Banana bunchy top virus

The *Banana bunchy top virus* (BBTV) is a circular single-stranded DNA virus (18-20 nm in diameter) that causes Bunchy top in bananas. Although the disease was first reported in the late 1880s\(^1\), the virus itself, which was originally classified as a *Luteovirus*, was isolated in the late 1980s and reassigned to the *Nanoviridae* family in the genus *Babuvirus*\(^2\).

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Transmission

BBTV is not mechanically transmissible, but it can be transmitted locally by the banana aphid *Pentalonia nigronervosa* or over long distances by infected planting material\(^1\). Transmission by the aphid is in a persistent, non-propagative manner, with an acquisition feeding period of at least four hours and inoculation feeding period of at least fifteen minutes (Hu *et al.*, 1996). The efficiency of transmission ranges between 46 and 67% (Magee, 1927; Hu *et al.*, 1996), with nymphs than adults in transmitting the virus (Magee, 1940). Retention of infectivity in the aphid has been reported up to 20 days after removal from the virus source (Magee, 1927). Bunchy top symptoms are evident approximately 25 days following the transmission, although this varies depending on temperature and age of plants (Magee 1927; Allen, 1978).

Host range

Alternative hosts for BBTV have been investigated since the aphid vector colonises numerous plant families including Araceae, Commelinaceae, Musaceae and Zingiberaceae (Blackman and Eastop, 1984). *Colocasia esculenta* (taro; Araceae) has been reported to be a symptomless host of BBTV in India (Ram and Summanwar, 1984), while *Canna indica* (Canna; Cannaceae) and *Hedychium coronarium* (white ginger or garland flower; Zingiberaceae) were reported to be hosts for BBTV in Taiwan (Geering and Thomas, 1997; Yasmin *et al.*, 2001).

In India, especially the hill bananas are highly susceptible to BBTV. BBTV has been the sole cause for drastic reduction in hill banana cultivation from 18,000 ha in 1970’s to 2,000 ha at present. Broad survey on BBTD during 2006 and 2007 showed the incidence of 20–30% in northern zones of banana cultivation (Lucknow, Barabanki, Bahraich, Kanpur, and Etawah districts of Uttar Pradesh) (Vishnoi *et al.*, 2009).

Genome organisation of BBTV

Its genome consists of at least six components of circular single stranded DNA (ssDNA), designated
as DNA-R, -U3, -S, -M, -C and -N, each with a similar organisation and size (approximately 1 kb) (Harding et al., 1991; Burns et al., 1995; Herrera-Valencia, 2005; Vetten et al., 2005) (Plate 7). The genomic components comprise an intergenic region (IR) and at least one open reading frame (ORF) that is transcribed in the virion sense (Burns et al., 1995). DNA-R encodes the master replication initiation protein (Rep) which is essential for trans-replication of the BBTV genomic components (Horser et al., 2001 a) through its nicking and joining activity (Hafner et al., 1997b). DNA-S encodes the coat protein (CP) (Wanitchakorn et al., 1997), while DNA-M and DNA-N are believed to encode the movement protein (MP) and nuclear shuttle proteins (NSP) respectively (Wanitchakorn et al., 2000). DNA-C encodes the cell cycle link protein (Clink) that has plant retinoblastoma-like binding ability to switch the host plant cells to S phase to make them more permissive for viral replication (Aronson et al., 2000; Wanitchakorn et al., 2000). The roles of the DNA-U3 gene product and that encoded by the small internal ORF of DNA-R are unknown (Burns et al., 1995; Beetham et al., 1997). Multiple satellite DNAs (otherwise known as deficient DNA-R components; Briddon and Stanley, 2006) encoding non-essential Reps, which are capable of autonomous replication but cannot trans-replicate any other BBTV genomic component, have also been identified associated with BBTV and are probably reliant on their helper virus to prepare cell conditions optimal for replication and movement within and between plants (Horser et al., 2001b).

The IR of each genomic component comprises a stem-loop common region (SL-CR), a major common region (CR-M), a TATA box and a polyadenylation signal (Burns et al., 1995). The 69 bp SL-CR shares 62% homology between all six genomic components (Burns et al., 1995), and contains a stem-loop (SL) structure which contains the nanonucleotide loop sequence (5' TA TTATTAC 3') that is conserved between all components (Burns et al., 1995; Hafner et al., 1997b) and iterative elements (iterons) that are potential Rep binding sites (Horser, 2000; Herrera-Valencia et al., 2006). The CR-M varies in size from between 62 and 92 bp and shares at least 76% homology between all six genomic components (Burns et al., 1995). The CR-M comprises three relatively conserved domains (domain I, II and III) and short primer sequences that map to this region (5' of CR-M, domain I and domain II) have been isolated from BBTV virions (Hafner ef al., 1997a), indicating its role in second strand synthesis of circular ssDNA genomic components. The promoter and terminator regions that drive the expression of encoded ORFs are located within the IR and have been shown to be active in both monocot and dicot embryogenic cells and plants with significant activity in vascular-associated tissue (Dugdale et al., 1998, 2000).

References


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