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The Netherlands. Zimbabwe isolate of *Cowpea aphid-borne mosaic virus* (CABMV-Z) in *Potyviridae* was analyzed in ultrastructural aspect. CABMV-Z induced pinwheels, scrolls, laminated aggregates and short curved laminated aggregates in cells of *Nicotiana benthamiana*. In cells of the upper leaves mainly pinwheels and scrolls that belongs to cylindrical inclusion body (CI) subdivision-I were maintained, and cells of the inoculated or the lower leaves having virions for a long time after infection contained short curved laminated aggregates (CI subdivision-IV) and a few laminated aggregates (CI subdivision-III) as well as pinwheels and scrolls. The cytopathological properties of CABMV-Z indicate that sampling time and stage is important to classify CI subdivision of *Potyvirus*.

C-26 HC-pro of *Cowpea Aphid-Borne Mosaic Virus* Aggravates Synergism in Mixed Infection with *Cowpea Mosaic Virus*. 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 Dong Campus, Tap Dong 540-41, Gweon-seon Gu, Suwon Gyeonggi-do, 441-440, Republic of Korea; [2] Laboratory of Virology, Department of Plant Sciences, Wageningen University, Building 504, Binnenhaven 11, 6709 PD Wageningen, The Netherlands.

Synergistic symptoms were produced on non-transgenic *Nicotiana benthamiana* infected with both *Cowpea mosaic virus* (CPMV) and *Cowpea aphid-borne mosaic virus* (CABMV), and transgenic plants of *N. benthamiana* inducted HC-pro of CABMV (*N. benthamiana*-HCpro) infected with CPMV. Single infection of CPMV revealed continuously typical symptoms on the upper leaves of non-transgenic *N. benthamiana*. However, in the *N. benthamiana*-HCpro the typical symptoms were decreased on the upper leaves at 14days post-inoculation. CPMV expressed green fluorescence protein (CPMV-GFP) could move in *N. benthamiana* and *N. benthamiana*-HCpro. In *N. benthamiana*-HCpro the fluorescence produced and moved faster along veins. The veinal movement of fluorescence on non-transgenic *N. benthamiana* infected doubly with CPMV-GFP and CABMV was occurred on the whole plants, and in the non-transgenic *N. benthamiana* infected singly with CPMV-GFP virions moved slower to

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 Masuta[2], Jang Kyung Choi[3], and Ki Hyun Ryu[1]. [1]Plant Virus GenBank, PVGABC, Division of Life and Environmental Sciences, Seoul Women's University, Seoul 139-774, Korea; [2]Graduate School of Agriculture, Hokkaido University, Kita-ku, Kita 9, Nishi 9, Sapporo 060-8589, Japan; [3]Division 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 characterizedSome 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.