

30,000 was observed after sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE). Indicator plant test showed mosaic, necrotic local lesion and sunken areas in leaves of *Nicotiana clevelandii* and *Tetragonia expansa*, while the others of indicator plants did not infect. An enzyme-aided purification protocol was used, which eliminated a highly viscous mucilage from extracts of the *Ornithogalum*. Total RNA extracted from infected *Ornithogalum* leaves were amplified of 411bp fragment in reverse transcription (RT)-PCR when primers specific for the coat protein gene. An isolate of *Ornithogalum mosaic virus* (OrMV) of the genus Potyvirus was identified as the causal agent of the disease on the basis of electron microscopic, biological and serological reaction.

4-33. Characterization of an Isometric virus Infecting Paprika (*Capsicum annuum* var. *glossum*) in Korea

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An Isometric virus was isolated from Paprika (*Capsicum annuum* var. *glossum*) showing necrosis spot and malformation on the fruit and the leaves, respectively, at yecheon in Korea. The virus could infect locally on *Chenopodium amaranticolor*, *C. quinoa*, *Petunia × hybrida* and *Nicotiana glutinosa*, but could not infect on *Gomphrena globosa* and *Physalis floridana*. The virus could infect systemically on red pepper and *Lycopersicon esculentum*. *Datura stramonium*, *N. clevarandii*, *N. rustica* and *N. tabacum* cvs. were produced necrosis or necrotic ring spot lesions on the inoculated leaves and mosaic, vein necrosis or lethal death on the upper leaves. The virus was not related serologically to *cucumber mosaic virus* (CMV). In RT-PCR assay, it could not be detected with specific primers of CMV and BBWV-II. The virions contain one molecule of genomic RNA, which was approximately 3.8Kb and the coat protein (CP) of the purified virion migrated as a single band with molecular weight of about 29KDa in SDS-PAGE.

4-34. Population of Rice Stripe Virus-Viruliferous Insect and Natural Weed Host of Rice Stripe Virus.

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Among over-wintering small brown planthoppers, population of the rice stripe virus (RSV)-viruliferous insects was surveyed throughout the country in late April of 2003 by using

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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