

B-37. Isolation and antifungal activity of Kakuol, a propiophenone from rhizome of *Asarum sieboldii*. J. Y. LEE¹, S. S. Moon², and B. K. Hwang¹. ¹Laboratory of Molecular Plant Pathology, College of Life and Environmental Sciences, Korea University, Seoul 136-701, Korea, ²Department of Chemistry, Kongju National University, Kongju 314-701, Korea.

The substance AsA active against *Colletotricum orbiculare* was isolated from the methanol extract of rhizome of *Asarum sieboldii* using various chromatographic procedures. The antifungal substance AsA, obtained as a white amorphous powder, was soluble in most of organic solvents, but insoluble in water. The HR-EI mass, NMR and UV spectral results confirmed that the antifungal substance AsA is kakuol, 2-hydroxy-4, 5-methylenedioxypropiophenone having a molecular formula of C₁₀H₁₀O₄ (M⁺, m/z 194.1878). *C. orbiculare* was most sensitive to the substance AsA, with MIC of approximately 10 g/ml. The substance AsA also completely inhibited the mycelial growth of *Botrytis cinerea* and *Cladosporium cucumerinum* at the concentration of 50 and 30 g/ml, respectively. However, no antimicrobial activity was found against yeast and Gram-positive or Gram-negative bacteria even at the concentration of 100 g/ml. The substance AsA exhibited a significantly high level of protective activity against development of anthracnose disease on cucumber plants.

B-38. Transcriptional regulation and mutational analysis of the aerobic C4-dicarboxylate transporter(*dctA*) gene of *Pseudomonas chlororaphis* O6. Nam, H. S., Kim, H. J., Cho, B. H., and Kim, Y. C. Agricultural Plant Stress Research Center, College of Agricultural & Life science, Chonnam National University, Gwangju 500-757, Korea

Pseudomonas chlororaphis O6 is an aggressive root colonizer that has abilities to inhibit fungal growth and to induce disease. Rhizosphere colonization is may be one of the crucial steps for them to have the efficient biological control activity. Generally organic acids are the preferred carbon source for *Pseudomonas* species. To investigate the role of organic acid in root exudate, a *dctA* gene encoding a dicarboxylate transporter was cloned from *Pseudomonas chlororaphis* O6. The *dctA* gene transcript was induced by dicarboxylates such as fumarate, succinate and malate in medium but not by glucose. Transcriptional induction of the *dctA* gene on glucose and succinate in minimal medium confirmed that *dctA* is subject to regulation by catabolite repression but of the *dctA* gene promoter has not been found yet CRP binding site. The *dctA*-deficient mutant of *P. chlororaphis* O6 was constructed by marker exchange mutagenesis. The *dctA* mutant did not grow on minimal medium containing succinate or fumarate and the growth was delayed on malate. The growth of wild type and the *dctA* mutant was similar on minimal medium containing glucose or citrate. The *dctA* mutant on cucumber roots in sterilized potting soil was colonized at levels comparable to those of the wild-type, but induction level of disease resistance by the mutant against target spot disease was decreased. These results may indicate that *dctA* gene is not essential for cucumber root colonization, but important for induction of disease resistance.

B-39. Selection of bacterial isolates in Jeju showing antifungal activities against

various plant pathogens *in vitro*. Y. C. Jeun and C. S. Lee. Department of Plant Resource Science, Cheju National University, Jeju 690-756, Korea.

A systemic resistance can be induced in plant by pre-inoculation with plant growth promoting rhizobacteria (PGPR) before challenge inoculation with plant pathogen. This PGPR-mediated resistance, defined as induced systemic resistance (ISR), is differentiated to systemic acquired resistance (SAR) which is induced by pre-treatment with plant pathogen or chemical activator. PGPR enhance growth of plant and most of them have a direct anti-fungal activity, whereas plant pathogens or chemical activators do not. Because using ISR is environment favorable and effective to broad spectrum of plant diseases, it has been regarded as a new strategy of plant protection against plant disease in the future. Until now, numerous bacterial strains showing anti-fungal activity have been reported, however, very rarely in Jeju. In the present study, 57 bacterial strains were isolated from the rhizosphere of the plant growing in various areas coast, middle and top of Halla mountain in Jeju. Anti-fungal effect of all bacterial strains were tested *in vitro* by incubating in a potato dextrose agar medium with 4 isolates of plant pathogens *Rhizoctonia solani*, *Fusarium oxysporum*, *Colletotrichum gloeosporioides* and *C. orbiculare*, respectively. Thirty four bacterial strains inhibited the hyphal growth of the plant pathogens, from which 17 isolates inhibited one of the tested fungi, 10 isolates two fungi, 6 isolates three and one isolate TRL2-3 inhibited all of the tested fungi. Especially, the inhibition by TRL2-3 was remarkably strong in all cases of this study. To select an effective ISR inducing agent more additional experiments, such as evidence of resistance expression in plants, should be carried out.

B-40. *Paenibacillus* sp. SD17, a new species with broad antimicrobial activity against plant pathogenic microorganisms. Dal-Soo Kim¹, Cheol-Yong Bae¹, Jae-Jin Jeon¹, Sam-Jae Chun¹, Hyun Woo Oh², Soon Gyu Hong², Keun-Sik Baek², Eun Young Moon² and Kyung Sook Bae². ¹Agrochemical Research Institute, LG Life Sciences Ltd. 104-1 Moonji-dong, Yusong-ku, Daejeon 305-380, ²Korean Collection for Type Cultures, Korea Research Institute of Bioscience and Biotechnology, #52, Oun-dong, Yusong-ku, Daejeon 305-333, Korea

A novel spore-forming bacterium with broad antimicrobial activity against plant pathogenic fungi was isolated from roots of *Perilla frutescens* in Korea. The isolate SD17T was facultatively anaerobic and variable in Gram reaction with the growth temperature at between 20 and 45 °C. DNA G+C content of SD17T was 51.7 mol%, and the major fatty acid was anteiso-C15:0 with 50-60% of the total composition. The 16S rDNA similarity of SD17T ranged from 97.9 to 91.6% with other *Paenibacillus* species and 98.9% with *Bacillus ehimensis*. Phylogenetic tree showed that the isolate SD17T formed a significant monophyletic clade with *P. koreensis*. DNA relatedness values of the strain SD17T with *P. koreensis* and *B. ehimensis* were 17.6% and 19.7%, respectively. Therefore, it is clear from polyphasic evidence that these isolates merit a species status within *Paenibacillus* (type strain, SD17T = KCTC 10016BPT). The 16S rDNA sequence data of the strains SD17T and SD18 are deposited in the GenBank database under the accession numbers AY090110 and AY081186.