



Distribution of Geminivirus in the Indian Subcontinent

Bhavin S. Bhatt, Fenisha D. Chahwala, Sangeeta, B. K. Yadav, B. Singh, and Achuit K. Singh

Abstract

Viral diseases cause havoc on crop yield, both qualitatively and quantitatively. *Geminiviridae* is the largest family of plant viruses and constitutes an important group of plant pathogens with genomes of ssDNA. Geminiviruses are characterized by particle morphology of twinned incomplete icosahedra. Geminiviruses derived their name from unique structure and geometry of virus particles, where two icosahedra are joined together. Family *Geminiviridae* is further classified into nine different genera on the basis of nature of genome, host plant infection, and vector requirements for disease transmission. These viruses cause significant yield loss to economically important plants. Disease outbreaks on cotton, cassava, tomato, and other important horticultural plants were reported to have major crop loss due to virus infection. Further, molecular interactions and presence of satellite molecules enable virus particles to break innate immunity of plants and revoke disease outbreaks. Also introduction of exotic species, transfer of plant materials across continents, and vector migration are also important factors which contribute to widespread distribution of geminiviruses. India and the Indian subcontinent have experienced and are experiencing major loss due to infection by geminiviruses. Novel recombinant viruses, host switching, and newer satellite molecules continue to be reported from the Indian subcontinent. Tropical humid atmosphere and crop diversity are major factor for vector multiplication and hence virus transmission too. This chapter reviews the major geminiviral crop infections in the Indian subcontinent.

B. S. Bhatt

Shree Ramkrishna Institute of Computer Education and Applied Sciences, Surat, India

F. D. Chahwala · Sangeeta · B. K. Yadav

School of Life Sciences, Central University of Gujarat, Sector-30, Gandhinagar, India

B. Singh · A. K. Singh (✉)

Crop Improvement Division, ICAR—Indian Institute of Vegetable Research, Varanasi, India

1 Introduction

Plants growing in the natural environment are sessile in nature and can be attacked continuously by omnipresent microorganisms, namely viruses, bacteria, and fungi. Plant viruses are intracellular parasites, which need the vector for movement from one plant to another plant. It directly affects the economy by reducing the production of plant products. Such losses due to viral diseases impact heavily on crop production and are one of the major thrust for the detailed study of plant viruses (Teng 1985). Chemically, viruses are nucleoprotein in nature, where viruses' genome is encapsidated in protein shell. Viral genome (DNA or RNA) encoded proteins modify host cellular machinery for their replication, movement and transmission efficiently. Small genome size and ability to multiply within host cell have made virus particles extremely dynamic and diverse. On the other hand, possessing a small genome and restricted host range made virus particles a model organism to understand the concepts and principles of molecular biology.

Structurally, plant viruses resemble other viruses. The viral nucleic acid is encapsidated in the closed shell or tube-like structure, made of protein, termed as the capsid. Plant viruses are intracellular parasites, which need the vector for movement from one plant to another plant. It directly affects the economy by reducing production of plant products, so in these cases, we can say it is the most dangerous guest of the host plant. Viruses are responsible for causing around the US \$30 billion loss in the yield every year (Valérie Nicaise 2014). According to *International Committee for Taxonomy of Viruses* (ICTV), there are around 49 families and 79 genera of plant viruses which have been discovered and reported to date.

2 Family *Geminiviridae*

Geminivirus constitutes an important group of plant pathogens with the genome of ssDNA. Geminivirus genome comprises a closed circular ssDNA of 2.6 kb–3.0 kb size with an intergenic region which has geminivirus signature nonanucleotide sequence that is recognition and initiation site for viral DNA replication. Geminivirus derived its name from unique structure and geometry of virus particles that look like small balls stuck together. A single molecule of covalently closed circular single-stranded viral sense DNA is encapsidated in each paired particle. This family is the most devastating to plants and is responsible for causing significant loss, especially in the tropical and subtropical regions.

Family *Geminiviridae* constitutes the largest number of viruses. Biological, genome partition and vector requirement for transmission have made the base for the partition of Geminivirus into nine different genera (Varsani et al. 2014, 2017).

3 Geminiviruses in Indian Subcontinent

The *Geminiviridae* family has been divided on basis of genome organization, host range and insect vector into nine genera: *Mastrevirus*, *Curtovirus*, *Topocuvirus*, *Begomovirus*, *Becurtovirus*, *Eragrovirus*, *Turncurtovirus*, *Grablovirus* and *Capulavirus* (Brown et. al. 2012) (Table 1).

Among nine genera of family *Geminiviridae*, prevalence of three genera viz. *Capulavirus*, *Mastrevirus* and *Begomovirus* is widespread in the Indian subcontinent. Due to tropical humid climate, vector population of these viruses is widespread in this area and hence reports of disease occurrence and outbreaks are available from the different parts of the Indian subcontinent. Amongst these three genera, occurrence of *begomovirus* is wide spread in the Indian subcontinent.

Table 1 Characteristics of genera of family *Geminiviridae*

Genus	Type Species	Acronym	Genome	Host range	Insect vector
<i>Becurtovirus</i>	<i>Beet curly top Iran virus</i>	BCTIV	Monopartite	Dicotyledonous plants	Leafhopper
<i>Begomovirus</i>	Bean golden mosaic virus	BGMV	Monopartite and Bipartite	Dicotyledonous plants	Whitefly
<i>Capulavirus</i>	caput-medusae latent virus	CMLV	Monopartite	Dicotyledonous plants	Aphid
<i>Curtovirus</i>	<i>Beet curly top virus</i>	BCTV	Monopartite	Dicotyledonous plants	Leafhopper
<i>Eragrovirus</i>	<i>Eragrostis curvula streak virus</i>	ECSV	Monopartite	Monocotyledonous plants	–
<i>Grablovirus</i>	Grapevine red-blotch associated virus	GRBV	Monopartite	Dicotyledonous plants	Treehopper
<i>Mastrevirus</i>	Maize streak virus	MSV	Monopartite	Mostly monocotyledonous plants (except for tobacco yellow dwarf virus and bean yellow dwarf virus which infect dicots).	Leafhopper
<i>Topocuvirus</i>	Tomato pseudo-curly top virus	TPCTV	Monopartite	Dicotyledonous plants	Treehopper
<i>Turncurtovirus</i>	<i>Turnip curly top virus</i>	TCTV	Monopartite	Dicotyledonous plants	Leafhopper

A large number of begomoviruses are continuously reported from different geographical regions. These begomoviruses either have newer more virulent features or they may have an infection on newer host species. Thus, careful examination on occurrence and spreading of diseases on continuous basis is vital need to design timely and efficient measures to manage viral infections.

The subsequent segments of this chapter highlight our current knowledge of occurrence of geminiviruses in the Indian subcontinent, their interaction and virulent strategies and major symptoms of the virus infection.

4 Genus *Capulavirus* (Type Species: Caput-Medusae Latent Virus, CMLV)

4.1 Introduction

Nowadays, high-throughput technologies for nucleotide sequencing methods are used to discover previously unknown viruses. *Capulavirus* genus name was derived from the virus *caput-medusae latent virus*. The viruses belonging to *Capulavirus* genus are transmitted by aphids. Four species are present in this genus: Alfalfa leaf curl virus, Euphorbia caput-medusae latent virus, French bean severe leaf curl virus (FbSLCV), and Plantago lanceolata latent virus (Varsani et al. 2017).

4.2 Important Capulavirus in Indian Subcontinent

4.2.1 French Bean Severe Leaf Curl Virus

Out of four virus species reported for genus *Capulavirus*, only one virus, French bean Severe Leaf Curl Virus (FbSLCV) reported from India was associated with severe leaf curl disease of French bean. Furthermore, Bernardo et al. (2016) reported virus *Caput-medusae latent virus* from South Africa which shares the maximum identity of 78% with this FbSLCV isolate.

5 Genus *Mastrevirus* (Type Species: Maize Streak Virus, MSV)

5.1 Introduction

Maize streak disease was first observed on maize in 1901 in South Africa in Hawaii region. Mastreviruses are leafhopper-transmitted monopartite viruses infecting monocots. Well-characterized subgroup I pathogens include maize streak virus (MSV) and wheat dwarf virus (WDV). Two other members of this genus, TYDV (Tomato yellow dwarf virus) and BeYDV (Bean yellow dwarf virus), also infect dicotyledonous species (Kraberger et al. 2013). They are generally monopartite in nature where sole DNA-A component is responsible for causing diseases. Recently,

Kumar et al. (2012a, b, c) for the first time proved association of two alphasatellite species, a Cotton leaf curl Multan alphasatellite (CLCuMA) and a Guar leaf curl alphasatellite (GLCuA), with *wheat dwarf India virus* (WDIV). Mastrevirus infection was first confirmed in 1992 in India (Horn et al. 1993). Mastrevirus infection was shown on sugarcane, wheat, and chickpea from various parts of the Indian subcontinent (Horn et al. 1993, 1994; Kumar et al. 2012b; Haider et al. 2011) (Table 2). However, the presence of Mastrevirus was shown on Bajra, that is, Bajra streak virus in 1972, but it is not yet confirmed and is designated as unassigned species.

5.2 Important Mastreviruses of the Indian Subcontinent

5.2.1 Wheat Dwarf India Virus

A very first time maize streak disease was observed in 1972 in India (Seth et al. 1972). During 2010 and 2011, wheat plants were found affected by dwarf diseases across the country. Plants were showing symptoms such as sterile spikes, yellowing of leaves and dwarfism. The presence of *Psammotettix* sp. (Leafhopper) in affected fields was suspected to be that of geminivirus. On the basis of PCR and RT-PCR studies, it was confirmed that there was absence of BYDV-MAV and BYDV-PAV in infected samples. However, association of a new species of mastrevirus named wheat dwarf India virus was identified (Kumar et al. 2012b). Agro-inoculation of wheat seedlings by infectious clones of virus results in the dwarfism of wheat plants, while mock inoculated control wheat seedlings were healthy and tall. Yet, typical streak phenotype was not observed in any of the inoculated wheat plants. Wheat dwarf India virus was also reported from Bihar, Maharashtra, Uttar Pradesh, Rajasthan, and Madhya Pradesh, which results in significant reduction in production of wheat (Kumar et al. 2012a, b, c, Kumar et al. 2014a, b).

There are reports that the association of begomovirus satellite molecules with mastrevirus increases severity in plants. During 2014, there was a report on the association of two alphasatellites and one betasatellite molecule with *wheat dwarf India virus* (Kumar et al. 2014a, b). This was the first report on the association of satellite molecule with WDV. Guar leaf curl alphasatellite and Cotton leaf curl Multan betasatellite were associated with WDV. Ageratum yellow leaf curl betasatellite is also associated with WDV. The satellite molecule tends to increase WDV accumulation in plant and suppresses the small RNAs' accumulation related to diseases (Kumar et al. 2014a, b). One study showed the co-infection of mastrevirus and begomovirus on cotton and *Xanthium strumarium*. In this way, WDV in association with alpha and betasatellites tends to cause severe symptoms in wheat.

5.2.2 Chickpea Chlorotic Dwarf Virus

Mastrevirus infection on dicot plant has been distributed in Asia, Africa, and Australia (Nahid et al. 2008). It infects important dicots (Kraberger et al. 2013). Horn et al. (1993) first reported the chickpea chlorotic dwarf virus (CpCDV) in

Table 2 List of major geminiviruses associated with various crops and weeds in the Indian subcontinent

Genus	Species	Abbreviation	Host	Country of origin
<i>Mastrevirus</i>	<i>Chickpea chlorotic dwarf virus</i>	CpCDV-C PK-Fai6-06]	Chickpea	Pakistan
	<i>Wheat dwarf India virus</i>	CpCDV-D PK-BGR-08]	Chickpea	Pakistan
<i>Capulavirus</i>	<i>French bean severe leaf curl virus</i>	WDIV-[IN-10]	Wheat	India
	<i>Ageratum enation virus</i>	F6LSV-[IN-10]	French bean	India
<i>Begonovirus</i>		AEV-IN IN-Kan-08]	Ageratum	India
		AEV-NP NP-99]	Ageratum	Nepal
		AEV-UP [IN-UP-Ag 10-10]	Ageratum	India
		AYVSLV-[LK-99]	Ageratum	Sri Lanka
	<i>Bhendi yellow vein Bhubaneswar virus</i>	BYVBhV-[IN-Ort-03]	Bhendi	India
	<i>Bhendi yellow vein Haryana virus</i>	BYVMV-Har IN-Har-07]	Bhendi	India
	<i>Bhendi yellow vein mosaic virus</i>	BYVMV-IN IN-mad]	Bhendi	India
		BYVMV-[IN-Mah-NOL751]	Bhendi	India
		BYVMV-[PK-Fai201-95]	Bhendi	Pakistan
		BYVMV-TN IN-Coi4-04]	Bhendi	India
		BYVMV-Tha IN-Tha-05]	Bhendi	India
	<i>Catharanthus yellow mosaic virus</i>	CaYMV-[PK-Jst-DR151]	Catharanthus	Pakistan
<i>Chilli leaf curl India virus</i>	ChiLCINV-[IN-08]	Chilli	India	
<i>Chilli leaf curl Kampur virus</i>	ChiLCKaV-[IN-Kam-08]	Chilli	India	
<i>Chilli leaf curl Vellamad virus</i>	ChiLCVV-[IN-Vel-08]	Chilli	India	
<i>Chilli leaf curl virus</i>	ChiLCV-PK PK-Mul-98]	Chilli	India	
	ChiLCV-IN IN-Amr-Pap-09]	Papaya	Pakistan	
	ChiLCV-chi IN-chi-05]	Chilli	India	
	ChiLCV BD-Gaz]	Chilli	India	
	ChiLCV-JO IN-Pon-Hib-07]	Hibiscus	India	
	ChiLCV-Kha PK-Kha-04]	Chilli	Pakistan	

<i>Clerodendron yellow mosaic virus</i>	CYMV-[IN-Iari-06]		India
<i>Corchorus golden mosaic virus</i>	CoGMV-[IN-Bah-08]	Corchorus	India
<i>Corchorus yellow vein mosaic virus</i>	CoYV-[IN-Mah-CEA8-11]	Corchorus	India
<i>Cotton leaf curl Allahabad virus</i>	CLCuAIV-A[PK-Ala804a-96]	Cotton	Pakistan
	CLCuAIV-ha[IN-Kar-OY77-0kr-05]	Okra	India
	CLCuAIV-Ka[IN-Kar-OY81B-0kr-05]	Okra	India
	CLCuAIV-loj[PK-Mul-Lob-06]	Cotton	Pakistan
	CLCuAIV-mu[PK-Mul-Pun-06]	Cotton	Pakistan
<i>Cotton leaf curl Bangalore virus</i>	CLCuBaV-[IN-Ban-04]	Cotton	India
<i>Cotton leaf curl Kokhran virus</i>	CLCuKoV-Ko[PK-Man806b-96]	Cotton	Pakistan
	CLCuKoV-Buj[PK-Veh-06]	Cotton	Pakistan
	CLCuKoV-La[PK-Lay-11]	Cotton	Pakistan
	CLCuKoV-Lu[IN-Luc-Ct-Beal0]	Cyamopsis	India
	CLCuKoV-Sha[PK-Sha-05]	Cotton	Pakistan
<i>Cotton leaf curl Multan virus</i>	CLCuMuV-Dar[PK-Mul-Dar1-06]	Cotton	Pakistan
	CLCuMuV-Faj[PK-Yaz62-95]	Cotton	Pakistan
	CLCuMuV-Hib[IN-Hib1-11]	Hibiscus	India
	CLCuMuV-his[PK-Mul-H65-1-97]	Hibiscus	Pakistan
	CLCuMuV-PK[PK-Mul-06]	Cotton	Pakistan
	CLCuMuV-Ra[IN-Sri-94]	Cotton	India
<i>Croton yellow vein mosaic virus</i>	CroYVMV-[IN]	Croton	India
<i>Dolichos yellow mosaic virus</i>	DoYMV-[BD-Gaz]	Dolichos	Bangladesh
<i>French bean leaf curl virus</i>	FbLCV-[IN-Kan-11]	French bean	India-
<i>Hemidesmus yellow mosaic virus</i>	HemYMV-[IN-Tir-H1-12]	Hemidesmus	India
<i>Hollyhock leaf curl virus</i>	HoLCV-[PK-Fai-20-4-06]	Hollyhock	Pakistan
<i>Horsegram yellow mosaic virus</i>	HgYMV-[IN-Coj]	Horsegram	India
<i>Indian cassava mosaic virus</i>	ICMV-Jat[IN-Dha-08]	Cassava	India
	ICMV-Ker[IN-Ker2-02]	Cassava	India

(continued)

Table 2 (continued)

Genus	Species	Abbreviation	Host	Country of origin
<i>Jatropha leaf curl virus</i>	<i>Jatropha leaf curl virus</i>	JLCuV-ND[JIN-ND-07]	Jatropha	India
		JLCuV-Gu[JIN-Guj-09]	Jatropha	India
		JMINV-[JIN-Luc-09]	Jatropha	India
		JYMV-[JIN-Kat-08]	Jatropha	India
		MeYVMBaV-[JIN-Bah-07]	Mesta	India
		MeYVMV-and[JIN-Ama27-08]	Mesta	India
		MeYVMV-[PK-CM-09]	Mesta	Pakistan
		MeYVMV-ben[JIN-Bar-06]	Mesta	India
		MYMIV-[JIN-ND-Bg3-91]	Mungbean	India
		MYMV-[TH-Mg2]	Mungbean	Thailand
		OELCuV-[JIN-SonEL10-06]	Okra	India
		PaLCrV-[JIN-Pan-08]	Papaya	India
		PaLCuV-Cir[JIN-PaND13-12]	Papaya	India
		PaLCuV-Asi[PK-Luc-as-11]	Papaya	Pakistan
		PaLCuV-A[JIN-WB-Cr-Cro-08]	Croton	India
PaLCuV-Amal[PK-Luc-am-11]	Amaranthus	Pakistan		
PaLCuV-Luc[JIN-Luc]	Papaya	India		
PaLCuV-Sik[jin-Sik-Cal-10]	Calotropis	India		
PaLCuV-Rh[PK-Mia-Rc-07]	Rhynchosia	Pakistan		
PaLCuV-soy[JIN-Luc-Soy-11]	Soybean	India		
PaLCuV-PK[PK-Cot-02]	Cotton	Pakistan		
PaLCuV-Pun[PK-Pun-Cro-06]	Croton	Pakistan		
PaLCuV-IN[jin-pat-Rad-09]	Radish	India		
PaLCuV-Lah[PK-Lah-HYDNA-A1c-06]	Hollyhock	Pakistan		
PaLCuV-Tob[JIN-Luc-Nic-10]	Nicotiana	India		
PaLCuV-tom[JIN-CTM-tom-06]	Tomato			

<i>Pedilanthus leaf curl virus</i>	PeLCV-[PK-Mul-06]	Pedilanthus	Pakistan
	PeLCV-Eu[PK-RYK1-To-04]	Tomato	Pakistan
	PeLCV-Sb[PK-NS-Sb-09]	Soybean	Pakistan
<i>Pepper leaf curl Bangladesh virus</i>	PepLCBV-BD[BD-Bog-99]	Pepper	Bangladesh
	PepLCBV-PK[PK-Kha-04]	Pepper	Pakistan
	PepLCBV-IN[IN-Coi-08]	Pepper	India
	PepLCBV-[PK-Lah-04]	Pepper	Pakistan
	PepLCLaV-[IN-Luc-11]	Pepper	India
<i>Pepper leaf curl Lahore virus</i>	RaLCuV-[IN-Var-03]	Radish	India
<i>Radish leaf curl virus</i>	RaLCuV-to[PK-Bih-To-09]	Tobacco	Pakistan
<i>Rhynchosia yellow mosaic India virus</i>	RhYMIV-[IN-Thi-JRH1-09]	Rhynchosia	India
	RhYMV-[PK-Lah33-07]	Rhynchosia	Pakistan
<i>Rose leaf curl virus</i>	RoLCuV-[IN-Raj-Sik-AS24-14]	Rose	India
<i>Spinach yellow vein virus</i>	SpiYVV-[IN-Sik-AS22]	Spinach	India
<i>Sri Lankan cassava mosaic virus</i>	SLCMV-LK[JK-Col-98]	Cassava	Sri Lanka
	SLCMV-IN[IN-Adi-03]	Cassava	India
<i>Sunn hemp leaf distortion virus</i>	SHLDV-[IN-Bar-08]	Sunn hemp	India
<i>Tobacco leaf curl Pusa virus</i>	TbLCPuV-to[IN-Pus-09]	Tobacco	India
<i>Tomato leaf curl Bangalore virus</i>	ToLCBaV-A[IN-Ban1]	Tomato	India
	ToLCBaV-[IN-Hes-TC265-10]	Tomato	India
	ToLCBaV-B[IN-Ban5]	Tomato	India
	ToLCBaV-D[IN-KerII-05]	Tomato	India
	ToLCBaV-C[IN-Ban4-97]	Tomato	India
<i>Tomato leaf curl Bangladesh virus</i>	ToLCBV-[BD-BD2]	Tomato	Bangladesh
<i>Tomato leaf curl Gujarat virus</i>	ToLCCuV-[IN-Var-01]	Tomato	India
<i>Tomato leaf curl Joydebpur virus</i>	ToLCJV-[IN-Var-Caa-10]	Chilli	India
<i>Tomato leaf curl Karnataka virus</i>	ToLCKaV-ban[IN-Ban-93]	Tomato	India

(continued)

Table 2 (continued)

Genus	Species	Abbreviation	Host	Country of origin
	<i>Tomato leaf curl Kerala virus</i>	ToLCKeV-[IN-Ker3-07]	Tomato	India
	<i>Tomato leaf curl New Delhi virus</i>	ToLCNDV-[IN-ND-Svr-92]	Tomato	India
	<i>Tomato leaf curl New Delhi virus 2</i>	ToLCNDV2-[IN-IANDS1-11]	Tomato	India
	<i>Tomato leaf curl New Delhi virus 4</i>	ToLCNDV4-[IN-Jun-TC306-11]	Tomato	India
	<i>Tomato leaf curl Palampur virus</i>	ToLCPaIV-[IN-pal-047]	Tomato	India
	<i>Tomato leaf curl Patna virus</i>	ToLCPatV-[IN-Pat-08]	Tomato	India
	<i>Tomato leaf curl Pune virus</i>	ToLCPuV-[IN-Pun-05]	Tomato	India
	<i>Tomato leaf curl Rajasthan virus</i>	ToLCRaV-[IN-Raj-05]	Tomato	India
	<i>Tomato leaf curl Sri Lanka virus</i>	ToLCLKV-[LK-Ban-97]	Tomato	Sri Lanka
	<i>Velvet bean severe mosaic virus</i>	VBSMV-[IN-Luc-08]	Velvet bean	India
	<i>Vernonia yellow vein virus</i>	VeYVV-[IN-Mad-05]	Vernonia	India

Pakistan on Kabuli type. This disease was later reported from Haryana, Punjab, Gujarat, Andhra Pradesh, and Madhya Pradesh regions in India. It was responsible for causing significant loss up to 75–90% in the field (Kanakala et al. 2013a, b). They also reported that CpCDV is responsible for stunt diseases in chickpea. CpCDV is responsible for causing symptoms in Kabuli- as well as Desi-type chickpea. The infected plants displayed symptoms like stunting, phloem browning, internode shortening, and leaf reddening in Desi-type, whereas leaf yellowing happens in Kabuli type. During field observation, different symptoms appeared at different times in plants like the initiation of reddening followed by discoloration and small leave phenotype after 45 days resulting in drying rot-like symptoms at the final stage (Kanakala et al. 2013a, b).

Orosius orientalis (leafhopper) is responsible for transmitting CpCDV in different families like *Solanaceae*, *Chenopodiaceae*, and *Leguminosae*. More recently, it also infected the *Capsicum annum*. An isolate of CpCDV from India shares a maximum nucleotide sequence identity with an CpCDV isolate from Pakistan. Initially, the agroinfected plants display symptoms such as small leaves, yellowing of terminal leaf and stunting of plants and later, they died before flowering. Constructed clones also caused symptoms on *N. benthamiana*, *N. glutinosa*, *N. tabacum*, *sesame*, soybean, black gram, mustard, French bean, and tomato (Kanakala et al. 2013a). There is no association of any alphasatellite or betasatellite molecule with CpCDV.

Recently, chickpea chlorotic dwarf virus was reported from spinach in natural field condition from Pakistan along with alpha- and betasatellites. Spinach is a very common vegetable crop. Presence of virus in symptomatic suspected leaves was confirmed by PCR amplification, and virus amplification was done by rolling circle replication (RCA) method. Sequencing analysis confirmed the presence of chickpea chlorotic virus in spinach. Apart from spinach, CpCDV infect many other dicot species, e.g., pepper (Akhtar et al. 2014), tomato (Zia-Ur-Rehman et al. 2015), cucumber (Hameed et al. 2017), cotton (Manzoor et al. 2014), and okra (Zia-Ur-Rehman et al. 2017).

5.2.3 Sugarcane Streak Virus

Sugarcane, the most important cash crop in Pakistan, was affected with geminivirus during 2012. PCR amplification studies revealed that Sugarcane maize streak virus was responsible for causing a significant loss in the field. Coat protein of sugarcane maize streak virus showed maximum identity with Mauritius isolate, Reunion isolate, and Zimbabwe SSV isolate. So, it was remarked as the same variants of the virus. This was the first report of mastrevirus infection sugarcane in Pakistan.

6 Genus *Begomovirus* (Type Species: Bean Golden Mosaic Virus, BGMV)

6.1 Introduction

Begomovirus is the largest genus in the family, *Geminiviridae*. Monopartite begomoviruses carry one genomic component, termed as DNA-A, while bipartite geminivirus possesses two genomic components, DNA-A and DNA-B. DNA-A component encodes for major proteins for virus replication and multiplication inside the host cell, while DNA-B cares for intra- and intercellular movement of virus particles (Brown et al. 2012; Hanley-Bowdoin et al. 2013). In the case of the bipartite genome, both genome components are essential for efficient disease transmission and systemic infection (Evans and Jeske 1993). Some of the monopartite geminiviruses are also associated with additional circular ssDNA molecules, such as betasatellite or alphasatellite, which are nearly half the size of DNA-A (Mansoor et al. 1999; Kumar et al. 2015, 2017).

6.2 Important Crops Affected by Begomovirus in the Indian Subcontinent

6.2.1 Tomato

Similar to other begomoviruses, tomato-infecting begomoviruses are also transmitted by an insect vector, white fly (*Bemisia tabaci* (*Gennadius*)). Lack of thick cuticle layer on tomato leaves, soft epidermal layer, fine hairs on the epidermis, and nutritionally rich leaf sap make tomato best-suited host for whitefly. Regarding the Indian subcontinent, ToLCV infection in tomato was reported by Vasudeva and Sam Raj for the first time in 1948 from the southern part of India (Vasudeva and Samraj 1948). Further, the disease was prevalent in tomato during the summer season in South India and autumn in North India (Saikia and Muniyappa 1986). So far, in the Indian subcontinent, 13 begomovirus species infecting tomato have been characterized, namely *Tomato leaf curl Bangalore virus* (ToLCBV), *Tomato leaf curl Gujarat virus* (ToLCGV), *Tomato leaf curl Karnataka virus* (ToLCKV), *Tomato leaf curl Kerala virus* (ToLCKeV), *Tomato leaf curl New Delhi virus* (ToLCNDV), *Tomato leaf curl Palampur virus* (ToLCPMV), *Tomato leaf curl Patna virus* (ToLCPaV), *Tomato leaf curl Pune virus* (ToLCPV), *Tomato leaf curl Ranchi virus* (ToLCRnV), *Tomato leaf curl Rajasthan virus* (ToLCRajV), *Tomato leaf curl Pakistan virus* (ToLCPkV), *Tomato leaf curl Sri Lanka virus* (ToLCSLV), and *Tomato leaf curl Bangladesh virus* (ToLCBDV) (Chatchawankanphanich and Maxwell 2002; Chakraborty et al. 2003; Kumar et al. 2008, 2016; Kumari et al. 2010; Pasumarthy et al. 2010). All these begomoviruses are monopartite except for ToLCNDV and ToLCPMV, whereas ToLCGV exists as both monopartite and bipartite nature. The primary host for ToLCV is tomato (*Solanum lycopersicum*). However, these begomoviruses are also recognized and infect more than 43 other plant species of families, such as *Cucurbitaceae*, *Solanaceae*, *Euphorbiaceae*, *Malvaceae*, and *Fabaceae* (Chigurupati et al. 2012).

6.2.2 Okra

Bhendi yellow vein mosaic virus (BYVMV) is one of the earliest reported begomovirus infecting okra; hence, most studies have been carried out on the BYVMV. BYVMV has been reported from different parts of the world but regarding the Indian subcontinent, the first report of BYVMV infection has been reported in 1924 from Mumbai, India (Kulkarni 1924), suggesting that India might be the origin of BYVMV. Later on, from a different part of India, BYVMV infection has been reported, but the incidence of the disease is frequently occurring in the southern part of India (Uppal et al. 1940; Verma 1955). BYVMV-infected okra plants showed vein enation, vein clearing, yellowing of mid veins, and typical mosaic symptoms of begomovirus infection. Reduced leaf size, fruit, and twisted fruit resulted in the significant loss of crop yield and in severe conditions crop yield loss is reported up to 96% (Pun and Doraiswamy 1999).

Molecular biology of BYVMV revealed the typical monopartite nature of begomovirus having a single component of circular single-stranded DNA of nearly 2.7 kb genome (Jose and Usha 2000). DNA- β of nearly 1.3 kb which encodes single protein β C1 is responsible for infectivity and symptom severity of the disease. In order to evaluate the role of DNA- β for disease severity, okra plants were agroinnoculated with BYVMV alone and BYVMV with its associated betasatellite molecule (BYVMB). Okra plants agroinnoculated with only BYVMV showed mild leaf curling symptoms. Whereas, okra plants agroinnoculated with BYVMV and BYVMB produced typical BYVMD symptoms of yellowing of veins (Jose and Usha 2003). These results clearly suggest an indispensable role of betasatellite in disease onset, progression, and severity. Although BYVMV is a typical monopartite whitefly-transmitted begomovirus having single genome component and associated betasatellite molecule but the association of DNA-B molecule with yellow vein mosaic disease of okra has been also reported from India (Venkataravanappa et al. 2013). Begomoviruses are very prone to undergo recombination and have a high rate of mutation. It replicates via rolling circle mode of replication with error-prone low fidelity DNA polymerase enzyme (Duffy et al. 2008; Duffy and Holmes 2009). The evolutionary analysis on BYVMV and associated betasatellite has revealed the ancestral relationship of BYVMV with cotton-infecting begomovirus. In mutation analysis study, the very high rate of nucleotide substitution in BYVMV (V1) and associated betasatellite (β C1) was observed indicating the mutation of BYVMV for host adaptation. Since cotton and okra belong to the same family of dicotyledonous plant group, there might be host adaptation of CLCuV for the evolution of BYVMV.

Okra enation leaf curl virus (OELCV) is another emerging monopartite begomovirus affecting okra production in India (Singh 1996). Almost in all parts of India, OELCV infection has been reported either from okra or other crops such as cotton and tomato. In Pakistan, okra enation leaf curl was reported in 1998 and was found to be one of the variants of begomovirus to cause cotton leaf curl epidemic during the 1990s (Zhou et al. 1998). The typical symptoms of OELCV infection are vein enation, curling of leaf blade and petiole, and stunted plant growth. In India, a geographical survey of begomovirus causing diseases in okra revealed the association of okra enation leaf curl betasatellite with okra enation leaf curl disease

(Krishnareddy et al. 2010). Intra-host infection enables OELCV with broad host range for evolutionary adaptation. Furthermore, infection of OELCV to intra-host cotton in Pakistan has been reported along with Cotton leaf curl Multan betasatellite and Cotton leaf curl Multan alphasatellite (Hameed et al. 2014). A study in Pakistan has shown the recombination between okra- and cotton (both crops belonging to *Malvaceae* family)-infecting begomoviruses resulting into the evolution of OELCV as a new species of virus (Serfraz et al. 2015). Bhendi yellow mosaic virus is the major parent of OELCV, which was not reported from Pakistan previously, and Cotton leaf curl Multan virus is the distant parent of OELCV.

Okra leaf curl virus (OLCV) is another monopartite begomovirus infecting okra. In the Indian subcontinent, OLCV, a potential pathogen of okra leaf curl disease, has been reported from Pakistan in 2001, and associated betasatellite was found to be involved in disease severity of okra (Mansoor et al. 2001). Alphasatellite is also found to be associated with okra leaf curl disease in Pakistan (Mansoor et al. 2003, 2006).

6.2.3 Legumes

Yellow mosaic diseases are a big constraint in crop productivity in the Indian subcontinent. *Fabaceae*, *Verbenaceae*, and *Malvaceae* families are the favorite host for yellow mosaic diseases. Mungbean yellow mosaic virus (MYMV), Horsegram yellow mosaic virus (HGYMV), and associated strains are causal agents for mosaic diseases. *Mungbean yellow mosaic virus*, *mungbean yellow mosaic India virus*, *Dolichos mosaic virus*, *Horsegram mosaic virus*, and *Rhynchosia yellow mosaic virus* are severely infecting agents.

Mungbean yellow mosaic virus and mungbean yellow mosaic India virus are the two major viruses infecting legume crops. Both viruses are isolated from India, Pakistan, and Sri Lanka. Interestingly, these viruses are restricted to the Indian subcontinent. Mungbean yellow mosaic virus “Indian” strain was first observed and reported in the late 1950s by Nariani (1960). It produces typical mosaic symptoms on leaves of infected plants and naturally transmitted by whitefly (Nene 1973). In addition to India, the virus is widely prevalent in the Indian subcontinent, Sri Lanka, Bangladesh, and Pakistan (Honda 1986). An epidemic of yellow mosaic disease of mungbean was also identified in Thailand in the 1980s (Honda et al. 1983). MYMIV infection is confined to Northern India, Pakistan, Nepal, Bangladesh, and Indonesia. Both viruses are transmitted by whitefly and mostly they are non-sap transmissible. Female whiteflies are a good transmitter of viruses compared to male whiteflies since females can retain virus up to 10 days compared to 3 days for male whiteflies. Disease occurrence through MYMIV infection is reported from Northern India, Pakistan, Nepal, Bangladesh, and Indonesia. While, MYMV infection is mostly restricted to Thailand, Vietnam, and Eastern Ghats and Deccan plateau of India (Islam et al. 2012; Tsai et al. 2013). MYMIV is important economically as it infects five major leguminous species, blackgram, mungbean, French bean, pigeonpea, and soybean, causing yield loss of about \$300 million annually (Varma et al. 1992). Natural infection of MYMV has been reported in *Dolichos* (Williams et al. 1968), urdbean (Ahmad and Harwood 1973), moth bean (Ahmad and Harwood 1973), mung bean (Nariani 1960), black gram (Vanitharani et al.

1996), French bean (Singh 1979), lima bean (Shahid et al. 2012), Horsegram, and pigeon pea (Biswas and Varma 2000).

MYMV and MYMIV produce yellow bright mosaic to golden bright mosaic symptoms on infected leaves. They produce a poor quality of seeds and fewer flowers. In French bean, it produces mosaic and downward leaf curling symptoms associated with stunted growth. Seed-borne nature of MYMV on black gram was first proved by Kothandaraman et al. (2016).

HgYMV was first reported by Williams et al. (1968) in India. HgYMV was found as the causal agent of yellow mosaic disease (YMD). The incidence of disease ranged from 60 to 100% in summer and early rainy season. YMD is characterized by yellow mosaic patches on leaves, reduced leaf size, and dwarfism in severely affected plants (Muniyappa et al. 1987). The occurrence of HgYMV was found limited to Southern India (Borah and Dasgupta 2012; Varma and Malathi 2003). HgYMV is reported to infect 15 plant species of 9 genera of *Fabaceae* family. This includes *Arachis hypogea* (Muniyappa and Veeresh 1984), *Cajanus cajan* (Muniyappa and Veeresh 1984), *Glycine max* (Muniyappa and Reddy 1976), *Dolichos biflorus* (Williams et al. 1968), *Phaseolus aconitifolius*, *Phaseolus aureus*, *Phaseolus mungo*, *Phaseolus vulgaris* and *Phaseolus lunatus* (Muniyappa and Reddy 1976), and *Phaseolus limensis* (Muniyappa and Veeresh 1984).

6.2.4 Chilli

Chilli leaf curl virus (ChLCV) is the most devastating agent for chilli production in the Indian subcontinent. India, Pakistan, and Bangladesh are majorly affected by ChLCV. ChLCV and associated strains, namely Chilli leaf curl Bangladesh virus and Pepper leaf curl Sri Lanka virus, are spread throughout the Indian subcontinent. Leaf curl disease on chilli was first recorded from Sri Lanka in 1939 and from India in 1930 (Senanayake et al. 2012; Husain 1932). But the authenticated first report was noted in 2007 from India (Senanayake et al. 2007). Chilli leaf curl virus showed symptoms of leaf curling, rolling of leaf, leaf curling, vein enation, stunting of leaf, and lower production and quality of fruits (Dhanraj and Seth 1968; Mishra et al. 1963). In this decade, chilli leaf curl virus is prevalent in central to south India. It showed prevalence in Maharashtra, Madhya Pradesh, and Andhra Pradesh. It causes about 90% yield loss in the infected field, whereas in Jodhpur, Rajasthan, chilli leaf curl diseases cause 14–100% loss in the field (Senanayake et al. 2012). *Chilli leaf curl virus*, *Chilli leaf curl India virus* (Saeed et al. 2017), *Chilli leaf curl Ahmedabad virus* (Bhatt et al. 2016), *Chilli leaf curl Vellanad virus* (Kumar et al. 2012a, b, c), *Chilli leaf curl Kanpur virus*, *Tomato leaf curl Joydebpur virus* (Shih et al. 2006), *Tomato leaf curl New Delhi virus* (Hussain et al. 2000), *Pepper leaf curl Bangladesh virus*, *Rhynchosia leaf curl virus*, and *Tomato leaf curl virus* are major begomoviruses infecting chilli in India (Kumar et al. 2012a, b, c, 2015).

An association of satellite molecules enhanced the severity of disease incidence in the field (Kumar et al. 2011). Approximately six satellite molecules are found from India recording the association with DNA-A component. Generally, chilli leaf curl virus is an old world monopartite begomovirus. Chilli leaf curl betasatellite, tomato leaf curl Joydebpur betasatellite, tomato leaf curl Bangladesh betasatellite, radish

leaf curl betasatellite, and tomato leaf curl Ranchi betasatellite are isolated with DNA-A component of chilli leaf curl virus. Among all these satellite molecules, tomato leaf curl Bangladesh is more prevalent and frequently involved with ChiLCV (Kumar et al. 2015). Many chilli-infecting isolates of begomoviruses are a combination of two or more begomoviruses. Apart from infection on chilli plants and on weed, they can also infect important vegetable crops, for example, tomato, bitter melon, eggplant, petunia, Mentha, and papaya (George et al. 2014; Saeed et al. 2014; Senanayake et al. 2012; Raj et al. 2008, 2010; Nehra and Gaur 2014).

6.2.5 Cassava

The first published record of the disease happened only in 1966 by Alagianaalingam and Ramakrishnan (1966). Later on, Malathi and Shrinivasaan reported severe cassava mosaic diseases in 1983 (Malathi and Sreenivasan 1983). In the Indian subcontinent, Indian cassava mosaic virus (ICMV) and its recombinant species, Sri Lanka cassava mosaic virus (SLCMV), are the most threatening species. Recently, cassava plants were infected with cassava mosaic virus in Ratnagiri, Reunion, Cambodia, etc. (Wang et al. 2015). Interestingly, India cassava mosaic virus and Sri Lanka cassava mosaic virus are restricted to the Indian subcontinent only.

Affected plants showed discoloration of pale green tissue to the mosaic pattern, stunted growth, and distorted curl leaves (Legg et al. 2015). For fulfillment of Koch's postulate, agrobacterium-based infection study was done on *N. clelandi* and *N. glutinosa*. Infected plants showed symptoms of stem swelling and leaf rolling. ICMV DNA-A alone can give expression of leaf curling by biolistic transfection. Studies showed that the SLCMV is more virulent compared to ICMV (Saunders et al. 2002). Cassava mosaic virus has wide host range. It can easily transmit to *Nicotiana*, *Nicandra physalodes*, and *Petunia hybrid*. Jose et al. (2008) did transreplication studies on *Solanaceae* family members among which 39 species developed symptoms upon infection with SLCMV. Infectivity studies of SLCMV were also done on *N. amplexicaulis*, *N. nudicaulis*, and *N. benavidesii*. These plants were easily infected by SLCMV (Jose A. et al. 2008). In natural condition, ICMV was also reported from bitter melon, jatropha, and mulberry (Rajinimala and Rabindran 2007; Sherry 2016; Aswathanaryana et al. 2007; Gao et al. 2010). There are reports of recombination events occurring between SLCMV and ICMV. When pseudo-recombination was done between ICMV DNA-A and SLCMV DNA-A, recombinant molecule induced significant disease symptoms in *N. benthamiana* (Rothenstein et al. 2006), whereas pseudo-recombinants of ACMV and ICMV were not too infectious to induce disease symptoms in *N. benthamiana*.

6.2.6 Cucurbits

Yellow vein mosaic disease on cucurbits is a serious threat to its cultivation (Maruthi et al. 2007). Begomovirus infects many cucurbits from different parts of the world. Watermelon, squash, pumpkin, chryote, cucumber, etc., are the host of begomovirus (Sohrab et al. 2006). They mostly belong to new world begomovirus

since they share less relationship with satellite molecules. Mosaic patterns on leaves, vein yellowing, leaf curling, vein clearing, stunting of stem, etc., are general symptoms appearing on cucurbits (Tiwari et al. 2011, 2012). *Pumpkin yellow vein mosaic virus* (Muniyappa et al. 2003), *Squash leaf curl China virus* (Saritha et al. 2011; Singh et al. 2009), *Tomato leaf curl New Delhi virus* (Zaidi et al. 2017), *tomato leaf curl Palampur virus* (Namrata et al. 2010; Ali et al. 2010), *Chayote yellow mosaic virus* (Mandal et al. 2000), and *Coccinia mosaic virus* (Nagendran et al. 2016) are the major viruses infecting cucurbits in India. Mixed infections of more than one begomoviruses, *Tomato leaf curl Palampur virus*, *Squash leaf curl China virus*, and *Tomato leaf curl New Delhi virus*, were reported from Varanasi, India, on pumpkin (Jaiswal et al. 2012). Chayote yellow mosaic virus, infecting Chayote (*Sechium edule*), shares maximum nucleotide identity with previously characterized Tomato leaf curl New Delhi virus (ToLCNDV). ChaYMV also infects other members of cucurbits, namely bitter melon, cucumber, and squash (Mandal et al. 2004).

6.2.7 Cotton

Cotton leaf curl virus is categorized as the most devastating virus belonging to the begomovirus genus. It is responsible for causing the most threatening effect in the world, especially to the Indian subcontinent. India, Pakistan, and Sri Lanka face a huge economic loss due to the infection of cotton leaf curl virus (Narula et al. 1999). Pakistan faces around 30% loss due to cotton leaf curl disease infection (Ahmad et al. 2018; Hassan et al. 2016). First report of cotton leaf curl virus infecting cotton was from Nigeria in 1912. A cotton leaf curl disease epidemic in the Indian subcontinent was first reported in 1967 from Multan, Pakistan (Husain 1932; Hussain and Ali 1975; Hassan et al. 2016). The begomoviral strain that acts as a causal agent of cotton leaf curl diseases was classified based on genomic identity into three strains, namely cotton leaf curl Multan virus, cotton leaf curl Burewala virus, and cotton leaf curl Kokhran virus (Chowdareddy et al. 2005; Radhakrishnan et al. 2004; Kirthi et al. 2004; Kumar et al. 2010; Rajagopalan et al. 2012; Zaffalon et al. 2012). In India, cotton leaf curl diseases were prevalent during 1993–1996 in northwestern India from Rajasthan, Punjab, and Haryana. Recombination between cotton leaf curl Multan virus and cotton leaf curl Kokhran virus is known as cotton leaf curl Rajasthan virus (Kumar et al. 2010; Rajagopalan et al. 2012; Zaffalon et al. 2012). It is designated as a different strain from India. Apart from these strains, Cotton leaf curl Bangalore virus, Cotton leaf curl Allahabad virus, Cotton leaf curl Barasat virus, and Cotton leaf curl Shahdadpur virus were reported from India (Datta et al. 2017; Sattar et al. 2013; Briddon 2003; Zhou et al. 1998; Mansoor et al. 1999). Apart from these, cotton plants are also sensitive to infection by tomato leaf curl Bangalore virus and tomato leaf curl Patna virus (Kirthi et al. 2004). Systemic reports of cotton leaf curl virus in India were available from Punjab and neighboring states in 1990s (Briddon and Markham 2000; Briddon 2003). Disease epidemic was spread and became prevalent toward south India and reported from the home garden in Bengaluru (Nateshan et al. 1996). It also infected

okra, tomato, cotton, and hibiscus plants. It is responsible for causing around 10–80% loss in seed production in different varieties of cotton.

There is no evidence of association of cotton leaf curl virus with DNA-B component from India but DNA-B component from ICMV and SLCMV showed association with DNA-A component of cotton leaf curl virus (Sattar et al. 2013). Cotton leaf curl Multan virus and cotton leaf curl Kokhran virus share 78–79% identity between them. It shows a close association with satellite molecules. The recombination between CLCuKoV and CLCuMuV strains resulted in Rajasthan, Shahdadpur, and Burewala strain. They are more virulent compared to the parent strand. Rajasthan strand is more prevalent in India and might originate from India. Burewala strain is more virulent in India and Pakistan and suspected to originate in Pakistan and travel via vector *B. tabaci* and enter India (Kumar et al. 2010).

6.2.8 Papaya

Papaya leaf curl disease was first reported from Tamil Nadu in India in 1939 (Thomas and Krishnaswami 1939), whereas it was noticed in Pakistan in 1997 (Nadeem et al. 1997). Initially, on the basis of symptom appearance on leaves, it is known as papaya leaf crumple disease. It shows symptoms like vein enation, stunted growth, and deformed and leathery leaf. Infected plants did not produce fruits (Summanwar and Ram 1993; Singh-Pant et al. 2012). Papaya leaf curl virus has wide host range of plant families, for example, *Apocynaceae*, *Malvaceae*, *Ephorbeaceae*, *Caricaceae*, and *Asteraceae* (Kumar et al. 2009; Srivastava et al. 2013; Varun et al. 2017). Furthermore, virus outbreak was observed in northern India and east India initially, which was then spread over Haryana, Maharashtra, Uttar Pradesh, Karnataka, Tamil Nadu, and Andhra Pradesh (Surekha et al. 1977; Pandey and Marathe 1986; Raj et al. 2008; Krishnareddy et al. 2010).

6.2.9 Mesta

Mesta, affected by begomovirus, was first reported from India in 2005 (Chatterjee et al. 2005). The symptoms were yellowing of vein and entire lamina turned into yellow. The similar kind of symptoms was found from Uttar Pradesh and West Bengal in 2007 and 2009, respectively (Ghosh et al. 2007; Das et al. 2008a, b; Roy et al. 2009). Mesta yellow vein mosaic virus and mesta yellow vein mosaic Bahraich virus are affecting in India. It can efficiently transmit up to 85% in *H. sabdariffa*. The association of betasatellite has been found in India in field condition (Chatterjee and Ghosh 2007). There was an association of cotton leaf curl betasatellite with MeYVMV.

6.2.10 Radish

Leaf curl disease in radish was first observed in India in 2003. It was observed in both kitchen garden and field from eastern Uttar Pradesh. The disease appeared as upward and downward curling in leaf, leaf distortion, and vein enation in infected plants (Singh et al. 2007, 2010). The disease incidence was noted to be 10–40% in field. It is a whitefly-transmitted disease. Scanning electron microscopy and PCR confirmed the presence of begomovirus. They also reported the presence of DNA-B

genome component and associated betasatellite molecule from the infected plants. Nonhost infection of radish leaf curl virus (RLCuV) was reported in okra plant in Bihar (Kumar et al. 2012a, b, c). Associated satellite molecules (alphasatellite and betasatellite) increased symptom severity. Nonhost infection was also seen in tobacco plants in field condition (Singh et al. 2012). The begomovirus genome experiences frequent recombination event which is a major factor for enormous viral genome diversity. As of other begomovirus, RLCuV also undergoes recombination, pseudo-recombination, and mutation. These strategies of virus made them feasible for surviving in multiple and nonhost plants (Singh et al. 2012).

6.2.11 *Jatropha*

Production of *jatropha* is increasing day by day due to its economic importance. The most important value of the plant is its role in fuel production. It is native to India, America, and Caribbean countries. The natural infection of begomovirus was by *jatropha* mosaic virus in Jamaica and Puerto Rico (Roye et al. 2006). It has also been reported from Kenya and Nigeria (Kashina et al. 2013). The disease incidence was more than 40% in *Jatropha curcas*. The infected plants were showing symptoms of leaf curling, leaf blustering, leaf mosaic pattern, leaf distortion, etc. In India, it spread over almost all *jatropha*-growing regions. Up to 25% of disease incidence in field condition has been reported from Uttar Pradesh. *Jatropha* mosaic India virus, *jatropha* leaf yellow mosaic Katarniaghat virus, and *jatropha* leaf crumple India virus have been reported to date (Srivastava et al. 2015; Snehi et al. 2016). Apart from these, *jatropha* plants also experience nonhost infection by Indian cassava mosaic virus, and croton yellow mosaic virus associated with betasatellite has also been reported in *J. gossypifolia* (Gao et al. 2010; Narayana et al. 2007).

7 Conclusion

Yield constraint, tremendous losses, and economical outbreaks lead researchers and policy makers to gain interest in geminiviruses. Sugar beet infection by beet curly top virus, cassava infection by African cassava mosaic virus, cotton infection by cotton leaf curl virus, bean golden mosaic virus of common bean, maize infection by maize streak virus, and finally tomato infection by tomato leaf curl virus are past pandemics that cause huge loss in the production of respective crops in one or the other parts of the world. Geminivirus infection is one of the major limiting factors for the production of cash crops. This chapter provides a review on geminivirus infections in the Indian subcontinent. Virus database and availability of full-length sequences are major prerequisites to develop long-term stable resistant variety against virus attack. Understanding host–pathogen interactions and mechanism of defense stratagems could be an important future aspect.

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