pXAG81 contained genes homologous to *avrBs3, tnpA, tnpR, repA, htrA,* two *parA* genes, *pemI, pemK, mobA, mobB, mobC, mobD, mobE, trwB, traF, traH, ISxac2,* and eleven hypothetical proteins. Based on DNA sequence analysis, we presume that pXAG81 is a conjugal plasmid. Interestingly, we found 0.5-kb truncated avirulence gene similar to *avrXacE3* on the right border of *avrBs3* homolgs of pAG1 and pXAG81. Two hundred twenty five isolates were analyzed to find *avrBS3* or *tra* gene homologs by Southern hybridization. The numbers of *avrBs3* homolog varied from 3 in AG1 to 8 in AG166. Two hundred seventeen isolates appeared to carry conjugative plasmids (pXAG81 type), and thirty eight isolates appeared to carry non-conjugative plamids (pAG1 type). This indicated that *avrBs3* gene homologs might be spread by conjugation in *X. axonopodis* pv. *glycines.*

4-25. Rapid identification of *Burkholderia glumae* from diseased seeds

Tae Hwan Noh[1], Wan Yeob Song[2], Mi Hyung Kang[1], Hyung Moo kim[2]. , Du Ku Lee[1], Jong Cheol Park[1] and Hyeong Kwon Shim[1]

[1]National Honam Agricultural Experiment Station, Iksan 570-080, Korea; [2]Department of Agricultural Biology, Chonbuk National University, Chonju 560-756, Korea

Bacterial grain rot by *Burkholderia glumae* cause severe damage in seedling and grain of rice after heading season. This seed-borne pathogen play a role as first infection agent that could be cause disease following cropping season. Until now the direct isolation of the bacteria has some trouble by interference of other bacteria existed inside seed. This study established convenient identification method as simple isolation with KB medium from seed showing symptom and using PCR identification. By this isolation method, *B. glumae* was isolated from 40 to 50% in brown rice and inner hull, however, there were saprophytic bacteria and fungi outer hull. In PCR identification with Ogf4 and Ogr3 primer to these 25 isolates, the amplified products were presented in all of the collections but not in 10 saprophytic germs. The isolation rate was constant to 3 months stored seeds. This result provide a rapid and convenient isolation and identification of *B. glumae.*

4-26. Phytoplasma specific primer for detection of jujube witches' broom group(16SrV) in Korea and China

Sangsub Han, Sanghun Lee, Mengjun Liu[1], and Byeongjin Cha

Dept. of Agricultural Biology, Chungbuk National University, Cheongju 361-763, Korea, [1]Research Center of Chinese Jujube, Agricultural University of Hebei, Baoding, China

In order to diagnose and differentiate jujube witches' broom (JWB) phytoplasma rapidly, oligonucleotide primer pair, 16Sr(V) F/R, for polymerase chain reactions (PCRs) was designed on the basis of 16S rRNA sequences of JWB phytoplasma. The PCR employing phytoplasma universal primer pair P1/P7 consistently amplified DNA in all tested phytoplasma isolates. But no phytoplasma DNA was detected in healthy jujube seedlings. The nested PCR, the primer pair 16S(V) F/R, about 460 bp fragment, amplified DNA in all tested JWB and related phytoplasmas including LiWB phytoplasma of the 16S rRNA group V, but no DNA amplification was detected from other

phytoplasma strains such as group 16SrI (Aster yellows) and group 16SrXII (Stolbur group) phytoplasmas in which mulberry dwarf phytoplasma and chrysanthemum witches broom phytoplasma are belonged to, respectively. The same results were obtained from both Korean- and Chinese-isolates of JWB. Nested-PCR using phytoplasma universal primer pair P1/P7 and 16S rRNA group V specific primer pair 16S(V) F/R could detect group V phytoplasma rapidly and easily, in particular JWB phytoplasma.

4-27. Replicase and movement protein of *Cucumber mosaic virus* are symptom determinants in zucchini squash

S. K. Choi[1], P. Palukaitis[2], and **K. H. Ryu**[3]

[1]Department of Biochemistry & Biophysics, Texas A&M University, TX 77843, USA, [2]Pathology Division, Scottish Crop Research Institute, Invergowrie, DD2 5DA, United Kingdom, [3]Plant Virus GenBank, Division of Environmental and Life Sciences, Seoul Womens University

A pepper strain of *Cucumber mosaic virus* (Pf-CMV) induces a mild chlorotic spot symptom in zucchini squash at 9 days post-inoculation (dpi), wile Fny strain of CMV causes severe mosaic and stunting symptom at 4 dpi in this host. Pseudorecombinants were constructed between the two strains, and assessments of symptom severity were indicated that both RNA2 and RNA3 were responsible for both mildness and the slow appearance of symptom elicited by Pf-CMV in zucchini squash. With various RNA2 and RNA3 chimeras between two strains of CMV, the genetic symptom determinants of phenotype of Pf-CMV were mapped to Tyr residue at positions amino acid 267 in 2a protein and at positions amino acid 168 in 3a movement protein (MP). Chimeras changed the sequences (both changed Tyr to Ile) in the codons of both amino acid 168 of 3a MP and amino acid 267 of 2a protein were resulted in the high RNA accumulation, severity of symptom, and the rapid systemic spread, suggesting that 2a replicase as well as MP is involved in virus movement. The RNA accumulation pattern of all pseudorecombinants and chimeras are identical in protoplast of zucchini squash, indicating the virus movement is responsible for the phenotypes of two CMV strains rather than virus replication.

4-28. Ultastructural Characteristics of Necrosis and Stunt Disease in Red Pepper by the Mixed Infections of *Tobacco mosaic virus* or *Pepper mild mottle virus* and *Pepper mottle virus*.

Dae. Hyun. Kim[1], Jeong. Soo. Kim[1], Jae. Hyun. Kim[1], Eui. Kyoo. Cho[2].

[1]National Horticultural Research Institute, RDA Suwon 441-440, Korea, [2]Department of Agricultural Biology, College of Natural Sciences, Andong National University, Andong, Kyungbuk 760-749, Korea

The commercial cultivars of red pepper were screened against *Tobacco mosaic virus* (TMV), *Pepper mild mottle virus* (PMMoV) and *Pepper mottle virus* (PepMoV) by seedling test. In single infection of TMV or PMMoV, mosaic symptom was produced on the cultivars of