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RESEARCH ARTICLE

GENOME SEQUENCE ANALYSIS OF DNA-A FROM OKRA YELLOW VEIN MOSAIC  
VIRUS ISOLATES

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ABSTRACT

Entire DNA-A of four *okra yellow vein mosaic virus* (OYVMV) Indian biotypes were isolated from virus infected leaf tissue of okra using PCR amplification. Isolated complete DNA-A from experimental biotypes were cloned and sequenced. DNA-A sequences from all these biotypes were compared and further analyzed using the bioinformatics tools. ClustalW analysis of these sequences confirmed variation into the DNA-A amongst OYVMV isolates. It is observed that out of the AV1 gene which encodes coat protein (CP) is the most conserved region, and AC4 protein the most variable. Results also concluded that there is variability in DNA-A of all four experimental biotypes. There are recombinational hot spots within DNA-A of these four biotypes. Among all four experimental biotypes of OYVMV, Madurai biotype was found to be more recombinant and formed by major genetic changes into its DNA-A.

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INTRODUCTION

Okra (*Abelmoschus esculentus* L) is commonly known as bhindi or lady's finger belonging to family *Malvaceae*. It is an important fruit vegetable crop cultivated in various states of India. Several species of the genus *Abelmoschus* are grown in many parts of the world among them *Abelmoschus esculentus* is most commonly cultivated in Asia and has a great commercial demand due to its nutritional values. The genus *Abelmoschus* was established by Medikus in 1787. However most authors followed De-Candolle (1824) and treated it as a section of *Hibiscus*. One of the major problems with this crop is infection and yield loss due to the fast growing, widely spread *okra (Bhindi) yellow vein mosaic virus*. The *okra yellow vein mosaic virus* (OYVMV) disease is characterized by a homogenous interwoven network of yellow vein enclosing islands of green tissue within its leaf. In extreme cases, infected leaves become yellowish or creamy color. If plants are infected within 20 days after germination, their growth is retarded, few leaves and fruits are formed and the loss may about 94%. The extent damage declines with delay in infection of the plants. Plants infected 50 to 65 days after germination suffer a loss of 49-84% respectively (Sastry and Singh, 1974). The vector transmitting the *okra yellow vein mosaic virus* is *Bemisia tabaci* Genn.

Several attempts have been made to manage the whitefly (Pun *et al.*, 1999). But the recombinations occurring within the genome of geminiviruses created difficulties to develop the resistance or effective tolerance against the *okra yellow vein mosaic virus*. Geminiviruses belongs to the family Geminiviridae and have circular single stranded (ss) DNA genome which is responsible for major crop losses worldwide (Moffat, 1999). Most of the Begomoviruses have bipartite genome, termed DNA A and DNA B. DNA A and DNA B share the region of ~200 nucleotides (nt) within the intergenic region called the common region. The DNA A component encodes the proteins required for viral DNA replication (Sunter *et al.*, 1987), while the DNA B encodes two proteins that are essential for systemic movement and symptom expression (Brown and Nelson, 1988, Noury *et al.*, 1994).

Recently certain monopartite Begomoviruses indicating *Agerantum yellow vein mosaic virus* (AYVMV), *Cotton leaf curl virus* (CLCuV), some Begomoviruses infecting tomato (TYLCV) and tobacco (TLCV) in China and *Okra (Bhindi) yellow vein mosaic virus* (OYVMV) in India have been found to require a satellite molecule called  $\beta$  (beta) for introduction of disease symptoms in the same host plants (Briddon *et al.*, 2001, Jose and Usha, 2003, Zhou *et al.*, 2003). Begomovirus genomes have either one (monopartite) or two (bipartite) DNA components ranging from 2.5 to 2.8 Kb in size. These viruses replicate in the host cell nucleus

via a double-stranded (ds) DNA intermediate, termed replicative form (RF). The RF is used as a template for transcription as well as replication. Both strands code for viral proteins (Hanley-Bowdoin *et al.*, 1999). The DNA A of bipartite begomoviruses and monopartite begomoviruses have a very similar genome organization and encode 5-6 overlapping open reading frames (ORFs). The virion-sense strand (V) of DNA A encodes the coat protein (CP, *AV1/V1*) that encapsidates the viral ssDNA. The DNA A of Old World begomoviruses encodes an additional ORF AV2/V2 that has been implicated in virus movement (Padidam *et al.*, 1996, Rigden *et al.*, 1993). The DNA A complementary-sense (C) strand encodes the replication-associated protein (Rep, *AC1/C1*), a transcriptional activator protein (TrAP, *AC2/C2*), and a replication enhancer protein (REn, *AC3/C3*). TrAP is involved in the control of both viral and host gene expression. Some DNA A of bipartite viruses and all monopartite viruses encodes *AC4/C4* that participates in cell-cycle control (Bridson & Stanley, 2006).

Natural recombination between TYLCV-Israel and TYLCV has been reported by Navas-Castillo *et al.*, (2000). Evidence has been provided by Kirthi *et al.*, (2002) that AV1, AV2, AC1 and intergenic regions of the viral genome contain potential sites of recombinations among TYLCV strains / species. In China, several Begomoviruses infecting squash, tobacco and tomato have been reported (Zhou *et al.*, 2001; Xie *et al.*, 2002). Jovel *et al.*, (2004) cloned and sequenced two molecules of DNA A (A1, A2) and three of DNA B (B1, B2, B3) of *Abutilon mosaic virus*. Their results demonstrated that the intergenic regions of DNA B2 appears to be the product of the recombination between DNA B1 and DNA A2. These results showed that a co infection of begomoviruses could persist over decades, producing a reservoir of partially recombined but distinct geminiviruses.

## MATERIALS AND METHODS

### Genomic DNA isolation from virus infected leaf

Whole genomic DNA extraction was carried out from the young tender leaf samples of Yellow Vein Mosaic Virus infected Okra. Four virulent biotypes were selected from India. These were from 1) Madurai, 2) Aurangabad, 3) Delhi and 4) Abohar. These different biotypes covered all different parts of India i.e. South, Central and North India. Okra yellow vein mosaic virus DNA A sequences were collected from various accessions from the NCBI (National Center for Biotechnology Information) site. The DNA A sequences were further analyzed using Bioinformatics tools. The genome specific primers were designed to get the DNA A genomes amplified through the PCR amplification.

Genomic DNA of okra was isolated by using protocol of Lodhi *et al.*, (1994) devised for genomic DNA isolation from Grape vine. Since okra plant contains latex type substance which may degrade the DNA, PVP was added to the extraction buffer during grinding of leaf samples. Quality of the isolated DNA of the entire four samples was checked on 0.8% agarose gel. 20  $\mu$ l of DNA loaded into the gel with the 5  $\mu$ l of gel loading dye.

### PCR amplification of DNA-A using genome specific primers

Master mix for PCR was prepared by adding 2  $\mu$ l of Taq Buffer (10X), 2  $\mu$ l dNTP's (10 mM), 0.4  $\mu$ l of Taq Polymerase (3U/ $\mu$ l), 7  $\mu$ l of BSA (1mg/ml), 0.2  $\mu$ l of Tween 20, 2  $\mu$ l of DNA-A genome specific forward primer reverse primer, 3  $\mu$ l of template DNA from each biotype and 3.4  $\mu$ l of SMQ to make final volume to 20  $\mu$ l. All the above components were mixed in a 0.2 ml PCR tube and PCR machine was set by giving the programs for first denaturation at 94°C for 3 minutes, second denaturation at 94°C for 15 seconds, annealing for 30 seconds and extension at 72°C for 5 minutes. Each PCR reaction was performed with 38 cycles.

All PCR amplicons were analyzed on 0.8% agarose gel in 1X TAE, agarose gel was prepared by dissolving the 0.8 gm of agarose. Agarose gel was stained with Ethidium bromide (EtBr). Ethidium bromide stain was prepared by adding the 5  $\mu$ l EtBr stock solution (10 mg/ml) to 100 ml TBE running buffer.

### Cloning of PCR amplicons

The ligation of the amplicon was carried out as per the user's manual provided with the pGEM-T Easy Vector Kit (Promega, USA). *Escherichia coli* JM109 and DH5 $\alpha$  was used as the host cell. The ligation mixture was prepared by adding 5  $\mu$ l of 2X rapid ligation buffer, 2  $\mu$ l of vector (100-150 ng), 6  $\mu$ l insert (300-400 ng) and 1  $\mu$ l T4 DNA ligase (3 U/ $\mu$ l). Final volume was made to 15  $\mu$ l with SMQ water and a ligation reaction was set up. For getting the maximum number of transformants, the reaction was performed overnight at 4°C. Plasmid DNA was isolated by using alkaline lysis method (Sambrook *et al.* 1989).

### Preparation of Competent Cell Lines

To get the pure culture for carrying the insert DNA, a single cell culture of *E. coli* JM 109 was developed. From these cultures, a single colony was inoculated in 2 mL of LB medium and grown overnight at 37°C. Then, 50 mL of LB medium was inoculated with a 5 mL overnight culture of the *E. coli* and grown at 37°C at 200 rpm. When an optimal density (OD<sub>600</sub>) of 0.5-0.8 was reached, cells were chilled on ice for 15-20 min and centrifuged at 4000 rpm at 4°C for 15 min. The cells were then washed with one volume (50 mL) of ice cold sterile water and centrifuged again. The pellet was resuspended in 1 mL of 100 mM CaCl<sub>2</sub>. This was then dispensed in 200  $\mu$ l aliquots to eppendorf tubes and kept at 4°C overnight. The cells were finally suspended in 0.004 volumes (2 mL) of ice cold glycerol. Aliquots of 25-50  $\mu$ l were placed into ice cold eppendorf tubes, snap frozen in liquid nitrogen and stored at -80°C.

### Transformation of *E. coli*

The competent *E. coli* JM109 and DH5 $\alpha$  cells were transformed as described by Sambrook *et al* (1989). DNA (~50 ng) was added to the competent *E. coli* cells, mixed and kept on ice for 30 min. The cells were then incubated at 42°C for 2 min. To each tube 800  $\mu$ l of LB broth was added and further incubated at 37°C for 1h. The cells were pelleted by centrifugation and resuspended in 200  $\mu$ l of LB broth and spread on LB medium plates containing appropriate antibiotic, IPTG (40  $\mu$ g/mL) and 40  $\mu$ g/mL X-

gal. In total, 13 transformed colonies were grown on the LB agar selective medium.

#### Isolation and Identification of Insert

Recombinant plasmids were isolated using alkaline lysis method as described by Sambrook *et al.* (1989) and characterized by restriction digestion. The plasmid was digested with *ApaI* and *SacII* restriction endonucleases to isolate the insert from the vector plasmid. The digested fragment was electrophoresed on 0.8% agarose gel for 45 min at 60 V and further the insert DNA was used for sequencing

#### Sequencing of DNA A genome

The insert DNA was bidirectionally sequenced using Beckman Coulter CEQ™ 8000 Genetic Analysis System. DNA sequencing reactions were set up using CEQ™ DTCS Quick Start Kit Dye Terminator Cycle sequencing kit. Sequences of viral genomes were confirmed by comparisons and alignments performed with the Basic Local Alignment Search Tool (BLAST; National Center for Biotechnology Information).

#### Bioinformatics for sequence analysis

Clustal analysis of all the DNA A and  $\beta$  DNA fragments was carried out by using ebi ClustalW analysis tool ([www.ebi.ac.uk/clustalw](http://www.ebi.ac.uk/clustalw)). ClustalW is a tool for aligning multiple protein or nucleotide sequences. The alignment is achieved via three steps: pairwise alignment, guide-tree generation and progressive alignment. Conserved regions within the DNA-A sequences were analyzed.

#### Recombination analysis by Recombination Detection Program (RDP3)

RDP3 is a Windows 95/98/NT/XP/VISTA program for detecting and analysing recombination signals in a set of aligned DNA sequences (Martin *et al.*, 2005). Once RDP3 has scanned an alignment and enumerated all detectable recombination signals, it begins the task of trying to distill all the detectable recombination signals down to a minimal set of unique recombination events that could account for the signals. This program helps to identify the site of recombinations within the sequences. This is available on the web <http://darwin.uvigo.es/rdp/rdp.html>. DNA-A and  $\beta$ -DNA sequences of all four biotypes were analyzed using the RDP3 tool (Martin and Rybicki, 2000).

## RESULTS AND DISCUSSION

### Genomic DNA isolation from okra leaf tissue

Isolation of genomic DNA from Okra leaf tissue is tedious due to presence of the high mucilage into the leaf. Genomic DNA was isolated by using Lodhi *et al.*, (1994) protocol for genomic DNA isolation. Genomic DNA isolation of all four *okra yellow vein mosaic virus* infected leaf samples collected from all the biotypes was carried out using the same method. Quality of isolated DNA was checked on 0.8% agarose gel. A good quality of DNA was seen under a UV transilluminator.

### PCR amplification of DNA

The forward primer 5'AGTGGTGGGTCCAGAAC3' of 17 nucleotides with 58% GC content and melting temperature (Tm) 59°C and a reverse primer

5'TATTATACGGATGGCCGC3' of 18 nucleotides with 50% GC content and melting temperature (Tm) 57°C was used for amplification of DNA-A from all the four OYVMV biotypes. DNA-A of OYVMV was amplified using the above mentioned forward and reverse primers with temperature gradient from 55°C to 60°C to study the exact annealing temperature. Finally primers produced a desired amplicon at annealing temperature of 58°C. Figure 1 reveals the PCR amplification products checked on 0.8% Agarose gel. After PCR amplification, out of OYVMV samples collected from the various regions of India produced a DNA-A genome amplicon of ~2700 bp.

More recently, Jose and Usha (2002) reported PCR amplification of DNA-A using begomovirus component equivalent to DNA-A in diseased bhendi plants. Again Jose and Usha (2003) have isolated a DNA-A and  $\beta$ -DNA component from BYVMV infected bhendi tissue, which together with BYVMV, causes typical yellow vein disease symptoms in bhendi. BYVMV was initially amplified using begomovirus specific primers. PCR amplicon were cloned, sequenced and the 2.7 kbp amplified product was compared with various other BYVMV isolates. Besides this, they have also reported the amplification, cloning and characterization of  $\beta$ -DNA component from Madurai isolate. An approximately 1.35 kbp  $\beta$ -DNA fragment was amplified from diseased bhendi plants using non overlapping primers located in the highly conserved region found in all  $\beta$ -DNA sequences and was clones into pGEM-T.

Ha *et al.* (2008) described molecular characterization of begomoviruses and DNA satellites from Vietnam. They collected samples from a range of crop and weed plants exhibiting characteristic geminivirus symptoms (vein yellowing, leaf curling, chlorosis and stunting). Total DNA was extracted and PCR amplifications were carried out using degenerate primers for amplification of DNA-A, DNA-B,  $\beta$ -DNA and Nanoviruses like DNA-1.

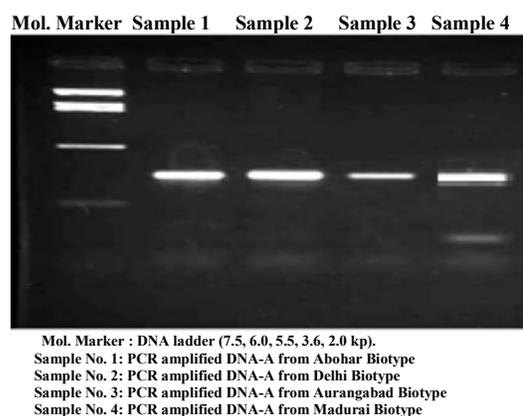


Fig. 1. PCR amplified DNA-A of OYVMV biotypes.

### Sequence Analysis of OYVMV DNA-A

The complete nucleotide sequences of DNA-A of four virus isolates were determined. Plasmid DNA from the pGEM-T vector was used for the DNA sequencing. The insert DNA was bi-directionally sequenced using Beckman Coulter CEQ™ 8000 Genetic Analysis System.





OYVMV/DNAA/ Delhi TTAGCTACTCTTAAGATTAGAAATATATTTTTATGACTCTGTAAACGAAC 1049  
OYVMV/DNAA/Abohar TTAGCTACTCTTAAGATTAGAAATATATTTTTATGACTCTGTAAACGAAC 1049  
OYVMV/DNAA/Madurai GTATGCTACGCTTAAGATTCCGATTTATTTTTATGACTCTGTAAACGAAC 1048  
OYVMV/DNAA/Aurangabad TTAGCTACGCTTAAGATTCCGATATATTTTTATGACTCTGTAAACGAAC 1049  
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OYVMV/DNAA/ Delhi AATATTAAAGTTAAATGCTATATCTGAATATTTGGTCTACATACATT 1099  
OYVMV/DNAA/Abohar AATATTAAAGTTAAATGCTATATCTGAATATTTGGTCTACATACATT 1099  
OYVMV/DNAA/Madurai GA-ATTAAAGTTGAAATTTATATCTGAATATTTGGTCTACATACATT 1097  
OYVMV/DNAA/Aurangabad ATATGATCTAGAGTTTAAATTTATATCTGAATATTTGGTCTACATACATT 1099  
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OYVMV/DNAA/ Delhi GTTTGATTAATTACATTGTACAATACATGTTCAACGGCTTTAATAACTAA 1149  
OYVMV/DNAA/Abohar GTTTGATTAATTACATTGTACAATACATGTTCAACGGCTTTAATAACTAA 1149  
OYVMV/DNAA/Madurai GTCTGATTAACTACATTGTACAATACATGTTCCGACGGCTTTAATAACTAA 1147  
OYVMV/DNAA/Aurangabad GTTTGATTAATTACATTGTACAATACATGTTCAACGGCTTTAATAACTAA 1149  
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OYVMV/DNAA/ Delhi ATTAATTGAGATTACACCTAGATTGTTGAGATGTTGAGGACTTGGGTTT 1199  
OYVMV/DNAA/Abohar ATTAATTGAGATTACACCTAGATTGTTGAGATGTTGAGGACTTGGGTTT 1199  
OYVMV/DNAA/Madurai ATTAAGTGAGATTACACCTAGATTATTGAGATATTTGAGGACTTGGGTTT 1197  
OYVMV/DNAA/Aurangabad ATTAAGTGAGATTACACTAGATTGTTGAGATACTTGAAGTACTTGGGTTT 1199  
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OYVMV/DNAA/ Delhi TGAATACCCCTTAAGAAAAGACCAGTCGGAGGGGTGAAGGTCGTCAGATT 1249  
OYVMV/DNAA/Abohar TGAATACCCCTTAAGAAAAGACCAGTCGGAGGGGTGAAGGTCGTCAGATT 1249  
OYVMV/DNAA/Madurai TGAATACCCCTTAAGAAAAGACCAGTCGGAGGGGTGAAGGTCGTCAGATT 1247  
OYVMV/DNAA/Aurangabad TGAATACCCCTTAAGAAAAGACCAGTCGGAGGGGTGAAGGTCGTCAGATT 1249  
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OYVMV/DNAA/ Delhi CGGAAGGTTAGACAACACTTGTGTATTTCCAGAGCTTTCCGTAGGTTGTA 1299  
OYVMV/DNAA/Abohar CGGAAGGTTAGAAAACACTTGTGTATTTCCAGAGCTTTCCGTAGGTTGTA 1299  
OYVMV/DNAA/Madurai CGGAAGGTTAGAAAACACTTGTGTATTTCCAGAGCTTTCCGTAGGTTGTA 1297  
OYVMV/DNAA/Aurangabad CGGAAGGTTAGAAAACACTTGTGCCTCCAGAGCTTTCCGAAAGGTTGTA 1299  
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OYVMV/DNAA/ Delhi GTTGAATGGATCCCTGAGTGTATTTATGTCATGTTCCGTCGTAATGGAC 1349  
OYVMV/DNAA/Abohar GTTGAATGGATCCCTGAGTGTATTTATGTCATGTTCCGTCGTAATGGAC 1349  
OYVMV/DNAA/Madurai GTTGAATGGATCCCTGAGTGTATTTATGTCATGTTCCGTCGTAATGGAC 1347  
OYVMV/DNAA/Aurangabad GTTGAATGGATCCCTCATTTGTTATGATGTCATGTTCCGTCGTAATGGAC 1349  
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OYVMV/DNAA/ Delhi GGTGTGCTGGTTGAGGATCCTTGAATAGAGGGGATTTGGAACCTCCAG 1399  
OYVMV/DNAA/Abohar GGTGTGCTGGTTGAGGATCCTTGAATAGAGGGGATTTGGAACCTCCAG 1399  
OYVMV/DNAA/Madurai GGTGTGCTGGTTGAGGATCCTTGAATAGAGGGGATTTGGAACCTCCAG 1397  
OYVMV/DNAA/Aurangabad GGTGTGCTGGCTGAGGATTTTGAATAAAGCGGATTTGGAACCTCCAG 1399  
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OYVMV/DNAA/ Delhi ATATAGACGCCATTCTTTGCTTGAGCTGCAGTGTGCGTTCCCTGTGCG 1449  
OYVMV/DNAA/Abohar ATATAGACGCCATTCTTTGCTTGAGCTGCAGTGTGCGTTCCCTGTGCG 1449  
OYVMV/DNAA/Madurai ATATAGACGCCATTCTTTGCTTGAGCTGCAGTGTGCGTTCCCTGTGCG 1447  
OYVMV/DNAA/Aurangabad ATAAAGACGCCATTCTTTGAAATGAGCTGCAGTGTGCGTTCCCTGTGCG 1449  
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OYVMV/DNAA/ Delhi AGAATCCATGGTTGTGGCAGTTGATGCTAAGATAATAAAAACACCCGCAT 1499  
OYVMV/DNAA/Abohar AGAATCCATGGTTGTGGCAGTTGATGCTAAGATAATAAAAACACCCGCAT 1499  
OYVMV/DNAA/Madurai AGAATCCATGGTTGTGGCAGTTGATGCTAAGATAATAACTGCATCCGCAT 1497  
OYVMV/DNAA/Aurangabad GGAATCCATGGTTGTGGCAGTTGATACTTAGTTAATAGCTGCATCCACAC 1499  
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OYVMV/DNAA/ Delhi TCAAGATCTACTCTCCTCCTGTTGCGTCTCTTCGCTTCCCTGTGCTG 1549  
OYVMV/DNAA/Abohar TCAAGATCTACTCTCCTCCTGTTGCGTCTCTTCGCTTCCCTGTGCTG 1549  
OYVMV/DNAA/Madurai TCAAGGTCCACTCGTCTCCTCCTGTCGACTCGCTTCGCTTCTCTGTGTTG 1547  
OYVMV/DNAA/Aurangabad TCAAGGTCCACTCGTCTCCTCCTGTCGCTCTCTTCGCTTCCCTGTGTTG 1549  
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OYVMV/DNAA/ Delhi TACTTTGATTGGTACCTGAGTACAACGGTTGGGTGAGAAAGACGAATGCT 1599  
OYVMV/DNAA/Abohar TACTTTGATTGGTACCTGAGTACAACGGTTGGGTGAGAAAGACGAATGCT 1599  
OYVMV/DNAA/Madurai AACTTTGATTGGTACCCGAGTACAACGGTTGGGTGAGAAAGACGAATGCT 1597  
OYVMV/DNAA/Aurangabad AACTTTGATTGGTACCGGAGTACGAGCGGTTGGGTGAGAAAGACGAATGTT 1599  
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OYVMV/DNAA/ Delhi GCATTTTTAAAGCCACGCTTCAAAGCTGAGTCTTTTCCCTCGTCCAG 1649  
OYVMV/DNAA/Abohar GCATTTTTAAAGCCACGCTTCAAAGCTGAGTCTTTTCCCTCGTCCAG 1649  
OYVMV/DNAA/Madurai GCATTTTTAAAGCCACGCTTCAAAGCTGAGTCTTTTCCCTCGTCCAG 1647  
OYVMV/DNAA/Aurangabad GCATTTCTTAAAGCCAGGATTTAATGCTGAGTCTTATCCCTCGTCCAA 1649  
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OYVMV/DNAA/ Delhi ATACTCTTTATAGCTAGCGTTGGGCCAGGATTCAGAGGAAGATTGTTG 1699  
OYVMV/DNAA/Abohar ATACTCTTTATAGCTAGCGTTGGGCCAGGATTCAGAGGAAGATTGTTG 1699  
OYVMV/DNAA/Madurai AAACCTTTTATAGCTTTCGTTGGGCCCTGGATTGCAGAGAAAGATTGTTG 1697  
OYVMV/DNAA/Aurangabad GAACCTCTTTATAGCTTGCATTGGGCCCTGGTTGCAGAGGAAGATTGTTG 1699  
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OYVMV/DNAA/ Delhi	GTATTCCA	CCTTTAATTGAACTGGCTTCCCGTACTTTGTGTT	C	GATTGC	1749
OYVMV/DNAA/Abohar	GTATTCCA	CCTTTAATTGAACTGGCTTCCCGTACTTTGTGTT	G	GATTGC	1749
OYVMV/DNAA/Madurai	GAA TGCCCT	CCTTTAATTGAACTGGCTTCCCGTACTTTGTGTT	T	GATTGC	1747
OYVMV/DNAA/Aurangabad	GTATGCCG	CCTTTAATTGAACTGGCTTCCCGTACTTTGTGTT	T	GATTGC	1749
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OYVMV/DNAA/ Delhi	CAGTCCCTTTGGGCCCCCATGAA	CTCTTTAAAGTGCTTGAGGAAGTGCGG			1799
OYVMV/DNAA/Abohar	CAGTCCCTTTGGGCCCCCATGAA	CTCTTTAAAGTGCTTGAGGAAGTGCGG			1799
OYVMV/DNAA/Madurai	CAGTCCCTTTGGGCCCCCATGAA	TTCTTTAAAGTGTTTCAGATAATGCGG			1797
OYVMV/DNAA/Aurangabad	CAGTCCCTTTGGGCCCCCATGAA	TTCTTTAAAGTGTTTTAGGAAGTGTTG			1799
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OYVMV/DNAA/Abohar	ATCTACGCCATCAATGACGTTATACCAAGCGTCGTTACTGTACACCTTTG				1849
OYVMV/DNAA/Madurai	GTC AACATCATCTATAATGTTGAACCCGCGATCGTTTGAATACACTTTAG				1847
OYVMV/DNAA/Aurangabad	ATCGACGTCATCAATGACGTTATACCAAGCGTCGTTACTGTACACCTTTG				1849
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OYVMV/DNAA/ Delhi	GGCTTAGATCTAGATGCCACATAAATAATTATGTGGGCCTAAAGACCTA				1899
OYVMV/DNAA/Abohar	GGCTTAGATCTAGATGCCACATAAATAATTATGTGGGCCTAAAGACCTA				1899
OYVMV/DNAA/Madurai	GGCTTAGATCC AAGTGC GCACATAAATAATTATGTGGCCCAAGGACGG				1897
OYVMV/DNAA/Aurangabad	GGCTTA ACTCCAGATGCCGCATAAATAGTTATGTGGGCCTAAAGACCTA				1899
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OYVMV/DNAA/Abohar	GCCCACATTTGCTTCCAGTACGACTATCACCCCTCAATTAATACTATTG				1949
OYVMV/DNAA/Madurai	GCCCATTGTGTTTTCCAGTCTAGACTCCCCCTCTAGA ACTAAACTCAA				1947
OYVMV/DNAA/Aurangabad	GCCCACATTTGTTTTCCAGTACGACTATCTCCCTCAATTAATACTATTG				1949
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OYVMV/DNAA/Madurai	AGGTCTCTGAGGGGCCGCGCAGCGCGTCCATGACGTTCTCCGACGCCACT				1997
OYVMV/DNAA/Aurangabad	AGGTCTCAGGGGCCGCGCAGCGGCATCGACAACTTCTCGCACGCCACT				1999
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OYVMV/DNAA/Abohar	CTTCAAGTACTTCTGGAACCTGATCGAAAGAAAGAGGAAAAAGGAGAA				2049
OYVMV/DNAA/Madurai	CTTCAAGTCTTCTGGAACCTGATCGAAAGAAAGAGATAAAAAAGGACAA				2047
OYVMV/DNAA/Aurangabad	CTTCAAGTCTTCTGGAACCTGATCGAAAGAAAGAAAAAGGAGAA				2049
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OYVMV/DNAA/ Delhi	ACATAAGGAGCTGGTGGCTCCTGAAAGATTCTGTCTAGATTGCATTTAA				2099
OYVMV/DNAA/Abohar	ACATAAGGAGCTGGTGGCTCCTGTAAGATTCTGTCTAGATTGCATTTAA				2099
OYVMV/DNAA/Madurai	ACATAAACCTCCTGAGGAGGAGTAAAAATCCTATCTAAATTTGAAATTTAA				2097
OYVMV/DNAA/Aurangabad	ACATAAGGAGCTGGAGGCTCCTGAAAAATCTATCTAAATTTGAAATTTAA				2099
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OYVMV/DNAA/Abohar	ATTATGAAATTGTAGTACAAAATCTTTAGGAGCTAGCTCCTTGATGACTC				2149
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OYVMV/DNAA/Aurangabad	ATTATGAAATTGAAGTAGAAAGTCTTTGGGGCTTTCTCCTTCAGTATAT				2149
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OYVMV/DNAA/Abohar	TAAAGCCCTCTGACTTACTTCCCGGTTAAGTGCTGCGGCGTAAAGCGTCG				2199
OYVMV/DNAA/Madurai	TAAAGCCCTCTGCTTACTTCCCGGTTAAGTGCTGCGGCGTAAAGCGTCA				2197
OYVMV/DNAA/Aurangabad	TGAGGGCCTGAGCTTTGGACCCTCGGTTGATTGCCCTGGGCAATGCGTCG				2199
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OYVMV/DNAA/ Delhi	TTGGCTGTTTGTGTCCTCCTCTTGCTGATCTTCCGTCGATCTGAAATTC				2249
OYVMV/DNAA/Abohar	TTGGCTGTTTGTGTCCTCCTCTTGCTGATCTTCCGTCGATCTGAAATTC				2249
OYVMV/DNAA/Madurai	TTGGCTGATTTGTTGTCCTCCTCCTTGCAGATCTGGCGTCGATCTGAAATTC				2247
OYVMV/DNAA/Aurangabad	TTGGCAGTTTGGCAACCTCCTCTAGCTGATCTTGCATCGACTTGGAAAAAC				2249
	*****	*****		*****	
OYVMV/DNAA/ Delhi	CCCCAGTCGAGAATGTCCCGTCCCTGGCGATGTAGGACTTGACGTCGG				2299
OYVMV/DNAA/Abohar	CCCCAGTCGAGAATGTCCCGTCCCTGGCGATGTAGGACTTGACGTCGG				2299
OYVMV/DNAA/Madurai	CCCCATTCAAGGGTATCTCCGTCCTTGTGATATAGGACTTGACGTCGG				2297
OYVMV/DNAA/Aurangabad	TCCATGATCAAGGATGTCTCCGTCCTTCTCGATGTAGGTTTGGACATCGC				2299
	**	*****		*****	
OYVMV/DNAA/ Delhi	AGCTGGATTTAACTCCCTGAATGTTCCGATGGAAAATGTCGTGACCTGGTT				2349
OYVMV/DNAA/Abohar	AGCTGGATTTAACTCCCTGAATGTTCCGATGGAAAATGTCGTGACCTGGTT				2349
OYVMV/DNAA/Madurai	AGCTGGATTTAGCTCCCTGAATGTTCCGATGGAAAATGTCGTGACCTGGTT				2347
OYVMV/DNAA/Aurangabad	TTGAGCTTTTAGCTCCCTGAATGTTCCGATGGAAAATGTCGTGACCTAGTT				2349
	*	*****		*****	
OYVMV/DNAA/ Delhi	GGGGATACGAGGTCGAAGAACTCTGTTATTTTTCACCTTGTATTTCCCTTC				2399
OYVMV/DNAA/Abohar	GGGGATACGAGGTCGAAGAACTCTGTTATTTTTCACCTTGTATTTCCCTTC				2399
OYVMV/DNAA/Madurai	GTGGCGCAAGTCGGAGAACTCTGATTTCTGGCACTTGTATTTCCCTTC				2397
OYVMV/DNAA/Aurangabad	GGGGAGGTGAGTTCGAAGAACTATTTGTTCTGCACTGGAACTTTCCTTC				2399
	* * *	*****		*****	

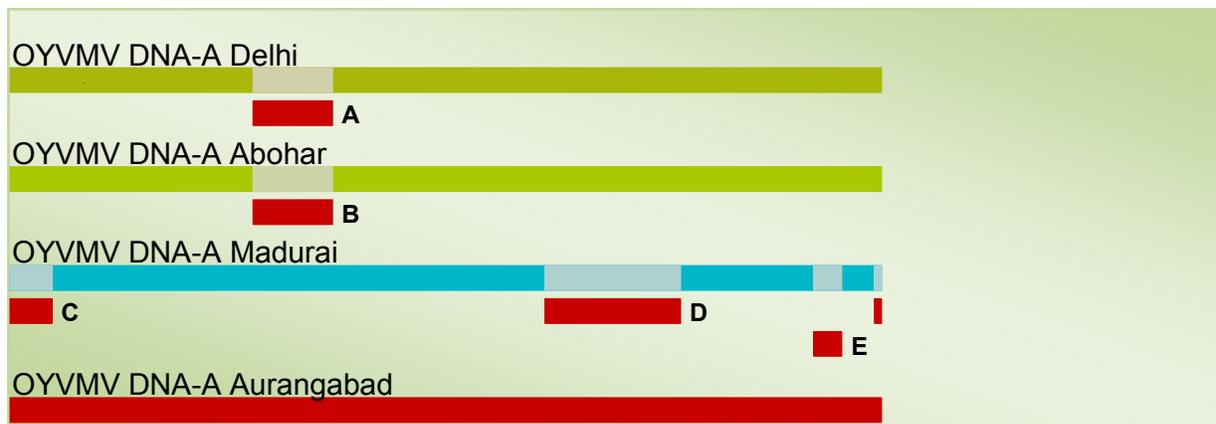


regions. In-depth analysis, it is also noticed that there is maximum conserved region between the DNA-A genome sequence of Aurangabad and Madurai biotypes. However, it has also been observed that Aurangabad isolate has an AV1 nonfunctional Pre-coat protein gene might have resulted through mutations.

**Table 1. Conserved regions between the DNA-A genome of four OYVMV biotypes.**

Complement		Total Nucleotides	Conserved region representing gene
Start Nucleotide	End Nucleotide		
34	49	43 nt	AV1 gene Coat Protein
51	76	26 nt	AV1 gene Coat Protein
274	301	28 nt	AV1 gene Coat Protein
327	377	51 nt	AV1 gene Coat Protein
560	605	46 nt	AV1 gene Coat Protein
813	840	28 nt	AV1 gene Coat Protein
926	990	65 nt	AV1 gene Coat Protein
1012	1101	90 nt	AC3 gene of Replication Enhancer protein
1190	1261	72 nt	AC3 gene of Replication Enhancer protein
1325	1360	36 nt	AC3 gene of Replication Enhancer protein
1421	1449	29 nt	AC2 gene
1451	1474	24 nt	AC2 gene
1574	1597	24 nt	AC1 gene of Rep protein
1708	1742	35 nt	AC1 gene of Rep protein
1744	1772	29 nt	AC1 gene of Rep protein

family (Keese and Gibbs 1993; Morse 1994; Gibbs *et al.* 1995; Holland 1998). It has now been accepted that recombination contributed to the diversity of geminiviruses and therefore, to the emergence of new variants and species\ reported worldwide. For instance, cotton leaf curl disease in Pakistan became severe during the past decade, causing extensive damage to cotton production. In Trinidad Tobago, a geminivirus disease on tomato observed in 1989 has reemerged throughout the country. A new cassava mosaic virus has devastated cassava production in Uganda. Tomato production in Spain and Italy is severely constrained by *Tomato yellow leaf curl virus-Sardinia* (TYLCV). All of these new viruses are recombinants (Umaharan *et al.* 1998). In India, Kirthi *et al* (2002) have detected recombination between strains of *Tomato leaf curl virus* from Bangalore. Girish and Usha (2005) have analysed recombination events in TLCV DNA-A. Recombinations within DNA-A of all four experimental biotypes were studied using the RDP3 program. Results of recombinations within DNA-A genome of *okra yellow vein mosaic virus* are reviewed in figure 4. From figure 4 and 5, it is observed that DNA-A sequence of Delhi biotype shows a sequence tract A portion where the recombination has occurred the sequence. Figure also reproduces that there is recombination between 766 nt and 1022 nt with a probability of 3.158. The present figure also represents that there is a major recombination between the Delhi and Madurai biotypes with a tract of Aurangabad biotype as a



**Fig. 4. The schematic display of recombination. Shows sites recombinations within DNA-A Genome sequence of OYVMV biotypes. The piece of sequence from major parent and piece of sequence from minor parent is highlighted. Piece of minor parent shows the site of recombination.**

A: Site of recombination within DNA-A of Delhi Biotype

B: Site of recombination within DNA-A of Abohar Biotype.

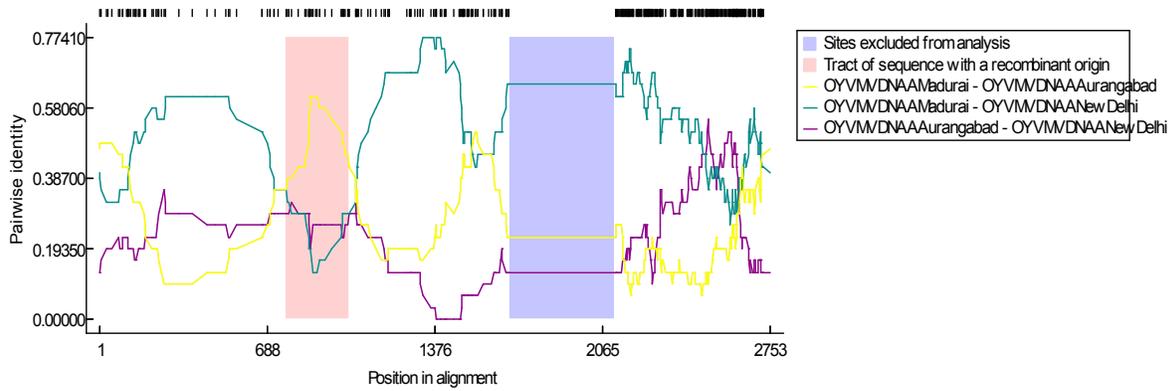
C, D & E: Sites of recombination within DNA-A of Madurai Biotype

As seen in table, there are two conserved regions of 29 and 24 nucleotides present in the AC2 gene. From table we also understand that there are three conserved regions amongst four biotypes within the AC3 gene which produces Replication Enhancer Protein. Results also highlight great similarity within three conserved regions from AC1 gene which codes for Rep Protein.

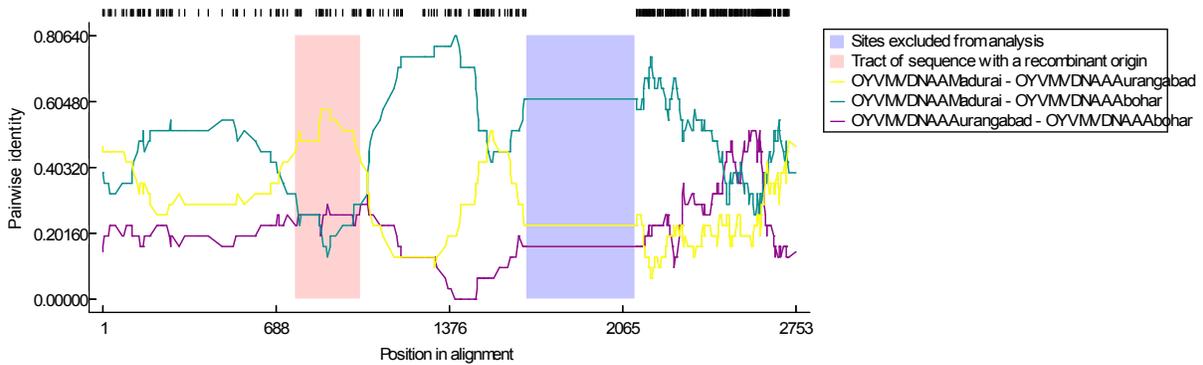
#### Detection of recombinations within DNA-A and $\beta$ -DNA genomes using Recombination Detection Program (RDP3) tool

Recombination can provide selective advantage in the evolution of viruses within strains, species, genera and

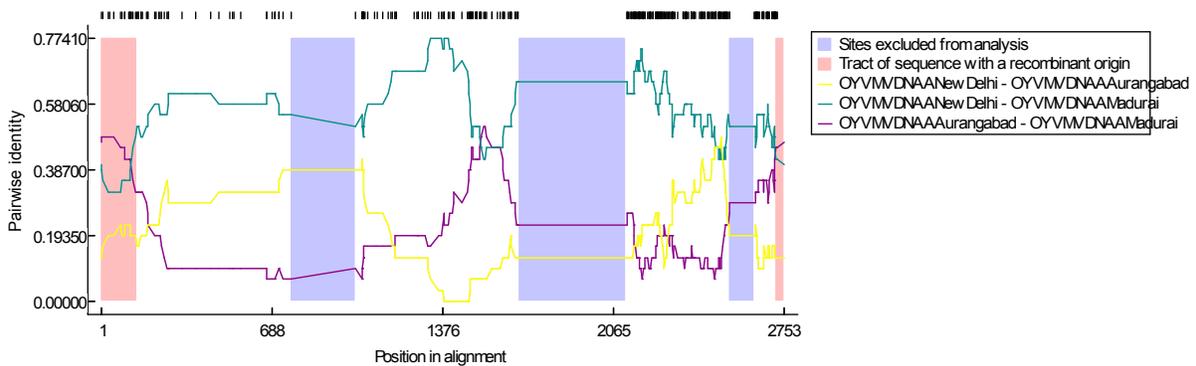
minor parent. Second strand from Figure 4 belongs to Abohar biotype. RDP3 tool showed that DNA-A sequence of Abohar biotype have a sequence tract B portion where the recombination has occurred within the sequence. Figure imitate that there is recombination between 766 nt and 1022 nt with a probability of 2.469 (Figure 6). The present figure also informs that there is a major recombination between the Abohar and Madurai biotypes with a tract of Aurangabad biotypes as a minor parent. From the Figure 4, third strand belongs to Madurai biotype. The bioinformatics program RDP3 showed that DNA-A sequence of Madurai biotype have three sequence



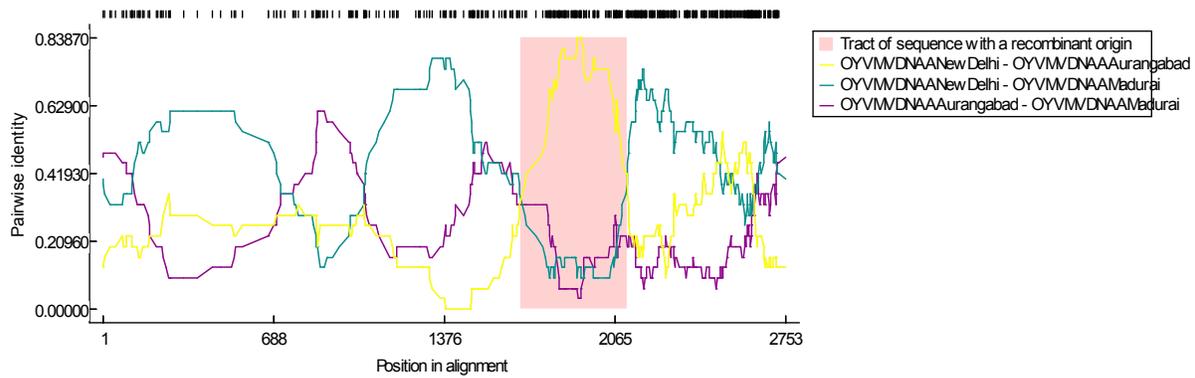
**Fig. 5. : The schematic display of nucleotides where the recombination is occurred. Tract of sequence with recombinations within DNA-A genome of OYVMV Delhi biotype.**  
**Beginning : 766 nt; Ending : 1022 nt; Daughter : OYVMV Delhi; Major Parent : OYVMV Madurai (88.3%); Minor Parent : OYVMV Aurangabad; Probability : 3.158**



**Fig. 6. The schematic display of nucleotides where the recombination is occurred. Tract of sequence with recombinations within DNA-A genome of OYVMV Abohar biotype.**  
**Beginning : 766 nt; Ending : 1022 nt; Daughter : OYVMV Abohar; Major Parent : OYVMV Madurai (89.7%); Minor Parent : OYVMV Aurangabad; Probability : 2.469**

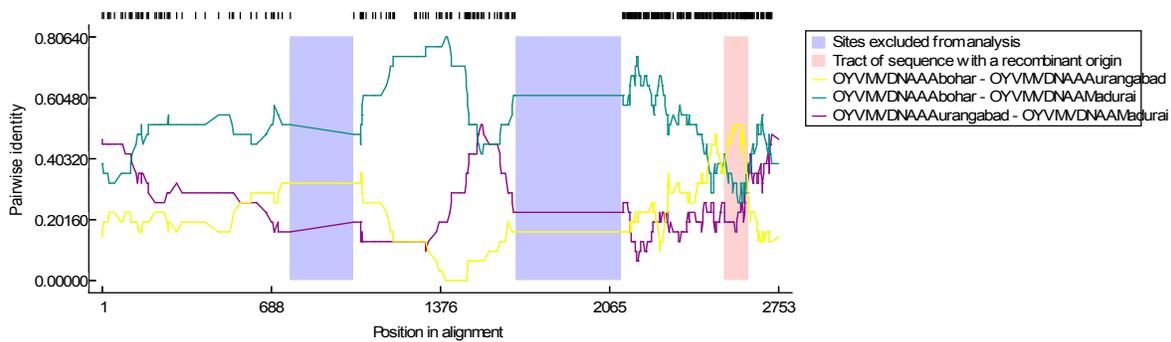


**Fig. 7. The schematic display of nucleotides where the recombination is occurred. Tract of sequence with recombinations within DNA-A genome of OYVMV Madurai biotype.**  
**Beginning : 2712 nt; Ending : 139 nt; Daughter : OYVMV Madurai; Major Parent : OYVMV Delhi (91.9%); Minor Parent : OYVMV Aurangabad (94.8%)**



**Fig. 8.** The schematic display of nucleotides where the recombination is occurred. Tract of sequence with recombinations within DNA-A genome of OYVMV Madurai biotype.

**Beginning** : 1683 nt  
**Ending** : 2114 nt  
**Daughter** : OYVMV Madurai  
**Major Parent** : OYVMV Delhi (90.2%)  
**Minor Parent** : OYVMV Aurangabad  
**Probability** : 1.485



**Fig. 9.** The schematic display of nucleotides where the recombination is occurred. Tract of sequence with recombinations within DNA-A genome of OYVMV Madurai biotype.

**Beginning** : 2532 nt  
**Ending** : 2627 nt  
**Daughter** : OYVMV Madurai  
**Major Parent** : OYVMV Abohar (91.3%)  
**Minor Parent** : OYVMV Aurangabad  
**Probability** : 1.971

tracts C, D & E portion where the recombination has occurred within the sequence. Figure also imitate that there is recombination between 2712 nt to 139 nt with a probability of 3.389 (Figure 7). During RDP scanning, tract of Delhi biotype was found to be a major parent and a tract of Aurangabad biotype as a minor parent. While from figure 8, it is also observed that there is recombination between 1683 nt to 2114 nt with a probability value of 1.485. During RDP scanning, tract of Delhi biotype was found to be a major parent and a tract of Aurangabad biotype as a minor parent. Apparently from figure 9 it seemed that there is recombination between 2532 nt to 2627 nt with a probability value of 1.971. During RDP scanning, tract of Abohar biotype was found to be a major parent and a tract of Aurangabad biotype as a minor parent. During this scanning, DNA-A genome sequence of Aurangabad biotype was used as a nome sequences from all other biotypes were scanned against DNA-A genome sequence of Aurangabad biotype.

Prasanna and Rai (2007) carried out the recombination breakpoint analysis using Recombination Detection Program. They detected the frequency of recombination in tomato-infecting Begomoviruses of South and Southeast Asia. Vadivukarasi *et al.* (2006) also studies the sequence and recombination analyses of the geminivirus replication initiator protein. To understand the frequent evolution of new geminiviruses, recombination detection analysis was carried out using RDP3. The recombinant regions predicted by both RDP and GENECONV were verified by constructing NJ tree, using ClustalW program. Seventy-seven potential/putative interspecies recombination events were predicted by both RDP and GENECONV. Geminiviruses infecting plants of the *Malvaceae*, *Asteraceae*, *Solanaceae*, *Euphorbiaceae*, *Cucurbitaceae* and *Fabaceae* families were included in recombination analysis. Among their predicted 77 events, 42 take place in the region spanning the 5' half of IR and the 5' end of *Rep* gene adjoining it. Thirty events take place only in the

5' region of *Rep* gene; three events in the IR alone and only two events were predicted in the 3' part of *Rep* gene. The length of the region of recombination ranges from 43 to 468 nucleotides.

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