Blackberry virus F

- Virus/pathogen name, including accepted acronyms and synonyms

  Blackberry virus F has a DNA genome and is a member of the family *Caulimoviridae*, Genus *Badnavirus*. The ICTV accepted acronym is BVF.

- Host range, including resistance or tolerance within the crop hosts, alternate hosts

  BVF has been identified in both wild and cultivated blackberry plants, with successful mechanical transmission to the following herbaceous hosts; *Beta vulgaris* Swiss chard 'H-32', *Chenopodium quinoa*, *Cowpea* 'Elegance 801', *Cucumis melo* 'Edisto 47' cantaloupe, *C. sativus* 'National Pickling', *Glycine man* 'William 82', *Gomphrena globose*, *Nicotiana rustica*, *N. tabacum*, *Pisum sativum* 'Wando', Pumpkin *Cucurbita pepo* 'Connecticut field', Pumpkin *C. pepo* 'National Pickling', *Solanum lycopersicum* 'Bradly', *Spinach* 'Meerkat" (Shahid et al., 2016). All infected herbaceous hosts showed no symptoms.

- Symptoms on crop host including varietal differences with images of symptoms when available

  BVF was identified in blackberry with blackberry yellow vein disease (BYVD) symptoms. The incidence of BVF is low (Shahid et al., 2016). Therefore it is unknown what role, if any, that BVF plays in BYVD symptom development. Mechanical inoculation of herbaceous hosts resulted in asymptomatic infections.

- Geographic distribution:

  BVF has only been found in the USA. A PCR test to detect BVF was positive in blackberry samples from Arkansas, Georgia, Mississippi, North and South Carolina. However, the majority of these samples were suspected of containing the integrated inactive form of the virus, rather than the active episomal form, due to further tests with DNase treated material being negative (Shahid et al., 2016). At least one blackberry plant in this study contained the active episomal form as the virus was sap transmittable to herbaceous hosts, and was further verified by southern hybridization.

- Means of spread:

  While the insect vector is currently unknown, other badnaviruses are vectored by mealybugs, aphids or lacebugs, suggesting these may be potential vectors of BVF.

As BVF is a badnavirus, there is a possibility that the inactive integrative form of the virus has the potential to become active and cause infection. Some, but not all, inactive badnaviruses species reactivate under stress conditions such as tissue culture (Dallot et al., 2001).

- Recognized diagnostic tests with cited references:

  Plants that test positive via PCR may be detecting the inactive integrated form of BVF. In order to detect the active form, DNAse treated nucleic acid extraction followed by RT-PCR, Rolling circle amplification and/or Southern hybridization can be used (Shahid et al., 2016). Sap transmission to herbaceous hosts will also detect the active form (Shahid et al., 2016).

- Sampling recommendations for each pathogen including timing and tissue to be sampled
  Spring to early summer (May-June) is the ideal time for sampling. Ideally, the samples should be taken from young but fully expanded leaves. Sampling from different sites of the same plant increases chances of detection since BVF may not be evenly distributed within plants.

- Management strategies for the pathogen and the vector(s) of the pathogen
  It is currently unknown whether BVF is able to be activated from the inactive form. Tissue culture propagation is often used in the production of virus-free planting material, which has the potential to activate integrated forms of Badnaviruses, as is seen with banana infecting badnaviruses (Dallot et al., 2001).

References

Dallot, S., Acuña, P., Rivera, C., Ramírez, P., CȏTe, F., Lockhart, B.E.L., Caruana, M.L., 2001. Evidence that the proliferation stage of micropropagation procedure is determinant in the expression of Banana streak virus integrated into the genome of the FHIA 21 hybrid (Musa AAAB). Arch. Virol. 146, 2179–2190. https://doi.org/10.1007/s007050170028

Shahid, M.S., Aboughanem-Sabanadzovic, N., Sabanadzovic, S., Tzanetakis, I.E., 2016. Genomic Characterization and Population Structure of a Badnavirus Infecting Blackberry. Plant Disease 101, 110–115. https://doi.org/10.1094/PDIS-04-16-0527-RE

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