transmission rate of watermelon was 24 % from symptomatic watermelon collected from 5 regions of Gyeongnam provinces. Cucumber green mottle mosaic virus (CGMMV) was detected by DAS-ELISA with specific monoclonal antibody of CGMMV-HY1 periodically from root stock, during the sequential process for nursery seedling in Haman. Necrotic spots, at root stock seedling progressively revealed to typical symptomatology appeared on grafted nursery. It is noticeable that greenhouse watermelon cultivation was introduced for the first time to Bongwha region at high altitudes 600 m during the summer of 2000, where CGMMV disease was epidemic. Average of detection rate of CGMMV was about 92 % from symptomatic watermelon samples collected from 8 regions of Gyeongnam provinces. This is suggested that CGMMV was a dominant virus on watermelon, of which most dominant over 97% from Haman and Changwon. In greenhouse of Gyeongnam province, watermelon produces slight or severe leaf mottling, mosaic, dwarfing, deformed fruit and induced serious internal discoloration and decomposition of fruit flesh (Piduli) and decreased yield.

C-30 *In situ* localization of P12 in rice dwarf phytoreovirus infected plant. Bong-Choon Lee, Yeon-Kyu Hong, Sung-Jun Hong and Sung-Tae Park National Yeongnam Agricultural Experiment Station, NICS, RDA. 1085, Milyang, Korea, 627-803

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). In order to locate P12, ultrathin sections of RDV-infected rice plant were labelled by the anti-P12 polyclonal antibody and the protein A-gold complex. When thin sections from infected tissues were treated with a preimmune serum, nonspecific gold labelling was not observed, nor did labelling occurred in the absence of the primary antiserum from the standard incubation procedure. Gold particles were observed with P12 throughout the cytoplasm of infected leaves, although labelling was not uniform. Densely labelled areas frequently occurred in patches in the cytoplasm where slightly electron-dense. Sections from healthy tissues exhibited no significant labelling. Immunocytotochemical studies showed P12 accumulated in the cytoplasm of infected cells.

C-31 Emergence of *Rsv*-resistance breaking *Soybean mosaic virus* isolates from Korean soybean cultivars. Bong Kum Choi[1], Jung Mo Koo[1], Hye .Jin Ahn[1], Hye .Jung Yum[1], Chang Won Choi[1, 2], Ki Hyun Ryu[3], P. Chen[4], S.A. Tolin[5]. [1]Department of Biology & Medicinal Science; [2]Bio-medicinal Research Center

(RRC), Pai Chai University, Daejeon, Korea 302-735; [3]Plant Virus GenBank, Division of Life & Environmental Sciences, Seoul Women's University, Seoul, Korea 139-774; [4]Department of Crop, Soil, & Environmental Sciences, University of Arkansas, Fayetteville, AR 72701, USA ;[5]Department of Plant Pathology, Physiology and Weed Science, Virginia Tech, Blacksburg, VA 24061, USA

Twelve *Rsv* resistance-breaking (RB) isolates of *Soybean mosaic virus* (SMV) were obtained from field-grown soybean plants showing mosaic symptoms and subsequently examined biologically and molecularly. All of these RB isolates were identified as SMV based on serological and infectivity assays, and the amplification of P1 gene products by reverse transcription-polymerase chain reaction (RT-PCR). Differential soybean cultivars, lines or accessions Lee 68 (*rsv*), PI 96983, York, Marshall, Ogden, Kwanggyo, Suweon 97 (*Rsv1* alleles), L29 (*Rsv3*), and V94-5152 (*Rsv4*), following inoculation with each RB isolate, showed similar systemic symptoms suggesting that these RB isolates can overcome *Rsv* resistance at three loci. To differentiate the twelve RB isolates molecularly, the P1 coding region for each isolate was amplified, cloned, sequenced and compared to known SMV strains. The P1 region from the RB isolates shared 86-90% and 90-99% similarities in amino acid (aa) and nucleotide sequence, respectively, with known SMV strains. Comparison of aa sequences indicated that these RB isolates are newly emerging isolates capable of breaking *Rsv* resistance. Phylogenetic analysis further suggested that the RB isolates can be classified as three major types. However, recombination was not observed within the coding region of P1 protein among the types. This is the first report on the emergence of SMV isolates capable of overcoming all of the known resistance alleles at the *Rsv1* locus, as well as distinct resistance genes at *Rsv3* and *Rsv4*.

C-32 Sequence Analysis of a Korean Isolate of *Soybean mosaic virus* That Overcomes the Soybean *Rsv* Resistance Gene. Bong Kum Choi[1], Hye .Jin Ahn[1], Hye .Jung Yum[1], Chang Won Choi[1,2], and Ki Hyun Ryu[3]. [1]Department of Biology & Medicinal Science; [2]Bio-medicinal Research Center (RRC), Pai Chai University, Daejeon, Korea 302-735; [3]Plant Virus GenBank, Seoul Women's University, Seoul, Korea 139-774

Recently, we have reported emerging *Rsv* resistance-breaking (RB) twelve isolates of *Soybean mosaic virus* (SMV) (Choi *et al.*, 2005). One of those RB isolates,