INTERNATIONAL JOURNAL OF APPLIED BIOLOGY AND PHARMACEUTICAL TECHNOLOGY

www.ijabpt.com Volume-4, Issue-4, Oct-Dec-2013 Coden : IJABPT Copyrights@2013

ISSN : 0976-4550

Received: 09th August-2013 *Revised: 18th August-2013* *Accepted: 29th August-2013*

Review article

A BRIEF REVIEW ON "MOLECULAR DETECTION AND CHARACTERIZATION OF YELLOW MOSAIC VIRUS (YMV) INFECTING BLACKGRAM"

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Blackgram (*Vigna mungo* (L.) Hepper) is one of the major pulse crops of the tropics and sub tropics. It is the third major pulse crop cultivated in the Indian subcontinent. Pulses and grain legumes are major sources of dietary protein. These crops are subjected to yellow mosaic and golden mosaic diseases caused by white fly transmitted geminiviruses (WTG's or begomovirus). Of these viruses, mungbean yellow mosaic virus (MYMV) is an important one, and it infects five major leguminous species, such as blackgram, greengram, Frenchbean, pigeonpea and soybean causing an annual yield loss of about US $ 300 million (Varma *et al.,* 1992). The MYMV causes 85-100 per cent yield loss in the plants that are infected at the seedling stage (Nene, 1973). MYMV was first observed in Delhi in the late fifties (Nariani, 1960). Virus particles were first observed by Thongmeearkom *et al.* (1981) and purified by Honda *et al.* (1983). Hence the characterisation of Yellow Mosaic Virus is essential to study the variability and to identify any new strains/ variants of YMV prevalent in India and Abroad at molecular level for developing the new resistant genotypes.

The work done in Abroad and India pertaining to characterisation of Yellow Mosaic Virus in Blackgram is critically reviewed and presented here under.

Nariani (1960) was the first person ever to report the mungbean yellow mosaic virus disease from the fields of IARI, New Delhi. The disease is characterised by the presence of bright yellow patches on leaves interspersed with green areas, complete yellowing and stunting of the plants and he reported 20-30 per cent incidence at institute areas. Singh and Verma (1977) reported that two different viruses namely mung urd mosaic virus 1 (MUMV 1) and mung urd mosaic virus 2 (MUMV 2) as the cause of mosaics of mungbean and urdbean causing considerable losses in Haryana. Murugesan and Chelliah (1977) reported a yellow mosaic on greengram sown during March to May months. The increased disease incidence might be attributed to the higher temperatures prevalent during these months, which was favourable for the vector, *Bemisia tabaci* to develop and multiply.

Thongmeearkom *et al.* (1981) reported association of virus like particles with yellow mosaic disease of mungbean in Thailand and observed presence of isometric virus like particles measuring about 15-30 nm in diameter. Further he observed the presence of loose aggregates of VLPs in phloem tissue. Honda *et al.* (1983) reported mechanical transmission of whitefly borne mungbean yellow mosaic virus (MYMV) in Thailand. He observed that purified virus preparations and leaf dip preparations contain geminate particles of 18x30nm. The purified preparation has ultraviolet light absorption spectrum typical of that of nucleoprotein with a A260/A280 value of about 1.3-1.4. Purified preparations and leaf-dip samples contained geminate particles of about 18×30 nm. Muniyappa *et al.* (1987) studied the isolation and characterization of a geminivirus causing yellow mosaic disease of horsegram. An antiserum for HYMV was produced and used in detection of virus in ELISA and ISEM tests, HYMV was also detected in leaf extracts of field infected bambara groundnut, Frenchbean, groundnut, limabean, mungbean, pigeonpea and soybean showing yellow mosaic symptoms. He further tested transmission of *B. tabaci* fed on purified HYMV through parafilm membrane transmitted the virus to all the above listed hosts but not to *Ageratum conyzoides*, okra, cassava, cowpea, fieldbean and tomato.

Krishna reddy (1989) reported that young unfolded leaves were a better source of the virus than old leaves for virus purification. Nath and Saikia (1995) reported that the main constraint for the cultivation of mungbean in Assam was MYMV and its incidence ranged from 8 to 45 percent. They also reported the effect of climate and whitefly population on MYMV incidence with a peak on August sown crop.

Padidam *et al.* (1995) studied the genomes and ORFs of 36 geminiviruses and were compared to obtain phylogenetic trees and frequency distributions of all possible pair wise comparisons with an objective to classify geminiviruses. Such comparisons show that geminiviruses forms two distinct clusters of leafhopper-transmitted viruses that infect monocots (subgroup-1) and whitefly-transmitted viruses that infect dicots (subgroup-III), irrespective of the part of the genome considered. They also showed that all the recognised strains of any one virus will have greater than 90% sequency identity. They also observed that approximately 200 nucleotide of inter cistronic regions (ICR) of geminiviruses are more variable than the remainder of the genome. The amino acid sequence of the coat protein (CP) of subgroup III viruses are more conserved than the remainder of the genome. However, a short N-terminal region (60-70 amino acids) of the CP gene is more variable than the rest of the CP sequence and this region is sufficient to classify a virus isolate or can be used for strains identification. They also used the PCR primers based on the conserved sequences for cloning and sequencing the N-terminal sequences of the CP of the geminiviruses.

Hoper *et al*. (1997) studied the Subgroup-III geminiviruses and are transmitted by the whitefly species *Bemisia tabaci.* An isolate of abutilon mosaic virus (AbMV), a bipartite geminivirus, was not detectable in the DNA extract from insects by Southern blot analysis, nor was the isolate transmissible by the B-biotype of *B. tabaci*, although the viral DNA was amplified (by PCR) from some insects. In contrast, sida golden mosaic virus (SiGMV-Co), a closely related geminivirus, was acquired and transmitted by *B. tabaci* to various host plants. The coat protein of AbMV was replaced with that of SiGMV-Co and the resulting chimeric AbMV was acquired and transmitted to various host plants by *B. tabaci,* indicating that the coat protein plays an essential role in the transmission process by *B. tabaci.*

Asthana (1998) evaluated germplasm and identified PDM-11, PDM-54, PDM-84-139, PDM-84-143 as yellow mosaic resistant varieties that can be utilized in breeding programmes. Basandrai *et al*. (1999) evaluated one hundred diverse stocks of blackgram (*Phaseolus mungo* (L.) for resistance against five different diseases widely prevalent in Himachal Pradesh. They found HPBU 38, HPBU 153, LBG 626 and UG 367 were resistant against mungbean yellow mosaic and web blight. WVG 108 was found resistant against *Cercospora* leaf spot and MYMV and UG 407 was resistant against *Cercospora* leaf spot, MYMV and powdery mildew.

Pant *et al.* (2001) obtained the complete nucleotide sequence of the begomovirus isolate of mungbean yellow mosaic virus (IMYMV-Bg), which infects legumes in India, was determined and compared at the amino acid level with those of other whitefly-transmitted geminiviruses. The genome organization of IMYMV-Bg was similar to that of the begomoviruses except sequence divergence of the common region (CR) between DNA-A and DNA-B. Phylogenetic analysis with other isolates at C-terminal region of coat protein gene gave >92% homology.

Brown *et al.* (2001) applied polymerase chain reaction (PCR) technique to detect and establish provisional identity of begomoviruses through amplification of a 575 bp fragment of the begomoviral coat protein gene (CP), referred to as the 'core' region of the CP gene (core CP). The core CP fragment contains conserved and unique regions, and was hypothesized to constitute a sequence useful for begomovirus classification. Virus relationships were predicted by distance and parsimony analyses using the A component (bipartite viruses) or full genome (monopartite viruses), CP gene, core CP, or the 200 nt of 5'-region of the CP gene. Reconstructed trees and sequence divergence estimates yielded very similar conclusions for all sequence sets, while the CP 5'-200 nt was the best strain discriminator. Alignment of the core CP region for 52 field isolates with reference to begomovirus sequences permitted provisional virus identification based on tree position and extent of sequence divergence. Ganapathy *et al*. (2003) in view of identifying resistance against mungbean yellow mosaic virus in urdbean, they evaluated 71 entries at NPRC, Vamban, Tamil Nadu. They found that RU 2229, VBG 86, 2KU 54, VBG 89, SU16 were highly resistant to MYMV. Pathak and Jhamaria (2004) evaluated fourteen mungbean varieties for resistance against yellow mosaic virus at ARS, Navgaon. They found that ML-5 and MUM-2 were resistant with only 2.22 and 3.12 per cent infection as against cent per cent infection in K-851, a check cultivar.

Peerajade *et al.* (2004) screened 85 genotypes against MYMV at MARS, Dharwad. Among them, GG 41 and GG 42 were found resistant and GG 52 showed moderate resistance. Balaji *et al*. (2004) cloned the mungbean yellow mosaic virus infecting blackgram in Tamil Nadu. He obtained one DNA- A (KA30) clone and five different DNA-B clones (KA21, 22, 27, 28 and 34) from same plant. The sequence identity in the 150-nt common region (CR) between DNA-A and DNA-B was highest (95%) for KA22 DNA-B and lowest (85.6%) for KA27 DNA-B. Agroinoculation of blackgram and mungbean with partial dimmers of KA27 and KA22 DNA-Bs with DNA-A caused distinctly different symptoms. Thus, DNA-B of MYMV-Vig is important determinant of host range between blackgram and mungbean. Karthikeyan *et al.* (2004) cloned one DNA-A and five different DNA-B components of mungbean yellow mosaic virus-Vigna (MYMV-Vig) from a pooled sample of field infected *Vigna mungo* plants from Vamban, South India. MYMV-Vig DNA-A (KA30) and one of the DNA-B components (KA27) exhibited 97% and 95% sequence identities respectively to those of MYMV reported from Thailand. However, the DNA-B components KA 21, KA 22, KA 28 and KA 34 exhibited only 71 to 72% sequence identity to MYMV DNA-B.

Usharani *et al.* (2004) studied the genomic components of the begomovirus causing yellow mosaic disease (YMD) in soybean in Delhi, cloned, sequenced and infectivity proved. Nucleotide sequence analysis of the virus isolate revealed more than 89% identity with mungbean yellow mosaic India virus (MYMIV) and therefore it is designated as soybean isolate of MYMIV (MYMIV- [Sb]). Based on nucleotide sequence analysis of MYMIV-(Sb) with other YMV isolates infecting legumes they established the involvement of at least two distinct viruses in the etiology of soybean YMD in India.

Hameed *et al.* (2004) studied epitope profiles from begomovirus infected cucurbitaceous and leguminous plants and also raised monoclonal antibodies against particles of African cassava mosaic virus, Indian cassava mosaic virus or okra leaf curl virus. They amplified DNA with nucleotide sequences typical of begomovirus DNA-A components from selected mungbean samples and they also done comparisons of the sequences of the amplified DNA with other begomovirus DNA-A sequences and phylogenetic analysis revealed that Pakistani mungbean viruses are isolates of MYMIV.

Surendranath *et al.* (2004) performed agro-inoculations with DNA-A and DNA-B components of mungbean yellow mosaic India virus (MYMIV) isolates differing in their infectivity on cowpea. The exchange of genomic components of the MYMIV isolates occurred in all the leguminous species but not in cowpea. This suggests that there are barriers in cowpea for both replication and systemic movement despite genetic similarity.

Kirthi *et al.* (2004) worked on cotton leaf curl disease (CLCuD) and it was caused by a virus belonging to the *Begomovirus* genus of the family *Geminiviridae*. Most of the begomoviruses are bipartite with two molecules of circular single standard DNA (A and B) encapsulated in icosahedral geminate particles. However, the begomoviruses associated with CLCuD have DNA- β instead of DNA-B. In this article they reported complete genomic sequence of DNA-A component of two CLCuD causing begomoviruses, cotton leaf curl Kokhran virus-Dabavali (CLCuKV-Dab), tomoto leaf curl Bangalore virus-cotton [Fatehabad] (ToLCBV-cotton[Fat]) and partial sequences of two other isolates namely cotton leaf curl Rajasthan virus-Bangalore (CLCuRV-Ban) and cotton leaf curl Kokhran virus Ganganagar (CLCuKV-Gang). They also constructed the phylogenetic tree of these isolates with the other related begomoviruses showed that ToLCBV-cotton (Fat) isolate was close to the tomato leaf curl Bangalore virus-5 whereas CLCuKV-Dab isolate was close to the cotton leaf curl Kokhran virus-Faisalabad1.The above results demonstrate that extensive variability exist in this group of viruses.

Shivaprasad *et al.* (2005) mapped promoters and transcripts and characterized regulatory proteins of mungbean yellow mosaic virus-*Vigna* (MYMV), a bipartite geminivirus in the genus *Begomovirus.* Sharma *et al.* (2005) studied the complete nucleotide sequence of the Indian isolate of cotton leaf curl geminivirus (CLCuV-HS2) coat protein (CP) gene component by using CP specific primers through PCR amplification from field infected cotton plants grown in Haryana, India. They compared amino acid sequence of the putative CP with some other mono and bipartite geminiviruses and revealed a maximum of 97.3% identity with Pakistan cotton leaf curl virus (CLCuV-62). They also determined the nuclear localisation signal located close to the N-terminal of CP gene.

Usharani *et al.* (2005) carried out host range studies by both whitefly transmission and agro-inoculation with a soybean isolate of MYMIV (MYMIV-[Sb]). MYMIV-[Sb] was similar to a cowpea isolate of MYMIV (MYMIV-[Cp]) in its ability to infect cowpea, thus differing from blackgram (MYMIV) and mungbean (MYMIV-[Mg]) isolates, which do not infect cowpea. Genomic analysis of DNA-A and DNA-B components of these MYMIV isolates showed characteristic differences in complete DNA-B nucleotide sequences correlating with host range differences. Girish *et al.* (2005) cloned and determined the complete nucleotide sequences of two soybean infecting begomoviruses from central and southern parts of India. Sequence analysis show that the isolate from Central India is a strain of mungbean yellow mosaic India virus (MYMIV) and the Southern Indian isolate is a strain of MYMV. Multiple DNA-B components could be detected with the soybean strain of MYMV species. The nucleotide sequence similarity between the DNA-A components of the two isolates is higher (82%) than that between the corresponding DNA-B components (71%). Analysis of the common region of the genomic components of these two virus isolates indicate considerable divergence in the origin of replication (*ori*), which did not impair their infectivity as demonstrated for the Central Indian isolate by agro-infection with partial tandem repeats (PTRs) of the genomic components. Detailed sequence and phylogenetic analyses reveal the distribution and possible recombination events among legume infecting begomoviruses from South-East Asia.

Maruthi *et al.* (2006) cloned and sequenced complete DNA-A components of dolichos yellow mosaic virus (DoYMV) isolates from Mysore and Bangalore. DoYMV isolates shared DNA-A nucleotide identities of 92.5-95.3% with previously described North Indian and Bangladesh isolates. They were most similar to mungbean–infecting begomovirus at 61-64% of DNA-A nucleotide identities. Phylogenetic analysis of DNA-A sequence grouped the *Dolichos*- infecting and mungbean infecting begomoviruses into a distinct cluster away from begomoviruses infecting non-leguminous plants in the Indian subcontinent. Singh *et al.* (2006) characterized the genome of bipartite virus associated with YMD of *Dolichos lablab*. They obtained full length clones of DNA-A and DNA-B and sequenced them. The DNA-A sequence analysis showed more than 97% homology with MYMIV-cowpea isolate reported earlier. The phylogenetic analysis of present isolate showed close relationship to legume geminiviruses.

Qazi *et al.* (2006) reported association of MYMIV with yellow mosaic disease in mothbean in Pakistan for the first time. To further confirm the identity of the virus, primers specific for the DNA-B encoded nuclear shuttle protein (NSP) gene of MYMIV (Hussain *et al.,* 2004) were used in PCR. These resulted in amplification of an approximately 800 bp fragment, that was cloned and sequenced. The complete 771 bp sequence of the NSP gene (Accession no AM 233490) showed 95-92% nucleotide sequence identity (94-92% amino acid similarity) to the NSP gene of other MYMIV isolates.

Girish *et al.* (2006) studied on replication-initiator protein (Rep) from a soybean-infecting geminivirus and was over expressed in *E. coli* as a fusion protein with maltose binding protein (MBP). In spite of the presence of the highly soluble MBP as the fusion partner, the over expressed MBP-Rep fusion protein formed insoluble inclusion bodies. The protein was solubilised from the inclusion bodies and refolded. The refolded MBP-Rep protein was purified using ion exchange and amylase affinity chromatography. The activity of the purified MBP-Rep was assessed using an *in vitro* cleavage assay. Soluble and stable MBP-Rep protein was obtained in high abundance, providing the feasibility of large-scale production of active Rep protein for functional characterization and X-ray crystallographic structure determination. Basher *et al.* (2006) screened mungbean germplasm lines against mungbean yellow mosaic begomovirus. Out of 110 mungbean lines, 85 were found as highly resistant (HR), 14 resistant (R) and 5 moderately resistant (MR). Only 6 accessions were graded as susceptible (S) to highly susceptible (HS). This study gave some additional new source of resistance in Pakistan. Choudhury *et al*. (2006) studied the rolling circle mode of replication of geminiviruses and the viral rep protein initiates RCR by the site-specific nicking at a conserved nonamer (TAATAT↓AC) sequence. The mechanism of subsequent steps of the replication process, e.g. helicase activity to drive fork-elongation, etc. has largely remained obscure. They also showed that rep of geminivirus, namely, mungbean yellow mosaic India virus (MYMIV), acts as a replicative helicase. The rep-helicase, requiring ≥6 nt space for its efficient activity, translocates in the 3`→5` direction, and the presence of forked junction in the substrate does not influence the activity to any great extent. Rep forms a large oligomeric complex and the helicase activity is dependent on the oligomeric conformation (~24mer). The role of rep as a replicative helicase has been demonstrated through *ex vivo* studies in *Saccharomyces cerevisiae* and *in Planta* analyses in *Nicotiana tabacum.*

Khan *et al.* (2007) reported association of begomovirus with sweet pepper in Oman by PCR using begomovirus specific degenerate primers (PAL I v 1978/PAR I c 496 and AV 494/AC 1048). The core region (74-604) of coat protein gene of the begomovirus was amplified by PCR with tomato yellow leaf curl virus (TYLCV) specific degenerate primers (Tycp V 369/ Tycp C 1023). The core region of coat protein gene contains highly conserved regions and is used to identify the begomovirus infecting sweet peppers. Shepherd *et al*. (2008) described a method for isolation and cloning of full length geminivirus genomes from dried plant material by combining an Extract-n-Amp based DNA isolation technique with rolling circle amplification (RCA) of viral DNA. Using this method an attempt was made to isolate and clone full length genome components of geminivirus from 102 plant samples including dried leaves stored at room temperature for between 6 months and 10 years with an average hands-on-time to RCA ready DNA of 15min per 20 samples.

McLaughlin *et al.* (2008) gave the first report on association of begomoviruses with sweet pepper and tomato in Belize. They collected virus infected crop plants and weed species from five districts in Belize over a three year period with the aim of determining the diversity of begomoviruses. Sixty five percent of the samples screened via DNA hybridization produced signals indicative of begomovirus infection. Subsequent PCR amplifications and nucleotide sequence analyses revealed the presence of four begomoviruses in Belize.

Rouhibakhsh *et al.* (2008) developed in-expensive protocol for the detection of genomic components of whitefly-transmitted begomoviruses in symptomatic legumes in the field. The method involves extraction with a modified CTAB buffer containing β-mercaptoethanol up to 5% and sodium chloride concentration from 1.4 to 2.0 M. Using this method, PCR amplifiable DNA could be extracted from mature leaves of legume hosts which contain rich in polyphenols, tannins and polysaccharides. The non coding region and full length DNA-A, DNA-B components of yellow mosaic viruses were consistently amplifiable from 97 samples out of 136 tested in PCR reaction, employing primers specific for intergenic regions and full-length genome. John *et al*. (2008) isolated, cloned and sequenced the components of begomovirus causing cowpea golden mosaic disease (CGMD) in Western India. Analysis of the sequences shows the virus to be an isolate of mungbean yellow mosaic india virus, but with a distinct DNA-B component with greater similarity to components of a second legume infecting begomovirus occurring in the region, mungbean yellow mosaic virus. The clones of the virus were readily infectious to cowpea, mungbean, blackgram and French bean by agro-inoculation. However, the wild-type isolate was shown to be easily transmissible by whiteflies between cowpea plants but not to blackgram and mungbean, suggesting that the insect vector plays a major role in determining the natural host range of these viruses.

Ilyas *et al.* (2009) identified a virus related to the LYMVs in a common weed, the legume *Rhynchosia minima* originating from Pakistan. Analysis of the sequence of the virus shows it to be a typical bipartite begomovirus. Sequence comparisons to all other begomovirus sequences available in the databases show the virus from *R. minima* to be distinct, with the highest level of sequence identity (69.5%) to an isolate of mungbean yellow mosaic virus. This indicates that the virus identified here is a new species in the genus *Begomovirus* for which they propose the name Rhynchosia yellow mosaic virus (RhYMV). Barnabas *et al.* (2010) studied the virus that causes horsegram yellow mosaic disease in India and considered as old world bipartite begomovirus. The viral origin of the disease has been established through agro-inoculation of horsegram using partial tandem repeat clones of both DNA-A and DNA-B. The DNA-A genome shows less than 89% identity with the corresponding sequences of all the begomoviruses in the databases. Hence horsegram yellow mosaic virus (HgYMV) may be considered to be a new species of the genus *Begomovirus.*

Briddon *et al.* (2010) described the relationship between the DNA-A and DNA-B components of bipartite begomoviruses with a view to unravelling their evolutionary histories and providing information on the possible origin of the DNA-B component. Comparative phylogenetic and exhaustive pair wise sequence comparison of DNA-A and DNA-B components of 212 geminivirus sequences all over the world demonstrates that the two molecules have very distinct molecular evolutionary histories and likely are under very different evolutionary pressures. The analysis has highlighted the greater genetic variation of DNA-B components, in comparison to the DNA-A components, and that component exchange is more widespread than previously demonstrated and confined to viruses from the old world. Although the vast majority of new world and some old world begomoviruses show near perfect co-evolution of the DNA-A and DNA-B components, this is not the case for the majority of old world viruses.

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Ilyas *et al.* (2010) determined the complete sequences of 44 components (23 DNA-A, 19 DNA-B and 2 beta-satellites) from Pakistan. The results show that only the mungbean yellow mosaic India virus (MYMIV) is of agricultural significance in Pakistan have been isolated from all cultivated grain legumes examined. MYMV a significant crop pathogen in India, was only identified in a weed, which together with a novel species of legume yellow mosaic viruses (LYMV) were reported earlier, represents the first LYMV identified in non-cultivated plants. MYMIV was shown to occur as two types in Pakistan that show phylogeographical segregation. Additionally, two begomovirus species not considered pathogens of legumes and a beta-satellite were isolated. This is of grave concern since it suggests that the presumed genetic isolation of the LYMVs in legumes may be being breached. LYMVs show little, if any, evidence of interspecific recombination with non legume infecting begomoviruses. Thus, either recombination with non legume viruses or interaction with beta-satellites, which are host range and pathogenicity determining satellites of begomoviruses, could lead to the appearance of more aggressive virus variants/strains affecting legumes.

Mahajan *et al.* (2011) studied on a blackgram isolate of MYMV and identified five variable and infective DNA-B components, of which KA22 and KA 27 DNA-Bs share only 72% nucleotide sequence identity between them. Agroinoculation of blackgram with partial dimmers of DNA A and KA27 DNA B caused severe stunting and an inordinate delay in flowering. Interestingly, co-agroinoculation of KA27+KA22 DNA-B components along with DNA A ameliorated severe stunting, rescued from the delay in flowering and caused the appearance of yellow mosaic symptom characteristic of KA22 DNA-B. Post-agroinoculation of KA-27 DNA B-infected blackgram plants with KA22 DNA-B also resulted in the amelioration from severe stunting and in the alleviation from the delay in flowering. Alleviation from KA27 DNA-B type of symptom by co-infection or post-infection with KA22 DNA B did not result in a corresponding reduction in KA27 DNA-B levels. Swapping of KA27 DNA B with the nuclear shuttle protein gene (NSP) of KA22 DNA-B abolished severe stunting and caused the appearance of mild yellow symptom, suggesting that the NSP is the major symptom determinant in MYMV DNA-B. Haq *et al.* (2011) reported that YMV disease in grain legumes in Indian subcontinent is caused by two important virus species namely MYMV and MYMIV. The genomic components of begomovirus causing yellow mosaic disease in blackgram in Southern India were cloned and sequenced. Nucleotide sequence comparison of DNA-A component shows the virus isolate to be a variant of MYMV. However, DNA-B component of the present virus isolate has greater similarity (92%) to MYMIV. Agro-inoculation of the viral clones produced typical yellow mosaic symptoms in blackgram and mungbean, severe leaf curl and stunting in French bean, similar to blackgram isolate of MYMIV.

Recently, it was reported that *Vigna mungo var. silvestris*, a wild species of black gram was infected with YMV disease. The incidence on this wild species is reported to be 100% according to Naimuddin *et al*. (2011). The symptoms on these plants characteristically resembled veinal yellowing and scattered bright yellow spots, suggesting the etiology of begomovirus. Comparative analysis of the coat protein (AV1) gene of the virus of the wild species (FJ821189) revealed 97 and 99% similarity with mungbean yellow mosaic India virus (MYMIV)-mungbean strain at the nucleotide and amino acid levels respectively. Comparisons of the genes of virus infecting wild species (AC1, AC2, AC3 and AC4) and cultivable blackgram indicated 94-97% similarity at nucleotide level, whereas the similarity is 91-99% for the amino acids sequence.

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