**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