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Original Research Article

COMPUTATIONAL ANALYSIS OF CHILLI INFECTING PEPPER LEAF CURL LAHOREVIRUS AND PEPPER LEAF CURL BANGLADESH VIRUS

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Abstract: *Since a few decades ago, the pandemic of the Chilli Leaf Curl Disease Complexes (ChiLCD) has caused enormous alarm. The investigations of various genomes isolated from various regions of the subcontinent in the current study revealed a vast expansion of ChiLCD. According to evolutionary research, genomes from the pepper leaf curl Lahore virus (PepLCLV) (JN880419 and JX524173) and the pepper leaf curl Bangladesh virus (PepLCBV) (DQ116881 and KY420149) are ancestors while others are descendants. The accessions JN880419, JX524173, DQ116881, and KY420149's sequences underwent evolution, giving rise to several strains and variations. According to the findings, the Indian subcontinent's chilli crop may be most severely affected by the extremely aggressive ChiLCV.*

Keywords: ChiLCD, Diversity, Geminiviruses, Mutation, Phylogenetic analysis

Introduction

Begomoviruses are generally significant and most destroying infections, spread by whiteflies (*Bemisia tabaci*). Around thirty years, *begomoviruses* infections have been arose significant pathogen in different crops like brinjal, papaya and American cotton etc. It's possible that the genomes of these diseases are either monopartite or bipartite. Designated as new world begomoviruses, bipartite genomes contain DNA-A and DNA-B portions. Monopartite genomes, also known as old world (OW) begomoviruses, contain only one DNA-A fragment. However, bipartite Begomovirus DNA-A can sicken a person alone and be responsible for further propagation in OW. DNA-A in gammoviruses is dependent on DNA-B for proper operation. Notwithstanding parts, some DNA satellites (betasatellites and alpha satellites) are likewise present (Briddon and Stanley, 2006). Betesatellites are assistant of *Begomoviruses* and have ss-DNA (Briddon *et al*., 2003). All capacities are done by CP. That CP has numerous capacities of inception and pathogenecity (Briddon, 2003). Dissimilar to betasatellites, alphastellites can reproduce freely and have size ~1400 nt (Mansoor *et al*., 1999). As per present day study, these are different in nature (Zulfiqar *et al*., 2012). The genome size is 2.8 kb long. DNA-A segment have five to six replication sites in the two sides that encode 10kDa protein. Protein is associated with numerous capacities like replication, hushing and transmission and so forth (Bisaro, 2006). Because of appearance of new terminology for *Begomoviruses*, these infections could be arranged into a few animal groups including: *Chili leaf twist multan infection* (ChilCMV), *Chili leaf twist India infection* (ChiLCINV), *Chili leaf twist Panipat* (ChiLCPP), *Chili leaf twist Oman infection* (ChiLCOV) and *Pepper leaf twist Lahore infection* (PepLCLV). Viruses like *PepLCLV* (JN135234, JN663864, and JX524173) have shown for disease significance. A few animal varieties spread in Pakistan as well as announced from different regions of the world, for example, Oman, Bangladesh, Sri Lanka and so forth. The genome of *Begomoviruses* ss-DNA gives an

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opportunity to decide their recombination and transformation rates. In this examination, transformative investigation of bean stew and pepper infections from various pieces of subcontinent have been provided. We have additionally created an information bank showing what succession was detached, when grouping was secluded, from where arrangement was confined.

Methodology and Materials

Sequences Organization

PepLCLV and *PepLCBV* complete sequences were gathered from National Center for Biotechnology Information. To compare the resemblance of different viruses (at the specie level), a BLAST is used (Muhire *et al*., 2014). Evolutionary dendrogram has been also given (Figure 1).

Evolutionary Examination

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). Remarkably similar separates were turned into triangles via MEGA 6's tree editor. The *PepLCLV* have eight genomes (Table 1), *PepLCBV* have four genomes. Using the Sequence Demarcation Tool (SDT) application, bilateral similarity was calculated (Muhire *et al*., 2014).

Results

Data bank analysis

Eight sequences of *PepLCLV* were reported in subcontinent. Equal number of genomes was isolated in each country that is four. Four sequences of *PepLCBV* reported from Bangladesh (Table 1).

Table 1: Presence of various *PepLCV* in various locations.

Count	Pathogen	Registration Number	Location		Reference
I.	Pepper leaf curl	JN135234	India	India	GB file*
II.	Pepper leaf curl	JN663864	India	India	GB file
III.	Pepper leaf curl	JX524173	India	India	GB file
IV.	Pepper leaf curl	NC_016984	Pakistan	Pakistan	GB file
V.	Pepper leaf curl	AM691745	Pakistan	Pakistan	GB file
VI.	Pepper leaf curl	AM491589	Pakistan	Pakistan	GB file
VII.7	Pepper leaf curl	AM404179	Pakistan	Pakistan	GB file
VIII.	Pepper leaf curl	JN880419	Pakistan	India	GB file

*GB file= Gene Bank file collected from NCBI.

Phylogenetic analysis

Eight complete genomes in all were examined. These genomes revealed the presence of four strains (SDT analysis). Only Pakistan and India were the countries that reported these (GB file).

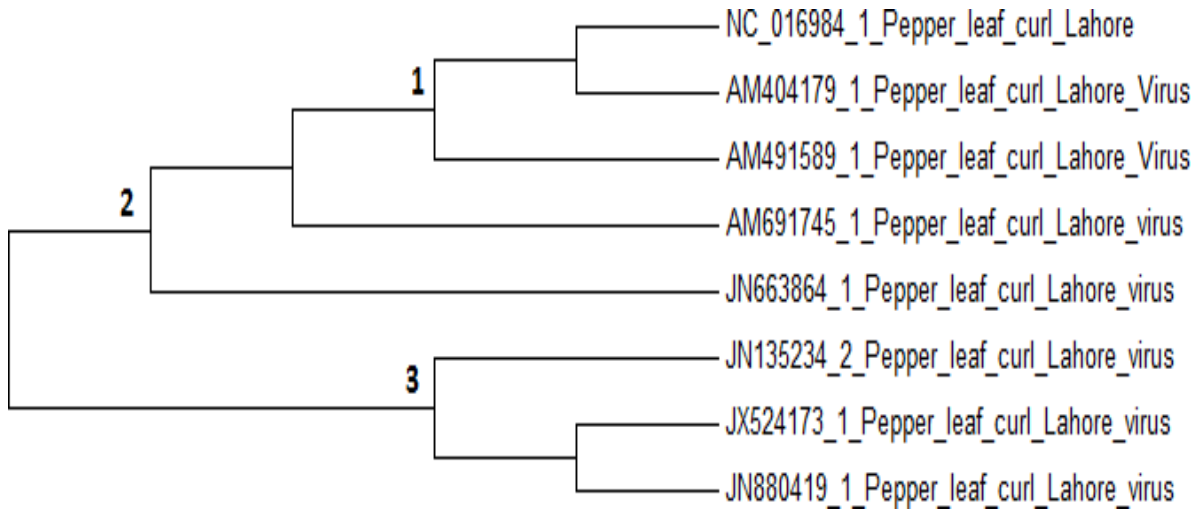

Figure 1. Dendrogram of *PepLCLV*

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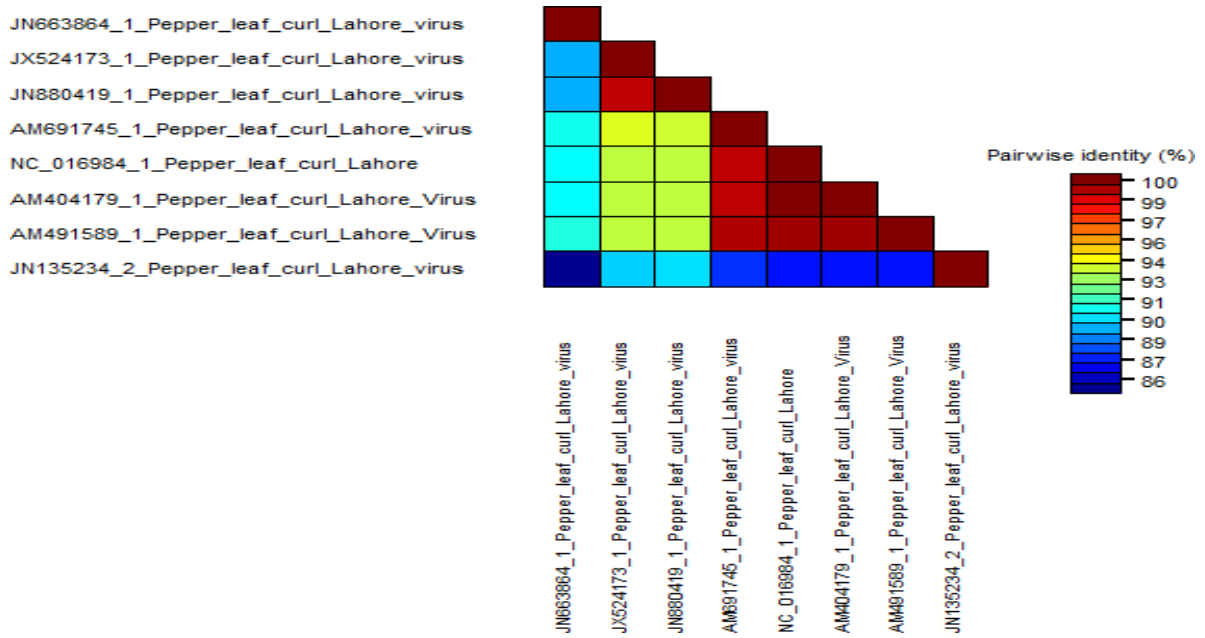

Figure 2. Grid (SDT Analysis) displaying evolution gap among *PepLCLV*. Grid values are maintained around 94 and 91 to identify species (New demarcation rule)

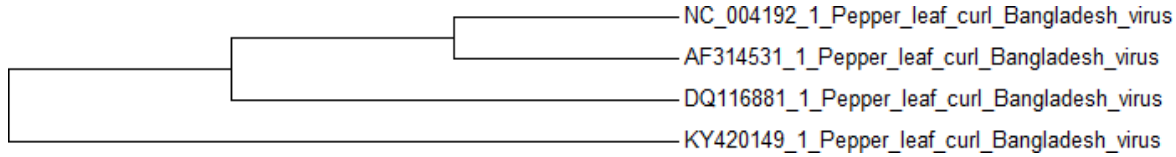

Figure 3. Dendrogram of *PePLCBV*

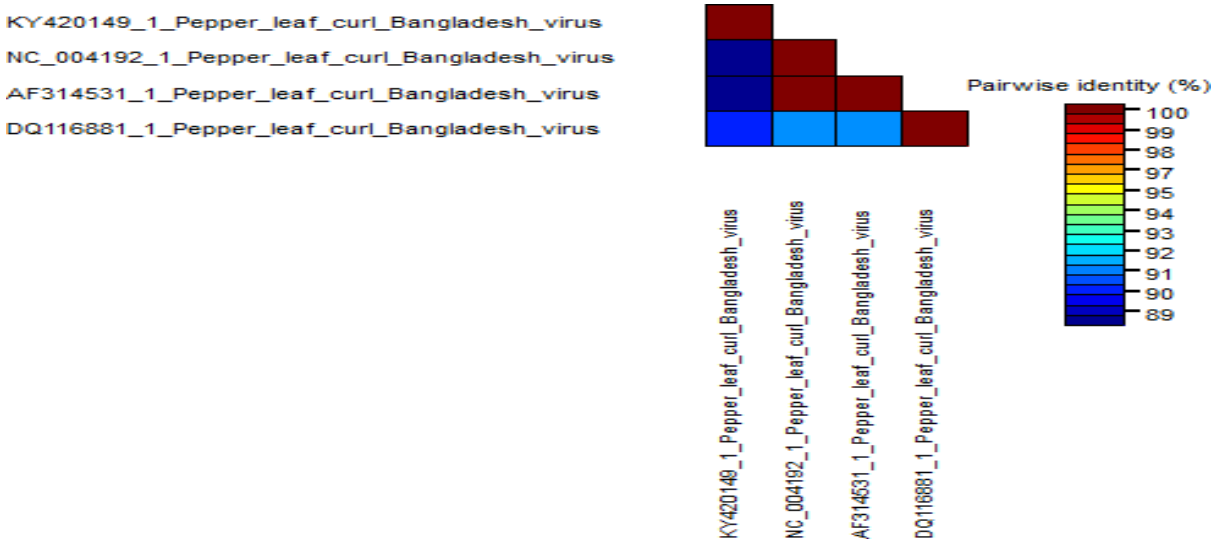

Figure 4. Grid (SDT Analysis) displaying evolution gap among *PePLCBV*. Grid values are maintained around 94 and 91 to identify species (New demarcation rule).

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A dendrogram was used to evaluate a set of eight genomes. Other genomes were offspring of the one whose registration number was JN880419. The rest genomes were obtained in Pakistan, while those with the identification codes JN663864, JN135234, JN880419, and JX524173 were separated from India. These genomes contained four distinct strains. The first strain, which was identified as coming from Nagpur (India), had just one genome, whereas the second and third strains each have two, four, and three genomes, respectively (GB file). Lots of factors might be at play in this variation and dispersion. These factors might include the emergence of new insect vectors, the exchange of contaminated goods among those 2 nations, and more. Some of these diseases were also found in plants besides stew, including other plants. It demonstrates that this pathogen has a variety of hosts. Whenever a microbe has a lot of different hosts, there is always a good reason for it. Because of various vector species, infections could advance as indicated by their vectors and become contagious (Figure 1). Four arrangements were characterized in phylogenetic tree. Two groupings were disconnected from Bangladesh and two from Pakistan. This infection was just detailed from bean stew crop up until now. Three arrangements were segregated by Chinese analysts and just one grouping was presented by Pakistani scientists.

Discussion

This examination has some remarkable focus when contrasted with past investigations. This investigation was showing changeability in *Pepper leaf twist infection* as species and strains. Our outcomes was showing huge variety. Our outcomes was showing change and recombination. That might be helpful at anticipating. That investigation might give development to next generation so that scientist may confine *Chili leaf twist infection* from different yields which was not influenced from this infection yet however are powerless against assault by this microorganism. More advancement could be possible on brinjal crop since it's anything but an equivalent group of stew crop. Hereditary variety is significant for huge populace sizes to exist (Biebricher and Eigen, 2006). The RNA infections transform quickly when contrasted with DNA infections (Holland, 1982). This was because of RNA infections give more destinations to hybridization (Worobey and Holmes, 1999; Eigen *et al*., 1988). Nonetheless, if there was an occurrence of single-abandoned DNA infections, development is probably going to be happened all the more quickly when contrasted with RNA infections (Shackelton and Holmes, 2006; Duffy *et al*., 2008). Infections have a place with *Geminivirideae* family showed tremendous hereditary variety. This was because of hybridization (Grigoras *et al*., 2010; Ge *et al*., 2007). Infections using DNA polymerase were heritably more varied, according to studies (Duffy and Holmes, 2009). The secret to inherited variation is transformation, notwithstanding (Balol, 2010). Hybridization is responsible for the spread of plant diseases, especially Geminiviruses, according to studies (Lefurve and Moriones, 2015). Actually, their dependent reproductive portion was the source of this fusion (Jeske et al., 2001). Due to the commitment of DNA fragments from different viruses, recombination occurred (Zhou et al., 1997; Barrie et al., 2001; Monci et al., 2002). Hereditary changeability and variation were brought about by this recombination (Silva et al., 2014). Our findings demonstrated that the exchange of sections across infections results in the creation of a new strain, adding to the enormous variety of viral population.

Begomovirus's genetic diversity resulted from two variables: their increased value of genome substitution (Duffy and Holmes, 2008, 2009) and ongoing crossover, which promotes advancement (Padidam et al., 1999; Pita et al., 2001). Therefore, metamorphosis and mixing play a crucial role in the hereditary diversity and instability of begomoviruses. Bipartite Begomovirus *Tomato Serious Rugose Infection* (ToSRV) and *Macroptilium Yellow Spot Infection* were explored by Lima et al. in 2013. A few studies suggested that begomoviruses merged often for a very long time (Martin et al., 2011). This resulted from the break focus's employment of a moving circular duplication instrument to replicate or improvement (Lefurve et al., 2007a; Prasanna and Rai, 2007). Results from our expanded analysis revealed that some configurations (LN845958 and LN845957) were not associated to cotton. Because of the diversity of viral groups, these infections could only be transmitted to cotton as a host. Geminiviruses' coat proteins provide important information regarding mixing and hereditary diversity (Unseld et al., 2001; Liu et al., 1997). Transmission required the coat protein. A few duplication errors could also lead to changes at certain grouping points (Zhang et al., 2001). Geminiviruses discovered across Brazil exhibited high hereditary variation and changeability through hybridization (Galvao et al., 2003; Inoue-Nigata et al., 2006; Ribeiro et al., 2007). Through recombination, new strains that trigger pandemics were given at fresh yields. Weeds were the Begomoviruses' mixing station, according to studies (Castillo-Urquiza et al., 2008; Roye et al., 1999).

It was later established that weeds serve as a foundation for hybridization. Begomoviruses develop, diversify, and then infect Jamaica (Paprotka *et al*., 2010b). Sections of the ssDNA of

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Geminiviruses appear to cause genetic material to mutate, according to some data (Harkins *et al*., 2009). In Brazil, numerous viruses, including the *BGMV*, exhibit little phenotypic mutations (Faria and Maxwell, 1999). However, when studies were carried out using the RCA method, this virus demonstrated increased heterogeneity within a species (Ramos-Sobrhino *et al*., 2010). Multiple new and aggressive variants of *CLCuV* have entered the cotton crop, according to diversity analysis of *CLCuV*, and *CLCKoV* and *CLCuMuV* are to blame for this (Ahmed, 2010; Ahmad, 2011; Briddon, 2003; Di Carli, 2012; Duffy, 2008; Ahmad, 2011; Bosco, 2004).

A begomovirus known as *PeLCV* infects 15 distinct host, including Pedilanthus. These hosts are primarily from Pakistan. According to certain investigations, it is evolved and originated in Pakistan (Moriones and Castillo, 2000; Zaidi *et al*., 2016). *Cucumber mosaic virus* (CMV), for example, has been found to infect a number of host plants (Palukaitis and Garca-Arenal, 2003). One of the finest viruses from the Geminivirus family to infect a variety of plants is the *pepper leaf curl virus* (PeLCV) (Shakir *et al*., 2018). The development or appearance in leaf curl infection are caused by *CLCuKoV* (Saleem *et al*., 2016). Research has demonstrated that begomovirus Rep genes are more translational and diverse than Cp genes (Lima *et al*., 2017; Zhou *et al*., 1997; Fondong *et al*., 2000; Patil and Fauquet, 2009). *EACMV* and *ACMV* are joined in South Africa and Angola, resulting in a novel variety of the begomovirus in both nations (Kumar *et al*., 2009; Bisimwa *et al*., 2012; Mabora *et al*., 2008; Cossa, 2010). *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).

Conclusion

Pepper leaf curl virus was a highly virulent virus. It was responsible for crop losses across subcontinent. Evolution played important role in its diversity. It had a strong ability to recombine with other viruses to evolve into a new strain. This study indicated that the spread of this virus into different areas of subcontinents was excellent.

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Conflict of interest

The author declared absence of conflict of interest.

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