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Original Research Article

EVOLUTIONARY ASPECTS EXPLIOTATION OF *CHICKPEA CHLOROTIC DWARF VIRUS* (CPCDV)INFECTING COTTON AND CHICKPEA

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Abstract: *The Chickpea Chlorotic Dwarf Virus (CpCDV) has been found highly devastating not only for chickpea crop but also for lentils, cotton and papaya. In recent past years, this mastrevirus caused a sublime pressure on the hosts and reduced yield up to 95%. This virus is most prevalence in dry regions and equally important pathogen in other parts of the world especially in America and Europe. This capability is due to rapid changes in DNA. Vector species also play an important role in spread of this virus. In our current study the evolutionary study of 53 genomes was performed. All genomes obtained from cotton crops are ancestors and rest is offsprings. According to our finding, CpCDV is very important pathogen not only for Fabaceae family but also for Malvaceae family.*

Keywords: Chickpea Chlorotic Dwarf Virus; *mastrevirus*; fabaceae; DNA; Species

Introduction

The *Mastrevirus* group of *Geminiviruses* can infect a wide range of grains, including corn, and spread illness. That group may transmit disease in dicots and and has a very diverse range of Genome variation. Geminivirus known as the *Eragrostis curvula streak virus* has just been discovered and has distinctive properties. Its CP has Mastrevirus-like action, as well as its method by making protein exhibits Begomovirus-like behavior. 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 are found in Africa, Europe, Asia and Central East (Adams, 2005b).

Various diseases in the Fabaceae family are brought on by the *chickpea chlorotic dwarf virus* (CpCDV). Phloem obstruction, discoloration, bruising that shortens height, and rotting are all effects of it. The signs of chickpea plants can vary based on the type. Many *Mastrevirus* variants have been identified in cotton crops (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). Evolutionary dendrogram is also given (Figure 1).

Phylogenetic Analysis

Using the MUSCLE alignment approach, every feature length sequences were mapped in MEGA 6 software. The maximum likelihood approach was used to build the dendrogram (Kumar *et al*., 2016).

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The virus has 53 genomes. Using the Sequence Demarcation Tool (SDT) application, bilateral similarity was calculated (Muhire *et al*., 2014).

Results

Phylogenetic Analysis

Complete 53 genomes were examined. Cotton genomes were the base of cause and further hybridization. This is due to environmental factors and vector species.

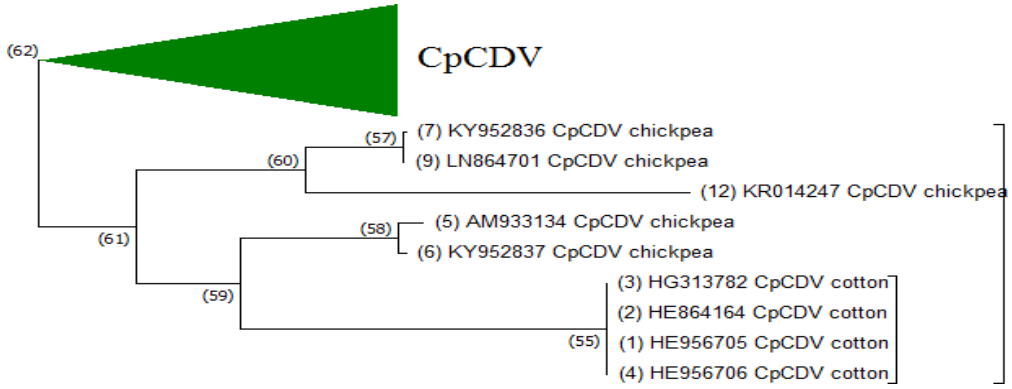

Figure 1. Dendrogram of *CpCDV*

53 whole genomes were examined. Pakistan was the source of the genomes with the registration number HE956705, HE864164, HG313782, and HE956706. The virus might have developed over time. Different strains and subtypes could develop for a variety of causes. These elements could include the development of the insect vectors, the cross-pollination of several strains from various genera, the hybridization of various variations within the same host plant, etc. Fragments that were gathered from various West Indian regions might be moved from one location to other using vectors. There are numerous opportunities for commerce in agricultural products across nations. Therefore, it would play a part in the spread of the virus throughout nations and continents (GB file).

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 2).

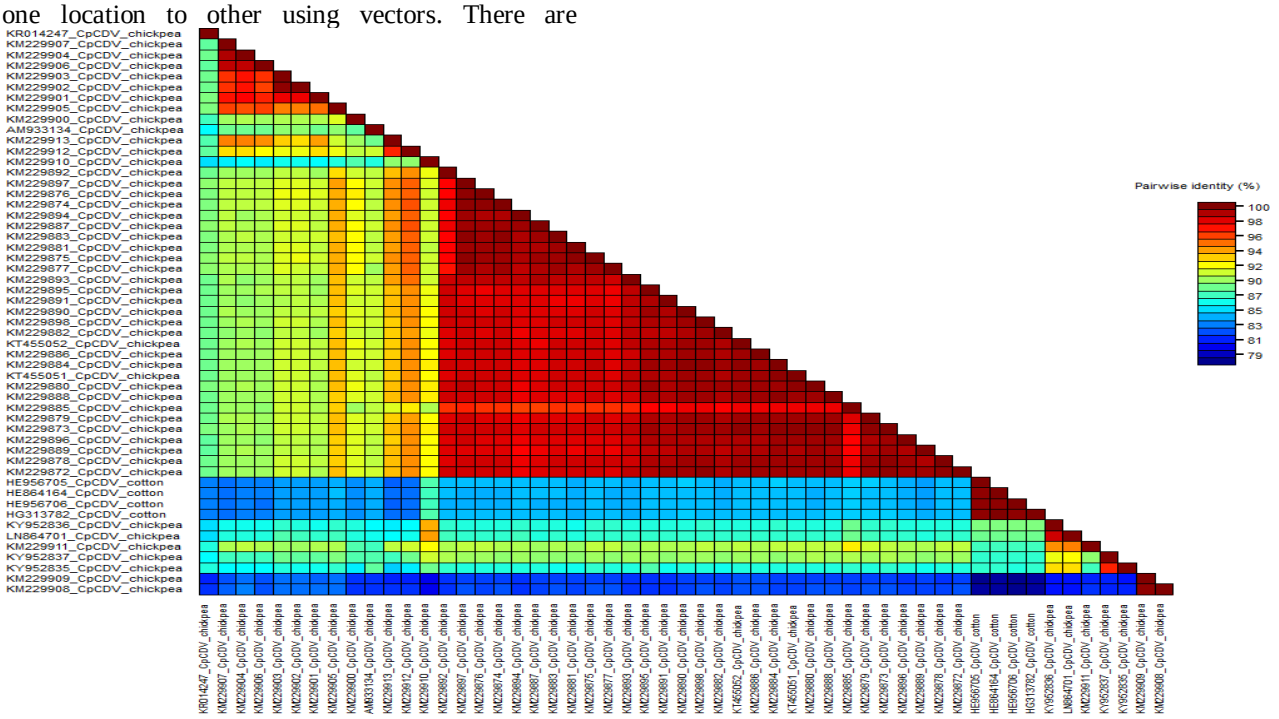

Figure 2. Grid (SDT Analysis) displaying evolution gap among *ChiRSV*. Grid values are maintained around 94 and 91 to identify species (New demarcation rule)

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RDP Analysis (Recombination Detection Programme)

There was no recombination found in any sequence of *CpCDV*. All sequences were unique sequences (RDP Analysis results).

Discussion

Evolution is very necessary for the survival of the organism generations. It acclimatizes the organisms into environment. Viral evolution makes viruses enable to adapt new crop plants, new varieties. Virus is a nucleoprotein in which replication plays an important role in evolution and changes in nucleic acid. During replication sometimes wrong nucleotides are added to synthesis process. If it remains as it is, it leads towards a new mutant which is slightly different from original one. Activity of DNA polymerase has also been considered as a factor in evolution. Its activities depend upon environment. During stress conditions, it is difficult to regulate polymerase activities to the right direction. In frequent changing environment viruses mutate very rapidly however evolutionary rates are different between DNA and RNA viruses (Ahmed, 2010). The replication of DNA viruses depend upon DNA polymerases whereas RNA is transcribed from DNA and requires some enzymatic activities. These enzymes, RNA replicases reverse transcriptases, are encoded by viruses/viral nucleic acid. These enzymes do not have any corrector activities which results in highly virulent strains. Highly virulent strains are responsible for emergence of new diseases.

Bhendi vein yellow mosaic virus (*BVYMV*) is common viral pathogen of Bhendi (okra) crop. Gene bank data analysis reveals that it not only present in Indo-Pak sub-continent but also in some parts of Europe and Northern America (NCBI gene bank data). Phylogenetic analysis indicates that *BVYMV* emerges as a result of recombination between two different viruses. Sequence demarcation analysis reveals that some sequences of *BVYMV* has unknown parents. Unknown parents are recombinant parents. These recombination events would be occurred in same host plant in which two different viruses would already present. Genomic phylogenetic analysis indicates that *BVYMV* coat protein have some adulteration in its nucleotide sequence. Some unknown parents would provide coat protein parts during recombination events. Evolutionary analysis indicates that *BVYMV* evolve from sub-continent. 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)

Sugarcane mosaic virus is one of most important *Potyvirus* of sugarcane crop. Diversity analysis of *SMV* indicates that it is most prevalent in Indian sub-continent and Brazil (NCBI gene bank data analysis). *SMV* transmits through aphid specie. 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). Phylogenetic analysis indicates that sequences at the bottom of the tree are reported from sub-continent which means that *SMV* emerges from sub-continent. Mutation rate of *SMV* is ($2.4gene/10^7$ genes). Evolutionary analysis reveals that it evolves parallel to its vector specie (Aphid). 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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