



Review Article

Transmission Specificity and Coinfection of Mastrevirus with Begomovirus

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Abstract

Coat protein (CP) of geminivirus is not requisite for replication of viral DNA yet it is multifunctional and have crucial role in virus transmission by insect vector, systemic infection and virion development. Although in geminivirus, systemic infection rely both on function of CP and specific host-geminivirus-vector interaction but in bipartite begomoviruses CP is dispensable for systemic infection and progression of symptoms. Nevertheless its role in spreading systemic infection cannot be neglected in monopartite viruses viz. mastrevirus, begomoviruses and curtoviruses, therefore any alteration in CP gene upshot in a new epidemiological adaptation hence worth to study. So the study was designed to present a better picture to view regarding coinfection within different Geminiviruses belonging to mastrevirus and begomovirus particularly due to vector inspecificity consequently resulted in revolutionary recombination events, which ultimately yield new viruses, have more drastic affects on crops. Moreover, co-evolution of both genera may open new horizons in understanding the complexity of cotton leaf curl disease and then to chalk out strategies to counter this emerging threat in Pakistan. © 2017 Friends Science Publishers

Keywords: Geminiviruses; Transmission; Insect specificity; Coinfection

Introduction

Viruses always have sound effect on the growth of plants, besides interacts with host defence mechanism, leads to the alteration of crop physiology. Agricultural production, around the globe has been continuously affected due to diseases spread by geminiviruses (Inouye and Osaki, 1980). Previously knowledge about the viral pathogens of diseases was restricted before the isolation, structure and morphology of virus particles linked with such diseases like maize streak and beet curly top (Bock *et al.*, 1974; Mumford, 1974). Cotton leaf curl disease (CLCuD) now become the subject of massive concern globally including Pakistan (Briddon and Markham, 2001; Mansoor *et al.*, 2003; Amin *et al.*, 2006). Intergenic recombinations due to coinfection of two different geminiviruses belonging to dissimilar genera have been reported to play major role in establishment of current taxonomic composition of the family *Geminiviridae* e.g., dicot-infecting mastreviruses are specifically prone to trans-encapsidation. Yet coat protein (CP) has a common role for all the members of family *Geminiviridae*; determinant of vector specificity because it is essential for insect transmission. THIS review broadens our knowledge about the diversity and distribution of mastreviruses across Pakistan and will provide the necessary

information regarding their control.

Cotton Leaf Curl Disease (CLCuD) in Historical Perspective

Gossypium virus-1 has been reported as causative viral agent for Cotton leaf curl and first report was documented in Nigeria infecting *Gossypium barbadense* L. (Farquharson, 1912). Later on, it was investigated that whitefly is a biotic agent in dispersal of this disease, after twelve years in Sudan (Jones and Mason; 1926; Bailey, 1934). Moreover, in 1960s long staple cotton production was significantly affected due to Cotton Leaf Curl Disease (CLCuD) both in Tanzania and Gezira whilst, in western part of India *G. hirsutum* was severely attacked by geminiviruses causing this disease (Singh *et al.*, 1996). Geminiviruses (genus *Begomovirus*; family *Geminiviridae*), also spread across northwestern India and Pakistan caused drastic reduction in cotton production and was reported to be caused by whitefly (*Bemisia tabaci* Gennadius) as one and only biotic constraint to all the cotton plants (Ahmad *et al.*, 2011). Abnormal and unusual symptoms of CLCuD were noticed on infected plants with reference plants like swelling of veins, downward or upward curling/cupping of leaves, enation formation on the lower surface of

leaves mainly midrib and leaves were greener than usual (Farooq *et al.*, 2011). These symptoms, however, are changeable with age of the plant at the time of infection and variety of cotton.

Geminiviruses

Recent research reports depict that Geminiviruses possess single stranded DNA (ssDNA) molecules (~2500 to ~3100 nucleotides) encapsidated in twinned icosahedral capsid, with circular monopartite or bipartite genomes but can encode only few genes and its replication mostly depend on host plant replication machinery. Furthermore, they are broadly disseminated viruses infecting both monocots (e.g. maize and wheat) and dicots like tomato and cassava (Hanley-Bowdoin *et al.*, 1999; 2004). Further geminiviruses has been divided into seven genera namely *Begomovirus*, *Curtovirus*, *Mastrevirus*, *Topocuvirus*, *Eragrovirus*, *Turncurtovirus* and *Becurtovirus* warp and woof on their (i) genome organization (ii) insect vector (iii) biological properties and (iv) host range (Varsani *et al.*, 2014) as depicted clearly in Table1. Whitefly (*Bemisia tabaci* Gennadius) has been reported as insect vector for the genus begomoviruses in contrast to Mastreviruses, which has been reported to transmit by leafhoppers (*Orosius albicinctus* Distant) to a range of host plants.

Begomoviruses cause a lot of economic losses and listed as largest genus of geminiviruses (133 known monopartite begomoviruses originating from the Old World - OW). Their genome consists of two components, one is called DNA-A and the other is DNA-B, both are ~2.7 kb in size (Lazarowitz, 1992). Both DNA-A and DNA-B perform different vital roles like viral DNA replication, encapsidation and transcription by DNA-A, while two movement proteins (BV1 and BC1) for translocation of virus by DNA-B (Levy and Tzfira, 2010). New world viruses related to the central and southern American strains such as *Tomato leaf deformation virus* is a new world virus. However, in the Old World (OW; including Africa, Europe, Australia, Japan, India, Pakistan and other Asian clades) just like bipartite begomoviruses are small in number, mostly have single genomic component similar to DNA-A of bipartite begomoviruses. Monopartite geminiviruses infecting monocots and dicots, with satellites in the Old World (OW), to strict bipartite geminiviruses infecting dicots without satellites in the New World (NW) (Nawaz-ul-Rehman and Fauquet, 2009). Data presented in Table 2 shows that some of viruses are truly monopartite (having only DNA-A) responsible for disease in host plant e.g., *Tomato yellow leaf curl Sardinia virus* (TYLCSV) (Kheyr-Pour *et al.*, 1991).

Mastreviruses

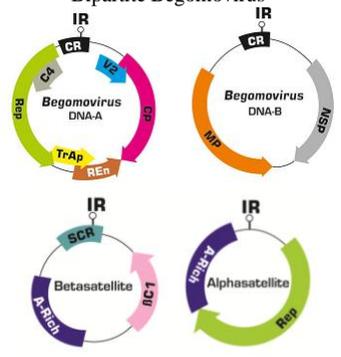
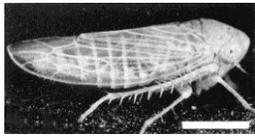
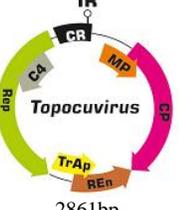
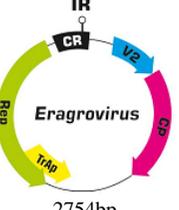
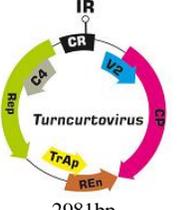
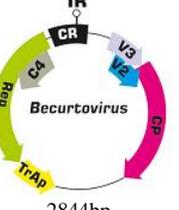
Mastreviruses are monopartite, ssDNA viruses with ~2.5–2.7 kb circular genomes, encapsidated in twinned isometric

viral particles but their genomes reported to express four proteins, encoded on the virion and complementary strand equally (Boulton, 2002). The virion strand encoded (1) movement protein (Mp) in plant, vital for cell-to-cell movement in and (2) coat protein (CP) necessary for systemic infection, encapsidation and for transmission of the insect. Cell to cell movement in plants along with vector specificity depends on structural proteins (Liu *et al.*, 1998; 1999; Boulton, 2002). While complementary strand has been reported to encode two replication associated proteins (instead of one, as in other geminiviruses), (1) RepA in trans-activation of late (virion-sense) genes as well as reported to establish a cellular environment conducive for virus replication and (2) RepB, which may be translated from alternatively spliced sense transcripts and required for replication, initiating and terminating rolling circle DNA replication and for the interference of the cell cycle. RepA and RepB shared ~70% amino acid sequence homology with each other (Schalk *et al.*, 1989; Heyraud-Nitschke *et al.*, 1995; Wright *et al.*, 1997; Hanley-Bowdoin *et al.*, 2004; Ruschhaupt *et al.*, 2013). Further compactness of mastrevirus genomes is highlighted due to its multiple known proteins and their functions, with the exception of MP. Anyhow rate of mastrevirus nucleotide substitution has been found relatively low as compared to basal mutation rates, hence mutation being less deleterious and therefore subject to negative selection (Jeske, 2009). A detailed comparison of protein functions between begomovirus and mastrevirus are depicted in Table2.

Mastrevirus Vector – *Orosius albicinctus* Distant

Considerable research efforts have been made which depict that Mastreviruses, occurs across the old world, do not replicate inside their insect vector and are transmitted in a persistent circulative and non-propagative manner (Boulton and Markham, 1986; Harrison *et al.*, 2002). Research reveals that *O. albicinctus* Distant (thought to be similar to *Orosius orientalis* Matsumura); leafhopper vector of plant viruses and phytoplasmas, successfully transmitted the *Chickpea chlorotic dwarf virus* (CpCDV). However, *O. orientalis* Matsumura has also been reported to transmit CpCDV to plant species of different families (like *Fabaceae*, *Solanaceae*, *Chenopodiaceae*) and induced CpCDV like symptoms (Horn *et al.*, 1996; Kumari *et al.*, 2004; Farzadfar *et al.*, 2008; Akhtar *et al.*, 2011). Nonetheless, Horn *et al.* (1993) reported first time the identification of CpCDV along with many reports from other countries like, Australia, Africa, Europe, the Middle East, Asia, and Far East, Arabian Peninsula and the Indian subcontinent (Horn *et al.*, 1993; Makkouk *et al.*, 1995, 1998; El-Muadhidi *et al.*, 2001; Farzadfar *et al.*, 2002; Makkouk *et al.*, 2003a,b; Kumari *et al.*, 2004; Nahid *et al.*, 2008; Thomas *et al.*, 2010; Muhire *et al.*, 2013; Akhtar *et al.*, 2014).

Table 1: Description of seven genera of Geminiviruses.

	Curtovirus	Begomovirus Bipartite Begomovirus	Mastrevirus	
Genome Organization	 <p>2927bp</p>	 <p>2647bp</p>	 <p>2787bp</p>	
Insect Vector	<p>Beet Leafhopper: <i>Circulifer tenellus</i> Baker.</p>  <p>http://www.dpvweb.net/dpv/showfig.php?dpvno=210&figno=03</p>	<p>Whitefly: <i>Bemisia tabaci</i> Gennadius.</p>  <p>http://www.gardeningknowhow.com/plant-problems/pests/insects/whitefly-control.htm</p>	<p>Leafhopper: <i>Orosius albicinctus</i> Distant.</p>  <p>Akhtar <i>et al.</i>, 2014.</p>	
Host Plants	<p>Dicot: Sugar beet <i>Beta vulgaris</i> L. <i>Phaseolus vulgaris</i> L.</p>	<p>Dicot: <i>Gossypium hirsutum</i> L. <i>Phaseolus vulgaris</i> L.</p>	<p>Dicot: Chickpea (<i>Cicer arietum</i> L.) Monocot: Maize (<i>Zea mays</i> L.)</p>	
Type Species	<p><i>Beet curly top virus</i> (BCTV) (Ball, 1909)</p>	<p><i>Bean golden mosaic virus</i> (BGMV) (van Regenmortel <i>et al.</i>, 1997)</p>	<p><i>Maize streak virus</i> (MSV) (Storey, 1925).</p>	
Monopartite/Bipartite	<p>Monopartite</p>	<p>Monopartite/Bipartite</p>	<p>Monopartite</p>	
Genome Organization	 <p>2861bp</p>	 <p>2754bp</p>	 <p>2981bp</p>	 <p>2844bp</p>
Insect Vector	<p>Treehopper <i>Microtalis malleifera</i> Fowler.</p>  <p>http://www.dpvweb.net/intro/</p>	<p>Unknown</p>	<p>Unknown</p>	<p>Leafhopper <i>Circulifer haematoceps</i> (Mulsant & Rey)</p>  <p>(Mulsant and Rey, 1855)</p>
Host Plants	<p>Dicot: Tomato (<i>Lycopersicon esculentum</i> Mill.)</p>	<p>Monocots: weeping lovegrass <i>Eragrostis curvula</i> (Schrad.) Nees <i>Eragrostis curvula streak virus</i> (ECSV) (Varsani <i>et al.</i>, 2009).</p>	<p>Dicots: Turnip <i>Brassica rapa</i> var. <i>rapa</i> L. <i>Turnip curly top virus</i> (TCTV) (Briddon <i>et al.</i>, 2010).</p>	<p>Dicot: Sugar beet <i>Beta vulgaris</i> L. <i>Beet curly top Iran virus</i> (BCTIV) (Gharouni <i>et al.</i>, 2013).</p>
Type Species	<p><i>Tomato pseudo-curly top virus</i> (TPCTV) (Briddon <i>et al.</i>, 1996)</p>	<p><i>Tomato pseudo-curly top virus</i> (TPCTV) (Briddon <i>et al.</i>, 1996)</p>	<p><i>Turnip curly top virus</i> (TCTV) (Briddon <i>et al.</i>, 2010).</p>	<p><i>Beet curly top Iran virus</i> (BCTIV) (Gharouni <i>et al.</i>, 2013).</p>
Monopartite/Bipartite	<p>Monopartite</p>	<p>Monopartite</p>	<p>Monopartite</p>	<p>Monopartite</p>

Dicot Infecting Mastreviruses

Members of the mastrevirus include species, which infect

monocotyledonous (monocot) but it has shifted its mood from monocot to dicotyledonous (dicot) plants. The change in the behaviour of viruses of this genus has made them

worthwhile for study. Mastreviruses, for example *Maize streak virus* (MSV), and *Panicum streak virus* (PSV) has been recorded to infect the monocotyledonous plant (Varsani *et al.*, 2009). Whilst dicots infecting mastrevirus *viz. Tobacco yellow dwarf virus* (TbYDV) from Australia and *Chickpea chlorotic dwarf virus* (CpCDV) from northern Africa and the Indian subcontinent were being isolated from dicots i.e., tobacco and chickpea respectively (Morris *et al.*, 1992; Horn *et al.*, 1993). Albeit *Bean yellow dwarf virus* (BeYDV) (Liu *et al.*, 1997a) (infect dicotyledonous plants) presence has been recorded in both Pakistan and South Africa (Halley-Scott *et al.*, 2007). However, Thomas *et al.* (2010) reported *Chickpea chlorosis virus* (CpCV-A, CpCV-B) and *Chickpea redleaf virus* (CpRLV) from Australia. Previously, CpCDV has been noted down to attack the legumes but with lapse of time, they expand their host range and infected other dicot families as well, like pepper (in India and Oman) and tomato (Byun *et al.*, 2014; Akhtar *et al.*, 2014; Zia *et al.*, 2015). Now CpCDV not only infect legumes but also the species of other important families like Solanaceae, Asteraceae, Malvaceae and Cucurbitaceae, have economic implications to Asia and the Arabian Peninsula. Likewise cotton (*Gossypium* L.) being important member of family malvaceae has always played an important role in lifting up the economy of any country including Pakistan (fourth largest cotton producing country). Yet for many members of family Malvaceae the CLCuD reported as a serious disorder in Pakistan and first report was recorded from Tiba Sultanpur near Multan in 1967 (Hussain and Ali, 1975). Unfortunately, CLCuD was ignored until it became a giant disaster for cotton crop in 1987 and turned into serious threat to most of the cotton producing areas of Pakistan such as Sahiwal, Multan, Khanewal, Vehari and Bahawalpur till 1990s (Mansoor *et al.*, 2003).

Mastrevirus Host Range

Number of plant scientists has reported natural hosts of dicotyledonous plant infecting mastreviruses in the field for example for (i) chickpea: [(*Cicer arietinum* L.) Horn *et al.*, 1993; Kumari *et al.*, 2004; Nahid *et al.*, 2008; Mumtaz *et al.*, 2011; Kraberger *et al.*, 2013] (ii) lentil: [(*Lens culinaris* Medik) Nahid *et al.*, 2008; Kraberger *et al.*, 2013] (iii) faba bean: [(*Vicia faba* L.) Makkouk *et al.*, 2003b; Kraberger *et al.*, 2013] (iv) field pea: [(*Pisum sativum* L.) Kraberger *et al.*, 2013] (v) french bean: [(*Phaseolus vulgaris* L.) Liu *et al.*, 1997a; Ali *et al.*, 2004] (vi) sugar beet: [(*Beta vulgaris* L.) Farzadfar *et al.*, 2008] (vii) pepper: [(*Capsicum annum* L.) Akhtar *et al.*, 2014; Byun *et al.*, 2014] (viii) cotton: [(*Gossypium* sp. L.) Manzoor *et al.*, 2014] (ix) squash: [(*Cucurbita pepo* L.) Fahmy *et al.*, 2015] and for (x) tomato: [(*Lycopersicon esculantum* L.) Zia *et al.*, 2015]. Additionally many researchers also claimed that weeds like '*Sesbania bispinosa* Jacq.', '*Rapistrum rugosum* L.' and '*Xanthium strumarium* L.' are favorite hosts of mastrevirus

(Nahid *et al.*, 2008; Schwinghamer *et al.*, 2010; Mubin *et al.*, 2012).

Reports of Coinfection of Mastrevirus with Begomovirus

Following research reports revealed that coinfection of viruses belonging to two different genera e.g. mastrevirus and begomovirus occurs very rarely and due to extreme genetic changes, intergenic recombinations are not viable and not as fit as their parents. The prerequisite of coinfection between begomovirus-dicot infecting mastrevirus intergenic recombination was shown first time by Mubin *et al.* (2012) in a weed (*Xanthium strumarium* L.: non-host of CpCDV) in Pakistan. This first report about recognition of co-occurrence of a defective mastrevirus was with speculation that they lack coat protein CP gene and depend on begomovirus for various activities (like encapsidation, cell to cell as well as plant to plant movement). The second evidence of coinfection between '*Cotton leaf curl burewala virus*' (CLCuBuV), a begomovirus with dicot infecting mastrevirus; '*Chickpea chlorotic dwarf virus*' (CpCDV) was reported by Manzoor *et al.* (2014) in cotton (non-host of mastrevirus). Recently a new study about begomovirus-dicot infecting mastrevirus co-infection in squash plants (non-host species of dicot infecting mastrevirus) has been reported by Fahmy *et al.* (2015) for full length complete genome of the CpCDV infected squash plants by studying its putative recombination events along with its phylogenetic analysis and molecular characterization. Such reports of co-occurrence of viruses put heavy pressure on recombination events between two different genera of same family but have been transmitted by dissimilar vectors. Begomoviruses are transmitted by whiteflies whereas CpCDV are transmitted by leafhopper *Orosius albicinctus* Distant (Akhtar *et al.*, 2011). Study of whiteflies and leaf hoppers for the presence of CpCDV isolates in their body will be good contribution. It may provide comprehensive information to perform some forced recombination experiments with a mastrevirus like '*Maize streak virus*' (Schnippenkoetter *et al.*, 2001; Martin and Rybicki, 2002).

Very few experiments have been performed so far to study the co-infection of a begomovirus together with a mastrevirus, infecting the same host plant. Hence to explore this aforementioned aspect we designed the study to replace coat protein (CP) gene of CpCDV (Genus: *Mastrevirus*, Family: *Geminiviridae*) with the CP gene of (CLCuBuV) (Genus: *Begomovirus*, Family: *Geminiviridae*). It is hypothesized that the *B. tabaci* might be able to acquire and transmit our chimeric 'MastreBegomo' confirming the observation that coat protein play an integral role in viral transmission by its specific vector. It is therefore suggested that co-evolution of both the genera may open new horizons in understanding the complexity of CLCuD and then to chalk out strategies to counter this emerging threat in Pakistan.

Table 2: Comparison of Protein functions between Mastrevirus and Begomovirus.

Geminivirus Genus	Orientation	Gene	Protein	Function	
Mastrevirus (Monopartite) <i>Maize streak virus</i>	Virion strand	V1	Movement Protein (MP)	Cell-to-cell movement in plant (Wright <i>et al.</i> , 1997; van Regenmortel <i>et al.</i> , 2000).	
		V2	Coat Protein (CP)	Systemic infection, encapsidation and insect transmission. This is the only structural protein that determines both cell-to-cell movement and vector specificity in plants (Mullineaux <i>et al.</i> , 1984; Boulton <i>et al.</i> , 1993).	
	Complementary strand	C1	Replication associated protein A (RepA)	Transactivation of late genes i.e., virion sense genes along with establishing a cellular environment conducive for replication of virus (Hanley-Bowdoin <i>et al.</i> , 1999; Boulton <i>et al.</i> , 1993).	
		C2	Replication associated protein B (RepB)	Translated from alternatively spliced sense transcripts, required for replication, initiate and terminate rolling circle DNA replication and interfere the cell cycle (McGivern, 2002).	
Begomovirus (Bipartite/monopartite.)	Virion strand	AV1	Coat Protein (CP)	Requisite for transmission of insect as well as mobility in plant (Rojas <i>et al.</i> , 2001) required for stability of genome, infectivity, transmission by insect vectors and systemic spread (Lazarowitz, 1992) need for accumulation of ssDNA (Qin <i>et al.</i> , 1998), determinant of the specificity of insect vector (Briddon <i>et al.</i> , 1990).	
		DNA-A	AV2	Precoat Protein	Only confined to old world begomoviruses and involved in movement of bipartite geminiviruses localized around the nucleus and at the cell periphery and co-localized with the endoplasmic reticulum (Padidam <i>et al.</i> , 1996), virus movement <i>in planta</i> (Rojas <i>et al.</i> , 2001).
	Complementary strand	DNA-A	AC1	Replication associated protein (Rep)	Need for replication of viral DNA particles that is the rolling circle replication initiator protein (Hanley-Bowdoin <i>et al.</i> , 2004).
			AC2	Transcription associated protein (TrAp)	Suppressor of post-transcriptional gene silencing (PTGS; Yang <i>et al.</i> , 2007). controls viral induced hypersensitive cell death (Hussain <i>et al.</i> , 2007; Mubin <i>et al.</i> , 2010).
		DNA-A	AC3	Replication enhancer protein (REn)	Initiate an environment helpful for replication of virus. (Settlage <i>et al.</i> , 2005).
			AC4	Multifunctional protein	Govern the pathogenicity, involved in movement of viral particles, overcoming host defenses as well as suppressor of PTGS (Gopal <i>et al.</i> , 2007; Saeed <i>et al.</i> , 2008; Vanitharani <i>et al.</i> , 2004; Nawaz-ur-Rehman <i>et al.</i> , 2010).
	Virion strand	BC1	Nuclear shuttle protein (NSP)	Need to alter the structure of plasmodesmata by accelerating the movement of virus inside host (Pascal <i>et al.</i> , 1993) and essential in determination of symptom severity due to crucial role of BC1 gene (Duan <i>et al.</i> , 1997).	
	Complementary strand	DNA-B	BV1	Movement protein (MP)	Confined only in nucleus of the host cell and require for binding to ssDNA, thus transporting it to cytoplasm (Pascal <i>et al.</i> , 1994).

AC1, AC2, AC3 and AC4 in bipartite and C1, C2, C3 and C4 in monopartite geminiviruses

Role of Coat Protein in Mastrevirus

Nucleus of the host plant has been reported as main place for the replication of the geminiviruses during which viral DNA particles move across the cell boundaries copulated with nuclear shuttling eventuate in infection of plant (Goodman, 1981; Davies *et al.*, 1987). In mastreviruses, MSV encode only one MP (PV1) in addition to the CP, requisite of maize infection (Boulton *et al.*, 1993, 1989; Lazarowitz *et al.*, 1989). Contrarily in bipartite geminiviruses, three genes are involved in movement of virus i.e., BR1, BL1 and CP (Jeffrey *et al.*, 1996). The CP of the genus Begomoviruses has one or more common antigenic epitopes signifying them as determinants of vector specificity indicating key role of the CP during transmission

of viruses (Roberts *et al.*, 1984; Briddon *et al.*, 1990; Hofer *et al.*, 1997). But transmission of viral particles could be enhanced due to relevant pathogens or parasites which may have ability to induce changes in behavior of host or its vector. As vectors are mobile and show their preferences on infection of host plant hence such effects mainly constraint to vectors. Nevertheless, pathogen spread also depend on different modes *viz.* mode of acquisition is promoted if non-infective vector has inclination toward infected plants in contrast to transmission where infective vector has preference for non-infected hosts (Ingwell *et al.*, 2012).

The potential role of geminivirus coat protein in determining infectivity (Briddon *et al.*, 1989) and vector specificity in the transmission of geminiviruses was first demonstrated by Briddon *et al.* (1990). Using gene

replacement (by using restriction enzymes) Chimera was construct between 'African Cassava Mosaic Virus' [(ACMV) whitefly transmitted Begomovirus] and 'Beat curly top virus' [(BCTV; leafhopper transmitted Curtovirus] where CP gene (AV1) of ACMV was excised by using restriction enzymes and replaced by V2 of BCTV. Successful transmission of both BCTV and chimeric virus was recorded via BCTV leafhopper vector [*Circulifer tenellus* (Baker)], whereas ACMV failed indicating that chimeric ACMV altered its insect specificity from whiteflies to leafhoppers. Therefore, it has been suggested that coat protein is an essential component for transmission and in identifying specificity of insect.

Further, Hofer *et al.* (1997) conducted an experiment by inserting CP gene of insect transmissible 'Sida golden mosaic virus' (SiGMV-Co) to non-transmissible isolate of 'Abutilon mosaic virus' (AbMV) that lacked specific region of coat protein by using specific primers designed in opposite orientation by PCR (polymerase chain reaction) amplification. So, *B. tabaci* successfully transmitted and acquired this resultant chimera to various host plants. Whereas research reports of Liu *et al.* (1998) and Azzam *et al.* (1994) was also supported the aforementioned report where they opined that geminiviruses capsids mutants are not acquired by whiteflies. Experiments of Azzam *et al.* (1994) clearly depict the role of CP of 'Bean golden mosaic virus' (BGMV) in systemic infection and vector transmission (whitefly). They produced three mutants by introducing two deletions and a restriction fragment inversion, in coat protein gene of BGMV. All the three mutants were non transmissible by whiteflies, non-sap transmissible and showed systemic infection by particle gun method when co-inoculated with DNA-B onto *Phaseolus vulgaris* L. In mutants, ssDNA accumulation was reduced to 25 to 50 fold in DNA-A and 3 to 10 fold in DNA-B.

Mastrevirus coat protein plays an important role for the infection of host plant but little is known about its function. It has been suggested that N-terminus is vital for nuclear accumulation of CP (Liu *et al.*, 1997b, 1999) and 13 amino acids of C-terminus is necessary for encapsidation and accumulation of ssDNA (Boulton *et al.*, 1989). Yet it has been also explored that CP of 'Maize streak virus' (MSV) along with most of other cereal-infecting mastreviruses posses a conserved motif of 180-182 amino acids i.e., proline-cysteine-lysine. Though, in previous studies role of lysine was reported as dendro-toxins or inhibitors of Kunitz protease (Dufton, 1985). Ultimately site directed mutagenesis in MSV was performed between lysine and valine in the CP region which was recorded as mutation of amino acid 182 and has been reported to affect the virion formation due to the absence of systemic infection. However, it does not affect the replication of ssDNA and/or dsDNA and other functions e.g., MP-CP interaction, nuclear accumulation and cell to cell movement (Liu *et al.*, 2001). Infectivity of MSV has also been abolished due to mutation or deletion of/in CP gene of

maize lead to non accumulation of ssDNA particles in protoplast (Boulton *et al.*, 1989, 1993).

Thereupon, Liu *et al.* (1997b) assessed the dual role of CP both in encapsidation as well as in transportation of ss and/or ds DNA. By contrast to CP of begomoviruses it was shown that CP of masriveruses is essential for systemic infection. Howbeit requirements for inter- and- intracellular movement of MSV is in accordance to begomoviruses, consequently even if there is deficiency of DNA B-encoded proteins, two proteins *viz.* CP and MP might have operative role similar to BV1 and BC1 (movement proteins) of begomoviruses yet their structure and manner of function might be dissimilar (Liu *et al.*, 1999). Nevertheless, a specific CP region (i.e., 1–104 amino acids) of MSV is mapped as DNA binding domain but any disruption or alteration of this area and subsequently deletion of 20 N-terminal amino acids that have an effect on refolding of protein so their DNA binding ability diminishes.

As recommended for BR1 of SqLCV, this coat protein region may bind viral ssDNA in the form of nucleoprotein which help both for cell to cell movement and in nuclear shuttling (Pascal *et al.*, 1994; Sanderfoot *et al.*, 1996). It is likely that CP binding function is helpful for encapsidation of viral (ss) DNA. Probably, CP complexed with dsDNA or ssDNA will interact with movement protein (MP) to carry out inter- and intra-cellular movement just like BL1 and BR1 of SqLCV (Pascal *et al.*, 1994). Later on a comparative study was performed by Benfey *et al.* (1996) in transgenic rice plants (*Oryza sativa* L.) to study the mastrevirus coat protein promoter activity with that plants transformed with the *gus* gene; downstream of the 'Cauliflower mosaic virus' (CaMV) 35S promoter. A *cp-gus reporter* gene replacement construct was made in order to study the tissue specificity and strength of MSV CP promoter region. The construct was theorized as MSV CP 'extended promoter' comprised of MSV (i) LIR and (ii) SIR, (iii) sequence of MP gene and (iv) replication associated regions of the genes. Though activation of MSV CP promoter was figured out inside the regenerating callus cells but for vascular tissues of regenerated plants such expression patterns were confined only to vascular tissues of above and below ground parts like stem, leaf, and flower and root. However, in phloem-associated tissues of the vegetative organs highest expression were assessed but no expression was observed in seedling roots (tip and elongation part). While working on transgenic rice Mazithulela *et al.* (2000) juxtapose the characteristics of MSV CP 'extended promoter' with that of CaMV 35S promoter to evaluate their utilization for tissue-specific expression.

For the host plants, two important stimuli *viz.* gustatory and olfactory stimuli are produced for which sensory receptors on the rostral apex of order Hemiptera were considered useful (Rani and Madhavendra, 1995, 2005) whilst chemosensilla is mainly found on the mouthparts and antennae. Members of order Hemiptera also enjoy the existence of contact chemoreceptive 'sensilla on

the labial tip' which give facts about nature of leaf surface to insect when it tap it on the leaf of host plant (Backus *et al.*, 1982). Previously chemosensory functions of such 'apical labial sensilla' have also been listed by Backus and McLean (1983) and Walker and Gordh (1989) in leafhoppers and whiteflies respectively. It is also insinuated that 'apical labial sensilla' have multiple role like in host selection, discriminate between host and non-host tissues and likely function in either chemo and/or mechano-sensory or both (Zhao *et al.*, 2010). Further research, however, is need of the hour to understand the more detailed and fine structure of the labial sensilla of leafhoppers.

Conclusion

In a nutshell it can be concluded that replacement of coat protein gene of CpCDV with CLCuBuV may help to broaden our understanding about the range and distribution of mastreviruses across Pakistan and will provide the necessary information regarding their control. Keeping in view the available information regarding mastreviruses, we have adopted advance molecular techniques, which aimed at to find out the possibility of co-infection of mastreviruses with begomoviruses. Hence may provide scientific community in depth knowledge about the diversity and prevalence of mastreviruses globally, not only in monocots but also in dicots together with begomoviruses. Whereas, it will further open avenues for researchers to find out the potential factors, which made the mastreviruses to evolve from monocotyledonous plants to dicotyledonous and their ability to cause infection in non-host plants, thus expanding its host range with the passage of time.

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