

# THE DEVASTATING *GEMINIVIRIDAE* - THE SECOND LARGEST FAMILY OF PLANT VIRUSES

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**Abstract :** *Geminiviridae*, the second largest family in the taxonomy of plant viruses, cause devastating plant diseases all over the world. Such devastating effect of geminiviruses to both staple food and cash crops is particularly predominant in tropical and subtropical countries exhibiting diverse types of symptom in plants. Based on the characteristics of their genome, host range and mode of transmission, the family *Geminiviridae* has been classified into four genera, i.e. *Mastrevirus*, *Curtovirus*, *Topocuvirus* and *Begomovirus*. Begomoviruses of a specific geographical region shares more sequence homology amongst them, than with begomoviruses from different geographical region infecting the same host. These viruses show rapid genomic variation. This variation could be due to mutation, recombination or pseudo-recombination, which was very much common phenomenon in begomoviruses.

**Index Terms -** Geminiviruses, begomoviruses, genomic variation.

## INTRODUCTION

Geminiviruses form the second largest family in the taxonomy of plant viruses, the *Geminiviridae*, and cause devastating plant diseases all over the world. Moreover, the present century faces severe disease epidemics caused by newly emerging geminiviruses infecting crops such as cassava, cotton, grain legumes and tomato and thus cause heavy economic losses (Boulton, 2003; Khan, 2000; Thottappilly, 1992).

The economic losses in cassava are estimated to be US \$1300-2300 million in Africa (Thresh *et al.*, 1998), US \$5 billion for cotton in Pakistan between 1992-97 (Briddon and Markham, 2000), US \$300 million for grain legumes in India (Varma *et al.*, 1992) and US \$140 million in Florida for tomato alone (Moffat, 1999). Such devastating effect of geminiviruses to both staple food and cash crops is particularly predominant in tropical and subtropical countries exhibiting diverse types of symptom in plants like vein yellowing, yellow mosaic, leaf curl etc.

Now-a-days geminiviruses are spreading in alarming proportion and adapt to new host because of high rate of recombination (Briddon *et al.*, 2003; Mansoor *et al.*, 2003). Control of the spread of these viruses is sometimes impossible as they are transmitted through insect vector like whitefly (*Bemisia tabaci* Genn.). In addition, several weed hosts serve as alternate hosts for these viruses especially when the main crops are absent in field.

## II. CLASSIFICATION OF GEMINIVIRUSES

Geminiviruses (family *Geminiviridae*) are plant viruses that have a circular, single-stranded DNA (ssDNA) genome of size ranging from 2.5 to 3.0 kilobases and are encapsidated within twinned isometric particles of 15-18 x 30 nm size (Brunt *et al.*, 1990; Goodman, 1977; Harrison *et al.*, 1977; Howarth, 1986; Morinaga *et al.*, 1987; Stanley, 1983; Stanley and Devis, 1985; Stanley and Gay, 1983).

Based on the characteristics of their genome, host range and mode of transmission, the family *Geminiviridae* has been classified into four genera, i.e. *Mastrevirus*, *Curtovirus*, *Topocuvirus* and *Begomovirus* (Fauquet and Stanley, 2003; Fauquet *et al.*, 2003).

The genus *Mastrevirus* is leaf hopper-transmitted and primarily infects monocotyledonous hosts; the monopartite genome of 2.5-3.0 kb has two virion-sense frames (Open Reading Frames, ORFs), with one long and one short intergenic region. The typical example is *Maize streak virus* (MSV).

The leaf hopper-transmitted *Curtovirus* infects dicotyledonous plants and the monopartite genome has three ORFs in the virion-sense and four in the complementary-sense with one intergenic region. The type species of this genus is *Beet curly top virus* (BCTV).

The leaf hopper-transmitted *Topocuvirus* has only one member, *Tomato pseudo curly top virus* which has a monopartite genome with two ORFs in the virion-sense and four in the complementary-sense.

Majority (over 80%) of the geminiviruses belong to the genus *Begomovirus* and are transmitted by whiteflies (*Bemisia tabaci* Genn.), infect dicotyledonous plants and have either mono- or bipartite genome. The type species of this genus is *Bean golden mosaic virus* (BGMV).

On the basis of sequence analysis of N-terminal region (60-70 amino acid) of the coat protein and biological properties, Padidam *et al.* (1995) had subdivided Whitefly Transmitted Geminiviruses (WTGs) into two groups: WTGs from the New World viz. Brazilian isolate - *Bean golden mosaic virus* (BGMV), Californian isolate – *Squash leaf curl virus* (SqLCV); and WTGs from the Old World viz. *Indian cassava mosaic virus* (ICMV), Thailand isolate of *Mungbean yellow mosaic virus* (MYMV-T).

### III. PHYLOGENETIC RELATIONSHIP

Phylogenetic relationships among different begomoviruses have been studied by comparing their either nucleotide or amino acid sequence. The analysis showed that the relationship is closest among viruses occurring in the same geographical area (Hong and Harrison, 1995; Padidam *et al.*, 1995, 1999; Rybicki, 1994).

Begomoviruses of a specific geographical region shares more sequence homology amongst them, than with begomoviruses from different geographical region infecting the same host (Harrison *et al.*, 1997; Nateshan *et al.*, 1996; Swanson *et al.*, 1992).

Region specific selection pressures are operating more efficiently than host range determinants. Based on amino acid comparison of CP, the phylogenetic tree of begomoviruses can be divided into two major branches, containing Old World and New World viruses respectively. Within them there are clusters depending on the region where they occur (Harrison and Robinson, 1999).

### IV. GENETIC VARIABILITY AND EVOLUTION OF NEWER VIRUSES

Begomoviruses have emerged as constraints to the cultivation of a variety of crops in various parts of the world. Investigations on begomoviruses revealed that these viruses are still being evolved and pose a serious threat to sustainable agriculture (Varma and Malathi, 2003). These viruses show rapid genomic variation (Harrison and Robinson, 1999). This variation could be due to mutation, recombination or pseudo-recombination, which was very much common phenomenon in begomoviruses (Isnard *et al.*, 1998; Liu *et al.*, 1998; Padidam *et al.*, 1999; Sanz *et al.*, 2000; Zhou *et al.*, 1998).

The spurt in molecular variation helping in increasing the biological fitness of the virus may lead to sudden outbreak of epidemics. The host genotypes, environmental condition and agricultural practices influence the interplay in the host-virus-vector relationship, by putting pressure on the genome of virus resulting in the

changes and that persist. In this respect begomoviruses differ greatly from plant viruses having RNA genome.

Different agro-ecological situations under which multiple infections with different begomoviruses and their satellites are caused in plants and that might be a suitable reason for emergence of newer recombinant viruses. Many new geminiviruses have emerged recently, and some geminiviruses have re-emerged as economically serious constraints in various agricultural systems around the world.

Several factors including evolution of new variants of the viruses, appearance of efficient vectors, weather events, changing cropping systems, movement of infected planting material and introduction of susceptible plant varieties have singly, or in combination, contributed to the emergence of geminivirus problems around the world (Verma, 1993; Varma and Malathi, 2003).

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