indicating that they could serve as specific symptoms of bacterial canker of sweet cherry. The gram negative, aerobic bacterium isolated from the lesion produced fluorescent pigments on King's B agar medium but did not grow at 37℃. The bacterium formed Levan-type colonies, and showed negative reactions in oxidase reaction, arginine dihydrolysis test, and pectolytic activity. Based on the biochemical and pathological characteristics, the causal organism was identified as *Pseudomonas syringae* pv. *morsprunorum*. This is the first report on bacterial canker of sweet cherry in Korea.

2-26. Screening of antifungal activities of *Bacillus thuringiensis* strains for the development of biocontrol agents of plant diseases

G. H. Kim[1], D. S. Kim[1], D.-H. Lee[1], J. S. Hur[2], Y. J. Koh[1].
[1]Dept. Applied Biology, Sunchon National University, Suncheon 540-742, Korea; [2]Dept. Environmental Education, Sunchon National University, Suncheon 540-742, Korea.

An attempt was made to screen antifungal activities of *Bacillus thuringiensis* strains on various plant pathogens, *Botryosphaeria dothidea, Diaporthe actinidiae, Botrytis cinerea, Glomerella cingulata, Colletorichum cocodes, Sclerotinia sclerotiorum, Alternaria alternata, Helicobasidium mompa, Bipolaris coicis, Fusarium graminearum* and *Rhizoctonia solani*. Ten and forty-five strains of *B. thuringiensis* were isolated from animal feces in Korea and Japan, respectively. Inhibitory effects of the strains on the mycelial growth of the pathogens were examined on the mixed media of potato dextrose agar and nutrient agar. Approximately half of the strains inhibited the mycelial growth of one or more pathogens. Most of the pathogens were inhibited by any of the strains but *Fusarium graminearum* and *Rhizoctonia solani* were not inhibited at all. This is the first report that *B. thuringiensis* shows a potent antifungal activity on plant pathogens in Korea.

2-27. A two-component sensor kinase (GacS) mediated signal transduction pathway involved in production of antifungal compounds in *Pseudomonas chlororaphis* O6.

Beom Ryong Kang, Jung Hoon Lee, Hyun Jung Kim, Baik Ho Cho, Young Cheol Kim.
Agricultural Plant Stress Research Center, College of Agriculture and Life Sciences, Chonnam National University, Gwangju 500-757, Korea.

*E. intermedium*Biocontrol activity of a *P. chlororaphis* rhizobacteium O6, depends to the synthesis of extracellular secondary metabolites and exoenzymes, thought to antagonize the pathogenicity of a variety of phytopathogenic fungi. The production of secondary metabolites and exoenzymes in O6, depends essentially on the GacS-mediated signal transduction pathway, which activates largely unknown signal transduction pathway. To exploit the GacS-mediated signal transdcution pathway involved in activation of *phz* genes that are necessary for biosynthesis of phenazine from *P. chlororaphis* O6, we cloned and sequenced the *phz* operon, *rpoS* gene encoding stationary specific sigma factor, *ppx* gene encoding polyphosphatase, and *lon* gene encoding lon protease. Expression of each gene in wild type and GacS mutant were analyzed by RT-PCR. Transcripts from *rpoS, phzI* enconing acylhomoserine lactone (AHL) synthase, and *phz* structural genes in the GacS mutant were reduced in each of these growth phases compared to the wild type.

The GacS or Lon mutant was found to be deficient in the production of phenzines, exoenzymes, and the acylhomoserine lactone. These mutants were not complemented by *phz* operon and addition of exogenous AHL. These results indicate that the GacS global regulatory systems controls phenazine production at multiple levels. Future research will focus to identifying the GacS-mediated regulatory cascade involving in production of phenazine in *P. chlororaphis*.

2-28. Transcriptional regulation and mutational analysis of a *dctA* encoding organic acid transporter protein from *Pseudomonas chlororaphis* O6.

Hyo Song Nam, Baik Ho Cho, Young Cheol Kim. Agricultural Plant Stress Research Center, College of Agriculture and Life Sciences, Chonnam National University, Gwangju 500-757, Korea.

A *dctA* gene encoding a protein with identity to a C4-dicarboxylate/H^+ was cloned from a beneficial biocontrol bacterium, *P. chlororaphis* O6. Expression of the *dctA* was induced in minimal medium by several organic acids and was repressed by glucose. Highest expression was observed in early-log cells grown on fumarate and succinate with decline as cells approached late-log phase. The *dctA* transcript accumulated weakly when cells were grown on malate but strong expression was observed with benzoate. Expression of the *dctA* transcript was repressed in early-log cells upon addition of glucose to fumarate, but was detected as the cell culture aged. A *dctA*-deficient mutant of O6, constructed by marker exchange mutagenesis, did not grow on minimal medium containing succinate, benzoate, or fumarate, and growth on malate was delayed. The *dctA* mutant and wild type grew equally on glucose. 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 leaf spot disease was decreased. These results may indicate that the *dctA* is essential for utilization of certain organic acids and its expression is controlled by the availability of sugars. In addition, the *dctA* is not essenitial for cucumber root colonization, but important for induction of disease resistance.

2-29. The global regulator GacS of a biological bacterium *Pseudomonas chlororaphis* O6 regulates expression of the stationary-phase sigma factor *rpoS* and reduces survival in oxidative stress.

Beom Ryong Kang, Baik Ho Cho, Young Cheol Kim. Agricultural Plant Stress Research Center, College of Agriculture and Life Sciences, Chonnam National University, Gwangju 500-757, Korea.

The global regulator, GacS (global antibiotic and cyanide sensor kinase), was required for the increased resistance to hydrogen peroxide occurring as cultures of the rhizobacterium, *P. chlororaphis* O6, matured. Specific stationary-phase peroxidase and catalase isozymes were absent in the GacS mutant, whereas a manganese-superoxide dismutase isozyme was expressed earlier and to a great extent than wild type. In the wild type cell, transcript accumulation of *rpoS* was higher in late logarithmic-phase cells than cells from mid logarithmic- or stationary-phase. Transcripts from