H-101. Roles of ascospores in the white root rot fungus, *Rosellinia necatrix*. J. S. Lee[1], J. H. Park, K. S. Han, Y. M. Choi. Div. Horticultural Environment, National Horticultural Research Institute, RDA, Suwon 441-440, Korea.

Rosellinia necatrix Prilleux, the ascomycetous white root rot pathogen, causes destructive damage to numerous woody and herbaceous plants, especially to fruit trees. The causal fungus produces teleomorph rarely on the diseased plants in nature. The production of its teleomorph on artificial media has not been reported yet. The role of ascospores as propagules remains unclear due presumably to the scarcity of teleomorph production. In this paper, we demonstrated that stromata in the white root rot fungus were easily produced in the open air when diseased root samples were placed on the ground in the shade, and compared the difference in virulence between single ascospore isolates and their presumed parents originating from vegetative hyphae in the tissues of diseased roots. Vertical transmission of dsRNA through sexual reproduction in the fungus was also investigated. The role of ascospores as propagules is discussed in terms of the life history of the white root rot fungus, *R. necatrix*.

H-102. Sporulating condition of *Alternaria panax* GAPM8 in vitro. Kee don Han[1], Tae soo Lee[2], and Min woong Lee[1]. [1]Dept. of Biology, Dongguk University, Chung-gu 100-715, Korea, [2]Dept. of Biology, University of Inchon, Inchon 402-749, Korea.

We investigated an effect of the light source, condition of media and pH on sporulation and mycelial growth of a pathogen of ginseng blight,*A. panax* GAPM8 comparing with *A. alternata* GINA4. *A. panax* GAPM8 showed highiest pathogenicity among 20 isolates from ginseng leaf at the ginseng field of Kumsan area, Chungnam. *A. alternata* GINA4 which did not show its pathogenicity was isolated from ginseng leaf at the same area of Chungnam. The mycelial growth of *A. panax* GAPM8 was favourable on V8 medium under the fluorescent light-illuminated(500lux) condition of 12 hours, whereas *A. alternata* GINA4 was good under the rotated condition of fluorescent light-illuminated condition(500lux) and dark condition of 12 hours in a day, and continuous dark condition. Sporulation of *A.panax* GAPM8 was good in non-sealed petri-dishes as compared with sealed petri-dishes under the fluorescent light-illuminated(500lux) condition. Under the fluorescent light-illuminated condition, the sporulation of *A. panax* GAPM8grown on V8 medium formed 106 spores/plate but the sporulation did not form any spores under the dark condition. Sporulation of *A. alternata*GINA4 was formed in both conditions. Based on pH ranges of medium, the mycelial growth of *A. panax* GAPM8 was optimal in the range of pH 4 - 6.

H-103. Ecology of rice brown spot caused by *Cochliobolus miyabianus*. Wan-Hae Yeh, Hoon-Seop Lee, Hong-Sik Shim, Ki-Woong Nam, Hyung-Jin Jee, Yong Ki Kim, and Choong-Hoe Kim. Plant Pathology Division, National Institute of Agricultural Science and Technology, Suwon 441-707, Korea

Occurrence of rice brown spot caused by *Cochliobolus miyabianus* was surveyed all over the country from 2001 to 2002. The percentage of infested rice fields with *C.*

miyabianus was recorded as 28% in 2001 and 12.5% in 2002. In order to confirm if how much rice brown spot pathogens could over-winter in the paddy field, detection ratio of rice brown spot pathogens on rice straw samples from the salt injury paddy fields and common paddy fields was investigated under different relative humidity condition. The pathogens were detected from 9.1% and 96.2% of rice straw samples collected from salt injury paddy fields and common paddy field, respectively. On incubating rice plants inoculated with spore suspension of *C. miyabianus* in dew chamber for 24 hours after inoculation, disease onset and development of rice brown spot was investigated on different rice cultivars including 'Chucheong', 'Daesan', and 'Tetep'. First symptom of rice brown spot was observed from 6 hours after inoculation(HAI) in all three cultivars, and the peak of disease development was reached 14 HAI, 24 HAI and 24 HAI in 'Chucheong', 'Dasan', and 'Tetep', respectively. To confirm whether disease development is dependent on rice seedling age, rice seeds were sown four times at 14-day intervals, rice seedlings were inoculated with spore suspension of *C. miyabianus* at 63days after first rice seeding. Susceptibility of rice leaves to rice brown spots at different rice leaf positions was more severe in high leaves than lower ones. In disease resistance of rice cultivars to rice brown spot 'Daesan' and 'Chuceong' turned out to be susceptible and 'Tetep to be resistance comparatively. The result showed that old seedlings were more susceptible than young ones in 'tetep'. To investigate the effect of light irradiation on disease development, 60-days rice seedlings were treated with lamp-light(6000lux and 3000lux) for 7days before inoculating *C. miyabianus* and compared with untreated rice seedligs. Light treatment resulted in much high disease incidence compared to untreated check.

H-104. Pre-penetration behavior of scab disease (*Elsinoe fawcettii*) on citrus. Jae Wook Hyun, Dong Hwan Kim, Seung Chan Lee, and Kwang Sik Kim. Department of Agricultural Environment, National Jeju Agricultural Experiment Station, RDA, Jeju, Korea

Pre-penetration behavior of *Elsinoe fawcettii* on citrus was investigated by scanning electron microscopy and fluorescence microscopy using aniline blue and Uvitex 2B. The conidia germinated and produced germ tubes from one and or both ends of the conidia from 1 day after deposition on the leaf surface of citrus. Globose appressoria were formed at the tip of germ tubes and mycelial swellingon germ tubes were also on the leaf surface, where no surface cracks and stomata were found. The germ tubes of the fungus seemed like to penetrate the leaf surface directly with forming appressoria or mycelial swellings, and sometimes entered the leaf through stomata. The leaf surfaces underneath appressoria or swelled germ tube were swelled and looked like degradated 3 day after inoculation, indicating possibility of direct penetration of the fungus by enzymatic degradation of the cuticle layers and relation of hormone in pathogenesis. And this is the first report of the formation of appressorium by *E. fawcettii*.

H-105. Cytology of cork layer formation of citrus and limited growth of *Elsinoe fawcettii* in scab development. K. W. Kim[1], J.-W. Hyun[2], and E. W. Park[3]. [1]National Instrumentation Center for Environmental Management, Seoul National University, Suwon, 441-744, Korea, [2]National Jeju Agricultural Experiment

Station, Rural Development Administration, Jeju-do, 699-803, Korea, [3]School of Agricultural Biotechnology, Seoul National University, Suwon, 441-744, Korea.

Ultrastructural aspects of host-parasite interactions were investigated in fruits and leaves of citrus (satsuma mandarin) infected with *Elsinoe fawcettii* by transmission electron microscopy. The fungal infection induced host tissues to form cork layers bordering necrotic areas below the infected sites. The cork layers were composed of compact host cells having convoluted cell walls with alternating lamellations, indicating ligno-suberized tissues in wound periderm of citrus. No hyphae were observed to invade healthy tissues below the cork layers. Hyphae grew intercellularly and intracellularly, often causing the hypertrophy and compartmentalization of infected host cells. The fungal invasion was usually accompanied by host cell wall modifications and cellular disruption. Host cells adjacent to invading hyphae showed the accumulation of electron-dense materials in host cells and the formation of host cell wall protuberances in intercellular spaces. Hyphae had concentric bodies that showed an electron-transparent core surrounded by an electron-dense layer with radiating filamentous structures on their surface. One or more intrahyphal hyphae were found in cytoplasm of intercellular or intracellular hyphae. These results suggest that the formation of wound periderm, particularly ligno-suberized cork layers, of citrus is closely associated with triggered host defense responses to invasion by *E. fawcettii*, and corresponding limited growth of the pathogen in scab lesions. Also, the fungus is thought to form concentric bodies and intrahyphal hyphae as a survival mechanism against water and nutrient-deficient environments including wound periderm formation of necrotic host parts.

H-106. Molecular phylogenetic analysis of *Alternaria* species isolated from solanaceous crops. B. R. Kim, H. S. Cho, and S. H. Yu. Plant Pathology, College of Agriculture and Life Sciences, Chungnam National University, 220 Gung-Dong, 305-764 Daejeon, Korea

The importance and diversity of the genus *Alternaria* highlights the need for accurate identification of species. However, many *Alternaria* isolates have been misidentified due to the use of spore size as the only identifying character. To elucidate phylogenetic relationships, fourteen isolates of *A. solani* and two isolate of *A. tomatophila* from solanaceous crops were segregated into morphological groups or species and then subjected to URP-PCR analysis, sequence analyses of histone H3 gene, nuclear internal transcribed spacer (ITS) and mitochondrial small subunit (SSU) ribosomal DNA (rDNA) together with 5 isolates of *A. porri, A. dauci, A. panax, A. elegans*, and *Alternaria* sp. Based on cluster analysis of URP-PCR fragment patterns, *A. solani* and *A. tomatophila* were placed distinct clades and *A. solani* were segregated into two groups. Based on analyses of histone H3, ITS and mitochondrial SSU rDNA sequence data, there were some variability in histone H3 gene, ITS and mt SSU rDNA sequences.

H-107. Molecular phylogenetic relationships amongst *Alternaria* species and related fungi based upon analysis of nuclear 28S rDNA and ITS

sequences. H. S. Cho, M. S. Park, B. R. Kim, and S. H. Yu. Plant Pathology, College of Agriculture and Life Sciences, Chungnam National University, 220 Gung-Dong, 305-764 Daejeon, Korea

Taxonomy of the genera *Alternaria, Ulocladium* and *Stemphylium* has been a subject of controversy because of their high variability in conidial morphology and their polymorphism displayed even in pure cultures. To elucidate relationships among *Alternaria, Ulocladium*, and *Stemphylium* species, nuclear 28S rDNA and internal transcribed spacer (ITS) sequences were analyzed. Phylogenetic analysis of 28S rDNA sequences, performed by the neighbour joining methods, revealed that the *Alternaria* and *Ulocladium* were closely related species and *Stemphylium* was clearly seperated to them. Based upon nuclear ITS sequences, *Stemphylium* species were phylogenetically distinct from *Alternaria* and *Ulocladium* species and *Alternaria* and *Ulocladium* species were placed together in a large *Alternaria/Ulocladium* clade. Within this large clade, the *Alternaria* spp. clustered into four distinct species-clade. Although ITS sequences differentiated among morphologically distinct species-groups within *Alternaria*, it did not provide a sufficient phylogenetic signal to resolve all of their relationships. The relationship between morphological and molecular taxa *Alternaria, Ulocladium* and *Stemphylium* spp. will be discussed.

H-108. Diversity of pathotypes and DNA fingerprint haplotypes in populations of *Magnaporthe grisea* in Korea over a 16-year period. Sook-Young Park[1], Michael G. Milgroom[2], Seong Sook Han[3], Seogchan Kang[4], and Yong-Hwan Lee[1]. [1]School of Agricultural Biotechnology, Seoul National University, Suwon 441-744, Korea, [2]Department of Plant Pathology, Cornell University, Ithaca, NY 14853, USA, [3]National Crop Experiment Station, Rural Development Administration, Suwon 441-100, Korea, [4]Department of Plant Pathology, The Pennsylvania State University, University Park, PA 16802, USA

Using isolates collected over 16 years, we determined the population structure and dynamics of the rice blast fungus, *Magnaporthe grisea*, in Korea at both the genetic and phenotypic levels. Pathotype analysis on 6,315 isolates collected from 328 rice cultivars from 1981 to 2000 revealed the presence of a total of 91 pathotypes. Among 91 pathotypes, nine pathotypes dominated, comprising 76.5% of the isolates collected during this period. The expected number of pathotypes (corrected for sample size) increased significantly over the time. On average six (ranging from 0 to 20) new commercial cultivars were introduced annually between 1981 and 1998. However, the overall cultivar diversity, which was estimated using the Shannon index, was low. Most of the new cultivars were not planted to a large area because the seven most common cultivars each year occupied over 70% of the rice-cultivated area. The frequencies of the nine dominant pathotypes from these seven cultivars were similar to those from entire set of cultivars (r = 0.95, P < 0.001). To understand genetic diversity within and between pathotypes, 176 isolates collected from 1984 to 1999 were randomly sampled and analyzed for their genetic relatedness by DNA fingerprinting. High levels of similarities were observed among isolates; overall similarities were greater than 63% in combined MGR586 and MAGGY DNA fingerprints. Unlike most other populations of *M. grisea*, DNA fingerprints showed no clear lineage structure. No groups were supported by

bootstrap values greater than 10%. There was no significant correlation between DNA fingerprint similarities and pathotypes. Although the difference in genetic similarity within and between years is not large, it is significant (P <0.001). Our data suggest that *M. grise* a populations in Korea have been mostly dominated by a single clonal lineage and that host selection and/or mutations of pathogen may have been a major force for changing pathotypes.

H-109. Molecular characterization of cDNAs encoding an enolase (PEG5) in *Magnapothe grisea*. Taesu Shin, Soonok Kim and Yong-Hwan Lee. School of Agricultural Biotechnology, Seoul National University, Suwon, 441-744, Korea

Enolase (2-phospho-D-glycerate hydrolase, EC 4.2.1.11) is a ubiquitous enzyme that catalyzes the conversion of 2-phosphoglycerate to phosphoenolpyruvate in glycolysis and gluconeogenesis. A cDNA clone encoding a enolase gene was isolated from cDNA library constructed from *Magnaporthe grisea* 70-15 infected rice leaves (cv. Nipponbare). PEG5 exhibited about 72% homologous amino acids to *enoA* of *Aspergillus oryzae*. PEG5 contains an open reading frame of 1570 nucleotides which encode 438 amino acid residues with 5 introns. Southern blot analysis of genomic DNA revealed that the *PEG5* exists as a single copy in the haploid genome of *M. grisea*. Expression of the *PEG5* was highly induced *in planta*. To evaluate the role of *PEG5* in fungal pathogenicity and morphogenesis at molecular level, the gene knock-out strategy is in progress.

H-110. Polymorphism of trichothecene biosynthesis genes in deoxynivalenol- and nivalenol-producing *Fusarium graminearum* isolates. H.-S. Kim[1], T. Lee[2], M. Dawlatana[3] S.-H. Yun[4] and Y.-W. Lee[1] [1]School of Agricultural Biotechnology and Research Center for New Bio-materials in Agriculture, Seoul National University, Suwon, 441-744, Korea. [2]Plant Biotechnology Div., National Institute of Agricultural Biotechnology, Rural Development Administration, 225 Seodoon-dong, Suwon, 441-100, Korea, [3]Institute of Food Science & Technology, Bangladesh Council of Scientific & Industrial Research, Dhanmondi, Dkaka 1205, Bangladesh, [4]Division of Life Sciences, Soonchunhyang University, Asan City 336-745, Korea.

Diversity in trichothecene mycotoxin production by 167 isolates of *Fusarium graminearum* was examined by chemical and molecular methods. *F. graminearum* isolates from barley, corn, and wheat grown in Korea produced either deoxynivalenol (DON) or nivalenol (NIV), whereas isolates from corn grown in the United States produced DON only. Southern blotting of *Mse*I-digested genomic DNA's from these isolates was performed using a 0.6-kb fragment of *Tri5*, a key enzyme for trichothecene production, as a probe. This technique revealed a single-band polymorphism between these isolates, with 1.8-kb and 2.2-kb bands arising from DON and NIV producers, respectively. The same set of isolates was subjected to previously developed PCR assays using primers derived from *Tri7* or *Tri13*. These assays also revealed a single-band polymorphism between NIV- and DON-producing chemotypes. The polymorphisms at *Tri5*, *Tri7*, or *Tri13* in all of the U.S. isolates were consistent with their chemotypes as identified by GC-MS. However, for seven Korean isolates, chemical

and molecular analyses yielded seemingly inconsistent results. This issue was resolved by Southern blot analysis with the *Tri5* probe using two other restriction enzymes and sequence comparison of a 3.8-kb region spanning *Tri5*. In addition, one of these exceptional isolates was found to carry both DON and NIV chemotype-specific regions, possibly resulting from recombination between the two chemotypes.

H-111. Characterization of two novel phytotoxins isolated from *Botrytis cinerea*. G.-J. Kim[1], H. T. Kim[2], G. J. Choi[1], S.-W. Lee[1], K. S. Jang[1], K. Y. Cho[1], B. Cha[2], and J.-C. Kim[1]. [1]Agrochemical Screening Research Team, Korea Research Institute of Chemical Technology, Taejon, 305-600, Korea, [2]Dept. of Agricultural Biology, Chungbuk National University, Cheongju, 361-763, Korea

Twenty five isolates of *Botrytis cinerea* were obtained from infected tissues of various plants and tested for their pathogenicities. Twenty two isolates showed strong or moderate pathogenicity on five plants such as cucumber(*Cucumis sativus* L.), tomato(*Lycopersicon esculentum* Mill.), red pepper(*Capsicum annuum* L.), tobacco(*Nicotiana tabacum* L.), and chinese cabbage(*Brassica campestris* subsp. *napus* var. *pekinensis* Makino), but 3 isolates had very low pathogenicity. When the liquid culture filtrates of 25 isolates were tested for their phytotoxicities in a tobacco leaf-wounding assay, isolate 2-16 exhibited the most potent phytotoxic activity. Two novel phytotoxins were purified from liquid cultures of *B. cinerea* 2-16 by ethyl acetate extraction, repeated silica gel column chromatography, Sephadex LH-20 column chromatography, preparative TLC chromatography and preparative HPLC. On the basis of mass and nuclear magnetic resonance spectral analyses, the compounds were identified as 3-*O*-acetyl botcinol and 3-*O*-acetyl botcinolide. They caused necrosis in a leaf-wounding assay and inhibited growth of the plants tested in a whole plant test. They also caused significant electrolyte leakage from leaf tissues of tobacco. In the bioassays tested, 3-*O*-acetyl botcinol exhibited stronger phytotoxic activity than 3-O-acetyl botcinolide.

H-112. Detection of 3-O-acetyl botcinol and 3-O-acetyl botcinolide in plant tissues infected by *Botrytis cinerea*. G.-J. Kim[1], G. J. Choi[1], S.-W. Lee[1], Y. H. Choi[1], K. Y. Cho[1], H. T. Kim[2], B. Cha[2], and J.-C. Kim[1]. [1]Agrochemical Screening Research Team, Korea Research Institute of Chemical Technology, Taejon, 305-600, Korea, [2]Dept. of Agricultural Biology, Chungbuk National University, Cheongju, 361-763, Korea

Production of two novel phytotoxins, 3-*O*-acetyl botcinol and 3-*O*-acetyl botcinolide, were investigated both *in vitro* and *in vivo* using 25 isolates of *Botrytis cinerea*, which were isolated from various plants. In liquid cultures, the two phytotoxins were not produced by three low pathogenic isolates. Among strong or moderate pathogenic isolates, some produced the two phytotoxins, but the others did not. *In vivo*, the two phytotoxins were detected in leaf tissues of cucumber(*Cucumis sativus* L.) and tomato(*Lycopersicon esculentum* Mill.) plants inoculated with conidial suspensions without wounding. The levels of two phytotoxins produced by various isolates of *B. cinerea in vivo* did not correlate with their pathogenicities. The two phytotoxins began

to detect in tomato plant tissues infected with *B. cinerea* 2-16 3 days after inoculation, increased gradually till 4 days after inoculation, and then decreased. The results suggest that 3-*O*-acetyl botcinol and 3-*O*-acetyl botcinolide are pathogenicity factors for *B. cinerea*, but not primary determinants of its pathogenicity.

H-113. Mutation of β-tubulin gene and genetic diversity of benzimidazole-resistant and sensitive *Monilinia fructicola* isolates in Korea. Tae Heon Lim, Jihee Jeong, and Byeongjin Cha *Department of Agricultural Biology, Chungbuk National University, Cheongju 361-763, Korea*

To analyze mutation in target site of benzimidazole fungicides, *Monilinia fructicola* isolates were isolated from peach fruits with brown rot. Benzimidazole-sensitive isolates did not grow on PDA with ≥ 1.0 ㎍ a.i./㎖ of the fungicides. However, benzimidazole-resistant isolates grew on PDA regardless of the concentrations tested. Benzimidazole-resistant isolates did not grow on diethofencarb-PDA, but sensitive isolates grew on the same PDA. In all 6 resistant isolates analyzed, only codon 198(GAG: glutamic acid) of target site (tubulin) gene was replaced with GCG. Other interesting codons such as 165 (GCT), 200 (TTC), and 241 (GCT) were not different among the isolates. The results using RAPD revealed low levels of genetic diversity between benzimidazole-sensitive and -resistant isolates of *M. fructicola* in the investigated regions.

H-114. Stem blight of brunfelsia Caused by *Fusarium oxysporum*. K. S. HAN, J. H. Park, J. S. Lee, Y. M. Choi. Div. Horticultural Environment, National Horticultural Research Institute, RDA, Suwon 441-440, Korea

Stem blight of brunfelsia(*Brunfelsia calycina*) caused by *Fusarium oxysporum* was found in greenhouse around Sungnam area, Kyunggi province, Korea in September 2001. The initial infection appears as a slight wilting of the foliage, turned yellow from the lower leaves. The yellowing leaves were fallen, resulting in blight of stem and eventual death of the entire plant. The vascular tissue of a diseased plants became dark brown and browning of the vascular system was characteristic of the disease and the pith remained healthy. Isolates obtained from the lesions of the diseased plant parts were identified as *F. oxysporum*, based on the morphological characteristics of conidia. Pathogenicity of the isolates was similar to the symptoms of naturally infected plants. This is the first report demonstrating the stem blight on brunfelsia caused by *F. oxysporum* in Korea. We proposed to name the disease of *Brunfelsia calycina* by *F. oxysporum* as "stem blight of brunfelsia.

H-115. Occurrence of fusarium wilt on cyclamen casued by *Fusarium oxysporum f. sp. cyclaminis*. J. Y. Kim[1], S. S. Hong[1], J. W. Kim[2], and K. Y. Park[2]. [1]Kyonggi-do Agricultural Research and Extension Services, Hwasung 445-972, Korea, [2]Dep. of Environmental Horticulture, The University of Seoul, Seoul 130-743, Korea.

A wilt disease of commercial cyclamen (*Cyclamen persicum*) which grown in greenhouse was found in Kyonggi province of Korea during the period from August, 2001 to july, 2002. The disease incidence was up to 42.7% in Kimpo, Kyonggi province. The disease was more severe in ebb and flow irrigation system than conventional overhead flooding's. The wilted cyclamen plants showed the chlorosis of leaves and followed by the death. The vascular tissues of the infected basal stem and bulb were discolored with black streaks. Fungal isolates from discolored vascular tissue were identified as *Fusarium oxysporum f. sp. cyclaminis* on the basis of mycological characteristics. Effect of infected soil shows 100% infection rate when the cyclamen plants were grown in potting with *F. oxysporum f. sp. cyclaminis* infested soil. This is the first report demonstrating the Fusarium wilt on cyclamen caused by *F. oxysporum in Korea.*

H-116. Occurrence of rhizoctonia web blight on soybean caused by *Rhizoctonia solani* in Korea. Sung Kee Kim[1], Seog Won Chang[2], and Jin Won Kim[2]. [1]Northern Agriculture Research Station, Kyonggido Agriculture Research and Extension Services, Yonchon 486-830, Korea, [2]Department of environmntal Horticulture, The University of Seoul, Seoul 130-743, Korea

Web blight symptoms caused by *Rhizoctonia* spp. were found on the soybean (*Glycine max* (L.) Merr.) cultivation field from late July to ripening stage in 2002 at Yonchon, Korea. The disease was usually initiated from plant organ (leaf, petiole and stem) lodged on soil, more severe in the field when humidity is high, rain is frequent. The pathogen produced the watersoaked, irregular and dark grey lesions that may enlarged and became a watery soft rot, then plant organ infected turned greyish brown followed by blight of the aerial part. White mycelia formed from lesions developed on higher stems, leaves, and pods and greyish brown sclerotia of small size numerously form in the mycelial mass. All the isolates obtained from the lesions of the diseased plant parts were identified as *Rhizoctonia solani* according to the criteria based on the cultural and morphological characteristics. Pathogenicity of the fungus was established by artificial inoculation on soybean plants. This is the first record of Rhizoctonia web blight on soybean caused by *R. solani* in Korea. Detailed epidemiological data are essential for the development of effective and economic control programs for disease caused by *R. solani.*

H-117. Occurrence of kalanchoe stem rot disease caused by *Fusarium oxysporum* and *F. proliferatum.* Jin-Won Kim, Mi-Seon Kang, and Sun-Yee Kim. Department of Environmental Horticulture, The University of Seoul, Seoul 130-743, Korea

A stem and root rot disease of kalanchoe (*Kalanchoe blossfeliana*) which is a potted hydroponic plants in ebb and flow irrigation system in greenhouse was found in Seoul, Korea during July 2001 and 2002. The diseased kalanchoe plants showed the typical symptoms including stems black rotted and covered with white to pinkish mycelia on infected stem. Fungal isolates from discolored stem tissue were identified as *Fusarium oxysporum* and *F. proliferatum* on the basis of mycological characteristics.

Pathogenicity tests by artificial inoculation method revealed that the isolates caused the same symptoms as observed in naturally infected kalanchoe plants. This is the first report of stem rot on kalanchoe caused by *F. oxysporum* and *F. proliferatum* in Korea.

H-118. Occurrence of powdery mildew on pear (*Pyrus serotina* var. *culta*) caused by *Phyllactinia mali*. Sang-Bum Lee, Sang-Yeob Lee, Weon-Dae Cho, and Choong-Hoe Kim. Plant Pathology Division, National Institute of Agricultural Science and Technology, Suwon 441-707, Korea.

Powdery mildew of pear, which rarely occurred in past decades, tends to increase in Gyeongbuk and Gyeongnam provinces in resent, while it did not occur in the other provinces. Incidence of the disease reached up to 60.0% at the average of 33.3% in fields in 2001. In general, the disease caused by *Phyllactinia mali* is not a problem for pear orchards. However, the disease caused leaf defoliation, decrease of fruit growth and quality, and decline of tree when severely occurred in pear orchards. Conidia of the causal fungus were clavate, non papillate but narrowed at the apex with 65~87×20~28 ㎛ in size. Conidiophores were mostly erect on superfical mycelium, 460㎛ in length, 5~7㎛ wide, and straight in foot cells. Dark brown ascomata were observed on lower leaves of pear. Cleistothecia were globose or subglobose with 150~210㎛ in size. Asci were 8~22 in a ascomata, and was olivaceous brown with 72~95×30~37㎛ in size. An ascus had 2 ascospores with shape of olivaceous brown to pale greenish oval. Ascospores were 30~37×16~23㎛ in size. The limited occurrence of the disease mainly in the east coast seems to be due to favorable weather conditions and decrease of fungicide application with the expansion of organic farming.

H-119. Occurrence of white rot caused by *Sclerotium cepivorum* and its pathogenicity. Mi Kyung Kwon, Yong Ki Kim, Weon Dae Cho, and Sang Bum Lee. Plant Pathology Div., National Institute of Agricultural Science and Technology, Suwon 441-707, Korea

This study was conducted to investigate the seasonal prevalence of white rot and pathogenicity of *Sclerotium cepivorum* isolated from 2001 to 2002, from garlics, onions, and nanking shallots. Seasonal prevalence of white rot was investigated in vinyl house plots contaminated artificially with *Sclerotium cepivorum* in Suwon. First symptom of white rot was observed in the middle of March on the tropical-type garlics and at late of March on the temperate-type garlics. Disease development lasted till the middle of May. Tropical-type garlics were more susceptible than temperate-type garlics. Sclerotial size of *Sclerotium cepivorum* isolates collected from various regions was of great difference according to the host. While most of sclerotia isolated from garlics and onions were large type, all ones isolated from nanking shallots were small type-sclerotia. To break dormancy of the sclerotia of *Sclerotium cepivorum*, influence of incubation temperature of sclerotia was examined. Optimal condition for germination of sclerotia under dormancy was to incubate sclerotia for 7 days at 35℃ and then 7 days at 10℃. An easy and simple method for pathogenicity test was established as follows; inoculating mycelial discs grown for 6 days at 20℃ into surface-sterilized bulb scales of onion. Mycelia were over-grown on onion scales on 7 days after inoculation (DAI) and

sclerotia started to form 16 DAI.

H-120. *Sclerotium* sp. associated with occurrence of a new disease, globular sclerotium rot of garlic. Weon Dae Cho[1], Wan Gyu Kim[2], Sung Kee Hong[1], and Woo Sik Kim[1]. [1]Plant Pathology Division, National Institute of Agricultural Science and Technology, RDA, [2]Applied Microbiology Division, National Institute of Agricultural Science and Technology, RDA.

White rot of garlic have occurred severely in southern part of Korea for many years. Isolates of *Sclerotium* spp. were obtained from white rot symptoms on garlic bulbs collected in eight locations in Korea to clarify the causal fungus of the disease occurrence. The 131 isolates out of the total 182 isolates were identified as *Sclerotium cepivorum* Berk. based on their morphological characteristics as previously reported. However, the other 51 isolates differed from *S. cepivorum* isolates in morphological and cultural characteristics but corresponded to *Sclerotium* sp. The *Sclerotium* sp. isolates produced lots of small sclerotia on PDA medium. The sclerotia were globular, black, differentiated into rind and medulla, and measured 340-570㎛ (average 440㎛) in diameter. Hyphae of the fungus were septate and 3.6-12.0㎛ in width. Optimum temperature for mycelial growth of the isolates ranged from 20℃ to 25℃. Pathogenicity of two isolates each of the fungus and *S. cepivorum* was tested to garlic bulbs. All the isolates induced severe rot symptoms on garlic bulbs. The symptoms induced by *Sclerotium* sp. isolates were similar to those by *S. cepivorum* but slightly different from those by *S. cepivorumin* formation of globular and black sclerotia on the bulbs. A new disease name of garlic caused by *Sclerotium* sp. is proposed as globular sclerotium rot. Further study is required to identify species of the causal fungus of the disease.

H-121. Anthracnose of sloumi caused by *Colletotrichum acutatum* in Korea. J. H. Kim[1], J. R.[1] J. S. Choi[1], Y. G. Choi[1], J. M. Kim[1], and W. H. Lee[2]. [1]Jeollabuk-do Agricultural Research and Extension Services, Iksan 570-704, Korea, [2]Faculty Biological Resources Science, Chonbuk National University, Jeonju 561-756, Korea

Anthracnose occurred on sloumi trees grown in Iksan areas of Korea in 2002. The disease incidence was ranged from 5.2 to 12.4%. Anthracnose of sloumi appeared as dark brown circular spots on naturally infected leaves and stems. The symptoms of infected leaves were small brown to dark brown spots and gradually enlarged larger cylindrical dark brown lesions. The causal fungus of anthracnose isolated from the diseased plants was identified as *Colletotrichum acutatum* based on the morphological and cultural characteristics. All isolates of *C. acutatum* were produced similar symptoms on the host leaves by artificial inoculation. The optimum temperature for mycelial growth and conidial sporulation were ranged from 25 to 30℃.

H-122. Decrease of fruits brix according to increasing of grape leaf spot caused by *Pseudocercospora vitis*. J. H. PARK, K, S Han, J. S. Lee, and Y. M. Choi. Division of Horticultural Environment, National Horticultural Research

Institute, RDA, Suwon 441-440, Korea

Cambell early is very susceptible grape cultivar to grape leaf spot caused by *Pseudocercospora vitis*. Leaf spot of grape (cv. Cambell rarly) is outbreak about 95% in ratio of diseased leaves according to the areas and management state of orchards in Korea(2000-2001, National Horticultural Research Institute). The diseased grapevine trees have some difficulty in raise of the trees by early defoliation, and decrease the quality of fruits by disadvantage of assimilation products accumulation. Severe outbreak of the grapevine leaf spot is the factor that decrease of brix of the fruits. The strong correlation was observed between disease incidence of grapevine and decrease of brix of the fruits. The regression equation was $Y = -0.023X + 18.8$ ($r^2 = 0.912$).

H-123. Rot of mungbean sprout caused by *Colletotrichum acutatum*. Seon-Chul Lee, Dong-Kil Kim, Chang-Ki Shim, Il-Kyo Seo, Dong-Won Bae, and Hee Kyu Kim. *Department of Agricultural Biology, Research Institute of Life Science and, Gyeongsang National University, Chinju, 660-701, Korea*

Decayed samples of marketed mungbean sprout were collected from Sacheon, Suncheon and Dangjin. Initial symptom on hypocotyls was diamond speck of dark brown color, which developed to enlarged sunken brownish black spot of irregular margin, followed by softening yellowish decay. Brown speck on cotyledon was further developed to irregular lesions. We isolated a fungus *Colletotrichum* sp. The colony was pale orange, later turn greenish gray, in a week at 25℃. Colony reverse was pink. Conidiomata was absent in culture and setae were not present. Typical fusiform conidia 7.5-15.0 x 2.5-2.9m, were hyaline, aseptate, smooth and appeared salmon color in mass. Conidiogenous cells were phialidic, hyaline, smooth, cylindrical with terminal distinct collarette. The causal organism was identified as *Colletotrichum acutatum* Simonds and Simonds. This is the first report of *Colletotrichum acutatum* as Mungbean sprout rot fungus, and we propose to name it *Colletotrichum* Mungbean sprout rot. Key words: Mungbean sprout rot, *Colletotrichum acutatum*