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Original Research Article

DENDROGRAMIC ANALITICAL STUDY OF REPORTED MASTREVIRUSES INFECTING MALVACEOUS AND FABACEOUS PLANTS USING BIOINFORMATICS TOOLS

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Abstract: *The Chickpea Chlorotic Dwarf Virus (CpCDV) has been found devastating not only for chickpea crop but also for lentils, cotton and papaya. It has been found that up to 95% yield of crop plants have been reduced in dry regions of world including America and Europe. The vector species have also been found to play an important role for spreading of this virus form crop to crop and region to region. In our current study an evolutionary study of about 53 genomes was performed. According to our finding, the CpCDV is an important pathogen not only for the Fabaceae family but also has been reported found in Malvaceae family.*

Keywords: biotic; stress; genome; yield loss; pathogen; virus

Introduction

Geminivirus known as the *Eragrostis curvula streak virus* has just been discovered and has distinctive properties. I ts CP has Mastrevirus-like action, as well as its method by making protein exhibits Begomovirus-like behaviour. Instead of hybridization, the odd genomic characteristics resulted from the mingling of alleles. 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 illnesses inside the *Fabaceae* family are brought on by the *chickpea chlorotic dwarf virus* (CpCDV). Many *Mastrevirus* variants were identified in cotton crops (Adams *et al*., 2011; 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 is used to build the dendrogram (Kumar *et al*., 2016). The virus has 20 genomes. Using the Sequence Demarcation Tool (SDT) application, bilateral similarity was calculated (Muhire *et al*., 2014).

Results

Phylogenetic Analysis

Complete 20 genomes were examined. Cotton genomes were the base of cause and further hybridization. This is due to environmental factors and vector species.

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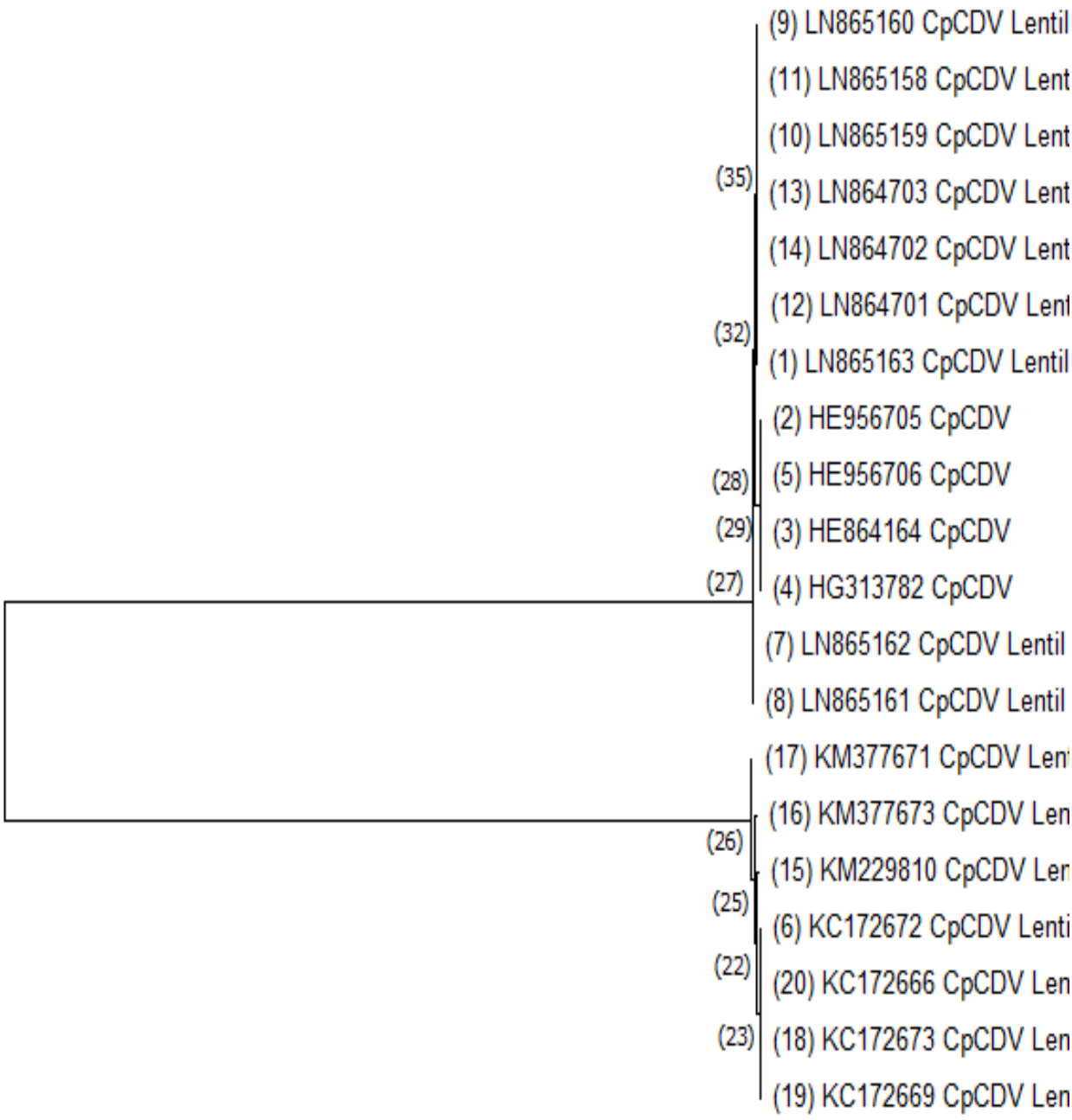

Figure 1. Dendrogram of *CpCDV* infecting Malvaceous and Fabaceous plants

Whole 20 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 another 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).

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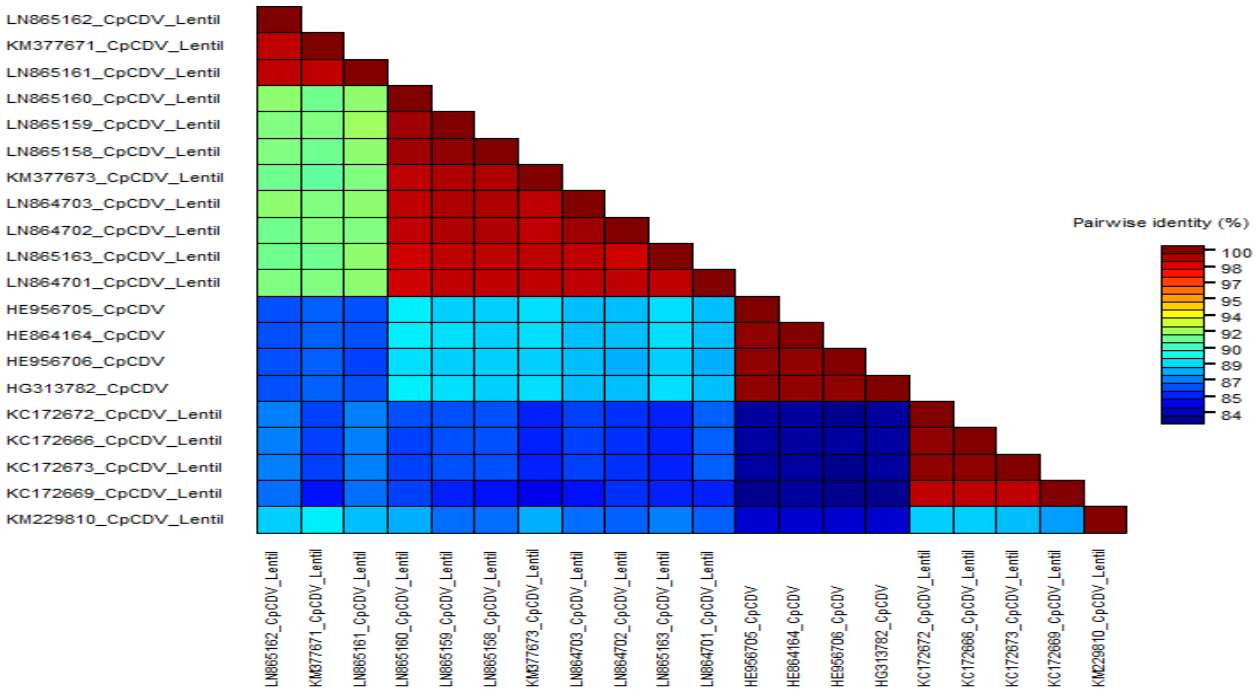

Figure 2. Grid (SDT Analysis) displaying evolution gap among *ChiRSV*. Grid values are maintained around 94 and 91 to identify species (New demarcation rule)

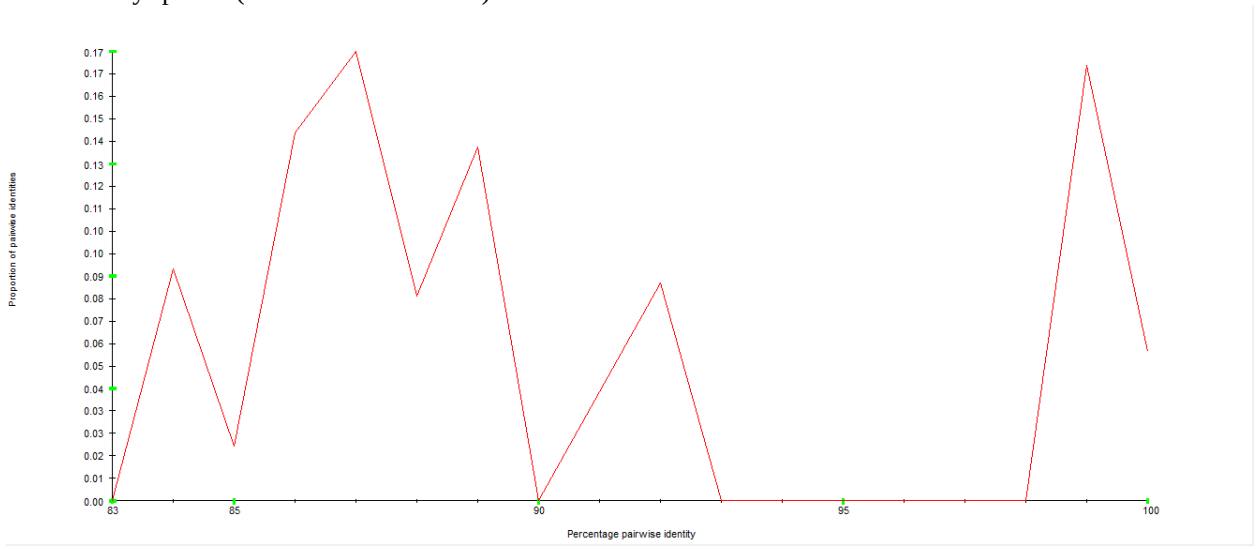

Figure 3. *CpCDV* infecting Malvaceous and Fabaceous graphical distribution. Plot is showing pairwise identity percentage. Vertical axis is showing proportion of matching percentage and horizontal axis showing extent of percentage.

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 generation. In frequent changing environment viruses mutate very rapidly however evolutionary rates are different between DNA and RNA viruses (Ahmed, 2010). 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. 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)

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).

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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