

Research developments in begomovirus in legumes : Past achievements, Present scenario and Future thrust areas

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Abstract - *Begomovirus* – A well recognized genus of plant viruses classified under Geminiviridae family of Group II (single stranded circular DNA) is known to cause virulence in a large range of hosts including tomato, okra, cotton, cassava, bittergourd, chilli, croton, cucumber, eggplant,

jatropha, mentha, mesta, papaya, potato, tobacco, legumes and many more. It is believed that organism has caused major economic losses on crops of all types. However, owing to today's demand of increased production, land area and productivity of pulses for future food and nutritional security, this paper will summarize collectively the research study and experiments conducted on legumes till date, present research work being conducted and future thrust areas on *begomoviruses* w.r.t. legumes like common bean (*Phaseolus vulgaris*), mung bean (*Vigna radiata*), urd bean (*Vigna mungo*), pigeon pea (*Cajanus cajan*), mothbean (*Vigna aconitifolia*), cowpea (*Vigna unguiculata*), velvetbean (*Mucuna pruriens*), frenchbean (*Phaseolus vulgaris*), soybean (*Glycine max*), long yard bean (*Vigna sesquipedalis*) etc. Prime focus areas of this review will include molecular characterization, DNA replication, phylogenetic analysis and infectivity patterns on host legumes.

Key Words: *Begomovirus*, legumes, *Bemisia tabaci*, yellow mosaic disease, bean common mosaic virus

1. Introduction-

Among all the diseases of plants, viral diseases are the most complex and the least known. Intensive research in the recent past has led to showcase some facts with clear understanding. This review will deal with morphology, taxonomy, genome, population genomics, gene expression, economic impact, host range, transmission, molecular characterization, antigenicity, infectivity and management of begomoviruses that forms largest group of disease causing viruses of plants and specifically of legumes.

2. Morphology-

Virions of geminivirus sub group III are germinate i.e. twinned with two incomplete icosahedra. They are non-enveloped in nature and have a common dimension of 30-38 nm * 18-28 nm (length*diameter) with 22 pentameric capsomers per nucleocapsid and 110 identical protein

subunits (Galvez & Castano, 1976; Goodman *et al.*, 1977; Qazi *et al.*, 2007).

3. Taxonomy-

Mungbean yellow mosaic virus, *Mungbean yellow mosaic India virus*, *Horsegram yellow mosaic virus* and *Dolichos*

yellow mosaic virus are bipartite begomovirus that are responsible for causing yellow mosaic diseases in legumes across southern Asia. MYMIV is a bipartite isolate of Begomovirus that is more widespread in tropical and subtropical climates (Chakraborty *et al.*, 2003; Usharani *et al.*, 2005; John *et al.*, 2008; Fazeli *et al.*, 2009; Haq *et al.*, 2011a, 2011b).

4. Genome-

Genome of begomovirus is bipartite (Honda and Ikegami 1986; Vanitharani *et al.* 1996; Mandal *et al.* 1997; Karthikeyan *et al.* 2004). Both the virions and complementary sense standards have coding regions, positive and negative respectively. Double standard intermediates are responsible for replication of the genome by rolling circle replication where component B is dependent on component A for replication with a common region consisting of two divergent promoters differentially regulating temporal expression of viral genes (SIB 2008).

5. Population genomics-

Experiments on global scale population structure of begomovirus concluded seven major sub populations that can be further divided into 34 entirely different yet genetically close minor sub populations (Prasanna *et al.*, 2010).

6. Gene expression-

Common region is responsible for bidirectional transcription in *begomovirus* while protein expression takes place at subgenomic RNA level. Bipartite *begomovirus* majorly a disease causing mesobiotic pathogen in legumes has two components- Component A encodes six proteins CP (on v-sense) & Rep, TrAP/AL2, REn, AC4, AV2 (on c-sense) and component B encodes 2 proteins BV1 (on v-sense) & BC1 (on c-sense) both involved in movement (Sunter and Bisaro 1992, Bisaro 2006, Sunter and Bisaro 1992, Noueiry *et al.*

1994, Fontes et al.1994, Laufs et al. 1995, Sanderfoot and Lazarowitz 1996, Hanley-Bowdoin et al. 2000, Arguello-Astorga et al. 2004, Bisaro 2006, SIB 2008, Hanley-Bowdoin et al. 2013, ICTV 2017).

7. Economic Impact-

After first report of yellow mosaic disease on major pulse group, its economic impact was expressed by various scientists. Yellow mosaic disease has a potential to cause 85-100% yield loss in black gram and mungbean (Nene, 1973). Yellow mosaic disease accounted for a total loss of 105,000 metric tonnes in soybean alone (Wrather et al., 1997). Total yield losses in blackgram, soybean and mungbean collectively are expected to be around \$ 300 million per year (Verma and Malathi, 2003).

8. Host Range-

Begomovirus are reported to hold a wider host range but in general it serves on dicotyledonous plant. Specific major legume genera includes Phaseolus, Vigna, Macroptilium, Calopogonium (Bird et al., 1972; Bird, Sanchez & Vakili, 1973; Meiners et al., 1973). Rarely infected legume genera are *Cassia*, *Cajanus*, *Glycine*, *Rhynchosia* and *Phaseolus* (J. Bird). Intrinsic research work led to identify Limbean or lablab bean (Capoor and Verma, 1948), Mungbean, urdbean and cowpea (Nariyani, 1960; Nene, 1973), soybean (Suteri, 1974, Fernandes et al. 2009), horsegram (Muniyappa et al., 1975), Frenchbean (Singh, 1979), wild bush bean or quail bean (*Macroptilium lathyroides*) (Lima et al. 2013).

9. Transmission-

Original transmission was reported by whitefly *Bemisia tabaci* (Hemiptera: Aleyrodidae) in a persistent, non-propagative manner across the globe (Costa, 1965). *Bemisia tabaci* race *sidae* is known to spread the virus (Bird et al., 1972). Both males and females are capable to act as a vector of the virus and no evidence of larvae acting as vectors has been found (Bird et al., 1973). Infection is possible in the hosts within six days of acquisition and inoculation (Bird, 1973). However longer feeding periods are needed to spread the disease effectively. 16-21 days approximately is the period to act as potential vectors after acquisition period of 10-15 minutes (Gamez, 1971; Bird et al., 1973). All whiteflies sub types *B. tabaci* MEAM1 (Middle East-Asia Minor 1) (Biotype B), *B. tabaci* NW (New World) (Biotype A), *B. tabaci* NW2 (New World 2), and *B. tabaci* MED (Mediterranean; Biotype Q) (Barbosa et al. 2015) are responsible for transmission of virus except biotype-b which acts as a vector only on monocots. Circulative transmission is known not to occur but replication of the virus inside the vector is questionable (Rosen et al., 2015).

10. Molecular characterization-

Molecular characterization and infectivity test led to the conclusion that viral isolates obtained from Indian cowpea were 94-98% similar in its genomic sequence of DNA-A and

DNA-B and shared a close relationship with the other isolates obtained so far, thus proving the Koch's postulates for *begomovirus* association with mungbean yellow mosaic disease-India in mungbean and cowpea (Singh et al., 2011).

11. Antigenicity

All the begomoviruses were put to test and serological tests evaluated them to be closely related. Harrison and Robinson, 1999 used monoclonal antibodies to group various begomoviruses geographically on the basis of shared epitopes.

12. Infectivity-

YMD's first incidence was marked in western and northern India in lima bean (Capoor and Verma, 1948). Nariyani, 1960 was the first to report yellow mosaic disease in mungbean in Indian subcontinent. Infection in legumes are caused by bean golden mosaic virus which is a type strain of begomovirus. It includes Mungbean yellow mosaic India virus, Mungbean yellow mosaic virus, Dolichos yellow mosaic virus which have bipartite genome and produce mosaic and leaf yellowing as the major symptoms in legumes (Varma and Malathi 2003; Balaji et al. 2004; Girish et al. 2005). Furthermore, Mungbean yellow mosaic India virus (MYMIV) and Mungbean yellow mosaic virus (MYMV) were reported to be more virulent, having more hosts and abundant (Fauquet and Stanley, 2003) and the other two strains Dolichos yellow mosaic virus and Horsegram yellow mosaic virus are specific and rare (Maruthi et al., 2005). Molecular characterization proved begomovirus subgroup-III isolates were responsible to cause mild mosaic infection on *Vigna mungo* var. *Sylvestris* L. (Naimuddin et al., 2011).

13. Management-

For the management of *begomovirus* it is important to lower down the inoculum and the vector population.

Cutting and destruction of infected portion of the plant in case of low or moderate infection and uprooting of the plant in case of severe infection is profitable.

Seed treatment with imidachlorpid @ 5ml/kg seed with two sprays of imidachlorpid @ 0.5 ml/l at 25 and 40 DAS were found to be effective against the infection (Jayappa et al., 2017). Another effective method is two sprays of neemazal @ 3ml/l after seed treatment with imidachlorpid @ 5ml/kg seed (Jayappa et al., 2017). Predators offer a better possibility of vector control. These predators include lacewings, bigeyed bugs, and minute pirate bugs. Lady beetles including *Clitostethus arcuatus* (on ash whitefly), the Asian multicolored lady beetle *Harmonia axyridis* and scale predators, such as *Scymnus* or *Chilocorus* species feed on whiteflies (UCIPM).

14. Conclusion and Future Prospects-

Begomovirus with their quantity, infectivity and strain differentiations have always attracted us to conduct exemplary research on them. The wide host range they share, the virulence they have developed and their close association with vector whitefly has brought them to immediate research action and work at present. Also as it fears nutritional security in vegetables like okra, brinjal, tomato, chili, cassava and food security through legumes and cereals, it has come up as an important and immediate research interest. Disease symptoms and particle morphology suggest that bean golden mosaic viruses (subgroup-III of begomovirus) from Puerto Rico, El Salvador, Colombia, Guatemala, and probably Brazil are the same virus, although possible strain relationships are not worked out. Causal agents of similar diseases in other tropical areas have not been characterized. Thus, future research should be emphasized to workout strain relationships and solve complexity of gene order of *begomovirus*. Another challenge is to mark the common gene pool, if any, of begomovirus to understand population distribution and gene flow to check increasing levels of virulent strains. The disease causing ability of the begomovirus has increased due to evolution of more virulent strains and is likely to increase due to uncontrollable spread of whitefly population, tropical climate and widespread cultivation of legumes. Hence, integrated approach towards the solution must be adopted to control the same. *B. tabaci* MEAM1 (Middle East-Asia Minor 1) (Biotype B) is found to violate rule boundaries of *begomovirus* and is found to transmit virus on monocots like maize which can later spread to legumes owing new threat to food security of future. Thus, thrust should be laid to limit strain of *begomovirus* on monocots. Extreme research work is also demanded in the field of protein mapping technology to mark both protein in a bipartite virus and understand their structure to break gene bond which would eventually control the disease spread. A new approach i.e. application of new generation sequencing (NGS) technology for better diagnosis by metagenomic analysis and deep sequencing is yet to be carried out in *begomovirus*. This will allow us to develop better understanding of viruses and their associations and control them to achieve food security.

REFERENCES

1. Arguello-Astorga G, Lopez-Ochoa L, Kong LJ, Orozco BM, Settlege SB, Hanley-Bowdoin L 2004 A novel motif in geminivirus replication proteins interacts with the plant retinoblastoma-related protein J Virol. 2004 May; 78(9) 4817-26.
2. Bagewadi B, Chen S, Lal SK, Choudhury NR and Mukherjee SK 2004 PCNA Interacts with Indian Mung Bean Yellow Mosaic Virus Rep and Downregulates Rep Activity. J. Virol. 78 11890-11903
3. Balaji V, Vanitharani R, Karthikeyan AS, Anbalagan S and Veluthambi K 2004 Infectivity analysis of two variable DNA B components of Mungbean yellow mosaic virus-Vigna in Vigna mungo and Vigna radiata. J. Biosci. 29 297-308
4. Bisaro DM Silencing suppression by geminivirus proteins. Virology. 2006 Jan 5; 344(1):158-68.
5. Chilakamarthi U, Mukherjee SK and Deb JK 2007 Intervention of geminiviral replication in yeast by ribozyme mediated downregulation of its Rep protein. FEBS Lett. 581 2675-2683
6. Choudhury NC, Malik PS, Singh DK, Islam MN, Kaliappan K and Mukherjee SK 2006 The oligomeric Rep protein of Mungbean yellow mosaic India virus (MYMIV) is a likely replicative helicase. Nucleic Acids Res. 34 6362-6377
7. Dasgupta I, Malathi VG and Mukherjee SK 2003 Genetic engineering for virus resistance. Curr. Sci. 84 341-354
8. Duraisamy R, Natesan S, Muthurajan R, Gandhi K, Lakshmanan P, Karuppasamy N and Chokkappan M (2012) Molecular studies on the transmission of Indian cassava mosaic virus (ICMV) and Sri Lankan cassava mosaic virus (SLCMV) in cassava by Bemisia tabaci and cloning ICMV and SLCMV replicase gene from cassava Mol. Biotechnol. DOI: 10.1007/s12033-012-9503-1.
9. Fauquet CM and Stanley J 2003 Geminivirus classification and nomenclature; progress and problems. Ann. Appl. Biol. 142 165-189
10. Fauquet CM, Maxwell DP, Gronenborn B and Stanley J 2000 Revised proposal for naming geminiviruses. Arch. Virol. 145 1743-1761
11. Fauquet CM, Bisaro DM, Briddon RW, Brown J, Harrison BD, Rybicki EP, Stenger DC and Stanley J 2003 Revision of taxonomic criteria for species demarcation in the family Geminiviridae, and an updated list of begomovirus species. Arch. Virol. 148 405-421
12. Girish KR and Usha R 2005 Molecular characterization of two soybean-infecting begomoviruses from India and evidence for recombination among legume-infecting begomoviruses from South-East Asia. Virus Res. 108 167-176
13. Girish KR, Palanivelu S, Kumar PD and Usha R 2006 Refolding, purification and characterization of replication initiator protein from soybean-infecting geminivirus. J. Virol. Methods 136 154-159

14. Govindu HC 1964 A review on virus disease of crop plants. Information pamphlet No.2 (Research series) (Bangalore: Directorate of Agriculture) p 13
15. Gutierrez C 1999 Geminivirus DNA replication. Cell Mol. Life Sci. 56 313–329
16. Gutierrez C 2000 Geminiviruses and the plant cell cycle. Pl. Mol. Biol. 43 763–772
17. Hanley-Bowdoin L, Bejarano ER, Robertson D, Mansoor S. 2013 Geminiviruses: masters at redirecting and reprogramming plant processes. Nat Rev Microbiol. 2013 Nov;11 PMID:24100361
18. Haq QMI, Rouhibakhsh A, Ali A and Malathi VG 2011 Infectivity analysis of a blackgram isolate of Mungbean yellow mosaic virus and genetic assortment with MYMIV in selective hosts. Virus Genes 42 429–439
19. Harrison BD, Muniyappa V, Swanson MM, Roberts IM and Robinson DJ 1991 Recognition and differentiation of seven whitefly-transmitted geminiviruses from India and their relationships to African cassava mosaic and Thailand mungbean yellow mosaic viruses. Ann. Appl. Biol. 118 297–308
20. Honda Y and Ikegami M 1986 Mungbean yellow mosaic virus; in AAB Descriptions of Plant Viruses No. 323 (Kew, England: Commonwealth Mycological Institute)
21. Idris AM Shahid MS Briddon RW Khan AJ Zhu J-K and Brown JK 2011 An unusual alphsatellite associated with monopartite begomoviruses attenuates symptoms and reduces betasatellite accumulation. J. Gen. Virol. 92 706-717
22. Jayappa, HK Ramappa and BD Devamani 2017 Management of Mungbean Yellow Mosaic Virus (MYMV) in Mungbean (*Vigna radiata* L.) Journal of Entomology and Zoology Studies 2017; 5(5): 596-601
23. Jeske H 2009 Geminiviruses. Curr. Top. Microbiol. Immunol. 331 185–226
24. John P, Sivalingam PN, Haq QMI, Kumar N, Mishra A, Briddon RW and Malathi VG 2008 Cowpea golden mosaic disease in Gujarat is caused by a Mungbean yellow mosaic India virus isolate with a DNA B variant. Arch. Virol. 153 1359–1365
25. Karthikeyan AS, Vanitharani R, Balaji V, Anuradha S, Thillaichidambaram P, Shivaprasad PV, Parameswari C, Balamani V, Saminathan M and Veluthambi K 2004 Analysis of an isolate of Mungbean yellow mosaic virus (MYMV) with a highly variable DNA B component. Arch. Virol. 149 1643–1652
26. Mandal B and Varma A 1996 Differentiation of natural variants of mungbean yellow mosaic geminivirus by host reactions and DNA-DNA hybridization. Intl. J. Trop. Plant Dis. 14 189–202
27. Mandal B, Varma A and Malathi VG 1997 Systemic infection of *Vigna mungo* using the cloned DNAs of the blackgram isolate of Mungbean yellow mosaic geminivirus through agroinoculation and transmission of the progeny virus by whiteflies. J. Phytopathol. 145 505–510
28. Mansoor S Briddon RW Zafar Y and Stanley J 2003 Geminivirus disease complexes: an emerging threat. Trends Plant Sci. 8 128-134
29. Maruthi, MN Manjunatha B Rekha AR Govindappa MR Colvin J and Muniyappa V 2006 Dolichos yellow mosaic virus belongs to a distinct lineage of Old World begomoviruses; its biological and molecular properties. Ann. App. Biol. 149 187-195
30. Nariani TK 1960 Yellow mosaic of mung (*Phaseolus aureus* L.). Indian Phytopathol. 13 24–29
31. Nene YL 1973 Viral diseases of some warm weather pulse crops in India. Plant Dis. Rep. 57 463–467
32. Noueiry AO, Lucas WJ, Gilbertson RL Two proteins of a plant DNA virus coordinate nuclear and plasmodesmal transport. Cell. 1994 Mar 11;76(5):925-32.
33. Pant V, Gupta D, Choudhury NR, Malathi VG, Varma A and Mukherjee SK 2001 Molecular characterization of the Rep protein of the blackgram isolate of Indian mungbean yellow mosaic virus. J. Gen. Virol. 82 2559–2567
34. Qazi J, Ilyas M, Mansoor S and Briddon B 2007 Legume yellow mosaic viruses: genetically isolated begomoviruses. Mol. Pl. Path. 8 343-348
35. Radhakrishnan GK, Splitter GA and Usha R 2008 DNA recognition properties of the cell-to-cell movement protein (MP) of soybean isolate of Mungbean yellow mosaic India virus (MYMIV-Sb). Virus Genes 13 152–159
36. Raghavan V, Malik PS, Choudhury NR and Mukherjee SK 2004 The DNA-A component of a plant geminivirus (Indian Mung Bean Yellow Mosaic Virus) replicates in Budding yeast cells. J. Virol. 78 2405–2413
37. Rouhibakhsh A, Haq QMI and Malathi VG 2011a Mutagenesis in ORF AV2 affects viral replication in

- Mungbean yellow mosaic India virus. *J. Biosci.* 36 329–340
38. Rouhibaksh A, Choudhury NR, Mukherjee SK and Malathi VG 2011b Enhanced nicking activity of Rep in presence of pre-coat protein of Mungbean yellow mosaic India virus. *Virus Genes* DOI: [10.1007/s11262-011-0701-x](https://doi.org/10.1007/s11262-011-0701-x)
39. Sarkar TS, Bhattacharjee A, Majumdar U, Roy A, Maiti D, Goswamy AM, Ghosh SK and Ghosh S 2011 Biochemical characterization of compatible plant-viral interaction: A case study with a begomovirus-kenaf host- pathosystem. *Plant Signal. Behav.* 6 501–509
40. Singh SK, Chakraborty S, Singh AK and Pandey PK 2006 Cloning, restriction mapping and phylogenetic relationship of genomic components of MYMIV from Lablab purpureus. *Bioresource Tech.* 97 1807–1814
41. Singh DK, Islam MN, Choudhury NR, Karjee S and Mukherjee SK 2007 The 32 kDa subunit of replication protein A (RPA) participates in the DNA replication of Mung bean yellow mosaic India virus (MYMIV) by interacting
42. Surendranath B, Usharani KS, Nagma A, Victoria AK and Malathi VG 2005 Absence of interaction of genomic components and complementation between Mungbean yellow mosaic India virus isolates in cowpea. *Arch. Virol.* 150 1833–1844
43. Usharani KS, Surendranath B, Haq QMR and Malathi VG 2004 Yellow mosaic virus infecting soybean in northern India is distinct from the species infecting soybean in southern and western India. *Curr. Sci.* 86 845–850
44. Usharani KS, Periasamy M and Malathi VG 2006 Studies on the activity of a bidirectional promoter of Mungbean yellow mosaic India virus by agroinfiltration. *Virus Res.* 119 154–162
45. Vanderschuren H, Stupak M, Futterer J, Grussem W and Zhang P 2007 Engineering resistance towards geminiviruses – review and perspectives. *Plant Biotech. J.* 5 207–220
46. Vanitharani R, Karthikeyan AS, Anuradha S and Veluthambi K 1996 Genome homologies among geminiviruses infecting Vigna, cassava, Acalypha, Croton and Vernonia. *Curr. Sci.* 70 63–69
47. Varma A and Malathi VG 2003 Emerging geminivirus problems: a serious threat to crop production. *Ann. Appl. Biol.* 142 145–164
48. Varma A, Dhar AK and Malathi VG 1991 Cloning and restriction analysis of Mungbean yellow mosaic geminivirus; in *Proceedings of the International Conference on Virology in the Tropics (Lucknow)* p 114
49. Varma A, Dhar AK and Mandal B 1992 MYMV transmission and control in India; in *Mungbean yellow mosaic disease (eds) S K Green and D Kim (Taipei: Asian Vegetable Research and Development Centre)* pp 8–27
50. Wrather JA, Anderson TR, Arsyad DM, Gai J, Ploper LD, Porta- Puglia A, Ram HH and Yorinori JT 1997 Soybean disease loss estimates for the top 10 soybean producing countries in 1994. *Plant Dis.* 81 107–110 Indian begomovirus research 805 *J. Biosci.* 37(4), September 2012
51. Yadav RK and Chattopadhyay D 2011 Enhanced viral intergenic region-specific short interfering RNA accumulation and DNA methylation correlates with resistance against a geminivirus. *Mol. Plant Microbe Interactions* 24 1189–1197
52. Yadav RK, Shukla RK and Chattopadhyay D 2009 Soybean cultivar resistant to Mungbean yellow mosaic India virus infection induces viral RNA degradation earlier than the susceptible cultivar. *Virus Res.* 144 89–95