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Original Research Article

EXPLOITATION OF INFECTIVITY POTENTIAL OF *CpCDV* A *GEMINIVIRUS* AGAINST DIFFERENT FRUIT CROPS AND WILD HOST PLANTS

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Abstract: *The Chickpea Chlorotic Dwarf Virus (CpCDV) has been found very much destructive not only for the chickpea crop but also for lentils, cotton, papaya and other wild hosts. During past few years, it has been found that the mastrevirus caused adverse effects on the hosts and caused to reduce crop plant yield up to 95%. This virus has been found as a most prevalence in the dry regions with an equally important pathogen in other parts of the world especially in American and European countries. The capability has been reported due to the rapid changes in viral genome. Vector species also played an important role in the spread of this virus. Here the evolutionary study of about 244 genomes was performed. All genomes obtained from food, fiber and wild plants. Genomes obtained from wild plants are ancestors and rest has been found as the offsprings. According to our finding, the CpCDV has been found an important pathogen not only for Fabaceae family but also for Malvaceae, Solanaceae, Cucurbitaceae and many more.*

Keywords: *mastrevirus*; pathogen; evolutionary; genome; species; virus

Introduction

The *Mastrevirus* group of *Geminiviruses* can infect a wide range of grains, including corn, and spread diseases. That group may transmit disease in dicots. Geminivirus has been known as the *Eragrostis curvula streak virus* which has been recently discovered and has distinctive properties. Instead of hybridization, the odd genomic characteristics resulted from the mingling of alleles. Such characteristics have made the virus a reliable indicator of the original geminiviral state. In addition to the *Rye dwarf virus*, *Wheat dwarf virus*, and *Barley dwarf virus*, all of the *Mastreviruses* that infect monocot plants have been found in Africa, Europe, Asia and Central East (Adams, 2005b).

Various diseases inside the *Fabaceae* family have been brought on by the *chickpea chlorotic dwarf virus* (CpCDV). Many *Mastrevirus* variants have been identified in cotton (Adams *et al*., 2011). In terms of host species, *mastrevirus* infects a large number of dicots, but it needs to be demonstrated at the cellular scale (Bisaro, 2006). They possess a few ORFs, including one for mobility, another for the protein that makes up their coat, and a few ORFs that make complementary sense (Botha, 2010). RepB is in charge of rolling circle replication, while RepA is in charge of creating a friendly climate. This article's main goal was to determine evolutionary changes in *CpCDV*.

Materials and Methodology

Data Arrangement

CpCDV complete sequences were gathered from the National Center for Biotechnology Information. To compare the homology of different viruses (at the specie level), a BLAST is used (Muhire *et al*., 2014).

Phylogenetic Analysis

Using the MUSCLE alignment approach, every feature length sequences were mapped in MEGA 6 software. The maximum likelihood approach is used to build the dendrogram (Kumar *et al*., 2016). The virus has 244 genomes. Using the Sequence Demarcation Tool (SDT) application, bilateral similarity was calculated (Muhire *et al*., 2014).

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Results

Phylogenetic Analysis

Complete 244 genomes were examined. Cotton genomes were the base of cause and further hybridization. This is due to environmental factors and vector species.

Total 244 sequences were classified in phylogenetic tree. This *mastrevirus* not only reported from chickpea crop but also from others crops. Sequences having accession number KF632712, KF111683 are reported from chilli and pepper crop (NCBI data bank analysis). Sequences having accession number AM933135, AM933134 are reported from chickpea crop (Hassan, 2000). Sequences having accession number HE956705, HG313782 are reported from *Gossypium hirsutum* (Manzoor, 2014). Being having different host plants, this virus has huge diversity. Multiple factors could be involved in this diversification. Because there is always a question mark how a virus becomes adapted to new host plants while its homology match only this crop? Mutation and recombination are the main sources involved in genomic diversity and different changes in DNA. These two factors not only brought changes in DNA of virus but also in vector species. The different crops have different insect vectors or in some cases single insect species affects many crops. In this case when a change is come in DNA, it becomes compatible to insect species and successfully transmitted to others crops and becomes a new virus of this crop. Recombination of different *genus* also creates new genera of viruses. These further become compatible to different crops. In, these 244 sequences, many sequences are reported from same crop but from different parts of the world. This thing shows that how this virus is successfully distributed in the world. For example sequence having accession number. KY817246 is reported from *Carica papaya* crop from Nigeria but another sequence also reported from *Carica papaya* crop but from Burkina Faso (NCBI data bank).

SDT Analysis

A grid was created, showing how distinct one genomes are from the others. The score for variance is displayed. SDT findings show the diverse species, mutations, and variants inside library (Figure 1).

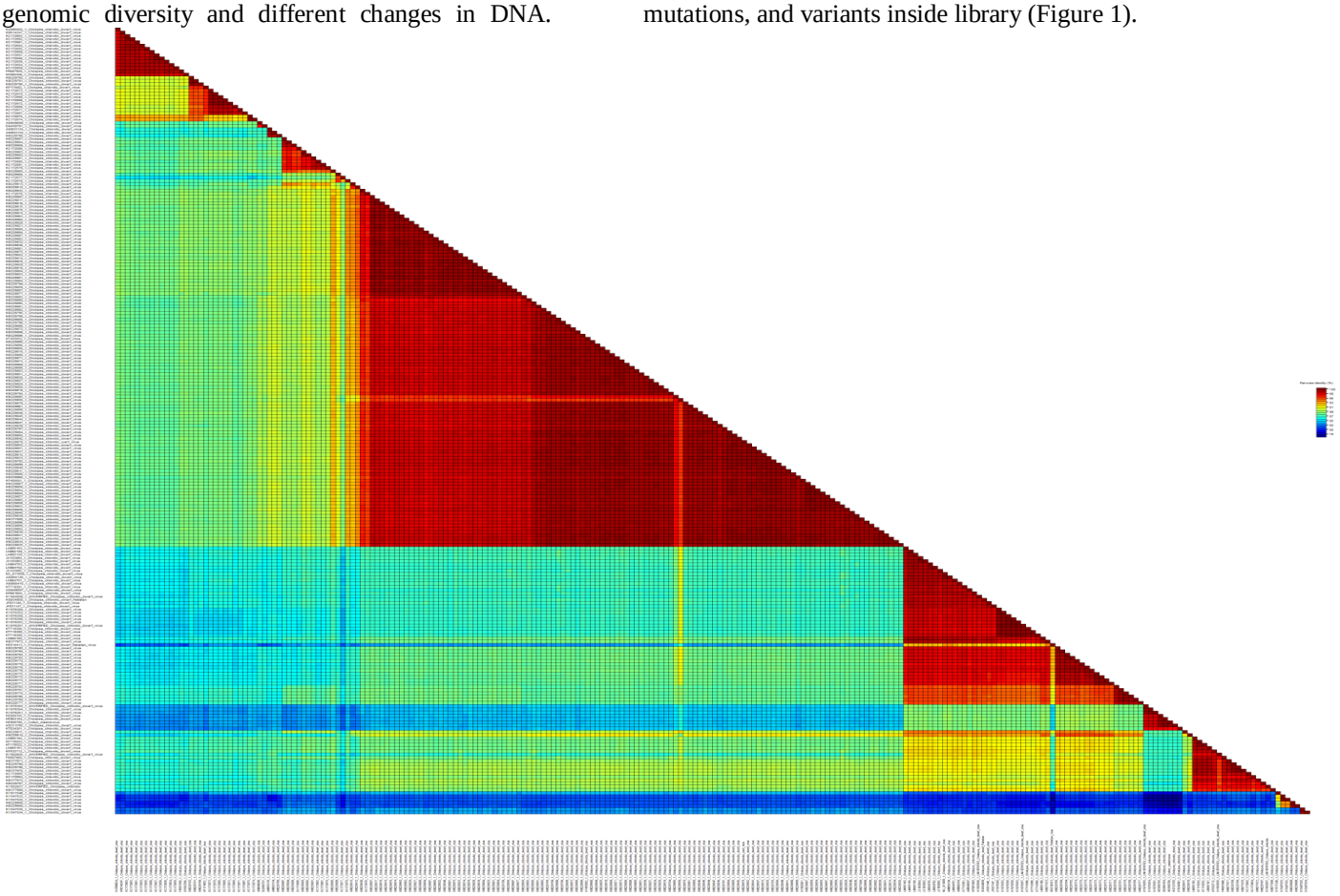

Figure 1. Grid (SDT Analysis) displaying evolution gap among *ChiRSV*. Grid values are maintained around 94 and 91 to identify species (New demarcation rule)

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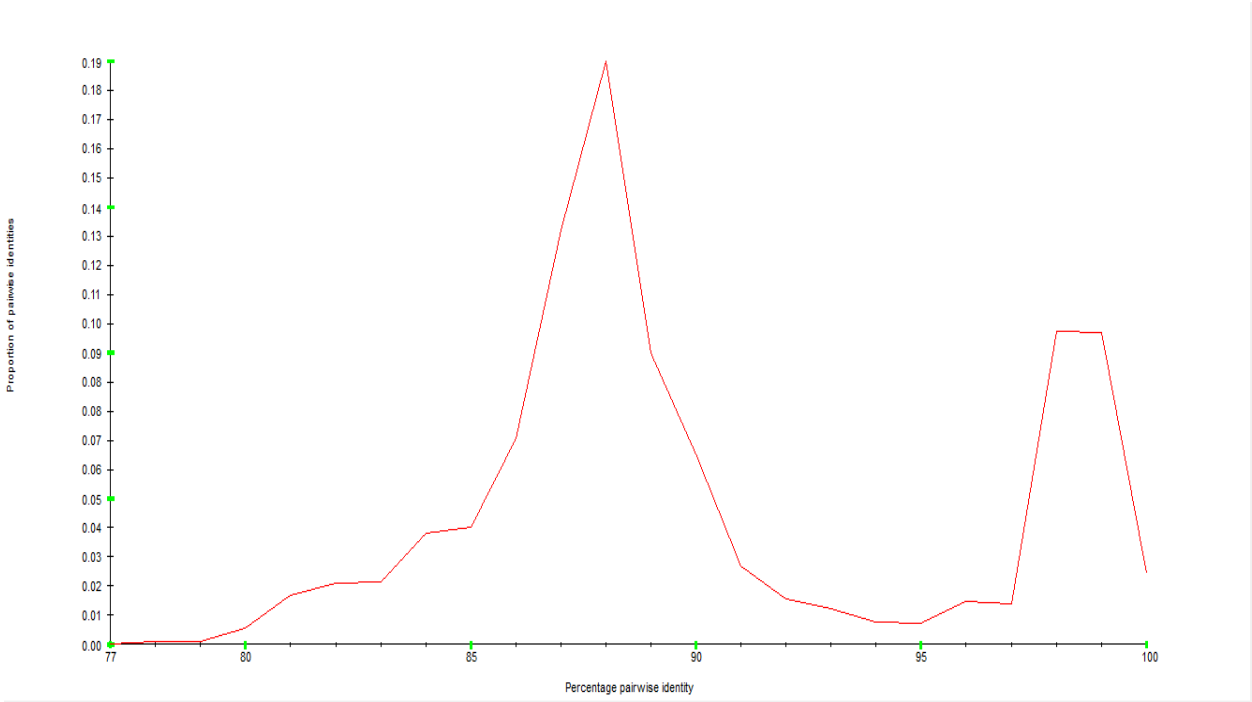

Fig. 2: Graphical representation of *chickpea chlorotic dwarf virus*. Vertical axis is showing proportion of changes and horizontal axis is showing scale of percentage between 77-100%.

Discussion

Evolution is very necessary for the survival of the generation. In frequent changing environment viruses mutate very rapidly however evolutionary rates are different between DNA and RNA viruses (Ahmed, 2010). Genomic phylogenetic analysis indicates that *BVYMV* coat protein have some adulteration in its nucleotide sequence. Evolutionary analysis of *BVYMV* and its vector (Whitefly) reveals great compatibility, several strains and species emerges which results in great diversity of this virus (Ong *et al*., 1980). Trade between two countries is also a factor of introduction of *SMV* into new locality (Rajamaki *et al*., 2009). Phylogenetic analysis of *SMV* indicates that it has great diversity. It is RNA virus and RNA viruses and RNA viruses evolve more quickly as compared to DNA viruses (Adams, 2005b). Due to evolution new species are able to overcome the resistance of existing varieties and cause huge economic losses.

The existence of huge populations depends on genetic diversity (Biebricher and Eigen, 2006). When contrast to DNA viruses, RNA viruses evolve more quickly (Holland *et al*., 1982). This is because RNA viruses offer more fusion sites (Worobey and Holmes, 1999; Eigen *et al*., 1988). However, compared to RNA viruses, diversification is more likely to have happened more quickly in the case of ss-DNA viruses (Shakelton and Holmes, 2006; Drake, 1991; Shakelton *et al*., 2005; Duffy *et al*., 2008). The *Geminiviridae* family of viruses exhibit a remarkably diverse genetic makeup. Hybridization and evolution are to blame for this (Ge *et al*., 2007; Grigoras *et al*., 2010).

There is increased genetic variety in viruses that use DNA polymerase, according to studies (Duffy and Holmes, 2009). But the essential component of genetic variation is evolution (Balol *et al*., 2010). Researchers have found that recombination, particularly in *Geminiviruses*, is key for diversification in plant pathogens (Bonnet *et al*., 2005; Fan *et al*., 2007; Lefurve and Moriones, 2015; Heath *et al*., 2006; Varsani *et al*., 2006). Examples of viruses that appear to have mutated as a process of recombination include *CLCuV*, *MSV*, *ToYLCV*, and *CMV* (Varsani *et al*., 2008; Sanz *et al*., 2000).

Apparently, their dependent replication process is what causes this recombination (Jeske *et al*., 2001). DNA pieces from different viruses were used to contribute to recombination (Zhou *et al*., 1997; Barrie *et al*., 2001; Monci *et al*., 2002). Due to this crossover, genetic variety and variability are produced (Silva *et al*., 2014). *Begomoviruses* are major cause of leaf curl diseases in India in chilli crop (Kumar *et al*., 2015). Combine attack of *ChiLCV* and *PepLCBV* has also been seen (Kumar *et al*., 2015). This is also found at six different places in India (Nagpur, Palampur, Ghazipur, Salem, New Delhi and Chapra) (Kumar *et al*., 2015).

Conflict of interest

The authors declared absence of conflict of interest.

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