

# Diversity dynamics of cotton infecting Begomovirus, a serious threat emerged due to assorted agro-climate of Pakistan

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## ABSTRACT

Pakistan is an agriculture based mono-crop economy largely dependent on cotton with 4th rank in production and 3rd in consumption globally. For last few decades cotton leaf curl disease (CLCuD) caused by a group of Begomovirus, is been proved to be havoc for cotton production in Pakistan with two major epidemic outbreaks after 1990s (\$5 billion loss in less than five years) and still a nightmare for country as they possess great evolving potential due to diverse and changing climate and cropping practices in cotton growing zone. Globally this virus has been reported from India, and several countries of Africa after Pakistan and now from China and Philippine too threatening the Australia and America with Large infestation of Begomovirus vector, White fly (*Bemisia tabaci*). The targeted virus has great recombination and resistance breaking capabilities specially therefore a constant eye is required on it to predict its genetic behavior and possible recombination. In current study diversity dynamics of Begomovirus has been study in different wild and cultivated hosts along with cotton with coat protein marker, to evaluate the host range of virus, either are they restricted to hosts or have multiple or shared host, in same way the viruses in cotton and non-cotton regions of Pakistan are evaluated. From 25 plant samples 13 different Begomovirus were identified. Six different samples were with mix viral infection, 7 different wild weeds were proved to be reservoir of Begomovirus. 7 viruses were common in different locations 4 plants were hosting different viruses in different locations, 7 viruses were found in multiple locations and There were 13 new reports of viruses and host which were not known before. Facts revealed that in favoring multiple cropping Begomovirus have developed utmost important infection patterns which favor them to recombine and evolve better to overcome host resistance in short time.

## Introduction:

Geminiviruses in the genus Begomovirus are among the most devastating pathogens worldwide of a variety of cultivated crops, including cassava, sweet potato, beans, tomato, cotton and grain legumes. Geminiviruses are distinct in having circular, single-stranded DNA genomes that are encapsidated within twinned icosahedral virions. Displaying substantial diversity in terms of their primary nucleotide sequences, genome structures, host ranges and insect vectors, the family Geminiviridae has been divided into four different genera. Besides the begomoviruses, these include the genera Mastrevirus, Curtovirus, and Topocovirus. The Begomovirus genus, with over one hundred and ninety two recognized species, contains more species than all the other geminivirus genera combined.

The primary species demarcation criterion for begomovirus classification is based on sequence similarity: to be classified as a new species a newly described DNA-A component must share less than 89% nucleotide identity with the DNA-A component of another previously recognised begomovirus species. At higher taxonomic levels the begomoviruses can be subdivided into New World and Old World members. New World viruses nearly all have bipartite genomes, with both components needed for infectivity. In contrast,

the majority of begomoviruses in the Old World apparently have monopartite genomes, and most of these interact with a class of ssDNA satellite molecules known as alpha- and betasatellites. A small number of Old World begomoviruses, such as Tomato yellow leaf curl virus and Tomato leaf curl virus, have true monopartite genomes containing only a DNA-A-like molecule that is sufficient to cause wild-type disease symptoms. Phylogenetically distinct from both Old World and New World begomoviruses are both a diverse group of bipartite begomoviruses infecting legumes are largely restricted to Asia, and a group of monopartite begomoviruses infecting sweet potatoes.

All begomoviruses are transmitted by the whitefly *Bemisia tabaci* in a persistent, circulative manner to eudicotyledenous plants. Worldwide, various begomovirus species are recognised as emergent threats to agriculture. Over the past three decades, the increasing threat posed by these viruses in a variety of cropping systems has been linked to the global spread of ultra-invasive members of the *B. tabaci* species complex. The global emergence of begomoviruses is, however, likely attributable to a combination of additional factors including the innate evolutionary adaptability of begomoviruses to novel host and geographical ranges, agricultural intensification that has favoured rapid whitefly population expansion and the modern international trade in horticultural products that has

spread host species, viruses and whitefly biotypes outside their natural geographical ranges.

Geminiviruses in general, but begomoviruses in particular, have the capacity to rapidly evolve via mutation and genetic recombination. It is through these processes of molecular diversification that widely distributed, normally weed-infecting begomoviruses, when transmitted into exotic cultivated host species, have the capacity to rapidly adapt to these new host species. Adaptive potential can also enable host-range switching when viruses are transmitted to novel alternative hosts within their natural environments by whitefly types or species that feed on an unusually broad range of plant species. Eventually, this concerted begomovirus evolution can lead to the emergence of new species with altered pathogenic potential and expanded geographical and/or host ranges.

Besides viral adaptation, the capacity of *B. tabaci* to adapt to and exploit modern agricultural systems has also been of paramount importance in the emergence of novel begomovirus plant diseases. *B. tabaci* is considered to constitute a cryptic species complex whose members are morphologically indistinguishable but exhibit a range of genetic, biological and behavioral variation. Population analysis using the mitochondrial cytochrome oxidase I gene sequence as a molecular marker have revealed 24 cryptic species that generally group phylogenetically according to their current geographical ranges. The exceptions, to this rule are the invasive B and Q whitefly types that now have a near global distribution. The extent to which *B. tabaci* populations vary genetically and biologically throughout sub-Saharan Africa has yet to be fully explored. Analysis of *B. tabaci* populations from nine African countries have revealed the existence of five endemic sub-Saharan Africa subclades, that are coexisting with the invasive B and Q types in a number of regions. The majority of SSAF clade members associate with cassava but some SSAF members have been documented to colonize indigenous plants and other vegetable crops. The relevant importance of each of these *B. tabaci* types as begomovirus vectors are however dependent on their host associations, fecundity and virus transmission characteristics. The cassava associated types transmit at least seven begomovirus species to cassava and the vegetable associated biotypes transmit a number of other different begomovirus species. It is however, the extremely polyphagous B and Q types that are considered the most important vectors of emergent begomoviruses. As is mentioned before, the spread of these invasive types has coincided with the emergence of new begomovirus diseases in many different regions around the world, including sub-Saharan Africa.

### Conclusion:

The phylogenetic and recombination studies concluded that the isolates of CLCuMuV genomes undertaken in this study have a potential recombinant origin. Remarkably, significant recombination was detected in almost all the genes with contribution of Cotton leaf curl Kokhran Virus (CLCuKoV) in IR, V1, V2, C1, C4 and C5 regions and of CLCuMuV in C2

region of CLCuMuV-SR14. CLCuKoV also donated in C2, C3 regions of CLCuMuV-ND14; V1, V2, C2 and C3 regions of CLCuMuV-ND15 and C1 of CLCuMuV-SR15. Altogether, these observations signify the uniqueness in Indian CLCuMuV isolates showing contribution of CLCuKoV in all the genes. An interesting observation was frequent identification of GLCuA in CLCuD leaf samples. The five Cotton leaf curl Multan virus (CLCuMuV) isolates investigated in this study showed monopartite organization of the genome typical of Old World begomoviruses. Nucleotide sequence analyses assigned them as the strains of CLCuMuV and were designated as CLCuMuV-SR13, CLCuMuV-SR14, CLCuMuV-ND14, CLCuMuV-ND15 and CLCuMuV-SR15. The genome of CLCuMuV-SR13 shared a highest level of nucleotide sequence identity (98%) with CLCuMuV (JN678804), CLCuMuV-SR14 and CLCuMuV-SR15 exhibited 96% with CLCuMuV (KM096471), while isolates CLCuMuV-ND15 and CLCuMuV-SR15 revealed 96% sequence identity with CLCuMuV (AY765253). The four betasatellite molecules investigated in this study shared 95–99% nucleotide sequence identity with Cotton leaf curl Multan betasatellite (CLCuMB) from India. The betasatellite molecules were designated as CLCuMB-SR13, CLCuMB-SR14, CLCuMB-ND14 and CLCuMB-ND15. Alphasatellite molecules in this study, designated as GLCuA-SR14, GLCuA-ND14 and GLCuA-SR15, revealed 98% identity with Guar leaf curl alphasatellite (GLCuA) reported from Pakistan. The emergence of cassava, tobacco and tomato-infecting begomoviruses throughout the SADC and SWIO regions was likely due to introduction and intensive cultivation of exotic crop species having been introduced into environments harbouring indigenous begomoviruses. Furthermore, the *B. tabaci* cryptic species complex, that transmit these begomoviruses between their natural hosts and the introduced plant species, has likely played a significant role in the emergence of cassava, tobacco and tomato-infecting begomoviruses in the SADC/SWIO regions. Given the propensity of begomoviruses to recombine, and frequent introduction of polyphagous whitefly types into novel regions and co adaptation to new cultivated crops, weeds and indigenous host plants, emergence of new recombinant begomoviruses with increased virulence can be predicted to occur. The emergence of several new tomato-infecting begomoviruses within the past 15 years in the SADC/SWIO regions and several new cassava begomovirus species, including SACMV, demonstrate the frequent occurrence of recombination events. The implications for agricultural productivity and economic losses in the future are enormous, and more attention is needed to study begomovirus diversity and epidemiology in the region in order to be able to strategize disease management programs.