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A Korean isolate of *Pepper mild mottle virus* (PMMoV-Kr) was isolated from a diseased pepper crop in Chunchon, Korea. The isolate was biologically purified on *Nicotiana tabacum* cv. Xanthi-nc by successive single local transfer steps, and propagated on *N. tabacum* cv. Samsun. PMMoV-Kr could systemically infect on *N. glauca*, *N. benthamiana*, *N. occidentalis* and *Lycopersicon esculentum*, which is typical of known isolates of PMMoV. PMMoV-Kr belongs to the pathotype P1,2 based on pepper-tobamoviral indicator experiments; *Capsicum chinense* harboring L3 gene revealed resistant (necrotic local lesion on inoculated leaf, HR) whereas L+, L1 and L2 pepper plants expressed susceptible reactions of mosaic systemic symptoms for the isolate. To confirm the pathology and delineate symptom determinant of the isolate, full-length cDNAs of PMMoV-Kr were amplified by RT-PCR with a primer set corresponding to the 5′- and 3′-ends of PMMoV. The RT-PCR molecules amplified from genome RNA of the isolate was cloned into the pUC18 vector. Full-length cDNA clones constructed under the control of the T7 RNA promoter could be successfully transcribed to produce in vitro transcript RNA. Infectivity of the capped transcripts and its progeny virus was verified by Western blot and RT-PCR analyses.

### 4-41. Functional assessment of attenuated mutants of *Pepper mild mottle virus*

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Attenuated viruses can protect their hosts against challenge to their related viruses. Increasing evidence shows that mutations of the tobamoviral 126/183 kDa protein play a major role in the viral attenuation and contribute to the cross protection mechanism. In this study, four mutants of *Pepper mild mottle virus* (PMMoV) have been constructed by mutagenesis; two mutants, pTPpoly348 and pTPpoly762, were substituted in the middle of replicase gene, and the others, pTPL3D::△6207 and pTPL3D::△6219, were deletion mutants made by deleting some parts of pseudoknot structures of the 3′ noncoding region (NCR) of the virus. Progeny viruses generated from the four mutants were infectious on *N. benthamiana* plants with symptomless or mild mosaic symptom. Replication efficiency and viral product accumulations of four mutants were assessed by Northern and Western blot analyses on BY-2 protoplast cells. Accumulation of CP for the pTPL3D::△6207 and pTPL3D::△6219 were lower than that of other mutants and wild type virus. These data suggest that the 3′-NCR mutations contribute to the viral gene expression in host tissues, while mutants of replicase gene rather govern the symptom expression.

### 4-42. Incidence and variability of *Hosta virus X* and seed-transmission in *Hosta* plants

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This study was performed to investigate the incidence of *Hosta virus X* (HVX), a *Potexvirus*, from cultivated hosta ornamental plants in Korea and to ascertain seed transmission of the virus from infected parent plant to progeny ones for breeding program of hosta plants. Infection rate of HVX in cultivated hostas was 25.6 % (11 out of 43 collected samples contained HVX) based on Western blot and RT-PCR detection methods. Most of HVX-infected hostas showed visible systemic leaf symptoms (mosaic, mottle, curling, stunting or combinations). Variability of HVX was confirmed by sequences of coat protein gene of individual isolates from different hostas. HVX was seed-transmitted on *Hosta* 'Blue Cadet'. The virus was detected from seeds, and sprouts and seedlings from the virus-contaminated seed sources. Over 7.5 % of seeds were HVX-contaminated surveyed in this study. Our data suggest that HVX can be transmitted by seed source, and indexing of the virus should be done for breeding program of *Hosta*.

**4-43. Variability in the coat protein genes of two orchid viruses from *Phalaenopsis* orchids in Korea**

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This study was conducted to designing conserved regions of molecules for virus-derived resistance to transgenic *Phalaenopsis* orchids to protect against two major orchid viruses, *Cymbidum mosaic virus* (CymMV) and *Odontoglossum ringspot virus* (ORSV). Infected leaf samples of *Phalaenopsis* were randomly screened by the RT-PCR with specific primers to both of viruses. RT-PCR products of the viruses were cloned and their nucleotide sequences were determined. Multiple alignments of coat protein (CP) genes of the viruses revealed that over the 88 % and 94 % identities with CymMV and ORSV, respectively, were observed. These data can be useful for selection of highly conserved regions of CP gene of the viruses for transgenic orchid experiments.

**4-44. Detection of citrus-infecting viruses and sequence analysis of *Satsuma dwarf virus* (SDV) and SDV-CiMV in Jeju island**

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To investigate occurrence and variability of satsuma mandarin (*Citrus unshiu*)-infecting viruses in Jeju island, several sets of diagnostic RT-PCR primers were designed and applied to samples collected randomly. Each primers set used in this survey was designed to detect *Satsuma*