# Characterizations of Broad Bean Wilt Virus isolated from *Rehmania glutinosa* Liboschitz

In-Sook Choi, Min-Kyoung Choi, Jong-Yeop Kim[1], Ju-Rak Lim[1], Kui-Jae Lee, Wang-Hyu Lee
Faculty of Biological Resource Science Chonbuk National University, Chonju, Korea
[1]Chinan Experimental Station of Medicinal Herbs, Chonbuk Provincial A.T.A, Chinan, Korea

The nucleotide sequence of a Korea isolate of broad bean wilt favavirus from *Rehmannia glutinosa* Lib., designated BBWV-RE, was determined. Direct amino acid sequencing of the virus coat proteins suggests that a comparison of several favaviruses in terms of nucleotide sequence and amino acid sequences showed that BBWV-2 isolates display high sequence identity. The small coat protein genes of RNA-2 were also determined for three other Japanese isolates(E, L, and 1-2) and two ATCC isolates(PV132 and PV176) of BBWV. the CP sequence suggested distinct evolution lineages. Serotype 2 favaviruses are more prevalent in Asia, Australia and North America, Wheres serotype 1 is more prevalent in europe.

So far, no favavirus CP sequence with homology spanning across the two serotypes has been reported. Genome organization of BBWV-RE was similar to other viruses in the comoviridae family. The nucleotide sequence of isolate BBWV-RE was compared with those reported for another BBWV-1 isolate(serotype 1) , BBWV-2 (serotype 2) and six comoviruses. Identification of the BBWV-2 was established by host range test, electron microscopy and serological reaction of the virus. BBWV-2 was inoculated systemic infection on the leaves.

In the host range test, *Nicotiana glutinosa*, *N. tabacum* cv samsun were systemically infected with the virus. BBWV-2 was wide host range. The virus was represented local lesions on inoculated leaves of *Datura stramodium*, *Vigna sinensis*, *Chenopodium amaranticolor*. However, *Pisum sativum*, Brassica rapa did not any symptoms. This virus reacted positive antiserum in ELISA test. We taken 600bp band by using the revers tanscription and polymerase chain reaction system.