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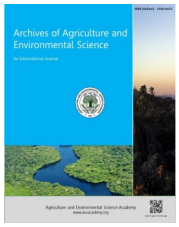

ORIGINAL RESEARCH ARTICLE

Transcriptional activator gene based phylogenetic analysis of dolichos yellow mosaic virus infecting lablab bean (*Dolichos lablab* L.)

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ABSTRACT

Lablab bean (*Dolichos lablab* L.) is one the important crop, cultivated as vegetable, pulses as it is rich in protein. It is affected from viral disease i.e. dolichos yellow mosaic virus. The causative agent is begomovirus belongs to geminivirus family. Begomovirus contain bipartite genome having two type of DNA-A and DNA-B. DNA- A helps in replication and DNA-B helps in movement. These DNA have six different type of gene coat protein gene, transcriptional activator gene, replication associated gene, replication enhancer gene, pre coat protein involved in different function associated with it. The present investigation was carried out to investigate the transcriptional activator gene based phylogenetic analysis of Dolichos yellow mosaic virus infecting *D. lablab*. This study is based on the transcriptional activator gene which is used in transactivation of genes, contains three conserved domains: a basic domain at N-Terminus, a central DNA binding domain and activator domain. The genome databases of dolichos yellow mosaic virus were taken from NCBI site total six genome was available and were used with Clustal W and CLC BIO were the bioinformatic tools for determining sequence homology among genome present in different geographical location. The absence of functional specificity suggests that all begomovirus contains a common element interacts with cellular proteins of other viruses reveals the phylogenetic analysis with the other species *Dolichos* in the different geographical location.

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INTRODUCTION

The lablab bean (*Dolichos lablab* L.) is most ancient cultivated crop plants. It is a multipurpose crop grown for pulse, vegetable and forage, widely cultivated due to it is having high nutritive value and having major sources of protein. It has ability of nitrogen fixation which helps in improving soil fertility, and drought resistance (Capoor and Varma, 1948, 1950; Maruthi *et al.,* 2006). In India, the lablab bean is grown in the peninsular region and cultivated to large areas of Karnataka and adjoining districts of Tamil Nadu, Andhra Pradesh and Maharashtra, Uttar Pradesh (Singh *et al.,* 2006, 2012). The lablab bean is extensively cultivated in the various climatic zones for example arid, semi-arid, sub-tropical and humid regions where temperatures vary between 22°C-35°C, low lands and uplands and many types of soils and the pH varying from 4.4 to 7.8. The dried seeds of lablab bean should be boiled in two changes of water earlier eating since they have toxins substance as Cyanogenic glucosides. It improves the soil condition and is relatively drought tolerant; it is also a good cover crop (Raj *et al.,* 1988; Singh *et al.,* 2006, 2012).

In dolichos disease named dolichos yellow mosaic disease and infected by virus named dolichos yellow mosaic virus (DoYMV) and was shown transmitted by the whitefly *Bemisia tabaci* (Capoor and Varma, 1950; Vanitharani *et al.,* 2004, 2005; Yadava *et al.,* 2010). It having symptoms like faint chlorotic specks on leaf lamina, which later develop into bright yellow mosaic patches with Small Island of green tissue. The leaves are seldom deformed, but yields are reduced significantly (Capoor and Varma, 1950; Bisaro, 1996; Zrachya *et al.,* 2006). The viruses

having bipartite genomes require these components differentiated into two diverse particles; consequently more than one virus particle is needed to infect a cell. The total size of the dolichos yellow mosaic virus is 2760 bp. (Maramorosch and Muniyappa, 1981; Muniyappa Muniyappa *et al.,* 2003; Stanley *et al.,* 2005). Its genome is divided into the two parts DNA-A and DNA -B and intergenic region or common region which is common in both the DNA. All the functions related for virus replication, control of gene expression and encapsidation are in coded in DNA-A and gene involved in intra and intercellular movement are encoded in DNA-B. DNA-A contains six different genes named AC1, AC2, AC3, AC4, AV1, AV2 and each gene have different function. AC2 interacts with itself and localizes to the nucleus and self interaction correlates with nuclear localization and efficient activation of transcription (Hayes and Buck, 1989; Yang *et al.,* 2007; Prajapat *et al.,* 2010). Its function as a transcriptional activator, three conserved domains has been recognized in this protein: a basic domain with a nuclear localization signal (NLS) at the N terminus, a central DNA-binding domain with a non classical Zn-finger motif, and an acidic activator domain at C-terminus (Hartitz *et al.,* 1999; Mansoor *et al.,* 2003; Dhakar *et al.,* 2010). A comparison of steady state transcript level and the transcript level determined by nuclear run on assay showed that activation of AV1 and BV1 gene expression by the AC2 protein primarily occurs at the transcriptional level. Mutational analysis of AC2 in begomoviruses showed that the mutation of this ORF prevented systemic movement of the virus, produced no capsid protein and accumulated reduced amount of ssDNA in the transient assay (Hanley-Bowdoin *et al.,* 1999; Harrison and Robinson, 1999; Markham *et al.,* 1994; Qazi *et al.,* 2007). Therefore, AC2 is functionally interchangeable among begomoviruses and the absence of active specificity suggests that either all begomovirus late promoters have a collective sequence element documented by AC2 or AC2 interacts with cellular proteins common to all begomovirus plant hosts to effect transcriptional activation. AC4 is highly variable among begomoviruses. AC4 of ACMV enhanced pathogenecity by increasing the levels of DNA accumulation of viruses and was also found to have anti-PTGS activity (Varma *et al.,* 1993; Vanitharani *et al.,* 2004; Yang *et al.,* 2007). They infect a wide range of plant species and are responsible for Geminiviruses are a major constraint to agricultural productivity in all tropical and sub-tropical regions of the world. The molecular phylogenetic analysis is the scrutiny of hereditary molecular alterations, mainly in DNA sequences, to gain evidence on an organism's evolutionary relationships (Yaraguntaiah and Govindu, 1964; Briddon *et al.,* 1990, 2001; Varma and Malathi, 2003). The result of a molecular phlyogenetic analysis is expressed in a phylogenetic tree (Dry *et al.,* 1997; Swanson *et al.,* 1992; Czosnek *et al.,* 2001). The tree was constructed by use of the various type of software. The CLUSTAL-W, CLC-BIO and BLAST were used to study the phylogenetic analysis. The multiple sequence alignment and phylogenetic relationship was done by the help of CLUSTAL-W and CLC-BIO and BLAST is used for the global sequence alignment helps in determining the maximum similarity within the other viruses (Rojas *et al.,* 2001; Rekha *et al.,* 2005; Saeed *et al.,* 2008; Govindappa *et al.,* 2011). Keeping in view, the present study was aimed to assess the transcriptional activator gene based phylogenetic analysis of Dolichos yellow mosaic virus infecting Lablab bean (*Dolichos lablab* L.).

MATERIALS AND METHODS

Description of study materials: There are different type's databases available on internet. The NCBI site was used for retrieving the genome of the dolichos yellow mosaic virus (NCBI, 2016). A total of six isolates of the gene AC2 and AC4 were identified for the diversity analysis (Table 1).

Phylogenetic analysis: Sequences were saved in the FASTA format in a notepad file. Software CLUSTAL-W and CLC-BIO was used for the phlogenetic analysis and making dendrogram. The neucleotide BLAST was done to determine the maximum similarity with the other species. The nucleotide sequences of the AC2 gene in the FASTA format were as follows:

>gi|41057586:c1631-1203 Dolichos yellow mosaic virus, complete genome
ATGCGGTCTTCGTCACCCTCGAACAGCCATT-
GTTCTTACCGAGCATCAAGGCACAGCATCGACAG
GCGAAGAAGCGCAAAACGATTCGGCGTAAGCGA
ATCGATCTGACCTGTGGCTGTTCGTATTACCTAAA
TATCAACTGCCGGAATGACGGATTCACGCACAGG
GGAATCCATCACTGCAACTCAACTACAGAGTGGC
GTGTTTATCTGGGAGCTAAAGAATCCCCTGTCTTT
CAAAATCCTGGAGCATCACGAGGGGTTCCTGTTC
GATCCGAACCAACACAGAACCAAGATCCGCATAA
TGTTCAACCACGGGTTGAAGAAAGCGTTGGGGAT
ACACAAGGCATTCTTGGATTTTGTGATTTACCATC
GATTGACTCCGCAATCTGGGCGGATCTTGAATGTA
TTCAGGAACTTCCTTTTTAA

>gb|AY309241.1|:c1631-1203 Dolichos yellow mosaic virus segment DNA-A, complete sequence
ATGCGGTCTTCGTCACCCTCGAACAGCCATT-
GTTCTTACCGAGCATCAAGGCACAGCATCGGCAG
GCGAAGAAGCGCAAAACGATTCGGCGTAAGCGA
ATCGATCTGACCTGTGGCTGTTCGTATTACCTGAA
TATCAACTGCCGAAATGACGGATTCACGCACAGG
GGAATCCATCACTGCAGCTCAACTACAGAGTGGC
GTGTTTATTTGGGAGCTAAAGAATCCCCTGTCTTT
CAAAATCCTGGAGCATCACGAGGGGTTCCTGTTC
GATCCGAACCAACACAGAACCAAGATCCGCATAA
TGTTCAACCACGGGTTGAAGAAAGCGTTGGGGAT
ACACAAGGCATTCTTGGATTTTGTGATTTACCATC
GATTGACTCCGCATTCTGGGCGGATCTTGAATGTA
TTCAGGAACTTCCTTCTTAG

>gb|AY271891.1|:c1631-1203 Hyacinth bean yellow mosaic Bangladesh virus DNA-A, complete sequence
ATGCGGTCTTCGTCACCCTCGAACAGCCATT-
GTTCTCTACCGAGCATCAAGGCACAGCATCGACA
GGCGAAGAAGCGCAAAACGATTCGGCGTAAGCG
AATCGATCTGACCTGTGGCTGTTCGTATTACCTAA
ATATCAACTGCCGGAATGACGGATTCACGCACAG
GGGAATCCATCACTGCAACTCAACTACAGAGTGG

CGTGTTTATCTGGGAGCTAAAGAATCCCCTGTCTT
TCAAAATCCTGGAGCATCACGAGGGGTTCCTGTT
CGATCCGAACCAACACAGAACCAAGATCCGCATA
ATGTTCAACCACGGGTTGAAGAAAGCGTTGGGGA
TACACAAGGCATTCTTGGATTTTGTGATTTACCAT
CGATTGACTCCGCAATCTGGGCGGATCTTGAATGT
ATTCAGGAACTTCCTTTTTAA

>gi|116077869:c1631-1203 Dolichos yellow mosaic virus DNA-A segment, complete sequence, isolate Bangalore-2

ATGCGGTCTTCGTCACCCTCGAACAGCCATT-
GTTCTCTACCGAGCATCAAGGCACAGCATCGACA
GGCGAAGAAGCGCAAAACGATTCGGCGTAAGCG
AATCGATCTGACCTGTGGCTGTTCGTATTACCTAA
ATATCAACTGCCGGAATGACGGATTCACGCACAG
GGGAATCCATCACTGCAGCTCAACTACAGAGTGG
CGTGTTTATCTGGGAGCTAAAGAATCCCCTGTCTT
TCAAAATCCTGGAGCATCACGAGGGGTTCCTGTT
CGATCCGAACCAACACAGAACCAAGATCCGCATA
ATGTTCAACCACGGGTTGAAGAAAGCGTTGGGGA
TACACAAGGCATTCTTGGACTTAGTAGTTTACCAT
CGATTGACTCCGCAATCTGGGCGGATCTTGAATGT
ATTCAGGAACTTCCTTTTTAG

>gi|116077862:c1631-1203 Dolichos yellow mosaic virus DNA-A segment, complete sequence, isolate Bangalore-1

ATGCGGTCTTCGTCACCCTCGAACAGCCATT-
GTTCTCTACCGAGCATCAAGGCACAGCATCGACA
GGCGAAGAAGCGCAAAACGATTCGGCGTAAGCG
AATCGATCTGACCTGTGGCTGTTCGTATTACCTAA
ATATCAACTGCCGGAATGACGGATTCACGCACAG
GGGAATCCATCACTGCAGCTCAACTACAGAGTGG
CGTGTTTATCTGGGAGCTAAAGAATCCCCTGTCTT
TCAAAATCCTGGAGCATCACGAGGGGTTCCTGTT
CGATCCGAACCAACACAGAACCAAGATCCGCATA
ATGTTCAACCACGGGTTGAAGAAAGCGTTGGGGA
TACACAAGGCATTCTTGGACTTAGTAGTTTACCAT
CGATTGACTCCGCAATCTGGGCGGATCTTGAATGT
ATTCAGGAACTTCCTTTTTAG

>gi|90185977:c1631-1203 Dolichos yellow mosaic virus complete DNA-A segment, strain Mysore

AATGCGGTCTTCGTCACCCTCGAACAGCCATT-
GTTCTCTACCGAGCATCAAGGCACAGCATCGACA
GGCGAAGAAACGCAAAACGATTCGGCGTAAGCG
AATCGATCTGACCTGTGGCTGTTCGTATTACCTAA
ACATCAACTGCCGGAATGACGGATTCACGCACAG
GGGAATCCATCACTGCAGCTCAACTACAGAGTGG
CGTGTTTATCTGGGAGCTAAAGAATCCCCTGTCTT
TCAAAATCCTGGAACATCACGAGGGGTTCCTGTT
CGATCCGAACCAACACAGAACCAAGATCCGCATA
ATGTTCAACCACGGGTTGAAGAAAGCGTTGGGGA
TACACAAGGCATTCTTGGACTTTGTGATTTACCAT
CGATTGACTCCGCAATCTGGGCGGATCTTGAATGT
ATTCAGGAACTTCCTTTTTA

Nucleotide sequence of AC4 gene in the FASTA format: >gi|41057586:c2480-2235 Dolichos yellow mosaic virus, complete genome

ATGGGACTATGCATCTCCATGCCCTCGTCCAG-
TTCAAGGGTAAGGCCCAGTTCCGAAATGCAAGAC
ATTTCGACCTTACCCATCCTCATAGCACACAGGTT
TTCCATGGAAATGTCCAGGGAGCAAAGAGCTCAT
CTGATGTCAAATCCTACATCACCAAGGACGGTGA
TTACGTCGACTGGGGAACATTTCAGATCGACGGA
CGATCTGCTAGAGGAGGTCGTCAGACAGCTGACG
ATGCTGTAG

>gb|AY309241.1|:c2480-2235 Dolichos yellow mosaic virus segment DNA-A, complete sequence

ATGGGA-
TATGCATCTCCATGCCCTCGTCCATTCAAGGGTAA
GGCCCAGTTCCGAAATGCAAGACATTTCGACCTT
ACCCATCCTCATAGCACACAGGTTTTCCATGGAAA
TGTCCAGGGAGCAAAGAGCTCATCTGATGTCAAA
TCCTACATCACCAAGAACGGTGATTACATCGACT
GGGGAACATTTCAGATCGACGGACGATCTGCTAG
AGGAGGTCGTCAGACAGCTGACGATGCTGTAG

>gb|AY271891.1|:c2480-2235 Hyacinth bean yellow mosaic Bangladesh virus DNA-A, complete sequence

ATGGGA-
TATGCATCTCCATGCCCTCGTCCATTCAAGGGTAA
GGCCCAGTTCCGAAATGCAAGACATTTCGACCTT
ACCCATCCTCATAGCACACAGGTTTTCCATGGAA
ATGTCCAGGGAGCAAAGAGCTCATCTGATGTCAA
ATCCTACATCACCAAGGACGGTGATTACGTCGAC
TGGGGAACATTTCAGATCGACGGACGATCTGCTA
GAGGAGGTCGTCAGACAGCTGACGATGCTGTAG

>gi|116077869:c2480-2235 Dolichos yellow mosaic virus DNA-A segment, complete sequence, isolates Bangalore-2

ATGGGACTATGCATCTCCATGCCCTCGTCCAG-
TTCAAGGGTAAGGCCCAGTTCCGAAATGCCAGAC
ATTTCGACCTTACCCATCCTCATAGCACACAGATT
TTCCATGGAAATGTCCAGGGAGCAAAGAGCTCAT
CTGATGTCAAATCCTACATCACCAAGGACGGTGA
CTACGTCGACTGGGGAACATTTCAGATCGACGGA
CGACCTGCTAGAGGAGGTCGGCAGACAGCTGACG
ATGCTGTAG

>gi|116077862:c2480-2235 Dolichos yellow mosaic viruses DNA-A segment, complete sequence, isolate Bangalore-1

ATGGGACTATGCATCTCCATGCCCTCGTCCAG-
TTCAAGGGTAAGGCCCAGTTCCGAAATGCCAGAC
ATTTCGACCTTACCCATCCTCATAGCACACAGATT
TTCCATGGAAATGTCCAGGGAGCAAAGAGCTCAT
CTGATGTCAAATCCTACATCACCAAGGACGGTGA
CTACGTCGACTGGGGAACATTTCAGATCGACGGA
CGACCTGCTAGAGGAGGTCGGCAGACAGCTGACG
ATGCTGTAG

>gi|90185977:c2480-2235 Dolichos yellow mosaic virus complete DNA-A segment, strain Mysore

GATGGGA-
TATGCATCTCCATGCCCTCGTCCATCAAGGGTAAG
GCCCAGTTCCGAAATGCCAGACATTTCGACCTTAC
CCATCCTCATAGCACACAGATTTTCCATGGAAATG
TCCAGGGAGCAAAGAGCTCATCTGATGTCAAATC
CTACATCACCAAGGACGGTGACTACGTCGACTGG
GGAACATTTCAGATCGACGGACGATCTGCTAGAG
GAGGTCGTCAGACAGCTGACGATGCTGTA

RESULTS AND DISCUSSION

The yellow mosaic diseases are challenging problems in the tropics and subtropics. The increase in *Bemisia tabaci*

Table 1. Isolates used for phylogenetic study.

S.N.	Accession No.	Gi.no	Description	Size of the gene	Place of isolate
1	NC-005338.1	41057586	Dolichos yellow mosaic virus isolate DYMV complete genome	AC2-1203-1631 AC4-2235-2480	South and South east Asia
2	AY309241.1	32187104	Dolichos yellow mosaic virus complete DNA-A segment	AC2-1203-1631 AC4-2235-2480	Mysore
3	AM157413.1	116077869	Dolichos yellow mosaic virus DNA-A, complete sequence.	AC2-1203-1631 AC4-2235-2480	Banglore-2
4	AM157412.1	116077862	Dolichos yellow mosaic virus segment DNA-A, complete sequence	AC2-1203-1631 AC4-2235-2480	India
5	AJ968370.1	90185977	Dolichos yellow mosaic virus DNA A, complete genome	AC2-1203-1631 AC4-2235-2480	Mysore
6	AY271891.1	33355890	Hyacinth bean yellow mosaic virus segment DNA-A, complete sequence	AC2-1203-1631 AC4-2235-2480	Bangladesh

Table 2. BLAST Score result showing maximum similarity with other viruses.

Accession	Description	Max score	Total score	Query coverage	E value	Max ident	Links
AY271891.1	Hyacinth bean yellow mosaic Bangladesh virus DNA-A, complete sequence	5099	5099	100%	0.0	100%	G
AJ968370.1	Dolichos yellow mosaic virus complete DNA-A segment, strain Mysore	4505	4505	100%	0.0	96%	
AM157413.1	Dolichos yellow mosaic virus DNA-A segment, complete sequence, isolate Bangalore-2	4447	4447	100%	0.0	96%	
AM157412.1	Dolichos yellow mosaic virus DNA-A segment, complete sequence, isolate Bangalore-1	4447	4447	100%	0.0	96%	
AY309241.1	Dolichos yellow mosaic virus segment DNA-A, complete sequence	4385	4385	100%	0.0	95%	G
GU591170.1	Dolichos yellow mosaic virus isolate DYMV-CpKn coat protein (AV1) gene, complete cds	1242	1242	28%	0.0	96%	
JN368437.1	Mungbean yellow mosaic India virus Indonesia isolate Rembang segment DNA-A, complete sequence	407	659	47%	3e-109	80%	
JN368432.1	Mungbean yellow mosaic India virus Indonesia isolate Bogor segment DNA-A, complete sequence	407	652	48%	3e-109	80%	
JN368433.1	Mungbean yellow mosaic India virus Indonesia isolate Purwakarta 1 segment DNA-A, complete sequence	401	652	48%	1e-107	79%	
FN543425.1	Velvet bean severe mosaic virus DNA A, complete genome	401	401	23%	1e-107	78%	G
JN368439.1	Mungbean yellow mosaic India virus Indonesia isolate Brebes 4 segment DNA-A, complete sequence	396	646	48%	6e-106	79%	
JN368434.1	Mungbean yellow mosaic India virus Indonesia isolate Purwakarta 2 segment DNA-A, complete sequence	396	646	48%	6e-106	79%	
JN368436.1	Mungbean yellow mosaic India virus Indonesia isolate Brebes 2 segment DNA-A, complete sequence	390	646	48%	3e-104	79%	
JN368435.1	Mungbean yellow mosaic India virus Indonesia isolate Brebes 1 segment DNA-A, complete sequence	390	641	48%	3e-104	79%	
JN368438.1	Mungbean yellow mosaic India virus Indonesia isolate Brebes 3 segment DNA-A, complete sequence	385	646	48%	1e-102	79%	
AY618902.1	Cowpea golden mosaic virus segment DNA-A, complete sequence	385	635	48%	1e-102	79%	
AY937199.1	Mungbean yellow mosaic India virus clone MB 0.9 segment DNA A, partial sequence	385	385	20%	1e-102	79%	
AY937195.1	Mungbean yellow mosaic India virus clone MBK-A25 segment DNA A, complete sequence	379	635	48%	6e-101	79%	
JN181006.1	Mungbean yellow mosaic India virus isolate Vizianagaram pre-coat protein (AV2) gene, partial cds; and coat protein (AV1) gene, complete cds	374	374	23%	3e-99	77%	
FJ685621.1	Tomato leaf curl Nigeria virus-[Nigeria:2006], complete sequence	372	372	22%	9e-99	78%	G
JQ398669.1	Mungbean yellow mosaic virus [Urdbean:New Delhi:2011] clone MF2 segment A, complete sequence	370	628	47%	3e-98	78%	
HE616781.1	African cassava mosaic Burkina Faso virus DNA-A complete genome, isolate BF:Oua:BF128C:08	368	368	22%	1e-97	78%	
HE616780.1	African cassava mosaic Burkina Faso virus DNA-A complete genome, isolate BF:Oua:BF128B:08	368	368	22%	1e-97	78%	
HE616777.1	African cassava mosaic Burkina Faso virus DNA-A complete genome, isolate BF:Oua:BF127:08	368	368	22%	1e-97	78%	
HE616779.1	African cassava mosaic Burkina Faso virus DNA-A complete genome, isolate BF:Oua:BF128A:08	363	363	22%	6e-96	78%	
FM208839.1	Mungbean yellow mosaic India virus, segment DNA-A, complete sequence, clone A14	353	624	47%	3e-93	78%	
AY049772.1	Mungbean yellow mosaic India virus-[Soybean] segment DNA A, complete sequence	353	353	20%	3e-93	78%	
GQ387509.1	Mungbean yellow mosaic India virus isolate MYMIV-Ub04 coat protein (AV1) gene, complete cds	351	351	20%	1e-92	78%	
AM992618.1	Mungbean yellow mosaic India virus, segment DNA-A, complete genome	351	351	23%	1e-92	77%	

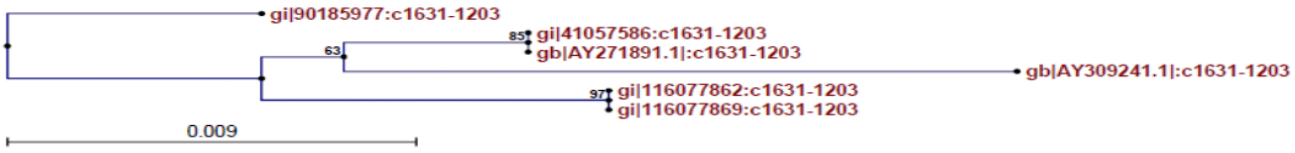

Figure 1. *Phylogenetic tree of AC2 gene created by CLC-BIO.*

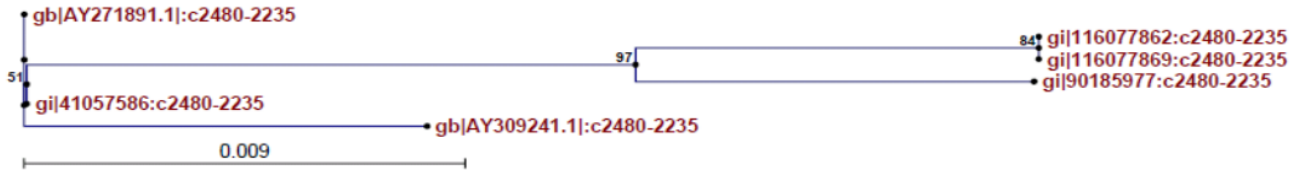

Figure 2. *Phylogenetic tree of AC4 gene created by CLC-BIO.*

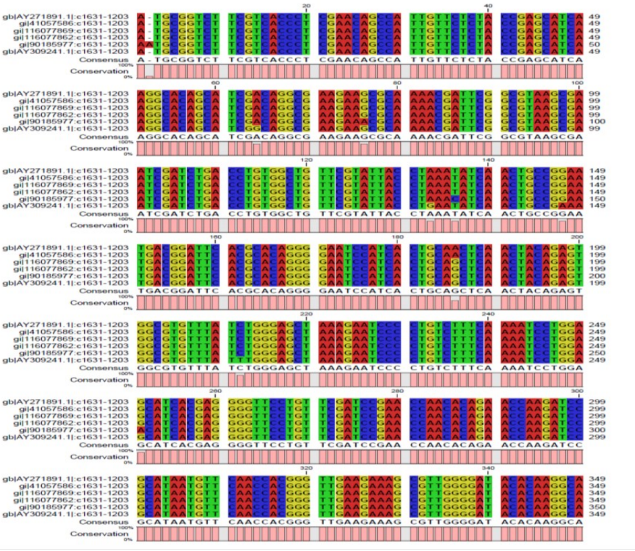

Figure 3. *Multiple sequence alignment result of AC2 gene.*

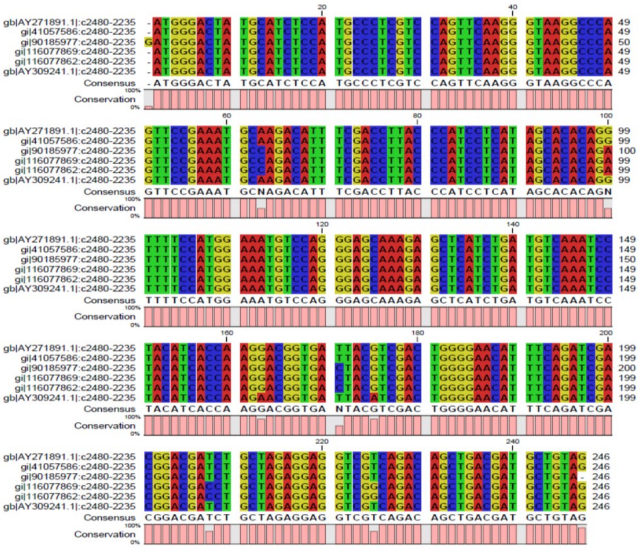

Figure 4. *Multiple sequence alignment result of AC4 gene.*

populations during the cropping season has also led to geminivirus problems in other countries evolution of new variants of the viruses depends upon the *v*ariability among viruses l, it arises through mutations, development of recombinants and pseudo recombinants. In the present study, we examine the influence of variability in Gemini viruses in relation to new disease problems. Variability in Gemini viruses is seen especially between isolates from geographically different regions. This has been shown for MSV, where emerging *Gemini viruses* 6 isolates genomic recombination in *Gemini viruses* may occur not only between variants of the same virus but also between virus species (Tables 1, 2). In the above case, six different evolutionary pathways are possible using an out group, each depicted by a different rooted tree. The sequence of one clone was determined to be 2760 nucleotides in length (accession number AJ968370) and to be most similar to the sequences of DoYMV-[Bangladesh] (AY271891) and a further clone of DoYMV originating from India (AY309241) at 95·2% and 93·4% nucleotide sequence identities, respective. The three DoYMV isolates examined in this study showed the highest levels of sequence identity (92.5–95.3%) with the previously described DoYMV isolates from North India and Bangladesh. DoYMV-[Ban1] and DoYMV-[Ban2] originated from two separate fields in Bangalore and were almost identical (99.1%) (Table 2). Iiyas *et al.* (2010) reported genetic diversity and phylogeography of begomoviruses infecting legumes in Pakistan. Moreover Maruthi *et al.* (2006) also reported genetic similarities in the different begomovirus causes Indian dolichos yellow mosaic disease. In an another study Maruthi *et al.* (2006) also concluded that dolichos yellow mosaic virus belongs to a distinct lineage of Old World begomoviruses and it showed variations in its biological and molecular properties.

During the present study, the sequences of the genomes (DNA-A components) of the two DoYMV isolates originating from Bangalore (DoYMV-[Ban1] and DoYMV -[Ban2]) were both 2762 nucleotides in length whereas the length of DoYMV- [Mys] was 2760 nucleotides it has been noted previously that the antigenic and genomic variation in begomoviruses is primarily correlated with geography rather than their host range. Viruses infecting different host plants but originating from the same geographical area are more likely to be closely related than viruses infecting the same host but from different

geographical areas Dolichos yellow mosaic disease was suspected to be caused by a geminivirus after the successful transmission of the pathogen from DYMD-affected plants by *B. tabaci*. The phylogenetic trees and multiple sequence alignment result of the gene AC2 and AC4 showed the geographical similarities (Figures 1-4). The findings are in agreement with Padidam *et al.* (1996) who reported the role of AV2 (precoat) and coat protein in viral replication and movement in tomato leaf curl geminivirus. In an almost similar study Muniyappa *et al.* (1987) also isolated and characterized of Dolichos yellow mosaic disease geminivirus causing yellow mosaic disease of Horsegram (*Macrotyloma uniflorum* (Lam.) Verdc.).

Conclusions

The present study concluded that variations in Gemini viruses were seen especially between isolates from geographically different regions and this is likely due to the MSV, where *Emerging Gemini viruses* 6 Isolates Genomic recombination in Gemini viruses may occur not only between variants of the same virus but also between virus species. The sequence of one clone was determined to be 2760 nucleotides in length (accession number AJ968370) and to be most similar to the sequences of DoYMV-[Bangladesh] (AY271891) and a further clone of DoYMV originating from India (AY309241) at 95·2% and 93·4% nucleotide sequence identities, respective. The three DoYMV isolates examined in this study showed the highest levels of sequence identity (92.5–95.3%) with the previously described DoYMV isolates from North India and Bangladesh. DoYMV-[Ban1] and DoYMV-[Ban2] originated from two separate fields in Bangalore and were almost identical (99.1%). The sequences of the genomes (DNA-A components) of the two DoYMV isolates originating from Bangalore (DoYMV-[Ban1] and DoYMV-[Ban2]) were both 2762 nucleotides in length whereas the length of DoYMV- [Mys] was 2760 nucleotides it has been noted previously that the antigenic and genomic variation in begomoviruses is primarily correlated with geography rather than their host range. Therefore, viruses infecting different host plants but originating from the same geographical area are more likely to be closely related than viruses infecting the same host but from different geographical areas Dolichos yellow mosaic disease was suspected to be caused by a geminivirus.

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