gene and most of the γb ORF have properties of defective interfering (DI) RNAs because they replicate to high levels and effectively interfere with the accumulation of wild type RNAs α and γ. However, these DI— like transcripts appear not to influence the course of systemic infections since they fail to inhibit systemic infections of barley plants when coinoculated with wild type transcripts and they also appear not to move systemically since they can not be detected uninoculated leaves of infected plants.

Purification, biophysical and biochemical characterization of broad bean wilt virus

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Broad bean wilt virus (BBWV) is known to be present in various countries and has been isolated from a number of cultivated plants and weeds. In China, this virus has been identified in many cultivated legumes including cowpea (*Vigna sinensis*), faba bean (*Vicia faba*), pea (*Pisum sativum*) and soybean (*Glycine max*). It has also been identified in spinach (*Spinacia oleracea*), pepper (*Capisum annum*), celery (*Apium graveolens*) and some weeds. The virus causes serious diseases on these crops, especially on faba bean and pea.

A virus isolate (B934) from faba bean was collected in Hangzhou, Zhejiang province, and identified as broad bean wilt virus (Serotype II). It was purified from *Chenopodium quinoa* by a method using triton X—100 and high molarity potassium phosphate buffer added with sucrose. The yield of purified virus was 128mg/g fresh tissue. Purified preparation of B934 contained isometric particles Ca. 25nm in diameter. When centrifuged in glycerol density gradients, preparations of virus formed three light—scattering bands called T(top), M (middle) , and B(bottom). The A260/A280 ratios of T, M and B were 0.75, 1.64 and 1.42, respectively. The capsid protein of virus contained two polypeptides with molecular weights of 425000 and 21200, respectively. The genome of B934 contained two types of single stranded RNAs. Double— stranded RNAs were isolated from BBWV infected pea leaves. Analysis by agarose gel showed two major species of viral dsRNA of approximately 6.2 and 4.1kb. The result confirm BBWV has bi— partite genome. The slow—migrating form and fast—migrating form were found When purified preparations were examined by electrophoresis, the electrophoretic forms were similar to that of comoviruses. The genome structure of BBWV is being investigated.