

Rice stripe virus causes severe damage to rice in Korea, Japan and China. RSV is a type member of the tenuivirus group and transmitted by the small brown planthopper, *Laodelphax striatellus*, in a persistent manner. Until now, occurrence of RSV is limited in the southern part of Korea. But recently occurrence of RSV is increasing and spreading in central part of Korea including Chungcheong and Kyonggi province. So we analyzed recent occurrence trend of RSV which is increased and cloned and sequenced coat protein gene for isolating of RSV strain. Infected rice of each species (Ilpumbyeo, Sindongjinbyeo, Keumobyeo-2, Dongjinbyeo, Jongnambyeo, Samcheonbyeo, etc.) is collected, we extracted total RNA from infected leaves and detected RSV viral RNA by reverse transcription (RT)-PCR using specific primer of coat protein gene. The result of RT-PCR, we observed specific band. We already cloned cDNA from the band, is analyzing sequence variety and homology of each species.

**3-08. Morphological and Genetic Characterization of *Penicillium* spp. associated with post-harvest decay of fruits. (oral)**

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Post-harvest decay, caused by *Penicillium* spp. is a serious problem of fruits worldwide. Morphological characteristics and molecular markers were used to characterize 22 *Penicillium* isolates from apples, 18 isolates from pears, 60 from oranges and 18 from grapes and 23 reference isolates representing related *Penicillium* spp. to assess their diversity and resolve their taxonomy. Based on morphological and physiological characteristics, the isolates were grouped as identical or very similar to *P. digitatum*, *P. italicum*, *P. ulaiense* or very similar to *P. crustosum*, *P. expansum*, *P. solitum* and unidentified *Penicillium* spp. Based on sequence comparisons of ITS region, variable site were presented within and among the species, but their variation were not correlated with the species. Cluster analyses of AP-PCR fragment patterns using URP and L45 primer and the  $\beta$ -tubulin gene sequence, the *Penicillium* species were segregated into distinct groups. Particularly, the  $\beta$ -tubulin partial sequence data provided support for species concepts based on morphological and physiological characteristics.

**3-09. Complete nucleotide sequence of genome RNA of *Daphne virus S* and its relationship in the genus *Carlavirus* (oral)**

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Complete genomic nucleotide sequence of *Daphne virus S* (DVS), a member of the genus *Carlavirus*, causing leaf distortion and chlorotic spot disease symptoms in daphne plants, has been determined in this study. The genome of DVS contained six open reading frames coding for long

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

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*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

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Late blight, caused by *Phytophthora infestans*, is one of the most destructive disease on potato and tomato cultivation. To analysis genetic diversity *P. infestans* 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