

SMV-CN18, which has ability to overcome resistance genes, *Rsv1*, *Rsv3* and *Rsv4*, of soybean cultivars, was analyzed by its genome full length. The complete genome RNA of CN18 was determined to have 9591 nt in length without poly (A) tail. A large single ORF (nt 141-9164) encoding 3068 aa was (Mr of 350 kDa) begins at 141 with AUG and ends with a UAA termination codon at nucleotides 9162-9164, followed by the 3' untranslated region (UTR). The full length of nt sequence identity of SMV-CN18 ranged between 93% and 94%, while aa of coding region ranged between 95 and 96%. The aa sequence similarities of respective eight protein-encoding regions of CN18 with known isolates were various depending on the gene and isolate. The decreasing order of the most similar protein is as following: 6K and CP (> 99% similarity) > NIa and NIb (98-99%) > HC-Pro (97-99%) > P3 (96-99%) > P1 (88-97%) > CI (89-92%). The 5' and 3' UTRs, determined by RACE were 140 and 253 nucleotides in length and their nt sequence identity, respectively, shared 54-60% and 84-94% in ranges with other isolates.

**C-33 Multiple recombination events in the evolution of natural population of *Soybean mosaic virus*.** Bong Kum Choi<sup>1</sup>, Hye Jung Yum<sup>1</sup>, L. Sumitra Vijayachandr<sup>1</sup>, and Chang Won Choi<sup>1,2</sup>. <sup>1</sup>Department of Biology & Medicinal Science; and <sup>2</sup>Bio-medicinal Research Center (RRC), Pai Chai University, Daejeon, Korea 302-735.

To determine the phylogenetic relationship between SMV-CN18 and other SMV isolates, amino acid (aa) sequences were submitted into both ClustalW and DNAMAN. The phylogenetic trees were distinguished three major clusters as three groups. An *Rsv* resistance-breaking (RB) isolate, SMV-CN18, clustered with subgroup I (G7d, -G7-2 and G7-1) and subgroup II (Aa and Aa15-M2), all together classed as Group I. Both G5b and G7H (subgroup IV), predominant RB strains in Korea that were clustered with a clade containing G2 and N strains (subgroup III), all of which belong to Group II. Group III was clustered by two Chinese isolates only (HH5 and HZ). Similar results were also obtained from the analysis of recombination events among SMV isolates by submission of nucleotide sequences into RDP Version 2. Recombination can be predicted at the numerous sites in the coding region of genome among SMV strains. This suggests that an *Rsv*-breaking isolate, SMV-CN18, has emerged through inter-isolate recombination.