viral replicase, triple gene block, 36 kDa viral coat protein (CP) and 12 kDa from the 5′ to 3′ ends, which is a typical genome structure of carlaviruses. Two Korean isolates of DVS isolates were 98.1% and 93.6% amino acid identical in the CP and 12kDa, respectively. The CP gene of DVS shares 25.2-55.2% and 42.9-56.1% similarities with that of 19 other carlaviruses at the amino acid and nucleotide levels, respectively. The 3′-proximal 12 kDa gene of DVS shares 20.2-57.8% amino acid identities with that of 18 other members of the genus. The 3′ noncoding region of DVS consists of 73 nucleotides with long excluding poly A tract, and shares 69.1-77.1% identities to the known carlaviruses. In the phylogenetic analyses of the two proteins, DVS was closely related to *Helenium virus S* and *Chrysanthemum virus B*. This is the first complete sequence information for the DVS, and further confirms the classification of DVS as a distinct species of the genus *Carlavirus*.

3-10. Evaluation of genetic affinities among *Fusarium oxysporum* f. sp. *fragariae* by RAPD and rDNA RFLP

Gopal Nagarajan[1], Myeong Hyeon Nam[2] , Yun Soo Lee[1], Woo Chung Lee[1], Sung Joon Yoo[3], Jeong Young Song[3] and Hong Gi Kim[1]

[1]Department of Applied Biology, College of Agriculture, Chungnam National University, Daejeon 305-764, Korea

[2]Strawberry Experiment Station, Chungnam ARES, Nonsan 320-862, Korea

[3]Bioshield Co. Ltd. HTVC KAIST, Daejeon 305-701, Korea

Fusarium oxysporum f. sp. *fragariae* is a fungal pathogen causing wilt disease on strawberry. The RAPD and RFLP of IGS region of rDNA were used to identify genetic affinity among 22 isolates of *F. oxysporum* f. sp. *fragariae* obtained from various location of major strawberry cultivating areas in Korea. Approximately 2.6kb DNA fragment was amplified with primer CNS1 and CNL12, and polymorphisms were observed with *Ava*II and *Hin*fI. A dendrogram was constructed using the UPGMA for cluster analysis. Eight distinct groups were clustered based on the banding pattern obtained from RAPD and rDNA RFLP. There was high level genetic variation among Korean isolates of *Fusarium oxysporum* f. sp. *fragariae*.

3-11. Genetic variation of *Phytophthora infestans* by RAPD analysis

Yun Soo Lee[1], Jeong young Song[2], Nam Kyu Kim[1], Nam Moon[1], Hye Jin Park[1] and Hong Gi Kim[1]

[1]Department of Applied Biology, College of Agriculture, Chungnam National University, Daejeon 305-764, Korea, [2]Bioshield Co. Ltd. HTVC KAIST, Daejeon 305-701, Korea

Late blight, caused by *Phytophthora infestans*, is one of the most destructive disease on potato and tomato cultivation. To analysis genetic diversity *P. infeatans* isolates were collected from potato and tomato fields in Korea. These pathogens contained both A1 and A2 mating type with metalaxyl-resistant and sensitive isolates. Polymorphisms showed base on RAPD (Random Amplified

Polymorphic DNA) in both potato and tomato isolates of *P. infestans*. Cluster analysis showed high level genetic variation in potato isolates of *P. infestans* than tomato isolates. *P. infestans* isolates were observed genetic diversity among them but not grouped among isolates related mating type and metalaxyl response. These results exhibited that *P. infestans* isolates showing genetic difference among them were distributed in Korea.

3-12. Genetic characteristics of *Phytophthora capsici* mutants induced by dimethomorph

Nam Moon[1], Kyoung Mi Lee[1], Kuang Il Jang[1], Jeong young Song[2] and Hong Gi Kim[1]
[1]Department of Applied Biology, College of Agriculture, Chungnam National University, Daejeon 305-764, Korea
[2]Bioshield Co. Ltd. HTVC KAIST, Daejeon 305-701, Korea

Phytophthora blight, caused by *P. capsici*, is very important disease of pepper. Many fungicides to control of Phytophthora blight have been developed, but most of fungicides disappeared in short periods. Nowadays dimethomorph was known as one of the most effective to control of this disease. *P. capsici* isolates from pepper fields were collected and surveyed their growth in dimethomorph amended V8 medium in order to evaluate their fungicides resistance. The fungicide resistant isolates were not founded among them. Most of the sensitive isolates were inhibited perfectly in V8 medium amended with 10ppm dimethomorph. Mutants of *P. capsici* by dimethomorph, was grown very well in 250ppm. The difference of pathogenicity, colony morphology, drug response, RT-PCR results was identified between sensitive and resistance isolates. This study should be provided a basic information about the occurrence of dimethomorph resistant isolates and genetic changes in *P. capsici* population.

3-13. Phylogenetic analysiccccccccc of the genus *Stemphylium* based on elongation factor -1 alpha and calmodulin gene squences

D. W. Kong, H. S. Cho, and S. H. Yu
Division of Applied Biology, Chemistry and Food Science, College of Agriculture and Life Sciences, Chungnam National University, Daejeon 305-764, Korea

The importance and diversity of the genus *Stemphylium* highlights the need for accurate identification of species. However, many *Stemphylium* isolates have been misidentified due to the use of spore size as the only identifying character. Molecular phylogenetic analyses were performed on fifty-four isolates covering 9 *Stemphylium* species collected in Korea. Phylogenetic analysis of the translation elongation factor -1 alpha (EF-1<alpha>) and the calmodulin gene sequence data showed that *Stemphylium* species were segregated into seven distinct groups, most of which correlated with species identified by morphology. Analysis of EF-1<alpha> in particular was useful for establishing well- supported relationships among the species of *Stemphylium*.

3-14. Complete genome sequence of *Fusarium hypovirus* DK21 strain and genomic diversity of dsRNA mycoviruses isolated from *Fusarium graminearum*