

the upper leaves and produced spots. The results of external symptoms and GFP movement indicated that HC-pro of CABMV accommodated the movement of CPMV greatly and it made aggravate symptoms. *N. benthamiana*-HCpro didn't show the CPMV particles in cells of upper leaves 14 days after inoculation and it was doubly conformed by immuno-cytochemistry. Gold particle conjugated CPMV antibody were bound a lot in cells infected mixedly with CPMV and CABMV in non-transgenic *N. benthamiana* and a little in cells infected singly with CPMV on non-transgenic tobacco. In *N. benthamiana*-HCpro, however, no clear signal was observed by gold particles binding in cells of upper leaves aged 14days after inoculation. It was visibly conformed that HC-pro of CABMV helped to move of CPMV and induced severe symptoms by the synergistic interaction.

C-27 Molecular evolution and adaptation of isolates of *Cucumber mosaic virus* isolated from soybean. Jin Sung Hong^{1,2}, Chikara Masuta², Jang Kyung Choi³, and Ki Hyun Ryu¹. ¹Plant Virus GenBank, PVGABC, Division of Life and Environmental Sciences, Seoul Women's University, Seoul 139-774, Korea; ²Graduate School of Agriculture, Hokkaido University, Kita-ku, Kita 9, Nishi 9, Sapporo 060-8589, Japan; ³Division of biological Environment, Kangwon national University, Chunchon 200-701, Korea

CMV that infects soybean [*Glycine max* (L.) Merr. ssp. *max* Ohashi] once called *soybean stunt virus* (SSV) and now called CMV soybean strain. SSV isolates from soybean was characterized. Some differences was observed, although they have a similar host range, serological properties and genome structure, and nucleotide sequence analysis of RNA3 of the virus were performed. Systemic infections were observed on *Nicotiana benthamiana* and soybean, but cucumber (cv. Model), and tomato (cv. Rutgus) were not infected. The full-length cDNA of SSV RNA3 was cloned and its complete sequence was determined, and the data were used to classify SSV isolates among known CMV strains. The 3a protein and coat protein of RNA3 was indicated a closer relationship with the CMV subgroup I. The phylogenetic analysis showed that the SSVs formed a distinct cluster separated from the other CMV strains. Comparison of the rates of synonymous and nonsynonymous substitutions revealed that the SSV group had evolved faster than the subgroup IA. Present study indicate that SSV group is a unique soybean-adapted novel strain and evolved from a common ancestor of the genus *Cucumovirus*.