C-22 The mixed infection with BBWV2 and ChyNMV or YMV in *Dioscorea batatas*. D. K. Kang[1], S. Fuji[2], M. U. Chang[3]. [1]Institute for bioresources research, Gyeongbuk Provincial A.T.A. Andong, 760-891, Korea; [2]Faculty of Bioresource Science, Akita Prefectural University, Akita, 101-0195, Japan; [3]Dept. Biology, College of Science, Yeungnam University, Kyongsan, 712-749, Korea

Dioscorea batatas which had both of BBWV2(broad bean wilt virus 2) and YMV(yam mosaic virus) or ChYNMV(chinese yam necrotic mosaic virus) showed mosaic, vein clearing, rugose and malformation on leaves. BBWV2 particles of about 28 nm in diameter and ChYNMV particles of about 760 nm in length from Dioscorea batatas cv Jang-Ma were detected by electron microscope. In the case of Dioscorea batatas cv Dung-Gun-Ma, the YMV virus particles of about 660 nm in length and BBWV2 virus particles of about 28 nm in diameter were confirmed. BBWV2, ChYNMV and YMV were identified on the base of particle morphology, immune responses and nucleotide sequencing of coat protein genes.

C-23 Differentiation of barley mild mosaic virus (BaMMV) isolates by single-strand conformation polymorphism analysis of the coat protein gene. M. K. Choi[1], H. M. Kim[1], K. J. Lee[1], J. C. Park[2], J. H. Seo[2], S. S. Han[3] and W. H. Lee[1]. [1]Division of Biological Resources Science, Chonbuk National University, Jeonju 561-756, Korea [2]National Honam Agricultural Research Institute, Iksan 570-080, Korea [3]Division of Forest Science, Chonbuk National University, Jeonju 561-756, Korea

Barley mild mosaic bymovirus (BaMMV) isolates of several geographical origins were compared for variations in their coat protein (CP) gene by analysis of single-strand conformation polymorphism (SSCP). Single-stranded RNA was extracted from the plants and used as a template for RT-PCR amplification of the CP gene. The CP amplicons were subjected to SSCP analysis with the other amplicons and nucleotide sequence analysis. These clones were sequenced and found to have between 94% and 98% sequence homology. The PCR amplified clones were denatured and compared by SSCP analysis in 8% polyacrylamide gels. The nucleotide sequence of several geographical isolates was determined. The results revealed that there was a complex relationship between the numbers of nucleotide differences and SSCP patterns. The

nucleotide sequence of two isolate (Puan and Yeonggwang) showed only 3 nt difference, where as the SSCP analysis gave different pattern. However, the nucleotide sequence was more (32 nt) between the two isolate (Gochang and gwangju), the SSCP patterns did not show the difference. SSCP analysis may provide a procedure to identify and differentiate BaMMV isolates based on comparisons of several genes. It is rapid and cheap and may drastically reduce the amount of sequencing necessary for accurate comparisons.

C-24 Characterization of the virus isolated from elderberry shrub, in Corea. S.G. Ye[1], H.M. Lee[2], S.K. Lee[1], H.J. Kim[1], S.B. Kwon[3], S.Y. Lee[1] [1]Dept. Forest Resources protection, Kangwon National University, Chunchon, 200-701, Corea; [2]Dept. Biological Environment, Kangwon National University, Chunchon, 200-701,Corea; [3]Gangwondo Agricultural Research and Extension Services, Gangwon, Chunchon 200-939, Corea.

Elderberry (*Sambucus nigra*, Family: Caprifoliaceae) is a shrub, which reproduce vegetatively by producing stolons is known to have medicinal properties, which is why it is grown all over the world. Elderberry carlavirus, elderberry latent carmovirus, cherry leaf roll nepovirus, the European strain of elderberry carlavirus and North American strain of elderberry carlavirus have been reported to infect elderberry plant. Elderberry (*Sambucus nigra*) showing line-pattern viral symptom was discovered in Hoengseong-gun Kangwon-do. When the virus was sap inoculated onto *C. amaranticolor*, it showed systemic infection after 7 days. Electron microscopic examination of the negatively stained preparation of virus revealed mixed infection. It showed flexuous rod-shaped particle of 680nm and isometric particles of 30 nm in diameter. The virus could infect systemically in *C.amaranticolor* and *C.quinoa*. It showed Systemic vein-clearing in *N. glutinosa* on the upper leaves. In case of *N. xanthi-nc*, it showed symptomless systemic infection, which was later confirmed by back inoculation onto *C. quinoa*. RT-PCR assay was not able to detect the virus by using specific primer for elderberry latent virus; however, further characterization of the virus is being done.

C-25 Cytopathological Characteristics of Zimbabwe Isolate of Cowpea Aphid-Borne Mosaic Virus in *Nicotiana benthamiana*. Jeom Deog Cho[1], Jan W.M. van Lent[2], Rob W. Goldbach[2]. [1]Laboratory of Plant Virology, Horticultural environment division, National Horticultural Research Institute, R.D.A. Tap