

## **Bacteriology and Bacterial Diseases (A1-A14)**

**A-01. Correlation between disease incidence of bacterial grain rot of rice and climatic factors.** Tae Hwan Noh<sup>1</sup>, Hyung Moo kim<sup>2</sup>, Wan Yeob Song<sup>2</sup>, Du Ku Lee<sup>1</sup>, Mi Hyung Kang<sup>1</sup> and Hyeong Kwon Shim<sup>1</sup>. <sup>1</sup>National Honam Agricultural Experiment Station, Iksan 570-080, Korea, <sup>2</sup>Department of Agricultural Biology, Chonbuk National University, Chonju 560-756, Korea

Disease occurrence rate of bacterial grain rot of rice caused by *Burkholderia glumae* was examined 5 regions for 3 years from 1998 through 2000. In the results, the disease incidence was 3.6% in 2000 which was higher than other examinations as 2.3% and 3.0% in 1998 and 1999 respectively. There was significant difference between investigated years but not regions by Duncan's multiple range test ( $p=0.01\%$ ). Among the examined regions, Kimje region recorded highest disease incidence as 3.5% in 3 years average rate in compare of other 4 regions. In the yearly examination result, the disease incidence was related to amount of rainfall as the rate was higher in case of more precipitation in 2000 than examined other seasons which suggest that the bacterial infection was established around heading date, and this could lead the different disease incidences. Climatic factors in October including heading time have wide variation yearly. In 1998 and 2000, showed higher disease incidence than 1999, the average temperature was higher 1.2 °C and have more 199.5mm and 540.4mm of rainfall than those of 1998 season. Number of rainfall date of comparative 2 seasons was more 2.2 and 1.2 days than 1999. In these results, the higher temperature, amount of rainfall and number of precipitation date were closely related to disease occurrence, and which suggest that the climatic conditions with humid, higher temperature and long-term rainfall were major factors to disease occurrence and spread.

**A-02. Evaluating disease resistance of major rice cultivars to *Xanthomonas oryzae* pv. *oryzae* races and surveying occurrence of bacterial leaf blight in Naju fields.** Kwang-Hong Cha<sup>1</sup>, Woo Yeop Ahn<sup>1</sup>, Yong-Hwan Lee<sup>1</sup>, Sug-Ju Ko<sup>1</sup>, and Baik Ho Cho<sup>2</sup>. <sup>1</sup>Jeonnam Agricultural Research and Extension Services, Naju 520-715, Korea, <sup>2</sup>Applied Plant Science Division and Institute of Biotechnology, Chonnam National University, Kwangju, 500-757, Korea

This study was conducted to test field disease resistance of major rice cultivars to *Xanthomonas oryzae* pv. *oryzae* races and to estimate occurrence of bacterial leaf blight disease in the fields for evaluating *X. oryzae* pv. *oryzae* races distributed in Jeonnam province. To test the resistance of major rice cultivars against K1 (HB01013), K2 (HB01014), and K3 (HB01015) races of *X. oryzae* pv. *oryzae*, 19 rice cultivars were planted at June 15, 2002 and managed by conventional method. Before heading period, each race of the pathogenic bacterium was inoculated by cutting flag leaves 2-3cm below from the top using scissors. Keumobyeyo I variety was susceptible to K1, K2, and K3 races. Six varieties including Nampyeongbyeyo, Odaeyeyo, and Ilpumbyeyo were susceptible to K1 and K3 races, but resistant to K2 race. Donjinbyeyo I, Saegyehwabyeyo, Hwayeongbyeyo, and Jongnambyeyo were resistant to K1 and K3 races, but susceptible to K2 race. Hojinbyeyo and Joonambyeyo were resistant to all races that used in this

experiments. Disease occurrence of bacteria leaf blight was investigated in 53 different fields(146,950 m<sup>2</sup>) at September 16th and September 30th, 2002 in Naju area in Jeonnam Province. The bacterial leaf blight in the fields occurred severely on Nampyeongbyeo, Donganbyeo, and Dongjinchalbyeo shown resistance to K2 race, but at low level on Donjinbyeo I, Saegyehwabyeo, and Hwayeongbyeo shown resistance to K1 and K3 races. The disease occurrence was not observed in Junambyeo and Hojinbyeo which shown resistance to all races, Our results implicate that recent occurrence of bacterial leaf blight disease in Jeonnam province may be caused mainly by K3 race.

**A-03. Bacterial soft rot of *Chamaecereus silvestrii* (Sanchui Cactus) caused by *Erwinia carotovora* subsp. *carotovora*.** Jung Ho Kim, Yong Ho Jeon, Sang Gyu Kim and Young Ho Kim. School of Agricultural Biotechnology, Seoul National University, Suwon 441-744, Korea

Occurrence of soft rots was observed on *Chamaecereus silvestrii* (Korean name: Sanchui) that were grown at the greenhouse in Suwon (National Horticulture Research Institute), Anseong, Eumseong, Cheonan, Daegu, and Koyang. Typical soft rot symptoms included a moist and a watery soft rot of *C. silvestrii*. Symptoms began as a small water-soaked lesion which enlarged rapidly to rot the whole stem. The causal organism isolated from the infected lesions was identified as *Erwinia carotovora* subsp. *carotovora* based on its pathogenicity, physiological and biochemical characteristics, fatty acid analysis and the results of the Biolog. Artificial inoculation of the bacterium produced the same soft rot symptoms on the cactus plants. The bacterial soft rot caused by *E. carotovora* subsp. *carotovora* was firstly described in *C. silvestrii* in Korea.

**A-04. Evaluation of the Biolog substrate utilization system to assess metabolic variation among strains of *Pectobacterium carotovorum* subsp. *carotovorum*.** I.-S. Myung<sup>1</sup>, M. H. Lee<sup>2</sup>, and D. S. Ra<sup>1</sup>. <sup>1</sup>Dept. Crop Protection, NIAST, RDA, Suwon 441-707, Korea; <sup>2</sup>Dept. Genetic Engineering, Sungkyunkwan University, Suwon 440-746, Korea.

Metabolic fingerprints of 45 strains of *Pectobacterium carotovorum* subsp. *carotovorum* originating from 8 countries were obtained by using by the Biolog substrate utilization system. Metabolic profiles were used to attempt strain identification. Eighty eight % of the studied strains were correctly identified when the commercial Microlog 4 N data base was used. The similarity coefficients of each strain of the subspecies estimated by the Biolog 4N software's data base were ranged from 0.41 to 0.83. The result is suggested that users supplement the commercial data base with additional data prior to or after using the program for identification purpose. In addition, metabolic profiles of the Biolog substrate utilization of *P. c.* subsp. *carotovorum* were compared with the strains of other subspecies of *P. carotovorum*, *atrocepticum*(n=9), *betavascularum*(n=4), *odoriferum*(n=1), and *wasabiae*(n=1). Substrates that can be used as a marker to differentiate the strains of *P. c.* subsp. *carotovorum* from the other subspecies among 95 substrates in the GN microplate were not observed. All strains of 5 subspecies of *Pectobacterium carotovorum* used in this study commonly utilized D-galactose, D-fructose, cellobiose, L-arabinose, N-acetyl-D-glucosamine, glycerol,

L-alanyl-glycine, L-alanine, bromo succinic acid, succinic acid, D-saccharic acid, methyl pyruvate, sucrose, α-methyl-D-glucose, and D-mannose.

**A-05. Halo blight of Kudzu (*Pueraria lobata*) caused by *Pseudomonas syringae*.**

Yong Ho Jeon, Sung-Pae Chang and Young Ho Kim. School of Agricultural Biotechnology, Seoul National University, Suwon, Korea

Occurrence of a bacterial halo blight disease of Kudzu (*Pueraria lobata*) was observed at several localities in Korea including Euiwang, Suwon, Daejeon, Gochang and Buan in 2002. Initial symptoms appeared typically as leaf spot with yellowish halo. Initial symptoms of a brown to black spot with a large yellowish halo appeared from early summer, which lasted till rainy season without much expansion. Symptoms became more necrotic with time, and were sometimes masked by high temperature in mid summer. It was conducted for pathogenicity and inducing hypersensitive response (HR). This organism induce symptom on kudzu and bean leaf for pathogenicity. In artificial inoculation test, this bacterium produced the same halo spot symptoms on kudzu and such as bean plants, induced HR on pepper and tomato leaves, but not tobacco leaves. The causal organism isolated from the diseased plants was identified as *Pseudomonas syringae* based on 16S rDNA sequencing, fatty acid and Biolog analyses. However, results of utilization of carbohydrate were not matched with known pathovars of *P. syringae* such as pathovars *phaeolicola*, *syringae* and *aptata*. This suggests that the bacterium may be a new pathovar. This is the first report of a bacterial disease of kudzu in Korea.

**A-06. A potential of bacterium agent which induce abnormal fermentation in oriental melon, Gumssaragi. J. E. Choi, S. K. Cha, J. H. Kim, J. A. Ryuk, and Y. S. Hwang. Chungnam National University.**

Fruit disorder associated with abnormal fermentation is usual in Oriental melon, Gussaragi, grown in Korea. Characteristic symptoms include water-soaking of placenta and pulp tissue in advance. In order to determine whether or not bacteria were the casual agents of this disorder, bacteria were isolated from infected melons and 25 strains were separated. Inoculation on melon and watermelon fruit with these isolates were identified as genera of *Enterobacter*, *Terrbacter*, *Knollia*, *Janibacter*, *Microbacterim*, *Pseudomonas* by stain reactions, morphological characterization, colony pattern, physiological and biochemical reactions, and 16s rDNA analysis.

**A-07. Occurrence of bacterial shoot blight of tea in Korea. J. E. Choi<sup>1</sup>, S. K. Cha<sup>2</sup>, J. H. Kim<sup>2</sup>, J. A. Ryuk<sup>2</sup>, and I. S. Nou<sup>1</sup>. <sup>1</sup>Chungnam National University, <sup>2</sup>Suncheon National University.**

In 2002 a bacterial disease of tea plants (*Thea sinensis* L.) was observed in Suncheon area. The primary symptoms of the disease include small, water-soaked and dark greenish-brown spot development on the young leaves. This spot gradually increases in size, especially taking on elongate shape along the midrib or vein of the

leaf, and then turns black. Such symptoms were also found on shoots and petioles. The diseased leaves were defoliated easily, but the shoots of first flush were scarcely infected. Ten strains were isolated from the infected leaf and shoot. Inoculation on tea leaf with these isolates produced the same symptoms of naturally infected plants. These isolates were identified as *Pseudomonas syringae* pv. *theae* by stain reactions, morphological characterization, colony pattern, physiological and biochemical reactions, and this disease was concluded as Bacterial shoot blight.

**A-08: Characterization of *Pseudomonas chlororaphis* O6 Tn5 mutants involved in production of secondary metabolites.** Kang, B. R., Cho, B. H., and Kim, Y. C. Agricultural Plant Stress Research Center, Chonnam National University, Gwangju 500-757, Korea

*Pseudomonas chlororaphis* O6 is a bacterium with potential to suppress plant pathogens through several secondary metabolites, such as phenazine, hydrogen cyanide(HCN), and protease. To investigate genes involved in production of phenazines, we isolated several Tn5 mutants, N7 and Org mutant. The N7 mutant did not produce phenazines and protease, lost their ability to inhibit the fungal pathogens and did not produce homoserin lactone(HSL) which is known as a signal molecule for induction of secondary metabolites. The Org mutant was not affected in their ability to secondary metabolites, but produced dark brown pigments, and increased their antifungal activity. When the Org mutant was treated on barley seed, a significant reduction of germination was observed. The flanking sequence of the N7 mutant showed high homology with *lon*, which encodes an ATP-dependent protease found in diverse organisms, including bacteria, plants, and animals. The flanking sequence of the Org mutant showed high homology with *hmgA* gene, encoding the enzyme homogentisate dioxygenase known to be involved in the degradation of tyrosine. *Lon* protease of *P. chlororaphis* may be one of the global regulators in production of secondary metabolites and homoserin-lactone. The *hmgA* gene of *Pseudomonas chlororaphis* O6 may involve in tyrosine metabolism in nutrient-starved condition. Mutation of *hmgA* may block tyrosine metabolism and thereby over-produce melanine as an intermediate. The melanine may enhance antifungal activity of the bacterium.

**A-09. Biochemical properties and rRNA operon analyses of Korean isolates of blackleg disease.** Jun-Hak Koo, Jung-Eun Kim, Duck-Hwan Park, Jang-Hyun Hur and Chun-Keun Lim. Division of Environmental Biology, Kangwon National University, Chuncheon 200-701, Korea

High peak zone of Gangwon Province is the most widely cultivated area for seed growing and production of potato in Korea. However, sudden outbreak of blackleg disease caused severe damage to potato production. The causal organism for blackleg diseases was identified as *Pectobacterium carotovorum* subsp. *atrosepticum* on the basis of biochemical tests and distinguished with the other soft-rot pathogens. Furthermore different strains of the causal organism were analyzed through 16S rRNA, 5S rRNA and 16S-23S intergenic spacer (ITS) studies. Sequences of 16S rRNA showed homology with that of the Japanese strain, but differed from those of European and ATCC strains.

Similarly, 16S-23S ITS sequence analysis showed homology with that of the Japanese strain, but it differed from those of Europe, ATCC and other strains. However, 5S rRNA sequence showed homology among all the studied strains. The reason for the similarity between Korean and Japanese strains and dissimilarity with other strains may be due to environmental factors of specific geographical locations.

**A-10. Genetic and phenotypic diversity of *Paenibacillus polymyxa* isolated from Korean ginseng.** Yong Ho Jeon, Ingyu Hwang and Young Ho Kim. School of Agricultural Biotechnology, Seoul National University, Suwon, Korea

Twenty-six isolates of *Paenibacillus polymyxa*, out of which 20 isolates were isolated from decayed Korean ginseng roots, were tested for genetic and phenotypic diversification. The genetic diversity was examined by 16S rDNA sequencing, BOX-PCR, and ERIC-PCR. Utilization of various carbohydrates and fatty acid composition of the bacteria were examined for the bacterial physiological characters. Pathogenicity to fleshy storage organs including ginseng root, resistance to antibiotics and antibacterial activity were also studied for examining their phenotypic variation. No relationship of the bacterial isolates between utilization of carbohydrates, resistance to antibiotics, fatty acid composition and production of antibacterial substances were evident. However, the bacterial isolate tested could be divided into two groups based on pathogenicity on ginseng, which coincided significantly with genetic groupings evaluated by BOX-PCR, ERIC-PCR and 16S rDNA sequence.

**A-11. Quorum sensing regulates toxoflavin biosynthesis and pathogenicity in *Burkholderia glumae*.** Jinwoo Kim, Suhyun Kim, Yongsung Kang, Ji Youn Jang, Jung-Gun Kim, and Ingyu Hwang. School of Agricultural Biotechnology, Seoul National University, Suwon 441-744, Korea.

*N*-Acylhomoserine lactone (acyl-HSL)-mediated gene expression, also called autoinduction or quorum sensing, is conserved among diverse gram-negative bacteria. *Burkholderia glumae* causing bacterial grain rot of rice produces two kinds of acyl-HSL, *N*-(3-oxooctanoyl)-L-homoserine lactone and *N*-octanoyl-L-homoserine lactone. We have cloned and sequenced the gene responsible for those two acyl-HSL biosynthesis, called *tofI*. An acyl-HSL receptor gene, *tofR*, was found upstream of *tofI*. The two genes are divergently transcribed and separated by 800 bp. *TofI* and *TofR* are homologs of *LuxI* and *LuxR*, respectively. *Tn3-gus* insertions in *tofI* abolished acyl-HSL production and subsequently resulted in loss of toxoflavin production and pathogenicity. Toxoflavin production and pathogenicity were restored by complementation with *tofI* or by adding acyl-HSL exogenously. This clearly indicates that toxoflavin biosynthesis and pathogenicity are regulated by quorum sensing.

**A-12. Toxoflavin produced by *Burkholderia glumae* causing rice grain rot is responsible for inducing bacterial wilt on many field crops.** Yeonhwa Jeong<sup>1</sup>, Jinwoo Kim<sup>1</sup>, Suhyun Kim<sup>1</sup>, Tomohisa Nagamatsu<sup>2</sup>, and Ingyu Hwang<sup>1</sup>.  
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Severe wilt symptoms similar to bacterial wilt caused by *Ralstonia solanacearum* were observed in tomato, hot pepper, eggplant, potato, perilla, sesame, and sunflower in 2000 and 2001 in Korea. From diseased crops at 65 different locations, we obtained 106 isolates that produced green pigment on CPG plates; 36 were isolated from discolored rice panicles. The causal pathogen was Gram negative and was identified as *Burkholderia glumae* based on its biochemical characteristics, fatty acid methyl esters analyses, and 16S rRNA gene sequence. All the isolates produced toxoflavin, as determined by electrospray ionization mass spectrometry using a direct inlet system and TLC analyses. All the isolates, except BGR12 and a toxoflavin-deficient mutant generated by *Tn5lacZ*, caused bacterial wilt on various field crops. BGR12 is a wild-type isolate lacking toxoflavin production. Synthetic toxoflavin caused wilt symptoms on hot pepper at 10 µg/ml, concentration 1 day after treatment. Cells of *B. glumae* and synthetic toxoflavin caused wilt symptoms on field crops, demonstrating a lack of host specificity. This is the first report of bacterial wilt on various crops caused by *B. glumae* and our results clearly demonstrate that toxoflavin is a key factor in wilt symptom development.

**A-13. Hrp pathogenicity island of *Burkholderia glumae* is chimeric.** Suhyun Kim, Yongsung Kang, Jinwoo Kim, Ji Youn Jang, Jung-Gun Kim, and Ingyu Hwang. School of Agricultural Biotechnology, Seoul National University, Suwon 441-744, Korea.

The Hrp Type III protein secretion systems are highly conserved among plant pathogenic bacteria and now designated as pathogenicity island (PAI). We have isolated the Hrp PAI of *Burkholderia glumae* BGR1 and partially characterized by sequencing and mutagenesis. We identified six *hrp*, nine *hrc*, and *hpaB* genes from the region. Mutations in the *hrp* and *hrc* genes abolished pathogenicity and the ability to induce hypersensitive response in non-host plants. The *hrp* cluster resembled most the putative Type III secretion systems of *B. pseudomallei*, which is the causative agent of melioidosis, a serious disease of man and animals. However, the upstream region of *hrcC* and downstream region of *hrcS* were very different between two pathogens. Features of *B. glumae* Hrp PAI were mosaic. The Hrp PAI core region showed high similarity to that of *Ralstonia solanacearum* and *Xanthomonas campestris*, however some aspects were dissimilar. Interestingly, we found a *hrpK* homolog of *Pseudomonas syringae* pv. *syringae* even though its role in pathogenicity remains to be answered. This mosaic nature of *B. glumae* Hrp PAI indicates horizontal transfer of Hrp PAI and instability in the genome.

**A-14. Preliminary analysis of the endophytic bacteria isolated from rice in Korea.** Soo-Young Park, Sung-Hyun Yang, Jihyun F. Kim, and Seung-Hwan Park. Korea Research Institute of Bioscience and Biotechnology (KRIBB), P.O. Box 115, Yusong, Taejeon 305-600, KOREA.

Numerous bacterial endophytes thrive in the interior of plants. Some of them are beneficial to the host; they can fix atmospheric nitrogen (diazotrophs), synthesize plant growth hormones, or even antagonize plant pathogens. To select strains well adapted to the environment inside plants, and effective in promoting plant growth and inducing plant defense against pests and pathogens, we collected paddy rice samples from 8 locations in the Chungcheong provinces, Korea, in years 2000 to 2001, and isolated bacteria from the roots surface-sterilized with 1% NaClO. Total of 43 distinct isolates from rice selected based on size, shape and color of the colonies, were used for further study. The estimated numbers of the isolates in rice were ca  $10^4$ - $10^5$  CFU per gram root tissue. For a tentative identification, the 16S rDNA sequences of the isolates were partially determined. BLAST searches of the sequences against databases suggested that they are taxonomically diverse 65% were Proteobacteria, 23% high G+C Gram positives, and 12% low G+C Gram positives. To obtain more definite evidence that the isolates can be endophytically established within plant tissues, we tried to fulfill Kochs postulates using gnotobiotically grown seedlings. Sixteen strains were successfully re-isolated from inside of the root tissue, and were identified as species of *Burkholderia*, *Enterobacter*, *Klesibella*, *Pantoea*, *Sphingomonas*, *Pseudomonas*, *Serratia*, *Herbaspirillum*, which are identical to the originally inoculated strains. The PCR cloning was performed to determine the presence of the nitrogenase gene. *nifH* could be cloned from five *Burkholderia* strains and two *Enterobacter* strains.

#### **Biological Control (B15-B42)**

**B-15. Control effect of N1E powder formulation using *Bacillus licheniformis* N1 to the naturally occurred gray mold rot in tomato plastic house.** Park, Jong Young, Lim, Eun Kyung, Kim, Hyun Ju, Song, Ju Hee, Jung, Soon Je, and Moon, Byung Ju. Faculty of Natural Resources and Life Science, Dong-A University, Busan 604-714, Korea

This study was carried out to investigate the control effects of N1E wettable powder formulation using *Bacillus licheniformis* N1 to the naturally occurred gray mold rot in the tomato plastic house, Kim-hae in Pusan. First of all, to select the application density of N1E for field trials, 1/100, 1/200, 1/300, 1/400, and 1/500 diluents of N1E were sprayed at every 7 days for an one month on tomato leaves, respectively. According to the results, 1/100 diluent of N1E was most effectually controlled gray mold rot as the control value of 92.5%, was more effective than those results of 1/200, 1/300, 1/400, and 1/500 diluents of N1E as the control value of 81.7%, 74.7%, and 61.8%, respectively. Thus, 1/100 diluent of N1E was selected as the most suitable density to control gray mold rot for further studies. Also, for the selection the spraying frequency of N1E, 1/100 diluent of N1E was sprayed at every 3 or 7 days with a different spraying frequency. the most suitable spraying frequency was the 3 times at every 7 days. Besides, for the comparison of control effect of N1E and chemical fungicide, Diethofencarb·Carbendazim (DC, W.P), 1/100 diluent of N1E and 1/1000 diluent of DC were sprayed at every 7 days for an one month, and measured the disease incidence of gray mold rot on tomato leaves. N1E showing the control value of 90.5% was more effective than that of DC as the control value of 77.0% to control the gray mold rot in the plastic house. In addition,

For the promotion of control effect in the plastic house, N1E and the DC were treated by turns at every 3 days for an one month. the control value of sole treatment of N1E was significantly higher than those of sole treatment of DC and crossing treatments with N1E and DC. To find the change of control effect with time, N1E was maintained as the control effect of 90.5% for 3 weeks. eventhough, DC showed 24% of decrement after 3 weeks. According to the all aforementioned results, N1E powder formulation was proved to be the most effective biofungicide for naturally occurred gray mold rot by *B. cinerea* at the tomato fields in a commercial plastic house.

**B-16. Postharvest control of gray mold rot, *Botrytis cinerea* on fruits with N1E and N1K powder formulations.** Bak, Jung Woo, Park, Jong Young, Kim, Hyun Ju, Song, Ju Hee, Jung, Soon Je, and Moon, Byung Ju. Faculty of Natural Resources and Life Science, Dong-A University, Busan 604-714, Korea

An antagonistic bacteria, *Bacillus licheniformis* N1 which effectively inhibited mycerial growth of gray mold rot pathogen, *Botrytis cinerea* LVF12 was isolated from the rhizosphere of the perilla crop. N1E and N1K powder formulation by *B. licheniformis* N1 was previously reported as a successful biocontrol agents on various crops. These agents were tried to control the postharvest decay by LVF12 and estimated their control effects on apple, pear, and tomato fruits in this study. First of all, for the pathogenicity test, conidial suspension ( $1 \times 10^7$  conidia/ml) of LVF12 was made by 30% tomato juice plus 0.1M KH<sub>2</sub>PO<sub>4</sub>, was selected as a suitable inoculum for the high disease incidence on the apple, pear, and tomato fruits. However, conidial suspension inoculum showed slightly effective than mycerial disc's. For the comparisons of the control effects among N1E and N1K powder formulations, and chemical fungicide, Iprodion (W.P). 1/100 diluents of N1E and N1K and 1/1000 diluent of Iprodion were treated. and then, conidial suspension ( $1 \times 10^7$  conidia/ml) of LVF12 was inoculated on fruits, respectively. According to the results, control value of N1E and N1K were significantly higher than that of Iprodion. N1E was finalized as a potent biocontrol agent to control gray mold rot on fruits, although there were no significant differences between the N1E and N1K. Otherwise, to select the most fruitful spaying density of N1E, N1E according to the various concentrations were sprayed on fruits, respectively. 1/100 diluent of N1E showed more effective than other diluents, and was selected most suitable density to control of gray mold rot on postharvest fruits. Therefore, N1E powder formulation was found to be the most suitable biofungicide for the postharvest control gray mold rot by *B. cinerea* LVF12 on Apple, Pear, and Tomato fruits.

**B-17. Biological control of pythium damping-off of cucumber by *Bacillus stearothermophilus* YC4194.** Hyun Sook Yang<sup>1</sup>, Hwang Bae Sohn<sup>2</sup>, and Young Ryun Chung<sup>1</sup>. <sup>1</sup>Division of Applied Life Sciences(BK21 Program), Gyeongsang National University, Chinju 660-701, Korea, <sup>2</sup>Applied Biology and Chemistry, Seoul National University, Suwon, 441-744, Korea.

*In vitro* and *in vivo* activities of a biocontrol agent, strain YC4194 was evaluated for the control of Pythium damping-off. Strain YC4194 inhibited mycelial growth, germination of cysts, and formation of zoosporangia of *Pythium aphanidermatum*



*in vitro*. Incorporation of a bentonite and talc based formulation(109cfu/g) of strain YC4194 to the nursery soils(10g/L soil) resulted in a significant( $p=0.01$ ) reduction in the disease severity of cucumber damping off after inoculation with *P. aphanidermatum*. The efficacy of YC4194 was significantly better than that of the fungicide, dimethomorph, metalaxyl dithianon, ethaboxan. When the cucumber plants were transplanted to the soil inoculated with *P. aphanidermatum* zoospores, the strain YC4194 maintained the population density in rhizosphere soil up to 107cfu/g. Strain YC4194 was identified on the basis of their biochemical and molecular biological characteristics. The strain YC4194 was identified as *Bacillus stearothermophilus*.

**B-18. Biocontrol of potato common scab in field trials using endophytic bacteria isolated from potatoes.** J. T. Kim<sup>1</sup>, J. S. Kim<sup>1</sup>, Y. I. Hahm<sup>1</sup>, and S. H. Yu<sup>2</sup>.  
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One hundred twenty-six bacterial strains, which isolated from internal tissues of potato stems and roots, were screened for biological control against common scab caused by *Streptomyces scabies*. Seven strains of which were selected by inhibitory activity to the pathogen *in vitro* on potato dextrose agar media. Potato yield and disease severity were compared with the non-inoculated plants at 95 days after planting. Four of the strains, PEP-57, PEP-59, PEP-114 and PEP-119, reduced the incidence and the severity of disease, and increased potato tuber yield. Among these, one for *Pseudomonas* sp. and three for *Bacillus* sp. were effective strains as biological control agent.

**B-19. Biological control of the basal stem rot of graft-cactus caused by *Fusarium oxysporum*.** H.-W. Choi, J.-M. Lee, and S.-C. Chun. Department of Crop Science, Konkuk University, Seoul 143-701, Korea.

The production of a graft-cactus as a stock and scion, *Gymnocalycium mihanovichii* grafted to *Hylocereus trigonus* (triangular cactus) in Korea has 70 ~ 80% proportion of the world. However, the basal stem rot caused by *Fusarium oxysporum* have been a major problem, resulting in the yield loss of 80~90% in severe cases, which may be attributed to continued cultivation without crop rotation. The sawdusts used up for the growth of oyster mushroom, which often infested with *Trichoderma* spp were amended into the infested field soil to control the disease of the cactus. In addition, the microbial population of suppressive soil was studied. The treatments of the sawdusts as organic amendments significantly decreased basal stem rot as much as the suppressive soil did, resulted in 3 ~ 6% incidence compared to 44% of the infested field soil (LSD,  $P=0.05$ ). Also, the fungal population of *Trichoderma* species was significantly higher in the suppressive soil than the disease conducive soil ( $t$  test,  $P=0.05$ ). In contrast, bacteria and actinomyces populations were not significantly different between the two soil. These results indicated that the suppressive soil might be due to the population of *Trichoderma* species, and that biological control using organic amendments could be very successful in the control of the basal stem rot of *Hylocereus trigonus* .