

cDNA clones that were confirmed infectious were sequenced their nucleotide sequences. We will discuss sequence analysis of the two Korean isolates of AMV genomic RNA3 and compare reported foreign isolates of AMV.

4-47. Some properties of *Cucumber mosaic virus* and a potyvirus isolated from *Freesia*

H.R. Lim, E.G. Shin, H.I. Ahn, and K.H. Ryu

Plant Virus GenBank, PVGABC, College of Natural Science, Seoul Women's University, Seoul 139-774, Korea

Freesia, a member of the *Iridaceae* family, has fragrant, tubular shaped flowers and is very popular ornamental plants in the world. Diseased freesia plants showing systemic leaf streak mosaic symptoms were collected from a cultivated farm in Kyonggi province, Korea in 2003, and its causal agents were investigated. Two viruses, Cucumber mosaic virus (Fr-CMV) and a potyvirus, were identified from the leaf tissues of the diseased freesia based on sequence analysis and host range tests. CMV-Fr could infect systemically on *Chenopodium quinoa*, *C. amaranticolor*, *N. glutinosa*, and *N. benthamiana*, and this biological property is distinguishable from ordinary strains of CMV. A filamentous potyvirus-shaped virus could not infect general indicator plants by mechanical inoculation. Single RT-PCR products was successfully amplified with a set of degenerate primers specific to the *Potyvirus* genus and total nucleic acids from the infected tissues, and was cloned into the pGEMT-Easy vector. Nucleotide sequences confirmed it belongs to the *Potyvirus* genus with either a new species or an isolate of *Freesia mosaic virus* (no information is available for the FrMV). This is the first report of FrMV in Korea and more characterizations of the two viruses are in progress.

4-48. Complete sequence of genome RNA of *Pepper mottle virus* Korean isolate

H.I. Yoon¹, J.Y. Yoon¹, G.S. Choi², J.K. Choi³, and K.H. Ryu¹

¹Plant Virus GenBank, PVGABC, College of Natural Science, Seoul Women's University, Seoul 139-774, Korea, ²Department of Horticultural Environment, National Horticultural Research Institute, RDA, Suwon 441-440, Korea, ³Division of Biological Environment, Kangwon National University, Chunchon 200-701, Korea

Complete nucleotide sequence of genome RNA of a Korean isolate of *Pepper mottle virus* (PepMoV-Vb) from field-collected diseased paprika (*Capsicum annuum* var. *grossum*) was determined in this study. Symptoms of isolates of PepMoV were divided largely into two groups, vein banding (Vb) and vein clearing (Vc) patterns. PepMoV-Vb RNA consists of 9,640 nucleotides excluding the poly(A) tail. A single open reading frame was identified beginning at nucleotide position 169 encoding a polyprotein of 3024 amino acids which is typical of the *Potyvirus* genus. The complete nucleotide sequence and coding regions of PepMoV-Vb were compared to that of 11 potyviruses within the genus *Potyvirus*. The overall nucleotide sequence identity was 94.7 and 94.1% identical to PepMoV-C and PepMoV-FL, respectively. Full-length cDNAs of PepMoV-Vb1 were synthesized from purified viral RNAs by RT-PCR and their genome structure was analysed

by RFLP analysis. This is the first report on complete nucleotide sequence of PepMoV isolated from paprika in Korea.

4-49. First report of *Cycas necrotic stunt virus* from cultivated *Daphne* plants

B.Y. Lee, and K.H. Ryu

Plant Virus GenBank, PVGABC, College of Natural Science, Seoul Women's University, Seoul 139-774, Korea

Natural virus infection of cultivated *Daphne odora* plants showing chlorosis and stunting was observed and their causal agent was investigated. An isolate of isometric virus was purified from infected leaf tissues, and it could infect systemic severe mosaic on *Chenopodium quinoa* and *C. amaranticolor*. cDNA library was generated from partially purified viral RNAs and oligo dT primer-pSPORT1 system, and recombinant clones were selected and their inserts were sequenced randomly. Nucleotide sequences of the virus were analyzed by BLAST, and it was closely related to members of subgroup B in the genus *Nepovirus*. The sequence analysis suggest that the virus was identified as an isolate of *Cycas necrotic stunt virus* (CNSV) because it was 89.7 % and 94.7 % identical to known CNSV for the CP and 3' noncoding region, respectively. RT-PCR was performed to screen disease incidence of CNSV in *Daphne* plants, and five out of 10 plants (50 %) were infected by CNSV. This is the first sequence information of CNSV from *Daphne* plants.

4-50. Transgenic cucumber expressing the 54-kDa gene of *Cucumber fruit mottle mosaic virus* is highly resistance and protect non-transgenic scions from soil infection

A. Gal-On¹, D. Wolf², Y. Antignus¹, L. Patlis², K.H. Ryu³, B.E. Min³, M. Pearlsman¹, O. Lachman¹, V. Gaba¹, Y. Wang¹, J. Yang¹, and A. Zelcer²

¹Department of Virology, ²Department of Plant Genetics, Agricultural Research Organization, Israel, ³Plant Virus GenBank, PVGABC, College of Natural Science, Seoul Women's University, Seoul 139-774, Korea

Cucumber fruit mottle mosaic tobamovirus (CFMMV) causes severe mosaic symptoms with yellow mottling on leaves and fruits, and occasionally severe wilting of cucumber plants. No genetic source of resistance against this virus has been identified. The genes coding for the coat protein or the putative 54-kDa replicase were cloned into binary vectors under control of the SVBV promoter. *Agrobacterium*-mediated transformation was performed on cotyledon explants of a parthenocarpic cucumber cultivar with superior competence for transformation. R1 seedlings were evaluated for resistance to CFMMV infection by lack of symptom expression, back inoculation on an alternative host and ELISA. From a total of 14 replicase-containing R1 lines, 8 exhibited immunity, while only 3 resistant lines were found among a total of 9 CP-containing lines. Line I44 homozygous for the 54-kDa replicase was selected for further resistance analysis. Line I44 was immune to CFMMV infection by mechanical and graft inoculation, or by root infection following planting in CFMMV-contaminated soil. Additionally, line I44 showed delay of symptom appearance following infection by other cucurbit-infecting tobamoviruses. Infection of line I44 plants with various