Zantedeschia mosaic virus (ZaMV-KR). However, low identity in amino acid sequences was found in the termini of CP genes between the two isolates of JHMV and ZaMV-KR.

4-38. Sequence variant of Hop Stunt Viroid(HSVd) detected from Plum trees cultivated in Korea and Phylogenetic Analysis

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Hop stunt viroid(HSVd) is a plant pathogen which infect a number of hosts such as grapevine, *Citrus* and *Prunus* plants. Sequence variants of HSVd have been divided into three types(i. grapevine and hop, ii. citrus, iii. plum, peach, apricot and almond). Purified RNAs from plum trees were used for the synthesis of cDNA with reverse transcription and amplified by polymerase chain reaction. Cloned cDNAs were sequenced and two different consensus sequence variants were detected. A neighbor-joining analysis was carried out on the sequence variants together with 62 previously described variants of HSVd from hop, plum and other species. Sequence variants from plum trees cultivated in Korea were clustered in HSVd-plum subtype and not in HSVd-hop subtype which were two Korean isolates belongs. These relationship between sequence variants from plum and two Korean isolates in HSVd-hop type supports the other origin for hop stunt disease.

4-39. Sensitive method for the detection of Apple scar skin viroid(ASSVd) by nested reverse transcription-polymerase chain reaction

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A rapid and sensitive assay for the specific detection of plant viroids using reverse transcription-polymerase chain reaction(RT-PCR) has been developed already. The nested RT-PCR assay cloud be applied for the detection of apple scar skin viroid(ASSVd) from young leaves and other tissues. ASSVd has central conserved region(CCR), terminal left(T_L) and terminal right(T_R) domain. Primers were designed from these regions. Primer sets were successfully applicable for the amplification of full length or partial region of ASSVd by nested RT-PCR. Nested RT-PCR assay was more sensitive and accurate method to detect ASSVd from young trees during the early time of apple cultivation.

4-40. Pathogenicity of a Korean isolate of *Pepper mild mottle virus* and development of full-length cDNA clone for infectious *in vitro* transcripts

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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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