



ISSN (E): 2277- 7695
ISSN (P): 2349-8242
NAAS Rating: 5.03
TPI 2018; 7(12): 218-222
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www.thepharmajournal.com
Received: 24-10-2018
Accepted: 26-11-2018

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A review on biology and study of major viral diseases in banana

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Abstract

The BSVs of family Caulimoviridae integrate into the host genome and resulting into splitting of several pseudo-stem of banana plant, ultimately leading to death of the plant. Banana and plantain are known to be susceptible to five more other viruses of minor significance, such as Cucumber mosaic virus (CMV), Abaca bunchy top virus (ABTV), Banana mild mosaic virus (BMMV), Banana virus X (BVX), and Abaca mosaic virus (AMV). Bananas and plantains (*Musa* spp.) are massive herbaceous plants produced in 10.4 million hectare in the tropics. Cultivar bananas or plantains are the world's top 10 staple food. They are both sterile and parthenocarpic fruit. All cultivated species are mostly triploid ($2n = 3x = 33$; whereas some are diploid or tetraploid). With a production of more than 100 million tons annually, banana is a staple food across the Asian, African and American Oceania, and the Pacific tropics. Cultivation of bananas occurs through vegetative propagation using suckers or tissue culture plants and grown almost as perennial plantations. These cultivars are prone to hoarding of pests, pathogens and especially viruses such as Banana bunchy top virus (BBTV), Banana streak Virus (BSV) and Banana Bract Mosaic Virus (BBrMV) which contribute to lower yield of cultivars and impediment to exporting of *Musa* germplasm. These viruses are known to cause the most serious economic losses in the "Old World," contributing to yield reduction up to 100% and also responsible for a dramatic reduction in cropping area. Evidences from past 50 years have contributed to significant knowledge about plant diseases causing microbes, their distribution, and spreading. Moreover research during the last 25 years have led to a better understanding of the virus-vector-host interactions, virus diversity, disease etiology, and epidemiology. There are thousands of domestic *Musa* cultivars and their genetic diversity indicate multiple origins from different wild hybrids between two principle ancestral species. Due to a lack of durable host resistance in the *Musa* spp. Phyto-sanitary measures and the use of virus-free techniques are the major methods for virus control. The present study on BBTV, BSVs, and BBrMV, disease spreading, and controlling measures are summarized in this review.

Keywords: Caulimoviridae, banana, plantain, triploid, virus-free techniques Phyto-sanitary etc.

Introduction

Botanical distinction between plantain and banana is not straightforward. In general, banana are eaten uncooked as a dessert, and unripe starchy fruits that are cooked and eaten are referred to as plantain and also known as cooking banana. Other cultivars are "beer banana" used for fermentation of the juice (Heslop-Harrison & Schwarzacher, 2007) [28]. Cooking banana or plantain is predominant sources of food and income in SSA (Nweke, Njoku, & Wilson, 1988) [29]. With 56.5% of the global area, Africa dominates the global *Musa* production area compared with 21.7% in Asia and 20.5% in Latin America. However, in terms of crop productivity, Africa is last, after Asia and America (Table 1). Dessert banana are cultivating for commercial trade in Latin America and the Caribbean; Plantain are widely grown in Asia-Pacific and dominant in Central and West Africa and Latin America; whereas the highland banana (triploid) are mainly produced in East Africa (Ortiz & Swennen, 2014) [20].

Banana and plantain grow, mature, and fruit without seasonality throughout the year. Suckers spring up from the underground rhizome to replace the main shoot that withers after fruiting, and this process of succession continues indefinitely (Morton, 1987) [30]. However, this exposes plantations to the effects of adverse environmental factors, pests, and pathogens. Farmers generally use young suckers plucked from old plantations to establish new fields. This practice has been among the major causes of outbreaks of several banana diseases and pests around the world (Lockhart & Jones, 2000) [17], especially viruses, which are perpetuated along with the planting material. Banana and plantain belonging to genus *Musa*, (Musaceae, Zingiberales) produced in 10.4 million ha in over 130 countries, across tropics mainly Africa,

Asia, America, Oceania, and the Pacific it provide staple food and one of the source of income for millions of smallholder farmers (Fig. 1). Total production was estimated at 145 million tons from 10.4 million ha in 2013; these two cultivars together rank on 6th after maize, rice, wheat, potato, and cassava (FAOStat, 2012)^[8]. All widely cultivated varieties are parthenocarpic, resulting from intra- and intercrops of the two species, *M. acuminata* (2n=2x=AA) and *M. balbisiana*

(2n=2x=BB) (Ortiz, 2013). Many of the domesticated cultivars are natural mutants with triploid genome (2n=3x=33) such as dessert banana (AAA) and plantain (AAB or ABB), and seedless cultivars of both diploids (AA and AB) and synthetic tetraploids (2n=4x=44) with genome constitutions of AAAA, AAAB, AABB, and ABBB (Heslop-Harrison & Schwarzacher, 2007)^[28].

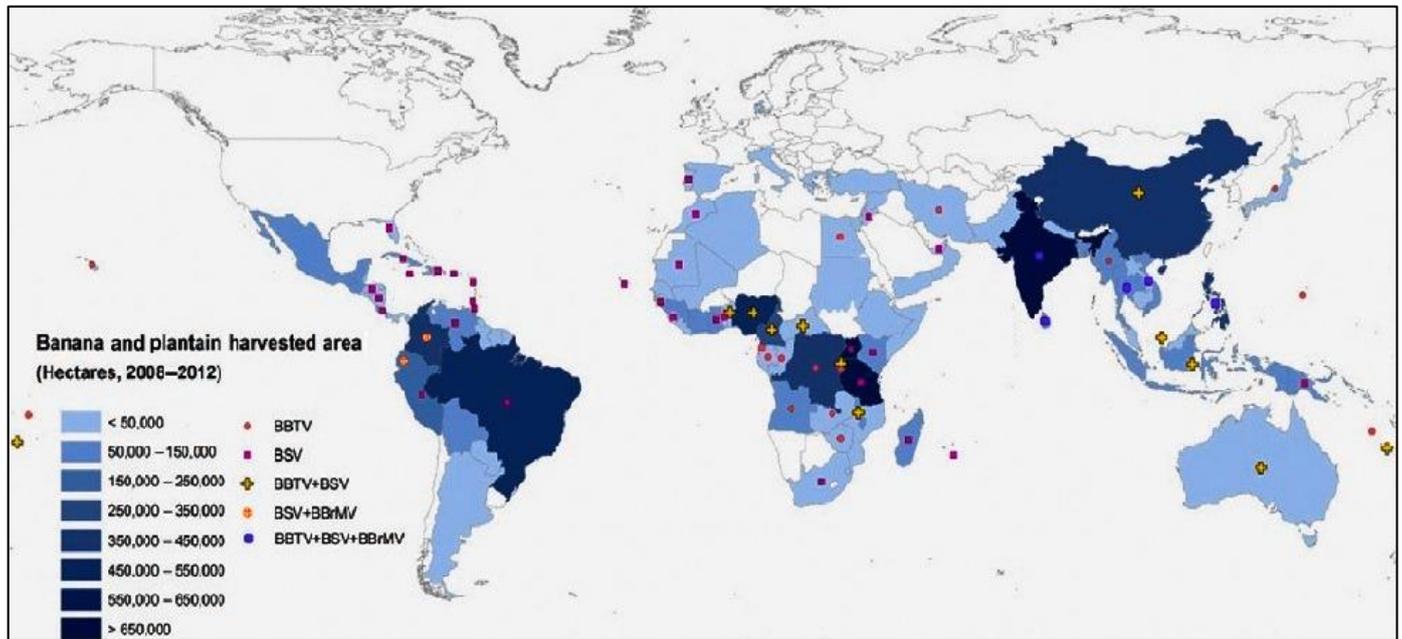


Fig 1: Banana and plantain production in various countries and distribution of the three major banana viruses, BBTV, BSVs, and BBrMV. (<http://faostat.fao.org/>)

Table 1: Combined area, production, and productivity of banana and plantain in 2012; production trend from 2002–2012

	Area		Production		Yield	
	Ha (X1000)	% Change	T (X1000)	% Change	t/ha	% Change
World	10,360.7	7.8	139,154.9	27.0	13.4	20.8
America	2133.1	0.6	36,089.2	14.1	16.9	13.6
Africa	5862.2	4.1	42,408.1	20.3	7.2	16.9
Europe	10.5	0.8	399.9	11.2	38.2	12.1
Asia	2258.0	24.2	58,731.0	40.3	26.0	21.3
Oceania	97.0	12.3	1526.7	19.4	15.7	8.1

Data source: FAO banana and plantain production statistics for 2012 (FAOStat, 2012)^[8].

% Change = Percentage increase or decrease compared with 2002 data.

Important Viral Diseases of Banana

1. Banana bunchy top disease

1.1 BBTV diversity

Various BBTV isolates characterized so far around the world have >85% homology (Banerjee *et al.*, 2014)^[4]. Although ABTV is also known to cause symptoms similar to those of BBTV in *Musa* spp., it is less prevalent and recognized so far only in the Philippines and Malaysia, mainly infecting abaca (Sharman *et al.*, 2008)^[25]. In general, the genetic diversity of BBTV isolates within the countries is very low (Vishnoi, Raj, & Prasad, 2009; Selvarajan & Balasubramanian, 2008)^[31], Pakistan (Amin, Qazi, Mansoor, Ilyas, & Briddon, 2008)^[32], Africa (Kumar *et al.*, 2011; Adegbola *et al.*, 2013)^[15, 1], and Oceania (Stainton *et al.*, 2012). However, in India, relatively greater diversity for BBTV was observed in the north-eastern region (Banerjee *et al.*, 2014)^[4], including the identification of a new Babuvirus—Cardamom bushy dwarf virus (CBDV)—in cardamom (Mandal, Shilpi, Barman, Mandal, & Varma, 2013)^[18]. Based on the phylogenetic relationships

among the DNA-R component sequences, various BBTV isolates were grouped into two different lineages: (i) the Pacific-Indian Oceans (PIO) group (formerly South Pacific group) comprising isolates in Africa, Australia, Hawaii, south Asia, Myanmar, and Tonga; and (ii) the South-East Asian (SEA) group (formerly Asian group) comprising isolates from China, Indonesia, Japan, the Philippines, Taiwan, and Vietnam (Banerjee *et al.*, 2014)^[4].

1.2 Symptoms and Spreading

BBTV induces discontinuous dark green flecks and streaks of variable length on the leaf sheath, midrib, leaf veins, and petioles. New leaves emerging from the infected plants are narrower with wavy leaf lamina and yellow leaf margins (Nelson, 2004)^[19]. Leaves are affected with progressively shorter, narrow, and brittle in texture; BBTV bunch together at the top of the plant and hence cause the disease (Thomas *et al.*, 1997)^[26]. Susceptible cultivars infected at a young stage and the suckers emerging from infected stems are severely

stunted. Severely infected plants usually won't give fruit. Occasionally, bracts of male flower buds turn into a leafy structure and exhibit dark green dots and streaks with splitting midrib (Thomas *et al.*, 1997) [26]. Emerging suckers from infected plants exhibit severe symptoms. Plants infected at a later stage do not normally show leaf symptoms, but dark green streaks can be seen on the tips of the bracts. Emerging suckers from such plants usually exhibit moderate symptoms or none. The incubation period from the time of virus inoculation to symptom expression varies between 19 and 125 days, depending on the stage of infection, cultivar, and weather. The shortest time for the diagnosis of BBTV using polymerase chain reaction (PCR) was 15 days after. However, suckers emerging from the infected stools show symptoms from the time of emergence.

2. Banana streak disease

2.1 BSV diversity

The genus *Badnavirus* is both the most complex and the most diversified genus within the family *Caulimoviridae*, with at least three major clades. A final phylogeny of BSVs has been established to clarify whether partial sequences distributed over the three main clades of the genus *Badnavirus* correspond to episomal viruses with or without an endogenous counterpart (Gayral *et al.*, 2010; Iskra-Caruana *et al.*, 2010) [9, 11] (Fig. 2).

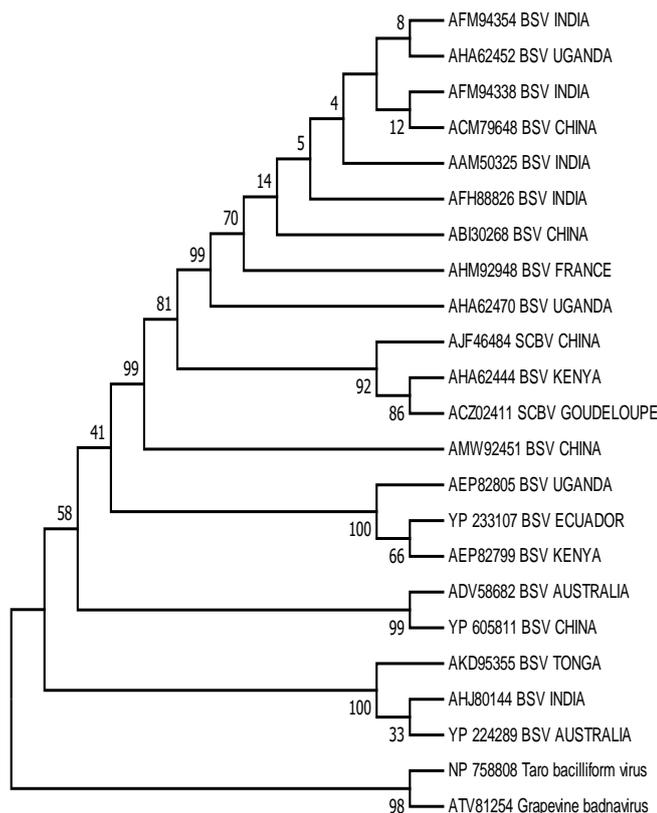


Fig 2: Maximum likelihood phylogeny of badnavirus sequences based on alignment of a 230-bp fragment of the RT/RNase H viral region. Bootstrap values of 1000 replicates are given when >50%. Taro bacilliform virus (TABV) and grapevine badnavirus (GVCV) are given as out groups. The Gen Bank accession numbers of sequences are given in parenthesis. Sugarcane bacilliform virus (SCBV) are also included

2.2 Symptoms and Spreading

BSV causes chlorotic streak disease and is known to be the

most widely distributed virus infecting banana and plantain around the world. The disease was first observed in the Niek valley on the Ivory Coast in 1958 (Lockhart & Jones, 2000) [17] and later, in 1964, severe BSV chlorosis disease was reported in the Gros Michel triploid *M. cuminata* (AAA) banana cultivar. Lockhart & Jones, 2000) [17] purified bacilliform particles from field-grown Dwarf Cavendish banana (AAA) in southern Morocco, confirming the viral etiology of the disease. The data currently available on the disease show a complex of distinct BSVs, each causing the same disease. BSVs are para-retroviruses belonging to the genus *Badnavirus*, family *Caulimoviridae*. The virus particles are bacilliform-shaped (120–150 × 30 nm), double-stranded non-covalently closed circular DNA genome approximately 7.2–7.8 kb long that uses a virus-encoded reverse transcriptase to replicate. Hull (1999) [10] were the first to describe the structure of the virus genome and named it Banana streak Obino l'Ewai virus (BSOLV). The virus genome has three consecutive ORFs on one strand (King *et al.*, 2012) [13]. ORF1 and ORF2 potentially encode two small proteins of unknown function of 20.8 and 14.5 kDa. ORF3 is a large polyprotein of 220 kDa encoding at least four proteins, encompassing a putative cell-to-cell movement protein, a coat protein (analogous to retroviral GAG), an aspartic protease, and a viral replicase consisting of RT and RNase H domains (Hull, 1999; King *et al.*, 2012) [10, 13]. This polyprotein is cleaved into functional units by the aspartic protease once it has been fully translated. In contrast to retroviruses, BSV does not encode integrase, neither does it require integration into the host genome to replicate. Two infectious forms of BSV exist: (i) the episomal form resulting from cells/plant infection following transmission by mealybugs and (ii) endogenous forms which are endogenous viral sequences of BSV (eBSV) integrated within the banana B genome (*M. Balbisiana*). Physical stresses have been reported to induce de novo viral particles (episomal form) from eBSV (Lheureux *et al.*, 2003) [16], possibly through intra-strand homologous recombination (HR) (Chabannes *et al.*, 2013; Iskra *et al.*, 2010) [11]. Both episomal virus and infectious particles from eBSV give rise to systemic plant infection (Hull, 1999; Iskra *et al.*, 2010) [10, 11]. BSV particles from both origins can be transmitted by mealybugs (Dahal *et al.*, 2000; Kubirib *et al.*, 2001) [6, 14].

3 Banana Bract Mosaic

3.1 Disease Symptoms and Spread

BBrMV noted on several banana cultivars in the Philippines in 1979 and thought to be different from all other recognized viruses of banana (Rodoni *et al.* 1997) [22]. Occurrence of the virus was discovered in a few other countries in Asia and the South Pacific, including Samoa, India, Thailand, Sri Lanka, and Vietnam (Rodoni *et al.*, 1997; Rodoni, 1999) [22, 23]. In Latin America, BBrMV occurrence was first reported in Colombia (Quito-Avila *et al.*, 2013) [21]. Kenyon *et al.*, (1997) [12] reported up to 40% yield loss on Mindanao island of the Philippines. High rejection rate of marketable fruit was associated with the higher disease incidence which causes misshapen fingers. In Hawaii (USA), BBrMV was detected in ornamental ginger plants (*Alpinia purpurata*) but not in *Musa* (Wang *et al.*, 2010) [27].

BBrMV causes characteristic spindle-shaped, purplish streaks on bracts, pseudostems, midribs, peduncles, and even fruits (Rodoni *et al.*, 1997) [22]. Bunches from infected plants unusually contain a long or very short peduncle BBrMV

belong to the genus *Potyvirus* and family *Potyviridae*. Flexuous filamentous virus particles measuring 750×11 nm have been detected (Bateson and Dale 1995) [5]. Purified virions contain a major coat protein of 38–39 kDa. The virus genome consists of single-stranded positive-sense RNA of 1197 nucleotides long excluding the 3'-terminal poly (A) tail. The viral genome contains a typical large ORF of 9378 nucleotides coding for a polyprotein of 3125 amino acids with 9 protease cleavage sites, potentially yielding 10 matured functional proteins that have motifs conserved among homologous proteins of other potyviruses.

BBrMV diversity

BBrMV belong to the genus *Potyvirus* and family *Potyviridae*. BBrMV particle is 750×11 nm in diameter have been detected are Flexuous and filamentous (Bateson and Dale 1995) [5]. Purified virions contain a major coat protein of 38–39 kDa. The virus genome consists of single-stranded positive-sense RNA of 1197 nucleotides long excluding the 3'-terminal poly (A) tail. The viral genome contains a typical large ORF of 9378 nucleotides coding for a polyprotein of 3125 amino acids with 9 protease cleavage sites, potentially yielding 10 matured functional proteins that have motifs conserved among homologous proteins of other potyviruses (Balasubramanian and Selvarajan 2012; Rodoni *et al.*, 1997) [2, 22]. The whole genome of BBrMV-TRY (India) and BBrMV-PHI (the Philippines) had 94% nucleotide sequence identity and 88–98% amino acid sequence identities (Balasubramanian and Selvarajan 2012) [2]. Studies of genetic analysis of the CP gene of 49 isolates revealed a greater variation among them, and two of the isolates from Tamil Nadu were distinct with 18–21% divergence (Balasubramanian and Selvarajan 2014) [3].

Conclusions

Banana is among 10 most important and high-priority food crops which provide staple food, nutrition and income for the millions of banana farmers globally causing high demands of banana at global level which have been raised as revealed by world banana production increasing for the last decade. Moreover, banana fruits are particularly valued in the tropics because they yield irrespective of the seasons. Viruses are considered a major constraint to banana plantation as they not only cause yield reductions but are also a major limitation to the exchange of germplasm. Among viruses that infect banana, BBTv and BBrMV and BSV are significant threats to banana production. Of these, BSV is more widely spread worldwide than BBTv, though the latter is so far the most economically damaging virus. Alongwith these several minor virus like Abaca bunchy top (ABTV) Abaca mosaic, Banana mosaic, Banana mild mosaic & Banana virus X are also reported to infect Banana (Kumar *et al.*, 2011) [15]. Tissue culture techniques have been used to develop virus-free planting material and using, strict regulation on movement of infected planting materials, and development of transgenic resistant cultivars to these viruses are the most effective means to control these virus diseases in banana. However, all banana viruses cannot be eliminated through tissue culture and traditional breeding because most of the commercially important cultivars are (tetraploid) mostly sterile and develop fruit through parthenocarpy. The development of transgenic plant with improved virus resistance has promising potential to incorporate in banana cultivars and currently gaining priority. RNAi-based resistance which is successfully

employed for transgenic control of several plant viruses (Sudarshana *et al.*, 2007) [34] has also been employed for transgenic control of BBTv in banana.

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