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More than 30 isolates of *Alternaria* were obtained from various solanaceous crops in Korea. For all isolates, morphological characteristics of the conidia were determined and compared with those of representative isolates of *A. solani* and *A. tomatophila*. Pathogenicity test was performed to potato, tomato, egg plant and red pepper and molecular characteristics of them including the representative isolates were determined using sequence analyses of ITS rDNA and histone H3 gene, and URP-PCR analysis. Based on morphological characteristics, the isolates from the solanaceous crops were grouped as identical or very similar to either *A. tomatophila*(ATO), *A. solani*(ASO), and unidentified *Alternaria* sp.(ASP). Among the molecular markers used in this study, the URP-PCR analysis was found to be appropriate for taxonomic resolution of these species. Based on the conidial morphology, pathogenicity test and molecular characteristics, *A. tomatophila*(early blight of tomato) could be distinguished from *A. solani*(early blight of potato), and the *Alternaria* sp.(ASP) from potato, which was closely related to *A. solani* in conidial morphology, was considered as a new species.

3-04. Complete genome sequence analysis *Hosta virus X* and comparison to other potexviruses

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A potexvirus, *Hosta virus X* (HVX-Kr), causing mosaic and mottle symptoms was isolated from hosta plants (*Hosta* spp.), and its entire genome RNA sequence was determined in Korea using cDNA library and RACE methods. The genome of HVX encodes five open reading frames coding for viral replicase, triple gene block (TGB), and viral coat protein (CP) from the 5' to 3' ends, which is a typical genome structure of potexviruses. The 3-terminal region of the virus includes the TGB1 (26 kDa), TGB2 (13 kDa), TGB3 (8 kDa), and 23 kDa coat protein (CP) and the 3-nontranslated region (NTR). The CP gene of the type isolate of HVX (HVX-U) was amplified by RT-PCR and its nucleotide sequence was determined. The CPs of HVX-Kr and HVX-U had 100% and 98.9% identical amino acids and nucleotides, respectively. Most of the regions of the genome HVX had over 50% nucleotide identical to other sequenced potexviruses. This is the first report of complete genome sequence information of HVX and molecular evidence supporting the virus as a distinct species of the genus *Potexvirus*.

3-05. Pathological and molecular comparisons of five distinct species of pepper-infecting Potyviruses (oral)

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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 etch 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 cloning of coat protein of korean strain.

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