J-146. Construction of full-length cDNA clones of RNAs 1, 3 and 3 of *Cucumber mosaic virus* strain Ly2 and generation of infectious RNA transcripts. Hye Jin Jung[1], Ki Hyun Ryu[2], Chikara Masuta[3], and Jang Kyung Choi[1]. [1]Division of Biological Environment, Kangwon National University, Chunchon 200-701, Korea, [2]Plant Virus Genbank, Division of Environmental and Life Sciences, Seoul Women's University, Seoul 139-774, Korea, [3]Graduate School of Agriculture, Hokkaido University, Sapporo 060-8589. Japan

Full-length cDNA to RNA1, RNA2 and RNA3 of cucumber mosaic virus strain Ly2 (Ly2-CMV) was amplified using the polymerase chain reaction (PCR). The PCR products were cloned into the BamHI and SphI sites of pUC18. Clones of each RNA were selected and RNA transcripts were synthesised in vitro from each clone using T7 RNA polymerase. All the transcipts were found to be infectious when inoculated onto Nicotiana benthamiana plant, corresponding to RNA1, RNA2 and RNA3. The complete nucleotide sequences of genomic RNAs of Ly2-CMV were determined from the infectious full-length cDNA clones. RNA1 and RNA2 of Ly2-CMV contain 3400 nucleotides and 3062 nucleotides, respectively. RNA3 of Ly2-CMV, 2226 nucleotides long. Ly2-CMV RNA1 and 1a protein are 71 to 97 % identical to those of Fny-CMV, NT9-CMV and Q-CMV. For RNA 2 and the 2a protein, identities between Ly2-CMV and three strains of CMV are calculated to be 60 to 94 %. RNA3 is 65 to 91 % identical to thoses of three strains of CMV. The 1a protein has the consensus sequences found in some helicases and methyltransferases and the 2a protein includes a sequence which exists in several RNA-dependent RNA polymerases.

J-147. Characterization of *Tobacco mosaic virus* isolated from *Solanum tuberosum* 'Chu-baeg' in Korea. Jeong-Soo Kim, Jae-Hyun Kim, Su-Young Chae, Gug-Seoun Choi, and Yong-Mun Choi. National Horticultural Research Institude, RDA, Suwon 441-440, Korea

An isolate of *Tobacco mosaic virus* (TMV) was isolated from potato 'Chu-baeg' cultivar showing vein clearing and mild mosaic at Namhae in Korea. This isolate, TMV-St, was differentiated from other tobamoviruses based on biological properties, serological relationships and partial nucleotide sequence analyses. TMV-St isolate caused typical symptoms on thirteen indicator plants as compared to the tobamovirus of TMV-U1, PMMoV, and ToMV, which caused economic losses in Solanaceous vegetables of tomato, pepper, and eggplant. Remarkably, the TMV-St induced distinctly different symptom of systemic chlorotic spots on *Chenophodium murale*. In *C. murale*, *Gomphorena globosa*, and *N. rustica*, the four viruses were classed by the virulence of systemic or local infections. In serological test TMV-St showed same precipitation lines with the tabamoviruses. The CP gene of TMV-St contain 477 nucleotides, and the nucleotides sequence was similar to that of TMV-U1.

J-148. Characterization of strain on *Banana streak virus* (BSV). Ryu, In-Hee[1] and Su, Hong-Ji[2]. [1]Division of Plant Virus, Jeno Biotech Inc., Chunchon 200-160, Korea, [2]Department of Plant Pathology, National Taiwan University, Taipei 106, Taiwan

The three symptom-expression types of *Banana streak virus* (BSV) was differentiated including (1) BSV-symptom expressing type on 9 % banana cultivars (AA, AAA and AAB), (2) chlorotic type on 23.3 % cultivars (ABB, AAB and AAA), and (3) symptomless type on 19.5 % cultivars (in all genotype bananas). The studies on the pathological natures of the three strains of different symptom-types revealed that the BSV-symptom expression type strain showed vector transmissibility, positive virion detection by ISEM, and ELISA detection, while negative results of the above-mentioned natures were found on BSV-materials of the cultivars showing symptom expression of chlorotic and symptomless type. Such two strains of A and B types were isolated from BSV-symptom expressing cultivars *i. e.* A strain isolated from BS-diseased Mysore (AAB) and Java (AAB) cultivars, caused typical BS-symptoms including typical chlorotic streaks and fine spindle-shaped spots, and B strain isolated from Java only, induced yellowish thick streaks with necrosis. The phylogenic identities among the present virus strains were investigated through the sequence homology by sequencing the DNA products (208 bp) of PCR amplification with the templates in DNA extracts from banana cultivars showing the three symptom expression types. The all DNA extract of banana plants A-type symptoms and vector fed on these plants, exhibited the same nucleotide sequence of 100 % homology. The fact different sequence homology (98.1 %) was found between strains A type and B type, revealed the both types were distinct strains. Different homologies were also examined among the sequences of PCR-products derived from the other strains of the chlorotic and symptomless types.

J-149. Genomic dsRNA pattern and nucleotide sequence of S12 to RDV-Kor. Bong Choon Lee, Jong Nae Hyun, Do Yeon Kwak, Yeon Kyu Hong, Jo Im Choi, Dong Chang Lee, and Soon Chul Kim. National Yeongnam Agricultural Experiment Station, RDA, Milyang 627-803, Korea

Rice dwarf phytoreovirus(RDV), a member of the family Reoviridae, has a genome composed of 12 segmented dsRNAs designated as S1 to S12 with an increasing order of mobility in polyacrylamide gel electrophoresis (PAGE). RDV isolate were collected from several locations in Korea, Japan, China, Philippines and Nepal. Genomic dsRNA segment profiles in PAGE differed among the isolates. This was the case even among isolates from the same region. The full-length S12 of Korean isolates was cloned and sequenced. It is 1,066 nucleotide long, with the longest open reading frame starting at nucleotide 42 and terminating at nucleotide 978. Nucleotide sequence identities were 94 to 99% with those of another isolates. Three open reading frames previously reported were present in RDV-Kor isolate, and the sequence identities were 83 to 98% for P12, 89 to 98% for P12OPa.

J-150. Transition of occurrence status of *Rice stripe virus* in Korea. D. B. Shin[1], J. W. Park[1], T. S. Jin[1], J. Y. Kim[2], I. S. Oh[3], B. C. Lee[4], T. H. Noh[5], S. J. Ko[6], and C. H. Kim[1]. [1]Plant Pathology Division, National Institute of Agricultural Science and Technology, Suwon 441-707, Korea, [2]Kyeonggi Agricultural Research and Extension Service, Hwasung 445-972, Korea, [3]Chungnam Agricultural Research and Extension Service, Taejon 305-313, Korea, [4]National

Yeongnam Agricultural Experiment station, Milyang 627-803, Korea, [5]National Honam Agricultural Experiment station, Iksan 570-080, Korea, [6]Jonnam Agricultural Research and Extension Service, Naju 520-715, Korea.

Rice stripe virus (RSV) was documented in 1935 at Yeongnam area, South East part of Korea. RSV was one of major diseases in rice with severe occurrence in the 1960s and 1970s in Yeongnam and Honam areas. In the last twenty years, the occurrence of RSV was declined to a chronic status since early 1980s. Though RSV was occurred in early 1990s around Yeongnam and Honam areas, the disease has been few or no occurrence since 1993. However, RSV was reoccurred at Kyeonggi and Chungnam areas in 2001. This indicates re-occurrence after the lapse of nearly twenty years since 1982 in Kyeonggi area. RSV is transmitted by small brown planthopper (SBPH), *Laodelphax striatellus*, in a persistant manner. The pattern of RSV occurrence was similar to that of SBPH, but the disease has a tendency to occur within 1 ~ 3 years later followed to the occurrence of SBPH. Based on this tendency, the re-occurrence of RSV in Kyeonggi and Chungnam areas may be due to the suddenly high occurrence of SBPH in 1998. The survey for the ratio of viruliferous insects among over-wintering SBPH was conducted nationwide in the middle of Apr. 2002 using ELISA test. The ratio of viruliferous insects in Kyeonggi and Chungnam areas was as high as 6.3%, 4.3%, respectively, while other areas were in average of 0.0 ~ 2.0%. Especially, Viruliferous insects ratio in Kimpo, Hwasung, and Kanghwa areas revealed 11.5, 9.4, 5.8%, respectively, indicating major occurrence areas of RSV. This result suggests that outbreak of RSV may occur in Kyeonggi area due to wide cultivation of susceptible varieties, Chuchung and Ilpumbyeo.

J-151. Construction of full-length cDNA clones of A*lfalfa mosaic virus*. J. H. Ha[1], K. H. Ryu[1], J. K. Choi[2], G. S. Choi[3], S. C. Lee[4], B. J. Oh[5], and D. S. Kim[3]. [1]Plant Virus GenBank, Seoul Women's University, Seoul 139-774, Korea, [2]Kangwon National University, Chuncheon, 200-701, Korea, [3]National Horticultural Research Institute, Suwon 440-310, Korea, [4]Sungkyunkwan University, Suwon, Korea, [5]Plant and Microbes, Inc, Co, Korea.

Full length cDNAs to RNA1, RNA2 and RNA3 of *Alfalfa mosaic virus* were amplified using the long-template polymerase chain reaction method. Each primer was designed from multiple-aligned analyses of 5′ nontranslated reion (NTR) and 3′-NTR region of all the known AMV strains. PCR products were cloned into the pGEM-T vector. Recombinant cDNA clones were selected and linearized by *Sph*I restriction site. RNA transcripts were synthesized in vitro from each clones using T7 RNA polymerase and infectivity test was performed in 5 sets of transcripts. All the transcripts were found to be infectious when inoculated onto *Nicotiana tabacum* cv. Samsun plants, and symptoms were not distinguishable to that of wild type. Infectivity test of pepper plants are now in progress.

J-152. Sequence analysis of *Lily mottle virus*, a lily-infection *Potyvirus*. B. Y. Lee[1], B. N. Chung[2], and K. H. Ryu[1]. [1]Plant Virus GenBank, Seoul Women's University, Seoul 139-774, Korea, [2]Div. Hort. Environ., National Horticultural

Research Institute, Suwon 440-310, Korea

To delineate molecular characterization of lily-infecting viruses, cloning and sequence analysis of genomic RNA of *Lily mottle virus* (LMoV-Kr), a lily-infecting *Potyvirus*, were performed. The cDNA library was constructed by using the LMoV-specific primer and purified viral RNA. Contig of nucleotide sequences was generated from partial sequences and entire sequences of selected cDNA clones for the virus. The contig consisted of 3,338 nucleotides long and encodes 1,112 amino acids residues for partial nuclear inclusion a, complete nuclear inclusion b (NIb) and coat protein (CP). Sequence analysis of the CP gene showed that LMoV-Kr was 94.6 %-98.1 % and 98.2 % identical at the nucleotide and amino acid levels, respectively, with Hangzhou isolate (LMoV-H) and Japanese isolate of LMoV. The NIb gene of LMoV-Kr shared 97.0 % and 98.3 % identities at the nucleotide and amino acid levels, respectively, to those of LMoV-H. Conserved domains of NIb and CP were found in all the isolates of LMoV.

J-153. Symptom variance in mixed infections by six *Turnip mosaic virus* isolates with *Ribgrass mosaic virus* (RMV-FG22) in crucifers. Jeom-Deog Cho[1], Hong-Soo Choi[2], Jeong-Soo Kim[3], Kook-Hyung Kim[1], and Kyung-Soo Kim[4]. [1]Seoul National University, Suwon 441-744, Korea, [2]National Institute of Agricultural Science and Technology, Rural Development Administration (RDA), Suwon 441-707, Korea, [3]National Horticultural Research Institute, RDA, Suwon 441-707, Korea, [4]Department of Plant Pathology, University of Arkansas, USA

Turnip mosaic potyvirus (TuMV) and *Ribgrass mosaic tobamovirus* (RMV) are major viruses infected on Crucifer crops in Korea. RMV-FG22 was isolated from oriental cabbage. TuMV isolates were TuMV-CA7 from oriental cabbage, TuMV-TU and TuMV-TU2 from turnip, TuMV-RA from rape, TuMV-ST from Stock, and TuMV-R9 from radish. The six isolates of TuMV were classified by symptom expression in inbred lines of Crucifers. TuMV-CA7 and TuMV-TU isolates infected mostly in oriental cabbages; three isolates of TuMV-ST, TuMV-TU2, and TuMV-R9 could infect radishes; TuMV-RA could infect both oriental cabbages and radishes. Six combinations of the mixed infections were made. External symptoms in oriental cabbage 'Tambok' and radish by each six single infections of TuMV showed similar results by bioassay. Synergistic response of necrotic death occurred within one week after inoculation in all combinations mixed with TuMV and RMV-FG22 on leaf mustard. In oriental cabbage 'SSD63', synergism of necrosis was occurred 4 TuMV isolates without TuMV-ST and TuMV-R9 isolates. In oriental cabbage 'Tambok', synergism was expressed only the two combinations of RMV-FG22+TuMV-CA7 and RMV-FG22+TuMV-TU, but other combinations had the same symptoms produced by RMV-FG22. In radish 'Daeburyungyeorum', only mild mosaic symptoms were induced by combinations of RMV-FG22+TuMV-CA7, RMV-FG22+TuMV-TU, RMV-FG22+TuMV-RA, and RMV-FG22+TuMV-R9. Mosaic and severe mosaic were induced in combinations of RMV-FG22+TuMV-TU2 and RMV-FG22+TuMV-ST, respectively.

J-154. Ultrastructural difference in mixed infections by six *Turnip mosaic virus*

isolates with *Ribgrass mosaic virus* (RMV-FG22) in crucifers. Jeom-Deog Cho[1], Hong-Soo Choi[2], Jeong-Soo Kim[3], Kook-Hyung Kim[1], and Kyung-Soo Kim[4]. [1]Seoul National University, Suwon 441-744, Korea, [2]National Institute of Agricultural Science and Technology, Rural Development Administration (RDA), Suwon 441-707, Korea, [3]National Horticultural Research Institute, RDA, Suwon 441-707, Korea, [4]Department of Plant Pathology, University of Arkansas, USA

Isolates of *Turnip mosaic potyvirus* (TuMV) were TuMV-CA7 from oriental cabbage, TuMV-TU and TuMV-TU2 from turnip, TuMV-RA from rape, TuMV-ST from Stock, and TuMV-R9 from radish, and *Ribgrass mosaic tobamovirus* (RMV-FG22) was isolated from oriental cabbage. Three kinds of characteristics in these 6 TuMV isolates were sorted by bioassay: TuMV-CA7 and TuMV-TU isolates infected mostly in oriental cabbages: Three isolates of TuMV-ST, TuMV-TU2, and TuMV-R9 could infect radishes: TuMV-RA could infect both oriental cabbages and radishes. Mixed infections of Crucifers were made as follows; RMV-FG22+TuMV-CA7, RMV-FG22+TuMV-TU, RMV-FG22+TuMV-RA, RMV-FG22+TuMV-ST, RMV-FG22+TuMV-TU2, and RMV-FG22+TuMV-R9. New specific ultrastructures by mixed infection with TuMV and RMV, nonagon-like ring (NLR) and spiral aggregates (SA) were formed in cells of Crucifer plants. The NLR was made by a TuMV surrounded loosely with 9 RMV particles and the SA was formed spirally by fully mixed of the two virus particles. The SA had some NLR in its center, which was observed from cross-sectioned SA. Host plants observed specific ultrastructures were mainly expressed synergistic symptoms. Specific ultrastructures of NLR and SA were formed in combinations of RMV-FG22+TuMV-CA7, RMV-FG22+TuMV-TU or RMV-FG22+TuMV-RA isolates that mostly infected in oriental cabbages. Whereas, no specific ultrastructures and hardly mixing of the two virions in a same cell were observed in combinations of RMV-FG22 and TuMV-ST, TuMV-TU2, or TuMV-R9 isolates having virulence in radishes.

J-155. 5 non-translated region of *Potato Virus X* required for assembly *in vitro*. Sun-Jung Kwon[1], Mi-Ri Park[1], Jeong Soo Kim[2], and Kook-Hyung Kim[1]. [1]School of Agricultural Biotechnology, Seoul National University, Suwon 441-744, Korea, [2]Horticultural Environment Division, National Horticultural Research Institute, Rural Development Administration, Suwon 441-440, Korea

The 5 non-translated region (NTR) of *Potato virus X* (PVX) contains single-stranded AC-rich sequence and stem-loop structure that has been known important for efficient plus-strand RNA accumulation and viral replication. To investigate the potential role of these cis-elements on virus assembly, we generated various deletion mutants at the 5 region using PVX cDNA clone, pMon8453. Transcripts containing each mutation were used for *in vitro* assembly using PVX coat protein (CP) subunit that was expressed *in Escherichia coli*. Virion formation was observed using transmission electron microscope. Deletion from 5 end and internal deletion of the 5 NTR of PVX genome (△8, △17, △36, △50, △84, 1N1, 1N2, 1N3 and 1N4; J. Virol. 7:5533) made differences on formation of assembled particles. Virion formation was observed in the transcripts of most mutants that contain the RNA secondary structure of stem-loop1 (SL1) or sequences therein, but the transcript of △84 and 1N4 mutants that disrupt SL1 RNA structure were insufficient for virion assembly. These results

suggest that the RNA secondary structural elements within SL1 or sequences therein of 5 NTR are crucial for formation of virion and required for efficient viral infection, related to virus assembly in PVX. Additional deletion and site-directed mutations are currently being tested to further define PVX assembly signal.

J-156. Occurrence of viruses infecting pepper in Korea. Gug-Seoun Choi[1], Jae-Hyun Kim[1], Ki-Hyun Ryu[2], Jang Kyung Choi[3], Soo-Young Chae[1], Hyun-Ran Kim[1], Bong-Nam Chung[1], Jeong-Soo Kim[1], and Yong-Mun Choi[1]. [1]National Horticulual Research Institute, RDA, Suwon 441-440, Korea, [2]Department of Horticultural Science, Seoul Womens University, Seoul 138-774, Korea, [3]Division of Biological Enviroment, Gngwon National University, Chunchon 200-701, Korea.

A survey on pepper virus diseases was investigated at the growing 17 regions in Korea during from November 2001 to October 2002. A total of 523 samples from peppers with virus disease-like symptoms were collected and identified using electron microscopy, test plant reaction, rapid immuno-filter papper assay (RIPA) and reverse transcription-polymerase chain reaction (RT-PCR). *Cucumber mosaic virus* (CMV), *Pepper mottle virus* (PepMoV), *Pepper mild mottle virus* (PMMoV), *Broad bean wilt virus II* (BBWV II) and *Tobacco mild green mosaic virus* (TMGMV) were detected in the pepper samples. Of the 523 samples analysed, 209 (40.0%) were infected with CMV, 87 (16.6%) with PepMoV, 75 (14.3%) with PMMoV, 5 (0.9%) with BBWV II, 3 (0.6%) with TMGMV, 82 (15.7%) with CMV and PepMoV, 31 (6.0%) with CMV and PMMoV, 13 (2.5%) with PepMoV and PMMoV, 5 (0.9%) with CMV, PepMoV and PMMoV, and 13 (2.5%) samples were not indentified. CMV was the most predominant in all inspected fields and the number of the samples infected with PMMoV was relatively low as compared PepMoV infection level in pepper. TMGMV were only found in the southern part of Korea. However *Alfalfa mosaic virus* (AMV), *Potato virus Y* (PVY), *Tobacco mosaic virus* (TMV) and Pepper vein chlorosis virus (PVCV) recorded in List of Plant Disease in Korea (1998) were not encountered in this survey.

J-157. First report of *Tobacco mild green mosaic virus* infecting pepper in Korea. Gug-Seoun Choi[1], Jae-Hyun Kim[1], Ki-Hyun Ryu[2], Soo-Young Chae[1], Hyun-Ran Kim[1], Bong-Nam Chung[1], Jung-Su Kim[1], and Yong-Mun Choi[1]. [1]National Horticurtual Research Institute, RDA, Suwon 441-440, Korea, [2]Department of Horticultural Science, Seoul Womens University, Seoul 138-774, Korea.

A rod-shaped virus was isolated from pepper showing mild mosaic in the winter growing seasons of 2001 and 2002 in Korea. Based on biological reactions, reverse transcription-polymerase reaction (RT-PCR) using specific primers, and partial nucleotide sequence of coat protein (CP) gene analyses, the isolate was identified as *Tobacco mild green mosaic virus* (TMGMV) and designed as Korean pepper isolate of TMGMV-KP. Crude sap from infected tissue was mechanically transmitted to various indicator plants, which produced characteristic symptoms of tobamovirus infection. However no symptom was observed in Gomphorena globosa. In RT-PCR assays with the specific primers for respective detection of TMGMV, *Tobacco mosaic virus* (TMV),

Pepper mild mottle virus (PMMoV) and *Tomato mosaic virus* (ToMV). A single strong band of about 500 bp in length was produced from the sample used with only TMGMV primers. The amplified DNA was cloned and the nucleotide sequence was determined. Sequence comparisons with the CP gene of other tobamoviruses in the GeneBank Database indicated that TMGMV-KP shared 99.3% identity with TMGMV Japanese isolate (GeneBank Database Accession AB078435) and only 59.1, 58.6 and 58.1% identity with TMV (AF103780), PMMoV (AB084456) and ToMV (AY063743), respectively. These data suggest that the virus isolated from red pepper is the first TMGMV reported in Korea.

J-158. Occurrence of *Tobacco Mild Green Mosaic Virus* on pepper in Korea. S. H. Lee[1], S. M. Kim[1], D. B. Shin[1], and K. W. Lee[2]. [1]Plant Pathology Division, National Institute of Agricultural Science and Technology, Suwon 441-707, Korea, [2]Department of Agricultural Biology, Kyungpook National University, Daegu 702-701, Korea.

In March 2002, unusual viral symptoms of yellow mottle and spots were observed on leaves of pepper (*Capsicum annuum* L.) grown in a greenhouse at Haman in Korea. Tobamovirus particles were consistently observed from the diseased plant tissues by electron microscopy and the virus was identified as *Tobacco mild green mosaic virus* (TMGMV) by the reverse transcription-polymerase chain reaction (RT-PCR) using tobamovirus specific primers and sequence analysis of coat protein (CP) gene. CP gene of the pepper isolate was 480 nucleotide residues that was identical to those of TMGMV reported previously. The CP region showed 97.9% and 98.1% nucleotide identities and 98.7% and 97.5% amino acid identities with TMV-U2 and TMGMV-KT1, respectively. Pathogenicity of the pepper isolate of TMGMV and its pathological impacts on pepper are being investigated. This is the first report of the TMGMV disease on pepper in Korea and the virus is designated as a pepper strain of TMGMV (TMGMV-P).

J-159. Occurrence of *Citrus mosaic virus* on Satsma mndarin (*Citrus unshiu*) in Jeju island. Jae Wook Hyun[1], Dong Hwan Kim[1], Seung Chan Lee[1], Kwang Sik Kim[1], and Suk Chan Lee[2]. [1]Department of Agricultural Environment, National Jeju Agricultural Experiment Station, RDA, Jeju, Korea, [2]Department Genetic Engineering, Sungkyunkwan University, Suwon, Korea

Citrus Mosaic Virus (CiMV) severely took place in some orchards in Jeju Island. The typical symptoms were pale green blotching of the fruit rind in early of ripening time, which then the oil grands became to necrosis. The symptoms mainly took place on 'Miyamoto' wase, very early satsuma mandarin, the most sensitive cultivar against CiMV and also 'Miyagawa' wase, early satsuma mandarin. In Miyamoto wase, many of the infected fruits were dropped eventually. We could not differentiate CiMV from satsuma dwarf virus(SDV) by ELISA because CiMV was serologically related to SDV. The symptoms appeared on 4 of 30 trees identified to SDV by ELISA using polyclonal antibody for SDV. The fruits quality was assayed between symptomed and healthy fruits. The contents of total sugar and acid were not different between

symptomed and healthy fruits but sarcocarps of fruits infected with CiMV were to be spongified and the peels of fruits infected with CiMV were harder than healthy. This is the first report of CiMV on citrus fruit in Jeju Island.

J-160. First report of identification of *Hosta virus X* (*Potexvirus*) from cultivated *Hosta* plants and its sequence analysis. Min Hye Park and Ki Hyun Ryu. Plant Virus GenBank, Division of Environmental and Life Sciences, Seoul Women's University, Seoul 139-774, Korea

A Potexvirus was isolated from cultivated *Hosta* plants such as Korean native Hosta species and some imported varieties. Virus-infected *Hosta* plants showed chlorotic mottle and/or severe mosaic systemic symptoms on their leaves. Virus consists of single unit of 25 kDa coat protein (CP) and a single-stranded genomic RNA over 6 kb long. The cDNA library for the viral RNA was constructed by using *in vitro* polyadenylated viral RNAs and oligo-dT-*Not*I primer adapter system. Sequences of selected cDNA clones were determined and contigs could be generated from overlapped nucleotide sequences. The 3'-terminal sequences containing CP gene and 3' nontrated region for the virus were compared in the BLAST analysis. The CP gene of the virus shares 15.4 % to 36.7 % and 29.0 % to 31.7 % amino acid identities with the known members of *Potexvirus* and *Calarvirus*, respectively. In the phylogenetic analysis, the virus could be clustered with the members of the *Potexvirus*. *Cactus virus X*, *Papaya mosaic virus* and *Alternanthera mosaic virus* were the closest ones with the virus among the genus. Comparison of the sequences with CP genes of the virus and *Hosta virus X* (HVX) which was previously reported in Hosta plant revealed that the virus was an isolate of HVX based on the nucleotide (99.2 %) and amino acid sequences (99.5 %) identities. This is the first report on the molecular characterization of HVX.

J-161. *Pepper Mild Mottle Virus* is a major Tobamovirus on pepper in Korea. S. H. Lee[1], S. M. Kim[1], H. S. Choi[1], J. W. Park[1], T. S. Jin[1], and K. W. Lee[2]. [1]Plant Pathology Division, National Institute of Agricultural Science and Technology, Suwon 441-707, Korea, [2]Department of Agricultural Biology, Kyungpook National University, Daegu 702-701, Korea.

In the spring of 2002, 155 pepper plants with various viral symptoms were collected from 49 greenhouse-grown pepper fields in Korea. Tobamoviruses were detected from 85 out of 155 plants with electron microscopy. For further identification of the causal agents, RT-PCR with specific primers was conducted. Among 85 tobamoviruses, 78 isolates were identified as *Pepper mild mottle virus* (PMMoV). Seven isolates were *Tobacco mild green mosaic virus* (TMGMV). However, *Ribgrass mosaic virus* (RMV), *Tobacco mosaic virus* (TMV), and *Tomato mosaic virus* (ToMV) were not detected. To determine genetic variation among the PMMoV isolates, the coat protein (CP) sequences were analyzed for 19 isolates of PMMoV, which were randomly selected. The CP gene of the isolates shared 97.7-100% nucleotide identities and 99.4-100% amino acid identities. This result indicates that PMMoV with little genetic variation is a major tobamovirus on greenhouse-grown pepper in Korea.