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A flexuous rod-shaped virus was isolated from *Cucurbita pepo* leaves showing green mosaic and puckering symptoms at Anseong, Korea. Based on the biological tests, electron microscopy, and reverse transcription-polymerase chain reaction (RT-PCR), the isolate was identified as Papaya ringspot virus type Watermelon (PRSV-W). In the biological test, host range of PRSV-W was limited in the families *Cucurbitaceae* and *Chenopodiaceae*. Most susceptible cucurbit species, such as *Cucurmis lanatus, Cucurmis sativus, Cucurbita pepo,* and *Citrullus lanatus,* responded to mechanical inoculation by PRSV-W that induce green mosaic, malformation, puckering, and narrow laminae. The local lesion symptoms were produced on the inoculated leaves of *Chenopodium amaranticolor* and *C. quinoa*. PRSV specific primers which amplifies the part of the coat protein (CP) genes, generated a 648 bp product from 6 isolates of PRSV-W, but no amplification had been detected in other viruses including CMV, CGMMV, KGMMV, ZYMV and WMV. In electron microscopy, PRSV particles were flexuous, approximately 780 nm in length and 12 nm in width. PRSV-W is one of the worldwide viruses which has the great economic importance in cucumber, melon, squash, watermelon, and other cultivated cucurbits with ZYMV and WMV. This is the first report of PRSV-W on cucurbits in Korea.

4-37. Japanese Hornwort Mosaic Virus in Ornamental Flower and Its Phylogenetic Analysis with Other Potyvirusess.

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Ammi majus (white lace flower, *Unbelliferae*) is an ornamental plant used for cut-flower arrangements worldwide. A potyvirus was isolated from its leaves with mosaic and chlorotic symptoms in the cultivated field of Chiba, Japan. Compared with *Japanese hornwort mosaic virus* (JHMV) previously isolated from *Cryptotaenia japonica*, it showed similar characteristics in host reactions and molecular properties. The nucleotide sequences of coat protein and 3′- nontranslated region were highly homologous and shared 87% and 91% identities with those of JHMV, respectively. This virus was thus supposed to be an isolate of JHMV and designated as JHMV-Am. Phylogenetic tree was constructed using CP nucleotide sequences of the two isolates and other potyviruses previously reported. JHMV-Am and JHMV fell into a cluster with Korean strain of

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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