon[4]. [1]Department of Forest Biology and [3]Special Purpose Trees, Forest Research Institute, Seoul, Korea 130-012., [2]Division of Forest Resources, Kangwon National University, Chunchon, Korea 200-701, [4]Faculty of Natural Resources and Life Science, Dong-A University, Pusan 604-714, Korea

Recently, chestnut trees planted in various areas are severely damaged by chestnut cankers in Korea. Field surveys for elucidating the relationships between disease occurrence and environmental factors, such as tree age, temperature, rainfall precipitation, direction, degree of slope, chemical properties of planted soils, and so on, were carried out in chestnut plantations located at Kyungnam, Chunnam, Chungnam, and Kyunggi-Do Province. One thousand and one hundred thirty seven trees from 36 experiment plots were investigated. Among these, trees infected by at least one of the canker fungi was up to 66%. The most severely infected area was Sunchon in Chunnam with 80% infection rate, while the most lightly infected area was Kongju in Chungnam with 39% infection rate. Disease occurrence was found to be related with tree age. The Disease occurred most frequently on trees ranged from 7- to 12-year old. The disease occurrence rate was relatively low on trees below 5-year-old or above 25-year-old. Canker positions formed by the pathogenic fungi were most often at 1.6-2.0 m above ground. Over five hundreds bark samples from canker area on the tree were collected and the pathogenic fungi were isolated. The most commonly isolated fungus was *Cryphonectria parasitica*, the chesnut blight fungus.

B-13. Assessment of Tree Susceptibility to Chestnut Blight Fungus(*Cryphonectria parasitica*) of Various Chestnut Varieties. Jong Kyu Lee[1], Hoon-Yong Lee[1], Sang-Hyun Lee[2] and Myoung-Soo Hwang[3]. [1]Division of Forest Resources, Kangwon National University, Chunchon, Korea 200-701, [2]Department of Forest Biology and [3]Special Purpose Trees, Forest Research Institute, Seoul 130-012, Korea

Various hybrids between Japanese chestnut tree(*Castanea crenata*) and Chinese chestnut tree(*C. mollissima*) and selected varieties are planted in Korea. So far, oriental chestnut trees are known relatively resistant to *Cryphonectria parasitica*, the chestnut blight fungus. However, chestnut blight is still causing important losses in chestnut tree plantations in Korea. No data was available about susceptibility to chestnut blight of the different varieties. As a preliminary experiment, stems of 45 different varieties were collected from the research field of Forest Research Institute located at Suwon. Among these, disease susceptibility of 18 varieties, which belongs to 4 species, i.e., *C. crenata, C. mollissima, C. dentata, and C. sativa*, were investigated and compared by a rapid and simple inoculation method. Different levels of susceptibility was appeared among various chestnut varieties.

B-14. RAPD and PCR-RFLP Analysis for the Evaluation of Genetic Diversity Among the *Fusarium moniliforme* from Maize. S. J. Woo, K. S. Kim, H. J. Kim, H. S. Shin, D. H. O and Y. S. Lee. Kangwon National University, Chuncheon 200-701, Korea

Fusarium moniliforme, one of the major soil borne plant pathogens with world-wide distribution, can cause great damages on major maize cultivars. Some *Fusarium moniliforme* isolates used in this study were isolated from infected corn grains collected form several regions in Korea and other *Fusarium moniliforme* mating tester strains that Kansas State University gave Seoul National University were reobtained. RAPD(random amplified polymorphic DNA) and PCR - RFLP(polymerase chain reaction - restriction fragment length polymorphism) were utilized to analyze genetic relationships among *Fusarium moniliforme* isolation. As a result, we obtained 65 fragments and they were ranged from 0.5 Kb to 3.0 Kb in RAPD analysis. Sixty one bands of the total sixty five bands were detected and used to examine the relationships of *Fusaium moniliforme* isolates. Also, ITS(Internal transcribed spacer)Ⅱ and ITS Ⅰ+Ⅱ regions in rRNA of *Fusarium moniliforme* were amplifed with primers. The ITSⅡ and ITS Ⅰ+Ⅱ has 400 bp and 500 bp size, respectively. The two bands each restricted with eleven restriction enzymes, showed distinctly digested band polymorphisms.

B-15. Isolation of Differentially Expressed Genes from Hypovirulent Strain of *Cryphonectria parasitica*. Jin-Won Choi, Hyun-Seok Kang, Moon-Sik Yang and Dae-Hyuk Kim. Chonbuk National University

Ordered differential display using RT-PCR(ODD-PCR) was conducted to have a profile on the differently expressed genes between a hypovirulent strain of *Cryphonectria parasitica* (UEP1) as well as its isogenic wild type (EP155/2). ODD-PCR has advantages of high sensitivity, reproducibility, proportional representation, and limited number of primer combinations comparing with other differential display methods. RNAs were prepared from 1 and 5 days after the liquid culture of both strains and they were further verified with the known marker genes of *C. parasitica* such as cryparin and mating factor, MF2-1. Expressed genes were categorized to five groups according to their temporal expression patterns and those fives groups are CPC, CPE, CPL, CPD, and CPU which indicate constitutive, early-expressed, late-expressed, down-regulated, and up-regulated, respectively. Sixteen primer set out of a total of 192 set were tested for ODD-PCR and five to ten genes were identified as viral-regulated fungal genes per each primer set. Those viral-specifc genes were further analyzed by cloning and sequencing. Characterization of 114 clones were conducted and more are under investigation.

B-16. Analysis of Genes Expressed During *Magnaporthe grisea* / *Oryza sativa* Interaction. Soonok Kim, Sang-Geun Park and Yong-Hwan Lee. School of Applied Biology and Chemistry and RCNBMA, Seoul National University, Suwon 441-744, Korea

Expressed sequence tag (EST) analysis was applied to identify the genes involved in defense responses of rice against infection by the blast fungus (*Magnaporthe grisea*) during compatible interaction. Three hundreds and seventy ESTs were sequenced from cDNA library constructed from *M. grisea* 70-15 infected rice leaves (cv. Nipponbare). The sequences of 214 clones (about 58%) match to those in the NCBI database. One hundred and fifty seven among them showed a homology with previously identified plant genes, 48 clones with fungal genes, and 9 clones with genes not from both kingdoms. A relatively high portion (65 clones, about 41%) of the plant gene homologues was functionally assigned to gene category of cell / organism defense. Expression patterns of defense related genes were analyzed.

B-17. Molecular Cloning and Characterization of a Hydrophobin Gene *Magnaporin*, Highly Expressed During Interaction of Rice Blast Fungus (*Magnaporthe grisea*) with Its Host. Soonok Kim, Sang-Geun Park and Yong-Hwan Lee. School of Applied Biology and Chemistry and RCNBMA, Seoul National University, Suwon 441-744, Korea

A cDNA clone encoding a fungal hydrophobin, *Magnaporin*, was isolated from cDNA library constructed from *Magnaporthe grisea* 70-15 infected rice leaves (cv. Nipponbare). The *magnaporin* gene codes for a typical fungal hydrophobin of 102 amino acids containing eight cycteine residues spaced in a conserved pattern, including two cysteine doublets. Hydropathy pattern revealed that this gene belonged to class II hydrophobin where a stretch of hydrophobic amino acids followed cysteine doublets. The amino acid exhibited about 20% similarity to MPG1 (another hydrophobin gene previously described in *M. grisea*). *Magnaporin* exist as a single copy in the haploid genome of *M. grisea*. Expressions of the *mpg1* and *magnaporin* genes were analyzed. *Magnaporin* was only highly induced *in planta*, but not expressed upon nutrient starvation. However, *mpg1* was expressed during infectious growth as well as upon nutrient deprivation. Functional role of magnaporin by a gene disruption is in progress.

B-18. Vegetative Compatibility Groups and Pathogenicity Among Isolates of *Fusarium oxysporum* f. sp. *melonis*. Il-Pyung Ahn, Hoo-Sup Chung and Yong-Hwan Lee. School of Applied Biology and Chemistry and RCNBMA, Seoul National University, Suwon 441-744, Korea

Ninety-five isolates of *Fusarium oxysporum* f. sp. *melonis*, the causal agent of oriental melon wilt, were isolated from five provinces in Korea. All fields where the isolates obtained were grown melons for 2 years. These isolates were grouped into vegetative compatibility groups (VCGs) by demonstrating heterokaryosis by complementation using nitrate nonutilizing (*nit*) mutants. All isolates were grouped into three VCGs, A, B, and C. No self-incompatibility was observed in any of the isolates. As the cultivation period prolonged, the number of isolates belonged to VCG A was decreased, but those of VCG B increased. Isolates of VCG B were more virulent than those of other VCGs. These data indicate that the level of virulence in *F. oxysporum* f. sp. *melonis* is related to VCGs.

B-19. Pathogenicity and Vegetative Compatibility Groups Among Isolates of *Colletotrichum gloeosporioides*. Il-Pyung Ahn, Hoo-Sup Chung and Yong-Hwan Lee. School of Applied Biology and Chemistry and RCNBMA, Seoul National University, Suwon 441-744, Korea

Fifty-seven isolates of anthracnose pathogen, *Colletotrichum gloeosporioides*, were recovered from apples (*Malus haliana and M. pumila*), red pepper (*Capsicum annum*), and grapevine (*Vitis vinifera*) in Kyonggi province. These isolates were grouped into 5 vegetative compatibility groups (VCGs) with the use of nitrate nonutilizing (*nit*) mutants. VCG A was composed of 24 isolates and exhibited diverse host ranges including ornamental apple (*M. haliana*), three cultivars of *M. pumila*, 'Boosa', 'Kookkwang', and 'Hongok', and red pepper. On the other hand, the second largest group, VCG D was only pathogenic on red pepper. Isolates in VCG B were pathogenic on apple cultivar 'Boosa' and red pepper, whereas those in VCG C and E were pathogens of two apple cultivars 'Kookkwang' and 'Hongok', and grapevine, respectively. The *C. gloeosporioides* did not show clear relationship between pathogenicity and vegetative compatibility.

B-20. The Role of Integrins on Conidial Adhesion in *Magnaporthe grisea*. Cheol-Yong Bae and Yong-Hwan Lee. School of Applied Biology and Chemistry and RCNBMA, Seoul National University, Suwon 441-744, Korea

Conidial adhesion of *Magnaporthe grisea* to rice is an important early event in the infection process. A spore tip mucilage (STM) is expelled from the hydrated conidial apex before the germ tube emergence. However, the chemical properties of STM are not characterized. Treatment of human vitronectin antibody inhibited conidial adhesion and appressorium formation. Furthermore, this antibody was immunolocalized to conidial apex of *M. grisea*. In general, recognition and mediation of extracellular signals are via transmembrane glycoproteins known as integirns. They exhibit specific affinities to tripeptide sequence Arg-Gly-Asp (RGD) found in several extracellular matrix components. Treatments of RGD, RGDS, and RGES inhibited conidial adhesion and appressorium formation, but GGGG, GRGD, GRGDS, and GRGDSPK did not inhibit both cell differentiation in *M. grisea*. Elucidation of the mechanism involved in conidial adhesion is not only of biological interest but may also provide the basis for new disease control strategies.

B-21. Assay of $O_2 \cdot$ Generated on Tuber Slices Treated with Elicitor by Electron Spin Resonance. Hae-Jun Park[1], Furobumi Yoshioka[2], Kazuhito Kawakita[2], Noriyuki. Doke[2], Kyungseok Park[1] and Choong Hoe Kim[1]. [1]Division of Plant Pathology, NIAST Suwon 441-707. [2]School of Bioagriculture Sciences Nagoya Univ., Nagoya 464-860, Japan

We developed new assay method for quantitative measurement of oxygen radical $O_2 \cdot$ by using electron spin resonance (ESR) analysis during elicitor-induced oxidative burst (OXB) on the surface of plant tissues. The ESR analysis using an $O_2 \cdot$ trapper, Tiron (1,2-dihydroxy-3,5-benzenedisulfonic acid), provided a convenient assay for detecting only $O_2 \cdot$ during elicitor-induced OXB producing various active oxygen species (AOS) on plant tissue surface. Tiron was oxidized to Tiron semiquinone radicalby $O_2 \cdot$ Quantity of the radical signal measured by specific spectra on ESR spectroscopy. We detected high level of $O_2 \cdot$ from potato tuber tissue surface treated with hyphal cell wall components of *Phytophthora infestans*. There was no secondary OXB induction by H2O2 treatment.

B-22. Induced Systemic Resistance Against Anthracnose in Cucumber by Selected PGPR and Their Mechanisms. Kyung-seok Park, Hae-Jun Park and Choong-Hoe Kim. Division of Plant Pathology, NIAST, Suwon 441-707, Korea

Eight hundred isolates of rhizobacteria were isolated from various plant rhizosphere to select PGPR-mediated ISR strain against *Colletotrichum orbiculare*, cucumber anthracnose. As a result of greenhouse screening, Seven promising isolates were selected in which showed under fifteen percent of diseased lesion area compared to that of the control. They showed strong PR-1a GUS promoter gene expression in the cell culture plate assay. The most promising strain P-8-1 inhibited the growth of *Rhizoctonia solani*, *Phytophthora capsici*, *Pythium ultimum* and *Colletotrichum gloeosporioides* in dual culture as well as ISR activity. Formation of hydrogen peroxide formation was detected by luminol assay and lignification of cucumber root also was enhanced by treatment with P-8-1 strain. The PR-1a GUS promoter system and greenhouse test would be effective to investigate PGPR-mediated ISR.

B-23. Genetic Analysis on Metalaxyl Resistance, Mating Type, DNA Markers for Oospores Progenies of *Phytophthora capsici*. Jeong Young Song, Hong Gi Kim. Department of Agricultural Biology, Chungnam National University, Taejon 305-764, Korea

Phytophthora capsici, which cause a widespread and destructive disease of pepper(*Capsicum annuum* L.), heterothallic fungus, was known to be highly variable genetically. Due to experimental difficulties associated with oospore germination, few trials, however, was carried out to reveal inheritance characteristrics of this pathogen. For genetic analysis, we conducted crossing of isolates between A1 and A2 mating types as well as metalaxyl response, then detected their inheritance to progeny. 364 single-oospore progeny from four crosses were obtained from pairing both mating types after 2 month incubation. The segregation ratio of A1:A2 mating type of progenies in each cross showed to be 72:28(103), 56:44(82), 48:53(84), and 15:85(95). Progenies derived from crossing of parental metalaxyl-resistant(MR)×metalaxyl susceptible(MS) isolates and metalaxyl-susceptible(MS)×metalaxyl-susceptible(MS) isolates segregated with a ratio of 81:19 and 0:100 with respect to MR:MS for random oospore progenies, respectively. Genetic analysis of sexual progenies by DNA markers, RAPD, rDNA regions by PCR and RFLP probe, revealed to be a accomplishing genetic recombination at DNA level. These results suggested that genetic diversity of *Phytophthora capsici* population might be mainly affected by the sexual reproduction between the A1 and A2 mating type isolates coexisting in the same field.