

DAS-ELISA. Averaged population of the RSV-viruliferous insects in this year was 2.1%, which was lower than that of last year of 3.7%. However, the insect population in Seoul, Incheon and Gyeonggi areas were relatively high showing 6.7%, 6.2% and 2.6%, respectively. Based on the survey results, it was expected that overall occurrence of RSV on rice could be decreased in this year, except certain areas. Ovarial transmission rate of RSV by the insects on diseased rice samples collected from 10 areas ranged from 22.2% to 77.8%. Among 35 graminous weed species collected from rice fields in Ganghwa and Kimpo in 2002 and 2003, common reed and formosens were found to be infected by RSV. The result indicates that those weeds are potential alternative natural hosts of the RSV. Further studies on ecological and pathological impacts of the alternative natural host of RSV are being processed.

4-35. Virulence differentiation of bean common mosaic potyvirus in leguminosae crops.

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Forty six isolates of bean common mosaic virus (BCMV) collected from azuki bean, mungbean, kidney bean, cowpea, broad bean and peanut were classified into three groups based on biological, serological, cytopathological, and molecular characteristics. Group I induced vein-banding symptoms in cowpea which was similar to those produced by the BCMV-cowpea strain. Group II caused mosaic symptoms in azuki bean but not in peanut and tobacco. Since this character was different from that of previously described BCMV strain, group II may not belong to BCMV. Group III induced vein-clearing symptoms in azuki bean, kidney bean and peanut, which are typical symptoms for BCMV-peanut stripe virus strain. Virus inclusion patterns of BCMV groups were similar to those of *Potyvirus* subdivision III with the scroll, pinwheel and long laminated inclusions. However, the inclusions of laminated aggregates were never observed in mungbean isolates. Multiple alignment as well as cluster dendrograms of 3' noncoding region (3'-NCR) and a part of coat protein gene (CP) suggested that group I belongs to the BCMV-cowpea strain, group II to the BCMV-azuki bean strain, and group III to the BCMV-peanut stripe virus strain. Since molecular phylogenesis of BCMV based on nucleotides of 3'-NCR and coat protein differed from the grouping based on virulence differentiation, and BCMV groups are more closely related to each other with the same host origin, other characteristics of those strains are under investigation.

4-36. Identification of Papaya Ringspot Potyvirus type W infecting squash in Korea

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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 Potyviruses.

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Ammi majus (white lace flower, *Umbelliferae*) 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