

Studies on the diversity of *Blackberry yellow vein associated virus*

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Blackberry yellow vein disease (BYVD) is the most important virus disease in the southern US as it is prevalent in all fresh market blackberry-growing states. The disease affects blackberry longevity, increasing production cost in the long-run. BYVD is unique in that it is not caused by any particular virus but symptoms appear when two or more viruses are present in the plant. The most common virus in the complexes causing BYVD is *Blackberry yellow vein associated virus* (BYVaV), a virus predicted to be transmitted by whiteflies. The prevalence of BYVaV (about 70% of BYVD plants were infected with the virus), made us wonder whether the virus is moving in propagation material rather than active movement in the field.

For this reason we conducted a study to ‘fingerprint’ 30 isolates collected from Arkansas, Mississippi, North and South Carolina, Georgia and Tennessee from both cultivated and wild blackberries. To get a better representation of the virus diversity we used four regions of the virus genome, the most diverse areas of viruses in the BYVaV group. The study revealed isolate differences within and between states. Differences were as high as 10%, indicating that there is significant virus diversity and isolates infecting cultivated blackberry arrived to the fields from different sources, presumably, and in lack of alternative hosts for BYVaV, from wild blackberries. These results show that BYVaV is not moving primarily in plant material but there is active movement because of vectors in the field.