Five pepper-infecting potyviruses, *Pepper mottle virus* (PepMoV), *Chilli veinal mottle virus* (CVMV), *Pepper veinal mottle virus* (PVMV), *Pepper severe mosaic virus* (PSMV) and *Tobacco each virus* (TEV), are known filamentous virus and can be infected pepper crops systemically. To understand pathology and genome information of the five viruses on pepper plants, host reactions and sequences were compared to the 5 viruses. Five potyviruses were inoculated onto some typical cultivars of hot peppers and compared their symptoms, and virus accumulations. A set of degenerate primers for potyviruses were applied to 5 viruses and RT-PCR was performed. RT-PCR products containing partial nuclear inclusion b and coat protein (CP) genes were cloned. Then, oligo dT primer and species-specific primer were redesigned to amplify the C-terminal part of CP and 3′ noncoding regions of each viruses. Sequences of the viruses were analyzed and compared to serological relationships among the viruses. The data can be useful for screening of potyviruses in pepper plants and pathogen-derived transgenic pepper plant development.

3-06. Characterization and sequence analysis of half of genome RNA of a new *Tobamovirus* (Cactus mild mottle virus) from cultivated cactus plants in Korea

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A new isolate of rod-shaped virus was identified from grafted cactus, *Gymnocalycium mihanovichii* grafted onto *Hylocereus trigonus*, in Korea. The virus proved to be a new *Tobamovirus* and called previously as Tobamovirus-Ca for which we suggest the name Cactus mild mottle virus(CMMoV), because it produced systemic mild mosaic symptoms on its original host. CMMoV is distantly related to known species of the genus *Tobamovirus* on the basis of host range, serological and sequence analyses. Western blot analysis showed that CMMoV is serologically unrelated to *Sammons' Opuntia virus* which is the only known species of the genus found in cactus plants. The 3′-terminal 2,910 nucleotides have been sequenced for the virus. The coat protein (CP) and movement protein (MP) genes encode 161 and 306 amino acids residues, respectively. The nucleotide and amino acid sequences of the CP were 39.6 % to 49.2 % and 26.4 % to 40.3 % identical to other tobamoviruses, respectively. The MP and 3′ noncoding region shared 16.3 % to 23.3 % and 44.6 % to 63.4 % identities, respectively, with the members of the genus. Phylogenetic tree analysis of the CP gene revealed that CMMoV clusters with members of subgroup I of *Tobamovirus*. CMMoV particles contained genomic RNA along with two subgenomic RNAs, and this characteristics is common in the members of the subgroup II. This is the first information of sequence and comparative analysis of a *Tobamovirus* that infects cactus.

3-07. The occurrence trend of the RSV and its colning of coat protein of korean strain.

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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 persistant manner. Until now, occurrence of RSV is limited in of 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 23reference 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 there 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