Bulletin of Biological and Allied Sciences Research
ISSN: **2521-0092**
www.bbasr.org
DOI: https://doi.org/10.54112/bbasr.v2018i1.12
Bull. Biol. All. Sci. Res., *Volume,* ***3****: 12*
BBASR

Review Article

A DETAILED REVIEW ON BEGOMOVIRUS BASED ON ITS CLASSIFICATION, ASSOCIATED SATELLITES, PROTEIN FUNCTIONS AND MODE OF ACTION

AMJID N[1], AMJAD I[2], *KHALID MN[2]

[1]*Centre of Agricultural Biochemistry and Biotechnology, University of Agriculture Faisalabad, Pakistan*
[2]*Department of Plant Breeding and Genetics, University of Agriculture Faisalabad, Pakistan*
**Correspondence author email address:*noumankhalidpbg@gmail.com*

(Received, 14thMay 2018, Revised 5th November 2018, Published 6thNovember 2018)

Abstract: *The largest group of plant viruses is Begomovirus genus. It encompasses round about 100 species. Begomovirus is main genus of family Geminiviridae. Begomoviruses can produce severe infections in several economically important crops all around the world. These are single stranded DNA viruses which are transmitted by Whitefly (Bemisiatabaci). These viruses can cause infection in dicots only. Begomoviruses are divided into two groups. Old world Begomoviruses are existing usually in Asia, America and Europe comprising of monopartite and bipartite genomes and new world Begomoviruses are mostly distributed in the American continent having bipartite genome. There are several DNA satellites which are also associated with Begomoviruses. This review mainly focuses on the classification of the Begomoviruses, origin and evolution of the Begomovirus associated satellites and Begomoviruses proteins functions. This review also sheds light on mode of infection, replication mechanism and Begomovirus-host plant interactions.*

[Citation: Amjid, N., Amjad, I., Khalid, M.N. (2018). A detailed review on begomovirus based on its classification, associated satellites, protein functions and mode of action. Bull. Biol. All. Sci. Res. 3: 12. doi: https://doi.org/10.54112/bbasr.v2018i1.12]

Keywords: Begomoviruses, Ageratum conyzoides, satellites

Introduction

There are several definitions on behalf of different types of viruses, butthere is no clear understanding yet of any definition of the virus. Generally, a virus can cause diseases and producedifferent parasitic infection is expected to be in living organisms. The definition of virus in other prospect that isdefined as " very small parasitic particles within the cells, that can either containing RNA or DNA genome and surrounding protein coat is very useful to protect from danger another definition A type of the nucleic acid that is containing DNA or RNA is present inside the nucleoprotein structure," or in broad sense, "the parasite existing inside of the cell having the DNA or RNA to be able to control its own multiplications having no serving ability for othercrucial function for host.

Viruses of plants

By looking in the past, viruses were found the continuing vectors tocarry a major problem in different vegetable and other crops which were cultivatedaround the globe. By a very long time, those were under control by means of applying different conventional methods for example rotation of crops and tillage techniques, by initialrecognition, chemically controlled vector and devastation of infectious sources, cross-protection as well as resistance(Brunt et al., 1996). In recent time, natural defense mechanisms in plantsagainst viruses have been damaged resulting to increase in latestinformation of molecular genetics and plant viruses and new techniques to controlling the viral diseases in plants are developed in innovative ways(Panattoni et al., 2013).Now in present days, plant DNA viruses belonging to three families are mentioned; *Geminiviridae*, *Caulimoviridae* and *nanoviridae*. *Caulimoviruses* having ds DNA genomic, while other families are having a ssDNA genomic(Hull, 1989).

Nanoviridae

They are containing genome of ssDNA circular in shape. They contain 6 to 9 core DNA components partsencapsulated in co-hederal particles form.In which there are somemodules wereadjusted for Geminiviruses during process of its evolution, and single particles fully rely on assistant virus are titled α-satellite. Second type of satellites, betasatellites with size round about 1.4 kb DNA have different in morphological character in sequences as compared to Geminiviruses and other viruses. Though two types of satellites are established to be trans-replicated and transmitted only with the helping of old world Begomoviruses(Young et al., 2008).

Geminiviridae

Geminiviruses encompassing plant viruses belong to the family of *geminiviridae*. Theyare having single-stranded circular DNA genome in packed formin molecules. Now there are 133 Geminiviruses are familiar species, out of 133, 117 species are belonging to the Begomoviruses and approximately 401 full nucleotide sequence which are entered into databases(Banik & Sharma, 2011).

Geminiviridae is much diversified family, encompassing different varieties of plant viruses that are capable to cause infectionsinplants and canextensively damage the crops in all over theworld. Geminiviruses have the capacity to cause infection in variouscrops very significant in economic prospectsfor example, tobacco, potato and other. The transmission of Geminiviruses is proceeded by the help of vectors i.e., whitefly, could affect substantialloss in several other commercial plants. The report reveals that whitefly have round about 50 different kind of plant hosts in different areas in the world(Mansoor et al., 2003).

The Geminivirus genomics can be monopartite approximately many hundred hectares of agricultural fertile land in twenty countries is under the effect of > 30 Geminiviruses' species of having same sizes i.e., DNA-α and DNA-β), but in many othercircumstances, these are complemented by a circular ssDNA-β both the satellites. Geminiviruses having feature of containing promoter hat can move on both sides for moreproficient transcription and overlying genes for the encoding of synthesizing polypeptides. The Geminivirus is carrying more than one intervenes regions one of them holds the origin of replication as well as stem loop structuretaking a securenucleotide involved in rolling circle replication technique (Aragão& Faria, 2009).

The classification of Geminiviruses is proceeded in 7 classes with respect to sequence of nucleotide, organization of genome, and most importantly thedifferenthost and insect vectors. These are Begomovirus, Topocuvirus, Mastrevirus, Eragrovirus, Curtovirus, Turncurtovirus as well as Becurtovirus. Mastrevirus, Curtovirus and Topocuvirus is having the genomic. In dissimilarity, the viruses are either monopartite or bipartite genome present in the Begomoviruses(Chellappan et al., 2005).

Genus mastrevirus

The transmission of Mastreviruses is proceeded by leafhoppers and contain monopartite genomic size of1.4 kb. It was established that the associates of the Mastrevirus are existing only in the America, Asia and Australia, they can easily cause infection, although some members also cause infection in dicot plants(Gutierrez, 2000).

Virus's genomics are coding for four. The virus strand codes for coat protein. The new sense strand translates for t genes C1 as well as C2 associated with replication which are then in transcription process into Rep-αand Rep-β genes correspondingly. The Long intergenic region and short region present it can distinctly sensing gene and complementary sense strand. SIR possibly containing origin of replication for the newly sense strands. It is also containing terminate inadenylsequences(Shepherd et al., 2010).

Genus topocuvirus

Topocuvirusis consisting of monopartite viruses one them 3.0kb in size, whichare then transmitted through vector. They are existing only in New World (NW). Topocuviruses are looked to cause infection withthe collaboration and showingrecombination character (Lapidot et al., 2007). Topocuviruses holds 6 ORFS. Viral sense strand having V1 and V2 and corresponding strand containing C1, 2, 3 and 4, these are homologues of AC1, 2, 3 and 4, respectively.

Genus curtovirus

Curtoviruses consists of a monopartite genome (BCTV)can cause infection in dicotyledonous plants, and procedure of transmission is done by vector *Circulifertenellus*. Its genome holds 7-8 Origin of replication and one specificsection. The viral sense standtranslates for three ORFS i.e., V1, 2 and 3 and complementary sense strand translates for C1, 2, 3.Byparallel fashion to mastreviruses, curtovirus genomic holds abundant Adenylation signal around about 20 base pairs between V1 and diverged C3 ORFS (Rybicki & Martin, 2011).

Genus Begomoviruses

The largest group of plant viruses is Begomoviruses genus (type species bean golden mosaic virus) genus. It encompasses round about 100 species Begomovirusesismain genus of family Geminiviridae. Begomoviruses can produce overwhelming symptoms and infections in several crops which is having economic importance in all over theworldcontaininggrapes dates and tobacco (Baliji et al., 2004). Whitefly (Bemisiatabaci) is act as a vector for transmitting the Begomoviruses and these viruses can cause infection in dicots only(Heydarnejad et al., 2007).

The division of Begomoviruses into two other groups according to barrierscomprising the New World and Old-world viruses(Gutierrez, 2000). Old world Begomoviruses, are existing usually in Asia, America and Europe comprising of having the monopartite and bipartite genomes and new generation begomoviruse that are mostly distributed in the American continenthavingbipartite genome (Power, 2000).

Bipartite Begomoviruses

Begomoviruses binary scheme is developed from ancestors. They are monopartite virus as a consequence of new genetic material and itsacquirement. Consequently, the homology of sequencein proteinof coat and the nuclear shuttling protein sequences also holding comparable things on the alphasatellites and betasatellitescorrespondingly, couldspecify a mutualorigin of evolution.

Their Genome comprising of two different size DNA molecules (DNA-α and DNA -β, with a length of 2.7kb and 1,4 kb respectively DNA-αtake open reading frames (ORFS). Betasatellites hold 2ORFS, BV1 gene in viral-sense strand and BC1 in newly formed sense strand.Bipartite Begomoviruses were established with AV2 gene that are not established in the New World virus.

Viral DNA sense strand involves to code in the coat protein and protein V2/AV2, and corresponding DNA sense strand involve to code in a protein related to replication, or C1 /AC1, Transcription activator protein, or C2/AC, replication motifs Protein, or protein C3/AC3 and protein. All the genes are tangled in the viral replication and in causing different diseases. Itinvolves to code for2 proteins: locomotion Protein and nuclear shuttling, towhich the measure of viral particles within the cells can easily be controlled(Krupovic et al., 2009).

Up to2-4 hundred ntlong collective region exist, it is very highly unspoiled in viral component. It holdsstem loop structure along with asequence TAATTAC with highly unspoiled sequence and its presence at one loop end is very important. There are several regulatory elements present in it, of having two boxes. It also contains 6 repeats of 142 nt sequence which is involved to act as a replicating site for binding(Soto & Gilbertson, 2003).All the necessary sequences in CR for the replication and process of molecules, thus involve in stabilizing the bipartite genomebinder alphasatellites of the bipartite Begomviruses have ability to replicate without interference as well as involve in producing molecule, but i the products of BV\1 and BC/1 along with infectious molecule codded by betasatellites for the sake it is marked that necessity of both components is provided by alphasatellites on the other hand betasatellites plays the vital role in movement as well asinfection. In some other cases, as previously discussions reveal Begomoviruses, the DNA-α only is necessary for the locomotion and positive infection, whereas in case of New World Begomoviruses,it is more dependent on betasatellites Certain Begomoviruses, and cabbage leaf curl virus are the prominent examples of partite Begomoviruses containing the components of genomeencapsulated by coat protein in different fashion(Lam et al., 2009).

Monopartite Begomoviruses

Approximately round about 130 species abstaining monopartite under the process of identification in Begomovirus genus since then and more amazingly the origin of all these species belongs to the OW. Unusually, monopartite Begomovirus has been identified that is native to new World, although TCV familiarized in recent inadvertently. However, the identification of number of monopartite Begomviruses along with single component which is closely similar to DNA-A and have the ability of encoding all the necessary proteins which plays important role for virus to cause disease. Approximately 2800 nucleotide (nt) long is genomic size of monopartite Begomovirus(Morales, 2006).The viral-sense ORFS are paired sense strand ORFS are four genes present in monopartite begomovirus. DNA complementary sense strand make sure to encoding for protein associated with replication, also named as C1 protein/AC1, (TRAp), or C2/AC2 protein, replicating enhancer protein, which are involved to take responsibility inthe controlling of viral replication and transmission process(Schaumberg et al., 2016).

Some other examples like which are much important economically inmonopartite Begomoviruses. The first isolation of Ageratum yellow vein virus was begunfrom virion sense strand make sure to encode for the protein coat, and DNA *Ageratum conyzoides* plants grow in Singapore, exhibitingthe classicsigns of vein yellowing disease).Even though Begomoviruses holds only one component. They usually establishing correlation with two, it is referring as betasatellites and alphasatellites(Zhou, 2013).

Origin and evolution of the Begomovirus associated satellites

Lot ofschemes reveal that the origin ofα-satellites most likely comes from nanoviruses because ofthe ability ofencapsulated nano virus portionin protein Begomovirus necessary for the sake of transmission proceeded by vectors after nourishing on infected plants with individually Begomoviruses. It has been identified that there is association ofalphasatellites category. The viewpoint of origin of evolution for betasatellites is fruitive, even though, the earlier report had specified that the adaptation isexpecting to come from DNA molecules. The Southeast Asia exhibits great diversity of Begomovirusesbeta satellites, directing that this region may exhibited the main edge of foundation for beta satellites begomovirus(Czosnek et al., 2017).On the prospect of relation with ancestors there are two categories under the Betasatellites: one are those which isolated from the masses in the malvaceousfor most part, and other one that were recognized from the hosts. This theory suggestions indicates that in the betasatellites evolution, the plants may have manyessentialparts(Briddon et al., 2003).

The mechanism of recombination plays a vital role in begomovirus evolution prospective bythe viral components that may develop) hence recombination plays vital role in regression such viral ss DNA molecules which are upcoming from betasatellites are frequently present in disease-ridden plants holding begomovirus and Betasatellites (Chowda Reddy et al., 2005).

Betasatellites

Betasatellitescontainingrounded ss DNAfragments have a open reading frame (ORF), earliertermed as DNA-β, it wasindicated that there is association with many diseased begomovirus. Since there was first report in 2000, approximately more than 100 floor-length betasatellites molecules were to be duplicatedand sequenced(Briddon et al., 2008).The first isolation of Betasatellite was done in Australian region from plantsof tomato that infected with ToLCV begomovirus, and was mentioned to ToLCV. Sat was a very minor in size, as betasatellite molecules having partially base pair length of 712bpwith no open reading frames. Full set is round about 1347bpin length it was originated firstly 1998 in (*AYVV*) infected weed plant. These plants were displaying it(Nawaz-ul-Rehman & Fauquet, 2009).

Currently, it is broadly revealed that several diseases act as liable role for was fully main diseases in vast variety of plant species in America as well as Brazil, exclusively in the subcontinent in Asia. The Begomoviruses exhibit many warnings sign of the disease, containingyellow veins, paper, nets,enations in infections a wide range of dicotyledonous plants containing in 17 families having at least 36-37 different genus of significant crops and showy plants, and diverse weeds(Mubin et al., 2010).

Betasatellites composed with theobsessivedetermining factor molecules which aresupplementary with numerous plant diseases and major damage of numerous crops ultimately.Also, can cause these disease multiplexes involved to cause by utterly Begomoviruses It is completely relying on the assistant DNA for the sake of replication, encapsulations and transmission process. There is difference between Betasatellites and alphasatellites in that way, regardless of hosts and geographical distribution there is association with specific helper element (Lozano et al., 2016).

Until now, approximately four hundred betasatellites with full length are submitted to databank. Half of the full length begomovirus is Genomic size of Betasatellite. They didn’t show any sequence resemblance with assistant viruses this is astarting point of copying DNA virus strand. Betasatellites are well-organized and preserved in their organization of genome. It holds a betasatellite conserving region (SCR) conserved of our genomic organization is made of recognized as the satellite in the region, so they are equivalent in the middle of all satellites, is also well-kept both in arrangement and point are involved in encoding through the complementary strand sense strand. SCR 132bp long sequence and appositionally resembles to commonviruses(Venkataravanappa et al., 2011).

BC1 protein (having great ability of doing many functions) is important, it is involved to cause the overpowering of both TVG and PTG, and also involved in repressing of plant defense on trivances. Pathogenicity contributing factor gene which have ability toreins the pathogenicity. All recognized betasatellites hold A-rich region, which is round about 160-280-bp long in length, contain the content.The A-rich regionis prospective to play essential role in maintenance of the betasatellite particles, which may contain the role of stuff to enhance the size of these particles to permitcapsulationsinefficiency forgeneralmeasure.

Alphasatellites

Single stranded DNA circular molecules which are linked with begomoviruses holding the size identical to the betasatellites size.The first report revealed in 1999 in collaboration with yellowing leaf vein disease Ever sincenow, 200 alpha satelliteare existed in genebank databanks. Begomoviruses which are accompanying with alphasatellites are self-repeating molecules. Which totally dependupon thepartner virus for their locomotion, encapsulations, relocation via vectors. It is no recognizedprecise function which is particularly specificto alphasatellites. It is established there is association with Begomoviruses(Zhou, 2013).

It isdissimilarity within the two kinds of satellites, thealphasatellites are supposed to involve indistribute with andexhibit lessinvolvement in the development of disease Nevertheless, a very unusualclass of alphasatellite is established alongmonopartite yellow vein virus in Singapore whichis devoted to as the DNA 'type, involving insharing the sequence identity with the' DNA-1type The genomic arrangementsof both DNA-1 and DNA-2 type alphasatellites isexhibiting very parallel properties; but,it is seen that here is noconclusiveinvolvement inhelper viruspathogenic(Fiallo-Olivé et al., 2012).

The genomic range of Alpha satellite is round about 1375 nts is involved in coding ofone alpha Rep. These holds A- rich area and expected hairpin structure. The leadingDelegateORF involved in coding in a protein. It ‘shaving size about abstaining and display sresemblance to nanoviruses Rep. by the comparison, thealpha Rep is unspoiled and conserved.). The average percentage of ranges between 60% and is showing single feature that discriminates begomovirus alphasatellites from nanovirus Rep involved in coding elements. It isassumed to bethe singlepurpose of A-rich sequenceis involved to rise in the size of alphasatellite particle to partial size of the assistantparticlesAlphasatellites hair-pin structure exhibiting a nucleotide TTAC, of nanoviruses displaying correspondence with anucleotide (TAC)exist in curling structures of Begomoviruses. In recent times, alphasatellites were established to be associated with Begomoviruses(Mubin et al., 2010).

Common features between the Geminivirus components and satellites

All Geminiviruses display a unique common feature and their allies are the existence of curtailhoop with the NONA nucleotide structure as well as RCRappliance and reproduction (alpha satellites) process. RCR is the simplecontrivance involved in the replicating process of bacterial and Rachael plasmids and, bacteriophages, plants,human as well as animals. It relies on the linked replicating protein is veryvital factor to achieve the process participating in DNA replicating strand It has seen proteins participate in theequivalentroles as delivered through various other proteins. Though the Geminiviruses and their assistant elements displayvery high diversity in the nucleotide genomic sequence buttheir genomicconstruction, length of individual genes as well as locationand protein occupations are much more well-kept withinparticipants of every genus(Xie et al., 2010).

Variability in features of Gemini-virus components

The newdomains monopartite Begomoviruses are not holding the alphasatellite piece. Begomoviruses holds N-terminalengaged indicating signals PWRsMaGTs produced in the protein coat, Because of nonexistence, Begomoviruses which are progressed in starting process of evolution from a blood relation after the Gondwana continental separation by the allowance of AV2, both new world and Begomoviruses displayed parallel genomic arrangements and there is indication of the Begomoviruses have evolved from mutual origin regardless sof their geographic barriers(Nawaz-ul-Rehman et al., 2012).

Begomoviruses proteins functions

Replication-associated protein (ac1, c1)

The Geminiviruses, replication-enhancing protein play important role in code by the AC1on the other hand monopartite Geminiviruses, Rep is participating to encode throughC1.Rep is verywell-kept intheir roles and sequence and display in the influence of a promoterco-represent in nucleus(Kumar et al., 2017).

The translation of fully size replication is proceeded from anointer wovenopen reading frame. Replicating enhance protein is showing different functional abilities in natural surroundings and its service able dominions have been categorized Rep play vital role for rolling circle replication (RCR) and isaffianced in the modulation of gene expression Rep express quitrelated properties to some other bacteria and animal single stranded DNA viruses and plasmids. This indication shows that a powerful linkage between the protein's evolutionary process(Idris et al., 2011).

The minor step is the synthesizing of complementary strand through this genomic single stranded DNA during the process of replication in geminivirus. How thereplication is accomplishedis unknown and is supposed to catalyze viahost elements. A late gene takes the responsibility for Rep and provides viral-specification gratitude of its same foundation of replication and DNA replication begins. Recognizing mechanism seems to be differ among mastreviruses and Begomoviruses, The origin of replication comprises mastreviruses, that is necessary for numerous Rep sites while the starting point of replication in begomovirus holds a single Rep binding site as the rolling circle replication begins, which contains of astructurewithtranscription frightposition and TATA box the compound attaches apparently to three sites present in the closeness of the two otherboxesdown and up of the DNA replication startsite and at the sordid of well-kept stem-looping formation(Lozano et al., 2016).

The other Rep proteins have known to act as chief role in duplication. Assembly of proteins termedasretinobstoma proteins(RBR). It is accommodating for DNA replication of viruses.Rep also binding with multiplying cell nuclear antigenwhich participate in destructiveinstruction of the cell cycle and also involved in interaction with protein of several Gemini viruses help of itsconnections with as Rep cooperates with RCR, then dealings concerning RcR and F is no longer established. Thus, by the activation of repressed cell cycle to release of E2F with its interaction and triggering of genes expression happened. Expression of genes rely on required Retinoblastoma-related proteins subdues cell cycle progression with the for-replication process, excluding, which is necessary to initiate to collect in the g1 phase ofthe cell cycle, getting the top level in the S phase(Paprotka et al., 2010).

The replicating proteins are involved to interact with the copying protein.Areplicating proteintakes the responsibility forenrollment of vibrant replicatingproteins machinery,In collective prospective, theoutcomes have shown to clearunderstandings in starring part of Delegate of Gemini virus in replication and complexmechanism ofrolling circle replication (RCR).Theconclusions cleared the modelof well-designedlink between thereproductionorigination proteins ofsolitarydeserted viruses and geminiviral Rep and plasmids, and reinforced the analysis that Geminiviruses are progressed from plasmids with respect to sequence inquiry Latest study indicated to reject the hypothesis that Geminiviruses initiated from plasmids. DNA leads to mechanize the cellular element recruitment and chemical events to initiate genomic replication process are still abundantly indomitable(Malathi et al., 2017).

Transcriptional activator protein (AC2, C2)

The role of AC2 is more significant as a transcript activating protein The AC2 protein of s involved in interaction with the adenine and participate in RNAi in bipartite viruses. AC2 play important role in interaction with nuclear signal lead toimproved transcription level of TrAP avoid viral general locomotion to minimizeaddition of DNA and manufactured coat protein. There are no specifications of TrAP function to virus. Due to the absence of this well-designed specificity, it isrecommended that Some was seen in yellow vein mosaic disease It overcomes virus induced oversensitive cell decease getting on supporters of all Begomoviruses holds a conjoint structure is recognized by TrAP or TrAP protein which participate in the interaction withproteins present in cellulose of plant host to upset the transcriptional activation. The reports reveal that TGMV and TrAP are involved in destruction silencing. The report of another study illustrates the AC2 in a varioussubdual inamongstnew Gemini viruses(Ferro et al., 2017).

Replication enhancer protein (AC3, C3)

Similar to AC2, expression of AC3is driven through strong promoter situated within codingsequence of AC1. While not vital for replication of virus, REn enhances accumulation of viral DNA anddevelopment of symptom in plants, infected through Begomoviruses and curtoviruses consequently confirmation ofa utility for REn in copying of viral DNA(Romay et al., 2010).

AC4 protein

The frameinpartite and C4 in bipartite Gemini viruses (C4 isabsent) are enclosedentirelyinside AC1 open reading frames, but in other frame, are less unspoiled of all Begomoviruses protein, using roles in bipartiteGemini viruses. Distraction of these proteins open reading frame of TYCV involved to cause inclining in levels of viral DNA and symptom development, representingit also takes part in developing in viral movement. in adding these are main determining factor ofspecific vein swelling phenotype which isdetected in plantsinfected by these proteins. For the restraining ofthe RNA silencing the capacity of C4 and AC4 is highly stable for other mono as well as bipartiteGemini viruses. By usingexemplary,the exposure of AC4 proteins of EAMVvirus has involved to reducesilencing factor)(Zubair et al., 2017).

Coat protein (AV1, V1)

The requirement of coat proteins play vital role inencapsulation, beetlediffusion, movement of virusessurrounded by and in the middle of the plants to plants in Begomoviruses. and in Gemini viruses it involves to facilitate in the transferring of betasatellites within the cell nucleolus of host and is also participate in general virus measurein opposite side, CP is not necessary for general communication in Begomoviruses but some mutation examination revealed the expansion of disease ishindered to diminishingsigns after having the septicity along with mutative. Another key task of coat protein participates in the safety ofssDNA as insect vector transmission initiates(Azzam, 1994; Frischmuth & Stanley, 1998). It has been found that essential sequences for communication process in this protein that exhibit coat proteintaking part in vector. At unambiguous point, CP is responsible to involve in RCR; a process in Gemini virus. Clear cut as virus enters initially into the host cell, it is transported in the nucleusfor thereplication. The presence of coat protein in the nucleus recommendedthere is participation in involvement for nuclear export of viral DNA. When the CP is not present as result into minimum number of ssDNA thus involvement inregulating its copy digit(Akhtar et al., 2014).

AV2 protein

Protein ORF (V]2) existence, along with in monopartite Gemini viruses was established in the old domain whereverin new world bipartite Begomoviruses are seen of having no exact certainty in their function as ToLCV along with transfiguration in V2 with themetamorphosis in AV2 invades in plantsexhibit low level of DNA in sicksoft tissue of flower(Rigden et al., 1993). Both the types AV2 and 2 were seen to be cooperative in RNA silencing process as validated for and for V2 of *Ageratum yellow* vein virus have its place to thevirus (Briddon et al., 2010).

Movement protein (BC1, V2)

The undertaking protein are to be obliquealongwith the ORF present on the betasatellites of bipartite Begomoviruses. It is been coded by V2 in occasion of monopartite Begomoviruses and don't show any sequence connection with B. The combination and interaction of Protein and Shuttle Protein is more important for long distance movements and one to anothercell measure for virus in bipartite Begomoviruses. By current revisions, it hasdetected thatunitedrejoinder effect of NSP-MP exhibit indications of promising DNA of virus in nucleus and this transport modelmonitors "couple slithering. Programme proteins are to be coded by the open reading frame of V2, on the other hand the coat protein is to be coded by the V1 ORF and It involves on support of the DNA of virus between the cytoplasm as well as nuclei so it substitutes (NSP) functionally. This "coupting" model displays that there is strong bound in movement protein along with nuclear-DNA component in the portion of cytoplasm of cells or in microvesicles and permits the passage to the adjoining cells. In monopartite Gemini viruses (CP) show vital role and necessary for the virus movements. Likewise, it has been seen that differences concerning functions between mastreviruses and Begomoviruses. Just like as bipartite Begomoviruses, the binding of movement proteins of mono-partite Begomoviruses with the viral genome while they do not participate. Furthermore, C4 facilitates from one to other cell locomotion's in monopartite Begomoviruses(Leke et al., 2015).

Nuclear shuttle protein (BV1)

The 2 ORFs existing on the BV1 proteins or recognized as BV1 is established in bipartite Begomoviruses. The encoding of nuclear shuttle proteins proceeded by BV1 is obligatory for the handlingof virus among cytoplasm MP set up on cytoplasmic trap the viral-genomics and NSP complexes and from this point it redirects nucleus. It is revealed through the evidences that binding of NSP to DNA occurs is in a sequence of nonspecific manner.On behalf ofaccomplishment of the lengthy and cell to cell moments, to the neighboring parallel cells. The NSP there guides the viral genome for the process of new duplication in the cell. Nuclear protein of many viruses are necessary for the cooperation with enzymes in cytoplasm for the sake of export of complex. It is there transmitted to the apparent of cell to the association with virus(Rishishwar et al., 2015).

Transmission of begomovirus

Not like Gemini viruses which use insects as a vectors for the transmission of disease to various plants, arthropod vector important channels of transmission of viruses is essential for Begomoviruses. Underneathof species the specialty of vector is to be seen within numerous *B. Tabaci.* Explicit vector mixture was illuminated by Brwsdford. (1994) for nineteenBegomoviruses holding Btypes of the vectors. The reason behind that most of types can take part in transferring a diversity of viruses but with regardless this presented that few of these Begomoviruses are to be involved in development to be conceded more excellently by some otherprecise species. In previousdays there was the consideration of *B. tabaci*long time as a complex of different species. o into 11 renowned groups along with other species,these are not under the distinction. These indistinguished species of *B. tabaci* were characterize don the viral but lately after wards of complete characterization molecules of whitefly, it was more separated by De Bar transmission approach and host unambiguouschoice.Whiteflies instinctive to a section can participate in the vital role ofupsetting the dominance in the different specific areas. of arbitrary efficiencies of the host plant in which the transmission of germ is being occurred (Godara et al., 2017). On the basis of their clustering of coat protein and the vector with respect to gene as well as Begomoviruses according to their complete DNA sequences (cytochrome oxidase I) theexhibition of interaction or cooperation with respect to geographical origin in steading the origin of plant.

Begomovirusinfection

As whitefly vector nourishes on phloem tissues of host plants, the infection cycle of begomovirus begins. As Soon as after nourishing, viral particles moves into the plant movement system through the channel of vascular tissues .as particles enters into the cells, the movement of particles in direction towardsthe cells related to plant tissue. The binging of Replication of the viral DNA and transcription process after entering particles in the cell's nucleus and are unceasing there.The viral DNA are then shifting in plant cell and then into cytosol is through the CP in monopartite begomovirus. Instead, the usage of NS protein to travel virus from nucleus to cytoplasm, protein coating is not essential in bipartite begomoviruss. The formation of Harmonizingfeature is done in the nucleus of the cell which is involved to follow the primer manufacturing for the sake ofmanufacture of dsDNA intermediate that serve as template for protein transcription of the virus (Marwal, Kumar Sahu, et al., 2013). Various transcriptional direct saroses on the accomplishment of DNA with the support of supporterstructure at the IR. Texts from virus for the sake of rendition are then transferred to cytoplasm. After the translation that transfer towards nucleus for replication process the proteins are formed, packaging of protein and for movement of DNA. Replication of virus impasses and support in initiation. After accumulation of the DNA, the coat proteinconvulsions RCT and moves towards cytoplasm.DNA packaging of virus is completed by CP for the sake of manufacture of the virions. The viruses are then get rid of to next cell or are composed by whitefly for the communication to next host plant(Amrao et al., 2010).

Replication mechanism

Due to deficiency of DNA polymerase in Begomoviruses,thus they are relying on DNA of host for replication as Gemini viruses to escalate genomes in nuclei of the cell of plague-ridden plant. To start the replication Begomoviruses are totally depends on two mechanisms along with recombination needy replication.The materialization of R protein is done as the product of the rendition after that protein is moved towardsdisease-ridden to participatefrom virus. Rep protein is necessary to begin viral precise appreciation of similar ori. Replication route is totally depending on the 3 stages. First one is the binding of Rep to the virus IR initiation, which is important in the formation of the sable sequence and to start RCR, host factors that are DNA polymerases take part in formation of replication folk, PRTE, RF-C, etc. Next to initiation is the elongation route starts at 3' OH end where nick was produced through the Rep protein performing as enzymes. The last and final step is termination which is more important replication process in which protein slices and ssDNA is consigned to get circular the viral DNA of replication depends on collaboration between them. Comparisons of sequencesindicated that the Rep protein of Geminiviruses is quite similar to the protein synthesized by plasmids ssDNA necessary for DNA requisite. DNA is amplified when REn impasses with SINC1 transcription feature. Newly formed ssDNA monitors one of the passages(Marwal, Sahu, et al., 2013).

Begomovirus-host plant interactions

The Begomoviruses superficially demonstratesnear of flexibility which give the permit to them inmodification very rapidly in reaction to fluctuatingsystems of cropping.A particular host plant of specific area can play vital role in direct or indirect mode to upset the whitefly population. For example, research showing that there may be a difference in population of whitefly on farmers having plants including hairy leaves which will involve eventually to disturb the bio type specificity of whitefly. In India, report reveals, two differentpopulaces of white fly are involved for bitterroot vegetable and sooner or lateraltering the viruses host vague training changed within them. The predominance of these Begomovirusesare to be aggerated by the level of crop to crop due to the host range difference and ultimately involve to affect their proliferation in a particular region. As is infection triggered by two viruses, this interaction of viruses may either in specificmode ofincompatiblescheme which totallydependent on the selectof the host plant where interaction occurs, it exhibited main effect in *Nicotiana benthamiana* and tobacco while incompatible effect produced in pepper The evidence through researches revealed that is just due to theopening of the new plants. It might be possibility exist that there is already presence of virus their but at the time of interaction with other it became familiar(Mubin et al., 2009).

Roughcrops involve to act as dynamic source for Begomoviruses. Through the action as sentimentalrocks they participate inassistance in the manufacturing of new viruses and rinsing (The results come from these communications between multitude plants and the illnesses is count on the proficiency of the viruses to do “counter-act” the defense of plant like PTGS. There are the more planned of hybridizing as well as mutant in many diseases throughalternative weed hosts as they provide thepoolof many viral plesartics. So far in the currentstudy, the cloning ofall unlikely Begomoviruses viruses infecting *A. conyzoides* were proceeded and accomplishment ancestral linkage analysis to measure the diversity of viruses(Patil & Fauquet, 2010).

Conflict of interest

The authors declared absence of conflict of interest.

References:

Akhtar, S., Khan, A. J., Singh, A. S., & Briddon, R. W. (2014). Identification of a disease complex involving a novel monopartite begomovirus with beta-and alphasatellites associated with okra leaf curl disease in Oman. *Archives of Virology* **159**, 1199-1205. DOI: https://doi.org/10.1007/s00705-013-1926-x

Amrao, L., Akhter, S., Tahir, M. N., Amin, I., Briddon, R. W., & Mansoor, S. (2010). Cotton leaf curl disease in Sindh province of Pakistan is associated with recombinant begomovirus components. *Virus Research* **153**, 161-165. DOI: https://doi.org/10.1016/j.virusres.2010.07.003

Aragão, F. J., & Faria, J. C. (2009). First transgenic geminivirus-resistant plant in the field. *Nature Biotechnology* **27**, 1086-1088. DOI: https://doi.org/10.1038/nbt1209-1086

Azzam, O. (1994). Whitefly Transmission and Efficient ssDNA Accumulation of Bean Golden Mosaic Geminivirus Require Functional Coat Protein. *Virology*. **204**, 289-296. DOI: https://doi.org/10.1006/viro.1994.1533

Baliji, S., Black, M. C., French, R., Stenger, D. C., & Sunter, G. (2004). Spinach curly top virus: A newly described Curtovirus species from southwest Texas with incongruent gene phylogenies. *Phytopathology* **94**, 772-779. DOI: https://doi.org/10.1094/PHYTO.2004.94.7.772

Banik, S., & Sharma, P. (2011). Plant pathology in the era of nanotechnology. *Indian Phytopathol* **64**, 120-127.

Briddon, R., Brown, J., Moriones, E., Stanley, J., Zerbini, M., Zhou, X., & Fauquet, C. (2008). Recommendations for the classification and nomenclature of the DNA-β satellites of begomoviruses. *Archives of* virology **153**, 763-781. DOI: https://doi.org/10.1007/s00705-007-0013-6

Briddon, R. W., Bull, S. E., Amin, I., Idris, A. M., Mansoor, S., Bedford, I. D., Dhawan, P., Rishi, N., Siwatch, S. S., & Abdel-Salam, A. M. (2003). Diversity of DNA β, a satellite molecule associated with some monopartite begomoviruses. *Virology* **312**, 106-121. DOI: https://doi.org/10.1016/S0042-6822(03)00200-9

Briddon, R. W., Patil, B. L., Bagewadi, B., Nawaz-ul-Rehman, M. S., & Fauquet, C. M. (2010). Distinct evolutionary histories of the DNA-A and DNA-B components of bipartite begomoviruses. *BMC evolutionary biology* **10**, 1-17. DOI: https://doi.org/10.1186/1471-2148-10-97

Brunt, A., Crabtree, K., Dallwitz, M., Gibbs, A., & Watson, L. (1996). *Viruses of plants*. DOI: https://doi.org/10.1079/9780851987941.0000

Chellappan, P., Vanitharani, R., Ogbe, F., & Fauquet, C. M. (2005). Effect of temperature on geminivirus-induced RNA silencing in plants. *Plant Physiology* **138**, 1828-1841. DOI: https://doi.org/10.1104/pp.105.066563

Chowda Reddy, R., Colvin, J., Muniyappa, V., & Seal, S. (2005). Diversity and distribution of begomoviruses infecting tomato in India. *Archives of virology* **150**, 845-867. DOI: https://doi.org/10.1007/s00705-004-0486-5

Czosnek, H., Hariton-Shalev, A., Sobol, I., Gorovits, R., & Ghanim, M. (2017). The incredible journey of begomoviruses in their whitefly vector. *Viruses* **9**, 273. DOI: https://doi.org/10.3390/v9100273

Ferro, C., Silva, J., Xavier, C., Godinho, M., Lima, A., Mar, T., Lau, D., & Zerbini, F. (2017). The ever increasing diversity of begomoviruses infecting non-cultivated hosts: new species from Sida spp. and Leonurus sibiricus, plus two New World alphasatellites. Annals of Applied Biology170, 204-218. DOI: https://doi.org/10.1111/aab.12329

Fiallo-Olivé, E., Martínez-Zubiaur, Y., Moriones, E., & Navas-Castillo, J. (2012). A novel class of DNA satellites associated with New World begomoviruses. *Virology* **426**, 1-6. DOI: https://doi.org/10.1016/j.virol.2012.01.024

Frischmuth, T., & Stanley, J. (1998). Recombination between viral DNA and the transgenic coat protein gene of African cassava mosaic geminivirus. *J. Gen. Virol*.**79**, 1265-1271. DOI: https://doi.org/10.1099/0022-1317-79-5-1265

Godara, S., Paul Khurana, S., & Biswas, K. (2017). Three variants of cotton leaf curl begomoviruses with their satellite molecules are associated with cotton leaf curl disease aggravation in New Delhi. *Journal of Plant Biochemistry and Biotechnology* **26**, 97-105. DOI: https://doi.org/10.1007/s13562-016-0370-x

Gutierrez, C. (2000). Geminiviruses and the plant cell cycle. *Plant molecular biology* **43**, 763-772. DOI: https://doi.org/10.1023/A:1006462028363

Heydarnejad, J., Hosseini Abhari, E., Bolok Yazdi, H., & Massumi, H. (2007). Curly top of cultivated plants and weeds and report of a unique curtovirus from Iran. *Journal of Phytopathology* **155**, 321-325. DOI: https://doi.org/10.1111/j.1439-0434.2007.01234.x

Hull, R. (1989). The movement of viruses in plants. *Annual Review of Phytopathology* **27**, 213-240. DOI: https://doi.org/10.1146/annurev.py.27.090189.001241

Idris, A. M., Shahid, M. S., Briddon, R. W., Khan, A., Zhu, J.-K., & Brown, J. K. (2011). An unusual alphasatellite associated with monopartite begomoviruses attenuates symptoms and reduces betasatellite accumulation. *Journal Of General Virology* **92**, 706-717. DOI: https://doi.org/10.1099/vir.0.025288-0

Krupovic, M., Ravantti, J. J., & Bamford, D. H. (2009). Geminiviruses: a tale of a plasmid becoming a virus. *BMC Evolutionary Biology* **9**, 1-11. DOI: https://doi.org/10.1186/1471-2148-9-112

Kumar, R. V., Singh, D., Singh, A. K., & Chakraborty, S. (2017). Molecular diversity, recombination and population structure of alphasatellites associated with begomovirus disease complexes. Infection, *Genetics and Evolution* **49**, 39-47. DOI: https://doi.org/10.1016/j.meegid.2017.01.001

Lam, N., Creamer, R., Rascon, J., & Belfon, R. (2009). Characterization of a new curtovirus, pepper yellow dwarf virus, from chile pepper and distribution in weed hosts in New Mexico. *Archives of Virology* **154**, 429-436. DOI: https://doi.org/10.1007/s00705-009-0320-1

Lapidot, M., Weil, G., Cohen, L., Segev, L., & Gaba, V. (2007). Biolistic inoculation of plants with Tomato yellow leaf curl virus DNA. *Journal of Virological Methods* **144**, 143-148. DOI: https://doi.org/10.1016/j.jviromet.2007.04.011

Leke, W. N., Mignouna, D. B., Brown, J. K., & Kvarnheden, A. (2015). Begomovirus disease complex: emerging threat to vegetable production systems of West and Central Africa. *Agriculture & Food Security* **4**, 1-14. DOI: https://doi.org/10.1186/s40066-014-0020-2

Lozano, G., Trenado, H. P., Fiallo-Olivé, E., Chirinos, D., Geraud-Pouey, F., Briddon, R. W., & Navas-Castillo, J. (2016). Characterization of non-coding DNA satellites associated with sweepoviruses (genus Begomovirus, Geminiviridae)–definition of a distinct class of begomovirus-associated satellites. *Frontiers in Microbiology* **7**, 162. DOI: https://doi.org/10.3389/fmicb.2016.00162

Malathi, V., Renukadevi, P., Chakraborty, S., Biswas, K., Roy, A., Sivalingam, P., Venkataravanappa, V., & Mandal, B. (2017). Begomoviruses and their satellites occurring in India: distribution, diversity and pathogenesis. In A century of plant virology in India (pp. 75-177). *Springer*. DOI: https://doi.org/10.1007/978-981-10-5672-7_5

Mansoor, S., Briddon, R. W., Zafar, Y., & Stanley, J. (2003). Geminivirus disease complexes: an emerging threat. *Trends in Plant Science* **8**, 128-134. DOI: https://doi.org/10.1016/S1360-1385(03)00007-4

Marwal, A., Kumar Sahu, A., & Gaur, R. K. (2013). Molecular characterization of begomoviruses and DNA satellites associated with a new host Spanish Flag (Lantana camara) in India. *International Scholarly Research Notices* 2013. DOI: https://doi.org/10.5402/2013/915703

Marwal, A., Sahu, A. K., Choudhary, D. K., & Gaur, R. (2013). Complete nucleotide sequence of a begomovirus associated with satellites molecules infecting a new host Tagetes patula in India. *Virus Genes* **47**, 194-198.

DOI: https://doi.org/10.1007/s11262-013-0914-2

Morales, F. J. (2006). History and current distribution of begomoviruses in Latin America. *Advances in Virus Research* **67**, 127-162. DOI: https://doi.org/10.1016/S0065-3527(06)67004-8

Mubin, M., Briddon, R., & Mansoor, S. (2009). Complete nucleotide sequence of chili leaf curl virus and its associated satellites naturally infecting potato in Pakistan. *Archives of Virology* **154**, 365-368. DOI: https://doi.org/10.1007/s00705-008-0296-2

Mubin, M., Shahid, M., Tahir, M., Briddon, R., & Mansoor, S. (2010). Characterization of begomovirus components from a weed suggests that begomoviruses may associate with multiple distinct DNA satellites. *Virus Genes* **40**, 452-457. DOI: https://doi.org/10.1007/s11262-010-0470-y

Nawaz-ul-Rehman, M. S., Briddon, R. W., & Fauquet, C. M. (2012). A melting pot of Old World begomoviruses and their satellites infecting a collection of Gossypium species in Pakistan. DOI: https://doi.org/10.1371/journal.pone.0040050

Nawaz-ul-Rehman, M. S., & Fauquet, C. M. (2009). Evolution of geminiviruses and their satellites. *FEBS letters* **583**, 1825-1832. DOI: https://doi.org/10.1016/j.febslet.2009.05.045

Panattoni, A., Luvisi, A., & Triolo, E. (2013). Elimination of viruses in plants: twenty years of progress. *Spanish Journal of Agricultural Research*, 173-188. DOI: https://doi.org/10.5424/sjar/2013111-3201

Paprotka, T., Metzler, V., & Jeske, H. (2010). The first DNA 1-like α satellites in association with New World begomoviruses in natural infections. *Virology* **404**, 148-157. DOI: https://doi.org/10.1016/j.virol.2010.05.003

Patil, B. L., & Fauquet, C. M. (2010). Differential interaction between cassava mosaic geminiviruses and geminivirus satellites. *Journal of General Virology* **91**, 1871-1882. DOI: https://doi.org/10.1099/vir.0.019513-0

Power, A. G. (2000). Insect transmission of plant viruses: a constraint on virus variability. *Current Opinion in Plant Biology* **3**, 336-340. DOI: https://doi.org/10.1016/S1369-5266(00)00090-X

Rigden, J. E., Dry, I. B., Mullineaux, P. M., & Rezaian, M. A. (1993). Mutagenesis of the virion-sense open reading frames of tomato leaf curl geminivirus. *Virology* **193**, 1001-1005. DOI: https://doi.org/10.1006/viro.1993.1215

Rishishwar, R., Mazumdar, B., & Dasgupta, I. (2015). Diverse and recombinant begomoviruses and various satellites are associated with Bhendi yellow vein mosaic disease of okra in India. *Journal of Plant Biochemistry and Biotechnology* **24**, 470-475. DOI: https://doi.org/10.1007/s13562-015-0305-y

Romay, G., Chirinos, D., Geraud-Pouey, F., & Desbiez, C. (2010). Association of an atypical alphasatellite with a bipartite New World begomovirus. *Archives of Virology* **155**, 1843-1847. DOI: https://doi.org/10.1007/s00705-010-0760-7

Rybicki, E. P., & Martin, D. P. (2011). Virus-derived ssDNA vectors for the expression of foreign proteins in plants. Plant Viral Vectors, 19-45. DOI: https://doi.org/10.1007/82_2011_185

Schaumberg, K. A., Antunes, M. S., Kassaw, T. K., Xu, W., Zalewski, C. S., Medford, J. I., & Prasad, A. (2016). Quantitative characterization of genetic parts and circuits for plant synthetic biology. *Nature Methods* **13**, 94-100. DOI: https://doi.org/10.1038/nmeth.3659

Shepherd, D. N., Martin, D. P., Van der Walt, E., Dent, K., Varsani, A., & Rybicki, E. P. (2010). Maize streak virus: an old and complex 'emerging'pathogen. *Molecular Plant Pathology* 11, 1-12. DOI: https://doi.org/10.1111/j.1364-3703.2009.00568.x

Soto, M. J., & Gilbertson, R. L. (2003). Distribution and rate of movement of the curtovirus Beet mild curly top virus (family Geminiviridae) in the beet leafhopper. *Phytopathology* 93, 478-484. DOI: https://doi.org/10.1094/PHYTO.2003.93.4.478

Venkataravanappa, V., Lakshminarayana Reddy, C., Swaranalatha, P., Jalali, S., Briddon, R. W., & Reddy, M. K. (2011). Diversity and phylogeography of begomovirus-associated beta satellites of okra in India. *Virology Journal* **8**, 1-13. DOI: https://doi.org/10.1186/1743-422X-8-555

Xie, Y., Wu, P., Liu, P., Gong, H., & Zhou, X. (2010). Characterization of alphasatellites associated with monopartite begomovirus/betasatellite complexes in Yunnan, China. *Virology Journal* **7**, 1-10. DOI: https://doi.org/10.1186/1743-422X-7-178

Young, M., Debbie, W., Uchida, M., & Douglas, T. (2008). Plant viruses as biotemplates for materials and their use in nanotechnology.

Annu. Rev. Phytopathol. **46**, 361-384. DOI: https://doi.org/10.1146/annurev.phyto.032508.131939

Zhou, X. (2013). Advances in understanding begomovirus satellites. *Annual Review of Phytopathology* **51**, 357-381. DOI: https://doi.org/10.1146/annurev-phyto-082712-102234

Zubair, M., Zaidi, S. S.-e.-A., Shakir, S., Farooq, M., Amin, I., Scheffler, J. A., Scheffler, B. E., & Mansoor, S. (2017). Multiple begomoviruses found associated with cotton leaf curl disease in Pakistan in early 1990 are back in cultivated cotton. *Scientific Reports* **7**, 1-11. DOI: https://doi.org/10.1038/s41598-017-00727-2