

# Genome organization of satellite DNA beta molecule associated with Mungbean yellow mosaic India virus Gujarat, India

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# ABSTRACT

Recent advancements in genomics have unveiled fascinating insights into the intricate world of plant pathogens. The discovery of an intriguing association between the DNA beta and MYMIV-[IN:Ana: CpMBKA25:04], a strain containing 1367 base pairs of nucleotides, has sparked a wave of scientific curiosity. Through sequence identity matrix analysis, it was revealed that this strain shares a striking 96% similarity with the Potato apical leaf curl virus, closely followed by the Tomato leaf curl beta satellite virus [Accession No. AY230138] at 95.3%. In contrast, its relationship with the beta satellite Bhendi yellow vein beta satellite [Accession No. AJ308425] stood at a comparative 45.7% when compared against seventeen other DNA beta isolates infecting various crops. Noteworthy features of the beta satellite sequences include a distinctive putative stem-loop structure TAATATT/AC in the common region and a recurring GCTACGC repeat sequence. An A-rich region spanning from nucleotides 910 to 1120 further adds to the genetic complexity of this novel strain. Intriguingly, an analysis of the amino acid sequence unveiled additional residues V, C, and N at the carboxyl end of the  $\beta$ C1 protein, setting it apart from its counterparts. The identity matrix analysis established a 95.9% similarity between  $\beta$ C1 and the beta satellite associated with Tomato leaf curl Karnataka virus and Potato apical leaf curl virus, phylogenetic analysis placed the beta satellite linked with MYMIV-[IN:Ana: CpMBKA25:04] in a distinct category within the Papaya leaf curl virus family, shedding light on its unique evolutionary lineage and biological significance in the realm of plant virology.

 ${\it Keywords:} {\it An A-rich region spanning from nucleotides 910 to 1120 further adds to the genetic complexity of this novel strain.}$ 

# **INTRODUCTION**

Begomoviruses are known to be agreat threat to several agriculture crops. They include cotton, okra, tobacco, and tomato and yellow mosaic diseases in grain legumes in the tropics for a long time. Since the Green Revolution (GR) period, begomoviruses spread their host range enormously and spreading to weeds also [1] [2]. Grain legumes cultivated as rainfed and irrigated crops in Gujarat are severely affected by whitefly-transmitted yellow mosaic disease (YMD) which is a bipartite begomovirus relicating in a rolling circle mechanism [3] belonging to the family *Geminiviridae*. Monopartite and begomoviruses are associated with a small satellite designated as DNA- $\beta$ . Uptil now more than 200 satellite sequences have

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been established from variety of plants which includes a range of weeds, vegetables and fibre crops in Africa and Asia, reflecting their diversity and impact on agriculture throughout the Old World [4]. Basil Kassanis in 1962 used the term satellite virus for the 17 nm diameter particles associated with tobacco necrosis virus. There are three types of circular ssDNA satellite molecules. They are alphasatellites, betasatellites, and deltasatellites are associated with diseases caused by begomoviruses. The satellites, in general, may have originated from genetic elements that were once part of the viral genome but eventually lost their ability to replicate independently [1] and also replicate similar rolling circle and recombinationdependent replication mechanisms [5]. As there is no report on the molecular characterization of beta satellite viruses causing YMD in legumes in Gujarat, the present study is focused on molecular cloning of genomic components of yellow mosaic viruses (YMV) infecting legumes and establishment of their relationship with other reported beta satellite viruses.

#### **MATERIALS AND METHODS**

MYMIV infected legume samples were used for DNA using the modified CTAB method [6]. PCR amplification was done based on the sequence of DNA beta satellite region using universal primers [7] PCR products were cloned in pGEM-T Easy vector. Computer analysis of sequence was carried out using the software programme Bioedit version 5.0.9, CLASTALW, the neighbour-joining method by MEGA version 3.1.

Sr. No.	Name of Virus	Accession No
1	Mungbean yellow mosaic India virus associated DNA beta:IN:Ana: CpMBKA25:04	DQ118862
2	Tomato leaf curl virus-associated DNA beta	AY230138
3	Tomato leaf curl virus-associated DNA beta	AY438557
4	Tomato leaf curl virus-associated DNA beta	HM101175
5	Potato apical leaf curl virus associated DNA beta	EF043234
6	Papaya leaf curl virus associated DNA beta	AY244706
7	Cotton leaf curl Multan virus associated DNA beta	EU384579
8	Cotton leaf curl virus-associated DNA beta	AY083590
9	Bhendi yellow vein mosaic virus-associated DNA beta virus	AJ308425
10	Tomato leaf curl-associated DNA beta	AJ316035
11	Ageratum yellow vein virusassociated DNA beta	EF527824
12	Chilli leaf curl virus satellite DNA beta C1 gene	FN179279
13	Tobacco leaf curl virus-associated DNA beta	NC_013800
14	Zinnia leaf curl virus-associated DNA beta C1 gene	AJ542499
15	Tomato leaf curl Karnataka virus-associated DNA beta	AY754813
16	Tomato leaf curl Bangalore virus-[Ban5] satellite DNA beta	EU280314
17	Cowpea severe leaf curl-associated DNA beta	AY728263

Table 1:List of beta satellites associated with begomoviruses with their accession numbers from GenBank used for all sequence analysis

# **Results and Discussion**

The sequence analysis of the beta satellite of Mungbean yellow mosaic India virus-[IN:Ana: CpMBKA25:041350] showed 1367 base pairs of nucleotides and their genome analysis is shown in Fig. 1-4 and Table 2. The sequence analysis showed the presence of iteron-like elements homologous which help in the replication.TAATATTAC is also present in the  $\beta$  satellite which is a common feature of geminiviruses. The Gujarat isolate showed the presence of an adenine-rich region, a satellite-conserved region and a single ORF encoding βC1 protein. Several studies show that the symptom development depends upon  $\beta$ C1 protein. The present study supports the presence of  $\beta$  satellite which is occurring mainly in Africa and Asia with maximum diversity from the Indian continent. The similarity identity matrix showed that the whole genome had 96 % similarity with Potato apical leaf curl virus-associated DNA beta and approximately 96 per cent identity with Potato apical leaf curl virus-associated DNA beta and Tomato leaf curl virus associated DNA beta viruses (Karnataka isolate) in  $\beta$ C1 region. The amino acid sequence showed similarity with those of other viruses which consisted of extra amino acid residues V, C, N in the BC1 protein at the carboxyl end. Whne all the isolates were compared with MYMIV-[IN:Ana: CpMBKA25:04] isolates it is found to be a distinct isolate belonging to the Papaya leaf curl virus. Begomoviruses family Geminiviridae causes viral diseases in economically important crop plants. Genomically begomoviruses possess two genomic components DNA A and DNA B. DNA  $\beta$  components do not show any homology to helper

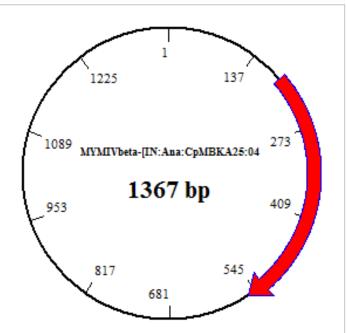
begomoviruses. But they depend upon them for replication, encapsidation and movement. DNA  $\beta$  play a role in the hostspecific symptoms in plants. Previous studies show that DNA  $\beta$ components exist in nature. So present paper also reveals the presence of DNA  $\beta$  component present in the legumes. Usually,  $\beta$ satellites are found to be associated with monopartite begomoviruses. Nowadays they are found to be spreading in bipartite begomoviruses spreading in the old world too. Earlier it has been reported from MYMIV infecting cowpea [8], mungbean [9] and tomato [10], chilli [11] [12] and kenaf [13]. Other part of the world showed the association of DNA  $\beta$  in Sri Lankan cassava mosaic virus [14], Tomato yellow leaf curl Thailand virus [15], and the New World bipartite Cabbage leaf curl begomovirus [16]. The presence of  $\beta$  satellite associated with begomoviruses was found to play a significant role in the evolution of begomovirus. Initiation of replication as well as the control of complementary-sense gene expression in DNA  $\beta$  is initiated by TAATATTAC [17]. TAATATTAC is a universally conserved region within the loop of a hairpin structure and it is a nonanucleotide sequence. Rep protein nicks at its downstream of the virion sense strand [18] [19]. Tobacco ring spot nepovirus was identified as the first satellite RNA in 1969 [20]. The first monopartite begomovirus satellite ToLCV-sat was isolated from tomato plants [21]. Different studies and its compilation shows that DNA satellites usually consists of 1350 nucleotides and they are called as DNA  $\beta$ . They are usually seen in the case of monopartite begomoviruses [7] [22] [23] [24] [25]. Betasatellites are usually the half of the genome size of the helper begomoviruses [26].

Satellite virus they depend upon the helper virus for its replication. Ageratum yellow vein virus (AYVV) infects ageratum plants when inoculated with the virus. But when it is inoculated in Nicotiana benthamiana, it produces asymptomatic infection and indicates the requirement of the presence of a helper virus like satellite molecule [27]. Cotton leaf curl Multan virus (CLCuMV) and Tomato leaf curl virus (ToLCV) showed severe symptoms in the plants in the presence of the helper virus [28] [29] [30]. This shows the role of  $\beta$  satellites in the disease symptoms [31)], virus movement in plants [32], binds DNA in a sequence non-specific manner [33], is a suppressor of RNA silencing [34] [35], forms homo-multimeric complexes in planta [35], inter feres with host gene expression [36] and has been shown to interact with a variety of host factors [37] [38]. So similarly at present too MYMIV infects legumes and its ability to infect Nicotiana benthamana is yet to be explored with its presence of  $\beta$  satellite virus. In the present studies, components contain an A-rich region suggesting that they may have originated as a bonafide component of another pathogenic agent before being captured by the begomovirus necessitating a slight increase in size as shown by earlier studies [4]. In addition to the above mentioned A-rich region,  $\beta$  satellite virus components usually in common posees a single gene  $\beta$ C1. It is a highly conserved sequence consisting of 80 nucleotideswhich is known as the satellite-conserved region (SCR) and PCR primers based on this sequence have provided a simple and robust method for the isolation of DNA-β components [23]. During the past years, it has been found from the database that more than one hundred full-length DNA- $\!\beta$  sequences have been deposited in from plant species belonging to the family Malvaceae and those associated with non-Malvaceae [39]. A similar trend also can be seen in the present study. The present study also shows its phylogenetic relationship showing as a distinct clade differing from the isolates of monopartite viruses like Tomato leaf curl virus and the Malvaceae family. Eralier studies showed that distinct betasatellite species share a high level of sequence identity with respect to  $\beta$ C1 gene which are responsible for inducing distinct symptoms. The whitefly performance is alaso dependenet on the serine-33, a conserved phosphorylation site in betasatellite-encoded  $\beta$ C1 protein which suppresses the plant terpenoid-based defense[40]. The identification of a relatively high level of diversity of beta satellites in okra showed possibility of development of resistance by both conventional breeding and transgenic approaches [26]. Previous studies interpret the possibility of monopartite begomoviruses of the other host might move legumes aided by the associated betasatellites. Still a lot of research is yet required to know association of betasatellites with MYMIV and MYMV will affect its host range, virulence and transmission to contain the YMD spread and mitigate the yield loss [41].



**Fig. 2** Iteron acharacteristics in the common region of beta satellite of Mungbean yellow mosaic India virus-[IN:Ana: CpMBKA25:04].

#### complement(189..557)



**Fig 1**Genome organization of beta satellite of Mungbean yellow mosaic India virus-[IN:Ana: CpMBKA25:04]

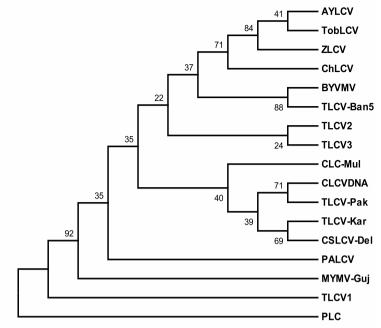
			<u> </u>					
	890	900	910	920	930	940	950	960
MYMV-Guj						TCACACATAA		
TLCV1						TCACACATAA		
TLCV2						TCACACATAA		
TLCV3						TCACACATAA		
PALCV						TCACACATAA		
PLC	ATGGCCCCCAGGGG/							
CLC-Mul						AGGACATAT		
CLCV						AGGATATAT		
BYVMV		GAA/	T-AGAG	GAAAAATGAA		AGGAAATATA	ТАТАААСТАА	GAAAA
TLCV-Pak		GAAG	TGAAGAG	GAAAAACAAA	GAAAAGAAAC/	AGGATATAT	TATTTA-TGA	AAGAA
AYLCV		ААААА	CTAATA-	-ATAAAAATA	ACTATCTATT	CATTGGAAATG	GGAGCGCAG	TCAAA
ChLCV	AAA	AAAATAAAAA	CGAAAA-	CATGAAAGGA/	ACC-AGAAAC	ATGAGCAGAAA	CAAAAATATO	ATGAG
TobLCV		AAAJ	TTAAAA-	-AAA <mark>T</mark> AAAAA	AA <mark>T</mark> AGAAAAC <sup>1</sup>	ACATAGACC-	CTAAATTCT/	TTATA
ZLCV	GA0	GAA <mark>T</mark> GTAAACA/		CATATAAAAA	AAAAGAAAAA	GGATAAAAGC	ATGGATAAT	TTGAG
TLCV-[Ban5]		CAGO	TTAAAA-	AAAAGGA/	AATAAATAAC/	ACTACACCTA-	CCAAACATT/	TTGAG
TLCV-[Kar]	AAAJ	AGAATTAAAAAA	ACAAAA	CATGGAAGGA/	AAAGACAAAT/	ATGAACACAAA	CAGAAATCT	TTGAG
CSLCV-Del	AAT/	AGAATTAAAAAA	ATAAAA-	CATGGAAGGA/	AAAGA <mark>C</mark> AAAC/	ATGAGCACAAA	GAGAAATCTO	TTGGG
	970	980	990	1000	1010	1020	1030	1040
MYMV-Guj	AAAATATGGCCCCGC/							
TLCV1	AAAATATGGCCCCGC/							
TLCV2	AAAATATGGCCCCGC/							
TLCV3	AAAATATGGCCCCGC/							
PALCV PLC	AAAATATGGCCCCGC/ AAAATATGGCCCCGC/							
CLC-Mul	ATGGGAGCGCGGCGA							
CLCV	ATGGGAGCGCAGCGA							
BYVMV	AAGAAAAGGGAGCGC							
TLCV-Pak	ATGGGAGCGCAGCGA							
AYLCV	CGAAAACAAAAATCAA							
ChLCV	AAAATATGGGAGCGC/							
TobLCV	TGAAAATGGTCGCGC/							ACAAC
ZLCV	AAAAAAGGGAGCGC	AGCGAAAAAAAA	AA	ААААААСААА	TGACTGAGAG	JAAAAATAAAA	G	
TLCV-[Ban5]	AAAACATGGCCCCGC/	AGGGGAACTGAA	GCCGA	ACAAGAAACAG	TGGACTAAA	CATCAGAAAC	ATACGAAATO	CATAC
TLCV-[Kar]	AAAATTTGGGAGCGC/	AGCGAAACGAAA	GCCCG	AAACTTGAGG/	AAGATATTA	ATAGAATAAAA	G-AAAAGC1	CACAT
CSLCV-Del	AAATTTTGGGAGCGC/	AGCGAAAAAAAA	CATCC	AAACAAGGAA	ACAACCGAAA	ACATGATCAGA	G-AAAA	
	1050	1060	1070	1080	1090	1100	1110	1120
MYMV-Guj	GTCACGGTTTTGA					AAATAAATTAA		
TLCV1	GTCACGGTTTTGA					AATAAATTAA		
TLCV2	GTCACCGTTTTGA					AATAAATTAA		
TLCV3	GTCACGGTTTTGA					AATAAATTAA		
PALCV	GTCACGGTGTTGA					AAATAAATTAA		
PLC	GTCACGGTTTTGA					AATAAATTAA		
CLC-Mul	GAAAACGTCATCGTT					ATATCCGAAAA		
CLCV	GAAAACGTCATCGTT					ATATCCGAAAA		
BYVMV	AAAAG					GTTTTGAGGA		
TLCV-Pak	GAAAACGTCATCGTT					ATATCCGAAAA		
AYLCV	AAAAGTTATTACATA					AAATAATTCTA		
ChLCV		ACACAAAACT				AAATACAGAAA		
TobLCV	ATATGAAACGTGAGA							
ZLCV	GTCTTCCGTA					AATAAAAGGG		
TLCV-[Ban5]	GTGTGGCTGCACGTG					AAATAAATCGT		
TLCV-[Kar] CSLCV-Del	ATCCACAACCATA/					GA-TAAAAAA		
CSLCV-Del	CGGA/	AAGACAAACG	AA	ACTGATAGGT	CETETIGTA	AAAATAAGAAA	ATCCUTACA	AGTAA

**Fig. 3A** – rich region in the genome of the beta satellite of Mungbean yellow mosaic India virus-[IN:Ana: CpMBKA25:04]

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	10	20	30	40	50	60	70	8
MYMV-Gui						TRSPALVKKK		
TLCV1			24		~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~			
TLCVI TLCV2		MTJ						
TLCV2 TLCV3								
						TRSPALVKKK		
PALCV						STRSPALVKKK		
PLC			24		~	STRSPALVKKK		
CLC-Mul						STKSPSLIKYE		
CLCVDNAR						STRSPSLIRYE		
BYVMV	MRISIHFIYIFISM							
TLCV-Pak						STRSPSLIRYE		
AYLCV		MT]	SHTNDRGVL	FIINVRLRSEI	RETVDVEVES	STRSPALVENK	PSIPYGHHGI	IPPFN
ChLCV		MQMT1	KYNNEKGME	FTINVKINDD	SLLVRVDLCS	TRSPALARET	PMI PYGHDGI	IPPF
TobLCV	]	TYEHSHNTMT]	KYKNQKGME	FIIDVRLKEDS	SILVQIQLFS	STGSPALATRK	<b>MIPYGHDGI</b>	IPPF
ZLCV		MTI	KYSNKKGMS	FIIDVRLRTT	RVSVEIDLFS	STTTPFLHKQR	<b>YIIPYGHQGL</b>	IGPF
TLCV-[Ban5]		MTI	<b>RYVNRNGLM</b>	FIINVRLKGDE	SIRVHIQLTS	TRSPALVERE	<b>VIPYGHNGL</b>	IPPF
TLCV-[Kar]		MTI	KYNTEKGME	TIDVKITRDN	SIIVQIELFS	TQSPALAKKT	MIPYGHDGI	ITPF
CSLCV-Del		MTI	KYNNKRGME	FTIDVKINEDN	SIVVOIELES	TOSSALARET	MIPYGHDGI	IPPF
	90 							
MYMV-Guj	FNNLEEGIRNILAI	MYRDSSFDEFE	DEDMTEIID	I LMMHEAPVFE	IQIFDEYGVO	TNVSARVCN		
TLCV1	THE REPORT OF TH	MYRDSSFDEFE	QEDMTEIID:	I LMMHEAPVFE	IQIFDEYGVO	TNVSA		
	FNNLEEGIRNILA							
	FNNLEEGIRNILAJ		QEDMTEIID:	I LMMHEAPVFE	IQIFDEYGVO	TNVSA		
TLCV2		IMYRDSSFDEF						
TLCV2 TLCV3	FNNLEEGIRNILAI	IMYRDSSFDEFE IMYRDSSFDEFE	QEDMTEIID	I LMMHEVPVFI	IQIFDEYGVO	TNVSA		
TLCV2 TLCV3 PALCV	FNNLEEGIRNILAI FNSLEEGIRNMLDI	IMYRDSSFDEFF IMYRDSSFDEFF IMYRDSSFDEFF	QEDMTEIID	I LMMHEVPVFT I LMMHEAPVFT	IQIFDEYGVO	TNVSA		
FLCV2 FLCV3 PALCV PLC	FNNLEEGIRNILAI FNSLEEGIRNMLDI FNNLEEGIRNILAI	IMYRDSSFDEFF IMYRDSSFDEFF IMYRDSSFDEFF IMYRDSWFDEFF	QEDMTEIID QEDMTEIID QEDMAEIID	ILMMHEVPVFI ILMMHEAPVFI ILMMHEAPVII	DIQIFDEYGVO DIQIFDEYGVO DIRIFDEYGVO	CTNVSA CTNVSA CTNVCA		
FLCV2 FLCV3 PALCV PLC CLC-Mul	FNNLEEGIRNILAJ FNSLEEGIRNMLDJ FNNLEEGIRNILAJ FNNLEEGIRNILDJ	IMYRDSSFDEF IMYRDSSFDEF IMYRDSSFDEF IMYRDSWFDEF FAYNGARIEEIF	QEDMTEIID QEDMTEIID QEDMAEIID SIEDIVHRLD	ILMMHEVPVFI ILMMHEAPVFI ILMMHEAPVII ILVLENPEILO	DIQIFDEYGVO DIQIFDEYGVO DIRIFDEYGVO MDVNEPYVFI	CTNVSA CTNVSA CTNVCA IKKFTV		
TLCV2 TLCV3 PALCV PLC CLC-Mu1 CLCVDNAR	FNNLEEGIRNILAJ FNSLEEGIRNMLDJ FNNLEEGIRNILAJ FNNLEEGIRNILDJ FNGFEGSIIANFLI	IMYRDSSFDEFI IMYRDSSFDEFI IMYRDSSFDEFI IMYRDSWFDEFI FAYNGAKIEEI FAYNGAKIEEI	QEDMTEIID QEDMTEIID QEDMAEIID XIEDIVHRLD XIEDIVHRLD	ILMMHEVPVFI ILMMHEAPVFI ILMMHEAPVII ILVLENPEILO ILVLENPEILO	DIQIFDEYGVO DIQIFDEYGVO DIQIFDEYGVO DIRIFDEYGVO MDVNEPYVF1 MDVNEPYLF1	CTNVSA CTNVSA CTNVCA IKKPTV IKKPTV		
FLCV2 FLCV3 FLCV FLC CLC-Mu1 CLCVDNAR BYVMV	FNNLEEGIRNILAJ FNSLEEGIRNMLDJ FNNLEEGIRNILAJ FNNLEEGIRNILDJ FNGFEGSIIANFLH FNGFEGSIIANFLH	IMYRDSSFDEFI IMYRDSSFDEFF IMYRDSSFDEFF IMYRDSWFDEFF FAYNGAKIEEIF FAYNGAKIEEIF FHYWGSKAEEII	QEDMTEIID QEDMTEIID QEDMAEIID SIEDIVHRLD SIEDIVHRLD EEDIIHMVD	ILMMHEVPVFI ILMMHEAPVFI ILMMHEAPVFI ILVLENPEILO ILVLENPEILO IIIIENPDIMO	DIQIFDEYGVO DIQIFDEYGVO DIQIFDEYGVO MDVNEPYVFI MDVNEPYLFI MDVNEPVTII	CTNVSA CTNVSA CTNVCA IKKPTV IKKPTV NKIII		
FLCV2 FLCV3 PALCV PLC CLC-Mul CLCVDNAR BYVMV FLCV-Pak	FNNLEEGIRNILAJ FNSLEEGIRNMLDJ FNNLEEGIRNILAJ FNNLEEGIRNILDJ FNGFEGSIIANFLH FNGFEGSIIANFLH FNGLEGTITSTFKH	IMYRDSSFDEF IMYRDSSFDEF IMYRDSSFDEF IMYRDSSFDEF PAYNGAKIEE PAYNGAKIEE PHYWGSKAEEI PAYNGAKIEEI	QEDMTEIID QEDMTEIID XQEDMAEIID SIEDIVHRLD EEDIVHRLD EEDIIHMVD SIEDIVHRLD	ILMMHEVPVPI ILMMHEAPVPI ILMMHEAPVII ILVLENPEILC ILVLENPEILC IIIIENPDIMC ILVLENPEILC	DIQIFDEYGV DIQIFDEYGV DIRIFDEYGV MDVNEPYVF MDVNEPYLF MDVNEPVTII MDVNEPYVF	TTNVSA TTNVSA IKKFTV IKKFTV NKIII IKKFTV		
FLCV2 FLCV3 PALCV PLC CLC-Mul CLCVDNAR BYVMV FLCV-Pak AYLCV	FNNLEEGIRNILAJ FNSLEEGIRNMLDJ FNNLEEGIRNILAJ FNNLEEGIRNILAJ FNGFEGSIIANFLI FNGFEGSIIANFLI FNGFEGSIIANFLI	IMYRDSSFDEFI IMYRDSSFDEFI IMYRDSSFDEFI IMYRDSWFDEFI PAYNGAKIEEIF PHYWGSKAEEI PAYNGAKIEEIF PAYNGAKIEEIF IMYRDSTIEEFI	QEDMTEIID QEDMTEIID CEDMAEIID SIEDIVHRLD EEDIIHRVD EEDIIHMVD SIEDIVHRLD CSEDMVEIID	ILMMHEVPVPI ILMMHEAPVPI ILMMHEAPVII ILVLENPEILC ILVLENPEILC IIIIENPDIMC ILVLENPEILC IMMQQEAPVII	DIQIFDEYGV DIQIFDEYGV DIRIFDEYGV MDVNEPYVF MDVNEPYVF MDVNEPYVF MDVNEPYVF DIQVNDEYHV	TTNVSA TTNVCA IKKFTV IKKFTV NKIII IKKFTV IKKFTV		
PLCV2 PLCV3 PALCV PLC CLC-Mu1 CLCVDNAR BYVMV FLCV-Pak AYLCV ChLCV	PNNLEEGIRNILAJ PNSLEEGIRNHLDI PNNLEEGIRNILAJ PNNLEGIRNILAJ PNGPEGSIIANPLI PNGPEGSIIANPLI PNGPEGSIIANPLI PNGLEEGIRNILRJ	IMYRDSSFDEFI IMYRDSSFDEFI IMYRDSSFDEFI IMYRDSWFDEFI FAYNGAKIEEIF FHYNGSKAEEII IMYRDSTIEEFF IMYRDSTIEFFI IMYRDSEIGEFF	CEDMTEIID CEDMTEIID CEDMAEIID SIEDIVHRLD SIEDIVHRLD SIEDIIHMVD SIEDIVHRLD CEDMVEID CEDMVEID	ILMMHEVPVFI ILMMHEAPVFI ILMMHEAPVFI ILVLENPEILO ILVLENPEILO ILILENPEILO ILVLENPEILO IMMQQEAPVFI ILMMHEAPVVT	DIQIFDEYGVO DIQIFDEYGVO DIQIFDEYGVO MDVNEPYVFI MDVNEPYVFI MDVNEPYVFI MDVNEPYVFI DIQVNEPYVFI DIQVNDEYHVY DIQVNDEYHVY	TTNVSA TTNVCA IKKFTV IKKFTV NKIII IKKFTV KKPTV TTNVYV		
TLCV2 TLCV3 PALCV PLC CLC-Mul CLC-Mul CLCVDNAR BYVMV TLCV-Pak AYLCV ChLCV TobLCV	PNNLEEGIRNILAJ PNSLEEGIRNHLAJ PNNLEGIRNILAJ PNNLEGIRNILAJ PNGPEGSILANFLI PNGPEGSILANFLI PNGLEGITTSTPKI PNALEGIRNILRI PNALEGIHNILKI PNALEEGIHNMLAI	MYRDSSFDEFF MYRDSSFDEFF MYRDSWFDEFF MYRDSWFDEFF FAYNGAKIEEIF FYWGSKAEEII MYRDSTLEEFF MYRDSTLEEFF MYRDSEIGEFF MYRDSEIGEFF	QEDMTEIID QEDMTEIID QEDMAEID SIEDIVHRLD SIEDIVHRLD SIEDIVHRLD SIEDIVHRLD SIEDIVHRLD SIEDIVHRLD SIEDIVHRLD SIEDIVELD	ILMMHEVPVFI ILMMHEAPVFI ILMMHEAPVFI ILVLENPEILO ILVLENPEILO ILVLENPEILO ILVLENPEILO IMMQQEAPVII ILMMHEAPVVI MLMMEEAPVII	DIQIFDEYGVC DIQIFDEYGVC DIQIFDEYGVC MDVNEPYVFN MDVNEPYVFN MDVNEPYVFN MDVNEPYVFN DIQVNDEYHV DIQVNDEYHV DIQVNDEYHV DIQVNDEYHV DIQVNDEYHV DIQVNDEYHV DIQVNDEYHV	TINVSA TINVCA IKKPTV IKKPTV IKKPTV TINVYV TINVYV TINVYV		
TLCV2 TLCV3 PALCV PLC CLC-Mul CLCVDNAR BYVMV TLCV-Pak AYLCV ChLCV TobLCV ZLCV	FNNLEEGIRNILAJ FNSLEGIRNILAJ FNNLEEGIRNILAJ FNNLEEGIRNILAJ FNGFEGSILANFLI FNGFEGSILANFLI FNGEGSILANFLI FNGEGSILANFLI FNGEGSILANFLA FNALEGIRNILAI FNALEGIRNILAI FNALEGIRNILAI	MYRDSSPDEFF MYRDSSPDEFF MYRDSSPDEFF MYRDSWFDEFF AYNGAKIEEIF PAYNGAKIEEIF MYRDSTIEEFF MYRDSTIEFF MYRDSTIEFF MYRDSTOEFF	QEDMTEIID QEDMTEIID QEDMAEID IEDIVHRLD SIEDIVHRLD SIEDIVHRLD SIEDIVHRLD SEDMTEID QEDMVESID QEDMVESID GEDMIELVD	I LIMHEVPYFI I LIMHEAPYFI I LIMHEAPYFI I LIMHEAPYFI I LVLENPEILC I LVLENPEILC I LVLENPEILC I LMMPELAPYFI I LIMHEAPYFI I LMMEAPYFI I LMMQEAHYFE	DIQIFDEYGVG DIQIFDEYGVG DIQIFDEYGVG MDVNEPYVFN MDVNEPYVFN MDVNEPYVFN MDVNEPYVFN JIQVNDEYHV JIQVNDEYHV JIRIGDEYDVG DINVMDAYDVJ SINLDEEYKVS	TTNVSA TTNVSA TTNVCA IKKPTV NKIII IKKPTV TTNVV TTNVV TTNVV KHTSV		
TLCV2 TLCV3 PALCV PLC CLC-Mu1 CLC-VDNAR BYVMV TLCV-Pak AYLCV ChLCV TobLCV ZLCV TLCV-[Kar]	PNNLEEGIRNILAJ PNSLEEGIRNHLAJ PNNLEGIRNILAJ PNNLEGIRNILAJ PNGPEGSILANFLI PNGPEGSILANFLI PNGLEGITTSTPKI PNALEGIRNILRI PNALEGIHNILKI PNALEEGIHNMLAI	IMYRDSSPDEFF IMYRDSSPDEFF IMYRDSSPDEFF IMYRDSWFDEFF IMYRDSWFDEFF AYNGAKIEEIF PHYNGSKAEEII MYRDSTIEEFF IMYRDSTIEFF IMYRDSTIEFF IMYRDSTIEFF IMYRDSTIEFF IMYRDSTIEFF	QEDMTEIID QEDMTEIID QEDMAEID IEDIVHRLD IEDIVHRLD IEDIVHRLD IEDIVHRLD GEDVFEID QEDMVEID GEDMTELD GEDMTELD	ILMMHEVPVFI ILMMHEAPVFI ILMMHEAPVFI ILVLENPEILG ILVLENPEILG ILVLENPEILG ILVLENPEILG ILMMHEAPVVI ILMMHEAPVVI MILMMEAPVVI MILMMEAPVV-	DIQIFDEYGVC DIQIFDEYGVC DIQIFDEYGVC MDVNEPYVFN MDVNEPYVFN MDVNEPYVFN MDVNEPYVFN DIQVNDEYHV JIRIGDEYDVC DINVMDAYDVN SINLDEEYKVC	TTNVSA TTNVSA TTNVCA IKKPTV NKI I I NKI I I IKKPTV TTVYV TTNYV TTHSSV KEATSV ILCVCV		

**Fig 4** Predicted Amino acid sequence of the beta satellite of Mungbean yellow mosaic India virus-[IN:Ana: CpMBKA25:04].



**Fig:5** Phylogenetic relationship between sequence of the beta satellite of Mungbean yellow mosaic India virus-[IN:Ana: CpMBKA25:04] with other ßDNA of begomoviruses

**Table2:** Percentage identity of the nucleotide sequence in the complete genome and ßc1 of the beta satellite of Mungbean yellow mosaic India virus-[IN:Ana: CpMBKA25:04] with other ßDNA of begomoviruses

<b>ßDNA of begomovirus isolates</b>	The whole genome of the Beta satellite	Beta C1
Tomato leaf curl virus-associated DNA beta	92.0	95.9
Tomato leaf curl virus-associated DNA beta	95.3	94.2
Tomato leaf curl virus-associated DNA beta	94.3	89.3
Potato apical leaf curl virus associated DNA beta	96.0	95.9
Papaya leaf curl virus associated DNA beta	80.8	85.2
Cotton leaf curl Multan virus associated DNA beta	48.1	24.5
Cotton leaf curl virus-associated DNA beta	50.4	24.5
Bhendi yellow vein mosaic virus-associated DNA beta virus	45.7	23.6
Tomato leaf curl-associated DNA beta	50.1	24.5
Ageratum yellow vein virus associated DNA beta	55.6	60.6
Chilli leaf curl virus satellite DNA beta C1 gene	61.5	66.9
Tobacco leaf curl virus-associated DNA beta	61.1	58.7
Zinnia leaf curl virus-associated DNA beta C1 gene	56.7	49.1
Tomato leaf curl Karnataka virus-associated DNA beta	73.3	68.0
Tomato leaf curl Bangalore virus-[Ban5] satellite DNA beta	59.8	61.4
Cowpea severe leaf curl-associated DNA beta	61.2	61.4

### **CONCLUSION**

Satellite DNA beta found to be associated with Mungbean yellow mosaic India virus-[IN:Ana: CpMBKA25:04]. Present study shows the presence of DNA- $\beta$  components that pose a threat to agriculture throughout the Old World. The recent isolation of novel satellite components suggests that other disease complexes and subviral components may exist and its role in symptom and transmission requires much exploration. DNA- $\beta$ and DNA-A and DNA-B can show the possibility of interacting with different begomoviruses.

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