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Etiology of major viral diseases in banana and plantain

Abhinay Singh*, R.M Mishra and U.K Chauhan
Centre of Biotechnology, APS University, Rewa, (M.P.) - India

Abstract

Cultivated bananas and plantains (Musa spp.), are giant herbaceous plants produced in 10.4 million ha in the tropics, are amongst the world's top 10 food crop. They are both sterile and parthenocarpic so the fruiting occurs without seed. 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. Propagation occurs vegetatively using suckers or tissue culture plants and grown almost as perennial plantations. These are prone to the accumulation of pests and pathogens, especially viruses which contribute to loss of yields and are also barriers to the international exchange of Musa germplasm. The most economically important viruses of banana and plantain are Banana bunchy top virus (BBTV), a complex of banana streak viruses (BSVs) and Banana bract mosaic virus (BBrMV). BBTV is known to cause the most serious economic losses in the "Old World," contributing to a yield reduction of up to 100% and responsible for a dramatic reduction in cropping area. Studies over the past 50 years have contributed to significant knowledge on disease biology, distribution, and spread. Research during the last 25 years have led to a better understanding of the virus–vector–host interactions, virus diversity, disease etiology, and epidemiology.

Keywords: Viral, Etiology, Disease

Introduction

Banana and plantain (Musa spp.), with a production of 10.3 million ha in the tropics, are among the world's main 10 nourishment crops. They are vegetatively engendered utilizing suckers or tissue culture plants and developed nearly as lasting manors. These are inclined to the amassing of vermin and pathogens, particularly infections which add to yield decrease and are additionally obstructions to the worldwide trade of germplasm. The most financially vital infections of banana and plantain are Banana bunchy best infection (BBTV), a complex of banana streak infections (BSVs) and Banana bract mosaic infection (BBrMV). BBTV is known to cause the most genuine financial misfortunes in the "Old World," adding to a yield decrease of up to 100% and in charge of an emotional decrease in trimming zone. The BSVs exist as episomal and endogenous structures are known to be worldwide in conveyance.

*** Corresponding Author**
E.mail: singh.abhinay@gmail.com

In India and the Philippines, BBrMV is known to be financially vital yet as of late the infection was found in Colombia and Costa Rica, consequently flagging its spread into the "New World." Banana and plantain are additionally known to be helpless to five different infections of minor criticalness, for example, Abaca mosaic infection, Abaca bunchy best infection, Banana mellow mosaic infection, Banana infection X, and Cucumber mosaic infection.

Banana and plantain having a place with genus Musa, (Musicale, Zingiberales) grown in 10.4 million ha in more than 130 nations, crosswise over tropics basically Africa, Asia, America, Oceania, and the Pacific it give staple sustenance and wage to a huge number of smallholder ranchers (Fig. 1). Add up to creation was assessed at 145 million tons from 10.4 million ha in 2013; the two yields together rank no. 6 after maize, rice, wheat, potato, and cassava (FAOStat, 2016). All broadly developed assortments are parthenocarpic, coming about because of intra- and intercrosses of the two dingy species, M. acuminata (2n=2x=AA) and M. balbisiana (2n=2x=BB) (Ortiz, 2013). A significant number of the trained cultivars are normal freaks with triploid genome (2n=3x=33, for example, dessert banana (AAA), cooking banana, and plantain (AAB or ABB), and seedless cultivars of the two diploids (AA and AB) and manufactured tetraploids (2n=4x=44)

with genome constitutions of AAAA, AAAB, AABB, and ABBB (Heslop-Harrison and Schwarzacher, 2007).

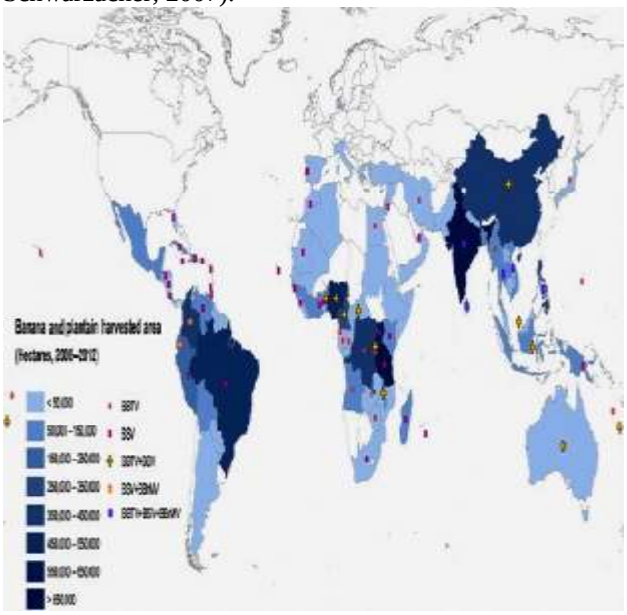

Fig. 1: Banana and plantain production in various countries and distribution of the three major banana viruses, BBTV, BSVs, and BBrMV. (Average production data for banana and plantain for the years 2008–12. http://faostat.fao.org/)

Botanical distinction between banana and plantain 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 cooking banana. Other cultivars are "beer banana" used for fermentation of the juice (Heslop-Harrison & Schwarzacher, 2007). Cooking banana and plantain are the most important sources of food and rural income in SSA (Nweke, Njoku, & Wilson, 1988). 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 production and productivity, Africa is last, after Asia and America (Table 1). Dessert banana are grown mainly for commercial trade in Latin America and the Caribbean; cooking banana are widely grown in Asia-Pacific; plantain are dominant in Central and West Africa and Latin America; whereas the highland banana are mainly produced in East Africa (Ortiz & Swennen, 2014).

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). However, this exposes plantations to the effects of adverse environmental factors, pests, and pathogens. Farmers generally use young suckers removed from the 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 (Jones, 2002), especially viruses, which are perpetuated along with the planting material.

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

	Area		Production	
	ha (×1000)	% Change	t (×1000)	% Change
World	10,360.7	7.8	139,154.9	27.0
Africa	5862.2	4.1	42,408.1	20.3
Americas	2133.1	0.6	36,089.2	14.1
Asia	2258.0	24.2	58,731.0	40.3
Europe	10.5	0.8	399. 9	11. 2
Oceania	97.0	12.3	1526.7	19.4

% Change = Percentage increase or decrease compared with 2002 data.
Data source: FAO banana and plantain production statistics for 2012 (FAOStat, 2016).

Major viral diseases of banana and plantain

1 Banana bunchy top disease

1.1 Disease etiology and biology

BBTV incites trademark spasmodic dull green specks and dashes of variable length on the leaf sheath, midrib, leaf veins, and petioles. New leaves rising up out of the contaminated plants are smaller with wavy leaf lamina and yellow leaf edges (Nelson, 2004). Leaves created are dynamically shorter, restricted, and fragile in surface; these cluster together at the best and subsequently give the name of the sickness (Jones, 1994). Helpless cultivars tainted at a youthful stage and the suckers rising up out of contaminated stools are extremely hindered. Seriously tainted plants more often than not won't natural product, however on the off chance that organic product is delivered, the hands and fingers are probably going to

be misshaped and curved (Nelson, 2004). Once in a while, bracts of male bloom buds swing to a verdant structure and show dull green spots and streaks (Thomas et al., 1994). Developing suckers from tainted plants show serious side effects. Plants contaminated at a later stage don't regularly indicate leaf side effects, however dim green streaks can be seen on the tips of the bracts. Developing suckers from such plants as a rule display moderate side effects or none. The hatching time frame from the season of infection BBTV initiates trademark intermittent dim green specks and dashes of variable length on the leaf sheath, midrib, leaf veins, and petioles (Fig. 2). New leaves rising up out of the tainted plants are smaller with wavy leaf lamina and yellow leaf edges (Nelson, 2004). Leaves created are logically shorter, limited, and weak in surface; these group together at the best and henceforth give the name of the illness (Thomas, Iskra-Caruana, and Jones, 1994). Vulnerable cultivars contaminated at a youthful stage and the suckers rising up out of tainted stools are seriously hindered. Extremely tainted plants for the most part won't natural product, yet in the event that organic product is delivered, the hands and fingers are probably going to be mutilated and turned (Nelson, 2004). At times, bracts of male bloom buds swing to a verdant structure and display dim green dabs and streaks (Thomas et al., 1994). Rising suckers from tainted plants show extreme indications. Plants tainted at a later stage don't regularly demonstrate leaf indications, however dull green streaks can be seen on the tips of the bracts. Developing suckers from such plants ordinarily display moderate indications or none. The hatching time frame from the season of infection immunization to manifestation articulation changes somewhere in the range of 19 and 125 days, contingent upon the phase of contamination, cultivar, and climate (Almeida, 2008). The most limited time for the analysis of BBTV utilizing polymerase chain response (PCR) was 15 days after contamination (Hooks et al., 2008). In any case, suckers rising up out of the contaminated stools demonstrate side effects from the season of rise.

1.2 BBTV diversity

Different BBTV segregates described so far around the globe have >85% homology (Banerjee et al., 2014). Despite the fact that ABTV is likewise known to cause manifestations like those of BBTV in Musa spp., it is less pervasive and perceived so far just in the Philippines and Malaysia, principally tainting abaca (Sharman et al., 2008). By and large, the hereditary assorted variety of BBTV segregates inside the nations is low [see thinks about in India (Selvarajan et al., 2010; Vishnoi, Raj, and Prasad, 2009), Pakistan (Amin, Qazi, Mansoor, Ilyas, and Briddon, 2008), Africa (Adegbola et al., 2013; Kumar et al., 2011), and Oceania (Stainton et al., 2012)]. In any case, in India, moderately more prominent assorted variety for BBTV was seen in the north-eastern area (Banerjee et al., 2014), including the recognizable proof of another Babuvirus—Cardamom ragged diminutive person infection (CBDV)— in cardamom (Mandal, Shilpi, Barman, Mandal, and Varma, 2013) (Fig. 2). In view of the phylogenetic connections among the DNA-R segment arrangements, different BBTV disconnects were gathered into two unique genealogies: (I) the Pacific-Indian Oceans (PIO) gathering (some time ago South Pacific gathering) containing secludes in Africa, Australia, Hawaii, south Asia, Myanmar, and Tonga; and (ii) the South-East Asian (SEA) gathering (once in the past Asian gathering) involving detaches from China, Indonesia, Japan, the Philippines, Taiwan, and Vietnam (Banerjee et al., 2014; Karan, Harding, and Dale.

2. Banana streak disease

2.1 Disease etiology and biology

BSV causes chlorosis of leafs and is recognized as the most widely dispersed virus infecting banana & plantain worldover. The disease was first identified in Nieky Valley on Ivory Coast in 1958 (Lockhart & Jones, 2000) and later, in year 1964, severe BSV chlorotic disease was reported in Gros Michel variety Musa acuminata (AAA) banana cultivar. Lockhart purified virus particles from field-grown Cavendish banana in Morocco, approving virus as the cause of disease. Currently available data on the disease signal a complex of diverse BSVs, each causing same disease.

Banana streak V are pararetroviruses falling in genus Badnavirus, family Caulimoviridae. The virus particles are bacilli-shaped (120–150 long & 30 nm wide), double-stranded non-covalently closed circular DNA (double stranded DNA) genome which is about 7.2–7.8 kb long it uses a virus-derived reverse transcriptase to replicate. (Harper and Hull 1998) defined viral genome structure and named it Banana streak Obino l'Ewai virus (BSOLV). The virus has three ORFs on sense strand (King et al., 2012). ORF1 and ORF2 encode two small proteins with function remain unclear of 20.8 and 14.5 kDa. ORF3 is a large poly-protein of 220 kilodaltons encoding nearly four proteins, including a putative coat protein, cell-to-cell movement protein, an aspartic protease enzyme and a viral replicase containing of RT and RNase H

domains (Harper & Hull, 1998; King et al., 2012). This poly-protein is sliced into functional protiens by the aspartic protease following translation. In distinction to other retroviruses, BSV does not code integrase, nor do it need integration into host genome to replicate.

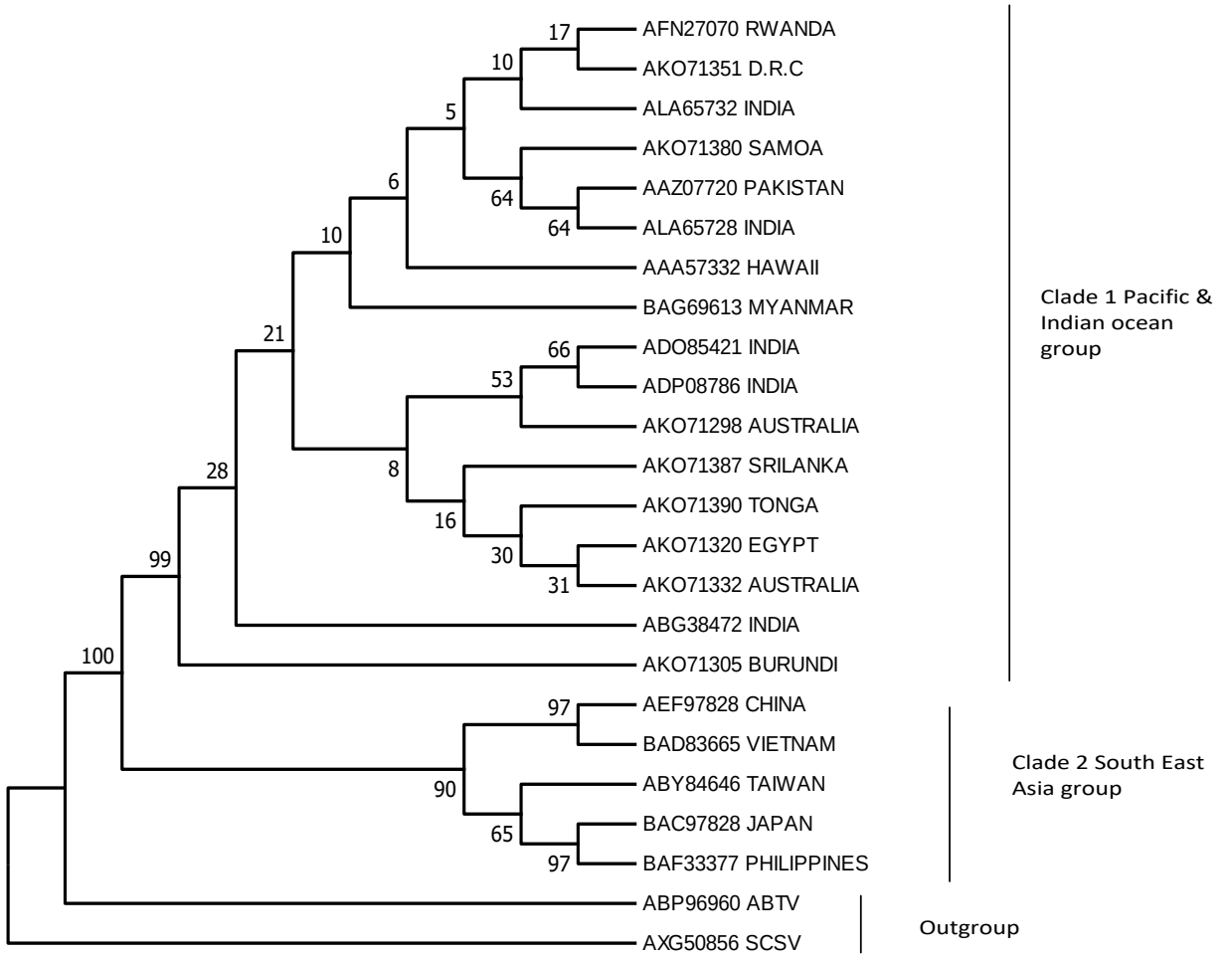

Fig. 2: The phylogenetic evolutionary history of BBTV inferred using Neighbor-Joining method based on the ClustalW alignment of the 240 base pairs of Banana bunchy top virus (BBTV) DNA-R master replication-protein of various BBTV isolates. Country of origin of the virus isolates and corresponding NCBI GenBank accession numbers are listed. Boot- strap values (1000 replications) are shown as percentages at the branch points. Abaca bunchy top virus (ABTV) and subterranean clover stunt virus (SCSV) are included as outgroup species using the Neighbor-Joining method. Phylogenetic analyses were conducted in MEGA7 (Tamura, Dudley, Nei, & Kumar, 2007).

Two contagious forms of BSV exist: (i) The episomal form of BSV resulting in cells or infection in plants following transmission by mealybugs and (ii) endogenous forms which are endogenous dna sequences of BSV (eBSV) integrated within the banana B genome (Musa balbisiana). Physical stresses have conferred to induce de-novo viral particles from eBSV (Cote et al., 2010), possibly by intra-strand homologous recombination (HR)

(Chabannes & Iskra-Caruana, 2013; Iskra-Caruana et al, 2010). Together infectious particles and episomal virus from eBSV give rise to complete plant infection (Harper, Hart, Moult, & Hull, 2004; Iskra-Caruana et al., 2010). BSV particles from both origins can be spread by mealybugs (Dahal et al., 2000; Kubiriba,et al., 2001)

2.2 BSV diversity

The variety Badnavirus is both the most perplexing and the most broadened class inside the family Caulimoviridae, with no less than three noteworthy clades (Harper et al., 2004, 2005; King et al., 2012). A last phylogeny of BSVs has been set up to clear up whether halfway successions dispersed over the three primary clades of the sort Badnavirus compare to episomal infections with or without an endogenous partner (Gayral and Iskra-Caruana, 2009; Iskra-Caruana et al., 2014). Clades 1 and 3 are devoted to BSV and Clade 2 collects most Musa endogenous badnavirus sequences, with no episomal counterpart reported so far Chabannes et al., in preparation. Clade 1 consist of four BSV species having an eBSV comparable in the B genome (BSIMV, BSGFV, BSOLV, and BSMYV); Clade 3 groups only BSV species of Uganda (Fig 3).

2.0 Banana bract mosaic

2.1 Disease symptoms and spread

BBrMV noted on a few banana cultivars in the Philippines in 1979 and thought to be unique in relation to all other perceived infections of banana (Magnaye and Espino 1990; Rodoni et al. 1997). Event of the infection was found in a couple of different nations in Asia and the South Pacific, including Samoa India, , Thailand, Sri Lanka, and Vietnam (Diekmann and Putter, 1996; Rodoni et al., 1997; Rodoni, 1999). In Latin America, BBrMV event was first detailed in Colombia (Alarcon et al., 2006, refered to in Quito-Avila et al., 2013. Kenyon et al. (1997) detailed up to 40 % yield misfortune on Mindanao island of the Philippines. High dismissal rate of attractive natural product was related with the higher sickness rate which causes distorted fingers. In Hawaii (USA), BBrMV was recognized in decorative ginger plants (Alpinia purpurata) however not in Musa (Wang et al. 2010).

BBrMV causes trademark shaft molded, purplish streaks on bracts, pseudostems, midribs, peduncles, and even organic products (Rodoni et al., 1997; Selvarajan and Jeyabaskaran, 2006; Bunches from tainted plants curiously contain a long or short peduncle BBrMV have a place with the variety Potyvirus and family Potyviridae. Flexuous filamentous infection particles estimating 750 × 11 nm have been recognized (Bateson and Dale 1995). Cleansed virions contain a noteworthy coat protein of 38– 39 kDa. The infection genome comprises of single-stranded positive-sense RNA of 1197 nucleotides in length barring the 3'- terminal poly(A) tail. The viral genome contains an ordinary extensive ORF of 9378 nucleotides coding for a polyprotein of 3125 amino acids with 9 protease cleavage destinations, conceivably yielding 10 developed utilitarian proteins that have themes saved among homologous proteins of different potyviruses.

BBrMV diversity

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Conclsions

Banana falls under 10 most critical and high-need nourishment crops which give staple sustenance, nourishment and wage for the a large number of banana ranchers around the world. That is the reason requests of banana at worldwide level have been raised as uncovered by world banana creation expanding for the most recent decade. Besides, banana organic products are especially esteemed in the tropics since they yield regardless of the seasons. Infections are viewed as a noteworthy imperative to

banana estate as they cause yield decreases as well as a noteworthy confinement to the trading of germplasm. Among infections that contaminate banana, BBTV and BBrMV and BSV are huge dangers to banana creation. Of these, BSV is more broadly spread worldwide than BBTV, however the last is so far the most financially harming infection. Alongwith these few minor infection like Abaca bunchy best (ABTV) Abaca mosaic, Banana mosaic, Banana gentle mosaic and Banana infection X are likewise answered to contaminate Banana (Kumar et al 2014)

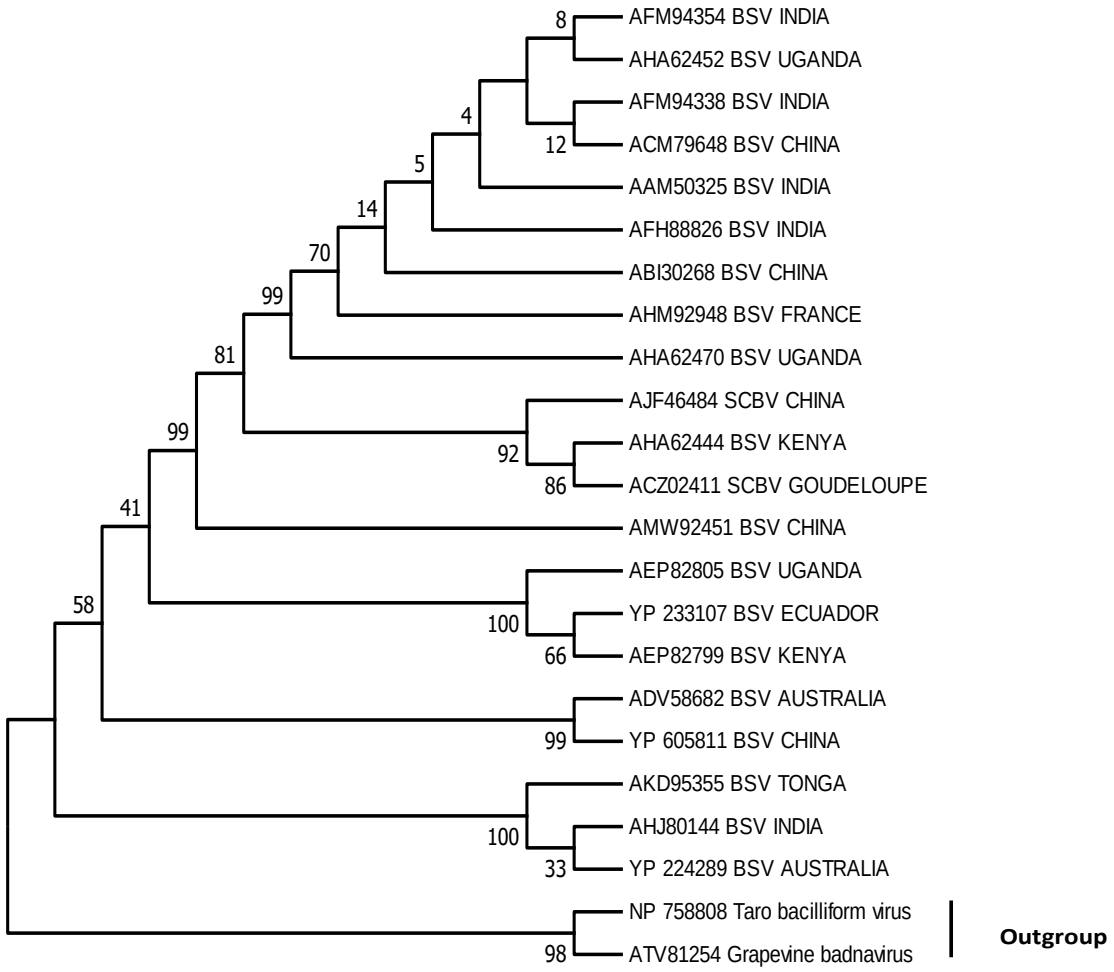

Fig. 3: Maximum likelihood phylogeny of badnavirus sequences based on alignment of a 230-bp fragment of the RT/RNase H viral region. Bootstrap values of 1000 replicates are given when >50%. Taro bacilliform virus (TABV) and grapevine badnavirus (GVCV) are given as outgroups. The GenBank accession numbers of sequences are given in parenthesis. Sugarcane bacilliform virus (SCBV) are also included

Tissue culture procedures have been utilized to create infection free planting material and utilizing, strict direction on development of tainted planting materials, and improvement of transgenic safe cultivars to these infections are the best way to control these infection sicknesses in banana. Be that as it may, all banana infections can't be killed through tissue culture and conventional reproducing in light of the fact that the vast majority of the industrially imperative cultivars are (tetraploid) for the most part sterile and create organic product parthenocarpally.

The advancement transgenics with enhanced infection opposition can possibly fuse in banana cultivars and at present picking up need. RNAi-based

opposition which is effectively utilized for transgenic control of a few plant infections (Sudarshana et al. 2007, Patil et al. 2016) has likewise been utilized for transgenic control of BBTV in banana. The International Network for the Improvement of Banana and Plantain (INIBAP) is a division of the International Plant Genetic Resources Institute (IPGRI) and has moved toward becoming as its order with the mission to enhance the efficiency and yield security of banana and plantain.

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