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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*

dwarf virus (SDV, *Sadwavirus*) and Citrus mosaic virus (CiMV) which is reclassified as an isolate of SDV (SDV-CiMV, *Sadwavirus*). RT-PCR methods could detect SDV-CiMV and CTV from leaf samples of unshui citrus. CTV was the prevalent and SDV-CiMV was not common in Jeju island. RT-PCR product of SDV-CiMV-JJ12 were cloned and sequenced. Sequence of the isolate revealed that it was 96.9 % identical to SDV-CiMV-Jp isolate at the nucleotide level. SDV-CiMV-JJ12 was propagated on *Physalis floridana* and sequencing of entire sequences of genome is in progress. Variability of SDV in Jeju island was confirmed by sequence comparisons and restriction mapping analysis.

4-45. Virus-resistant and susceptible transgenic *Nicotiana benthamiana* plants expressing coat protein gene of *Zucchini green mottle mosaic virus* for LMO safety assessment

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Transgenic *Nicotiana benthamiana* plants harboring and expressing coat protein (CP) gene of *Zucchini green mottle mosaic virus* (ZGMMV) were generated for both virus-resistant screening and complementation analysis of related viruses and environmental safety assessment (SA) of living modified organism (LMO) purposes. Transformation of leaf disc of *N. benthamiana* was performed using *Agrobacterium*-mediated method and the pZGCPPGA748 containing the ZGMMV CP and NPTII genes. Two kinds of transgenic homozygous groups, virus-resistant and -susceptible lines, were obtained by screening of challenging homologous virus for T1 generations. Complementation of CP-deficient related virus was analyzed using the susceptible line of ZGMMV. These two pathologically different lines can be useful for host-virus interactions and LMO environmental SA.

4-46 Pathogenicity of infectious *in vitro* transcripts and comparison of RNA3 of *Alfalfa mosaic virus* Korean isolates

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Two Korean isolates of *Alfalfa mosaic virus* (AMV-AZ, AMV-KR) were isolated from azuki bean and potato plants, respectively, and their pathologies were confirmed on some susceptible host plants including pepper, tobacco and red bean plants. Full length cDNAs to RNA1, RNA2 and RNA3 of the two Korean strains were amplified using the long-template reverse transcription (RT)-polymerase chain reaction (PCR) method. RT-PCR products covering entire regions for the three AMV genome RNAs were cloned. RNA transcripts were synthesized in vitro from each clones using T7 RNA polymerase and infectivity test was performed in 9 reassortment sets of transcripts. All the combinations of reassorted transcripts were found to be infectious when inoculated onto *Nicotiana benthamiana* plants, and were not distinguishable to those of wild types. The full-length