



Review Article

Overview of Chilli leaf curl virus disease: Breeding and advance genetic management strategies

Tejpal Singh Sran¹, S K Jindal*¹, S A H Patel¹, Abhishek Sharma¹ and Harpal Singh Bhullar¹

¹Department of Vegetable Science,
Punjab Agricultural University, Ludhiana (Punjab)-141004

*Corresponding author e-mail: saleshjindal@pau.edu

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Abstract

Begomovirus-caused chilli leaf curl virus disease has become a threat to chilli production across globe, resulting in significant output reduction and financial loss. Begomoviruses are a new class of plant viruses that are mostly spread by *Bemisia tabaci* complex whiteflies that in extreme situations, causes twisting of interveinal areas, altering the phyto-morphology or cause 100% yield loss due to leaf curl syndrome either by itself or in conjunction with thrips and mites. Its management through pesticides become futile as it quick develop resistance that demands integrated measures for its control effectively including utilisation of resistant genetic resources. Multiple reports exist on resistant variants in germplasm pools that reflect monogenic dominant, monogenic recessive, or two recessive loci interacting in duplicate dominance epistatic mode depending on genetic background. CRISPR/Cas-mediated virus resistance has several benefits over traditional methods, and has become more important in managing diseases caused by DNA and RNA viruses.

Keywords: ChiLCV, disease, resistance, vector, virus

Capsicum, a genus of flowering plants in the Solanaceae family, is native to the Americas and is now cultivated world wide for its edible fruit. The species of Capsicum include *C. annuum*, *C. chinense*, *C. baccatum*, *C. frutescens*, and *C. pubescens*, with *C. annuum* being the most widely cultivated. Further, *C. annuum* covers maximum cultivated area across the world on account of its nutritional and economic importance (Lata and Sharma 2024). These species have been integral to cuisines across the globe, providing not just heat but also depth and complexity to dishes (Dhaliwal *et al.* 2014). The chilli pepper, a fruit of Capsicum plants, has a storied history of influencing global cuisine since its introduction to Europe by the Spaniards in the 16th century, leading to its adoption in a variety of international cuisines, from Mexican to Thai to Korean. It is an important spice in tropical Asia and equatorial America based on its delightful and pungent taste and is consumed fresh or in dried form (Lata *et al.* 2023). The global production

of chillies is a testament to their significance, with an estimated 40.9 million tonnes produced annually. India, in particular, stands out as a major contributor to this figure, producing about two million metric tons of chilli in the fiscal year 2023, with Andhra Pradesh being the largest producer among Indian states (FAO 2023). This immense production reflects not only the culinary importance of chillies but also their economic impact.

However, this vital crop faces a formidable challenge in the form of viral diseases majorly caused by begomoviruses. Currently, about 75 viruses are known to infect chilli, of which 37 are recognised species by the International Committee on Taxonomy of Viruses (ICTV) and six are tentative species. As a result, viruses constitute the main limitation on chilli output globally (Kenyon *et al.* 2014; Thomas *et al.* 2021). The most troublesome disease in the Asiatic region is chilli leaf curl virus disease (LCVD), which is caused by the begomovirus Chilli leaf curl virus

(ChiLCV). On the other hand, the pepper golden mosaic virus (PepGMV) and the pepper huesteco yellow vein virus (PHYVV) significantly reduce pepper output yields in the Americas (Nalla *et al.* 2023). Furthermore, the worldwide production of chillies has become less sustainable due to the resurgence of new begomovirus strains caused by mutations and recombination (Shingote *et al.* 2022). This review's main objective is to analyse the threat of LCVD that affect chilli peppers, highlighting the major difficulties that farmers and breeders are now experiencing. ChiLCV is a member of the family Geminiviridae and genus Begomovirus. There are over 520 viral species in the Geminiviridae family. These species are further categorised into 14 genera based on factors such as host range, nucleotide sequence similarity, genomic organisation, and transmission (Thomas *et al.* 2021). Begomoviruses have single-stranded genomes made up of either two (bipartite) or one (monopartite) component, called DNA-A and DNA-B, each measuring 2.5–3 kb (Sakata *et al.* 2008; Zerbini *et al.* 2017). While most begomoviruses reported from the old-world regions (Africa, Asia, Australia, and Europe) have monopartite genomes, there are a few exceptions. Begomoviruses reported from the new world regions, like those in the American regions (Latin America and North America), typically have bipartite genomes (Nalla *et al.* 2023).

Most of the chilli LCVD due to monopartite DNA-A viruses that use ω -satellite molecules (Hussain *et al.* 2004; George *et al.* 2014). However, few bipartite types ChiLCV have also been linked to the development of chilli LCVD (Kushwaha *et al.* 2015). ChiLCV transmitted by the whitefly *Bemisia tabaci*. Characterized by symptoms such as upward leaf curling, crinkling, puckering, and stunting of plants, it leads to substantial yield losses. In cases where thrips or mites are also present, the severity of chilli LCVD is increased. Recent research has focused on understanding the molecular mechanisms of the disease, its impact, challenges, and management strategies, particularly in the Indian subcontinent where the disease is prevalent. Advances in detection systems and disease management, including CRISPR/Cas-mediated virus resistance, are at the forefront of current scientific inquiry, aiming to

mitigate the effects of this devastating disease on a crop that is so vital to both global cuisine and economy.

Epidemiology

It was initially claimed that TLCV was the cause of chilli leaf curl in its natural state (Mishra *et al.* 1963). There have also been reports of the appearance of a different kind of leaf curl symptoms in chilli leaves, which results in leaf enations (Dhanraj *et al.* 1968). Based on existing data, the leaf curl complex in chillies may be caused by thrips (*Scirtothrips dorsalis*), mites (*Polyphagotarsonemus latus*), and a virus carried by whiteflies (*Bemisia tabaci*) (Varma 1962). Begomoviruses were unknown at the time, but since 2003, many begomovirus species have been linked to the leaf curl disease that affects chilli peppers in India (Senanayake *et al.* 2007; Thakur *et al.* 2018). Since then, there have been other ChiLCD outbreaks in Central and Southern India, as evidenced by current reports (Shingote *et al.* 2022). Climate factors such as abrupt temperature increases, varied intensity precipitation, relative humidity, intensified cropping systems, and the existence of alternative hosts increase the number of whiteflies, which accelerates the transmission of begomoviruses and incidence of viral diseases. Also, the global distribution of begomoviruses is comparable to the spread of whiteflies (Brown *et al.* 1995). It encompasses nearly all of the equatorial areas of Australia, Europe, Asia, Africa, and the Americas.

Symptomology

Complex interactions between infecting viruses, insect vectors, and host plants result in infection. When pepper plants host ChiLCV, symptoms may appear depending on the virus's genetic resistance. Plants show immune (display no symptoms) to severe morphological distortions resulting in a complete loss of yield, depending on the alleles they contain. The typical symptoms of the virus include curling, rolling, and puckering of leaves. The most noticeable symptoms are thickening and swelling of the veins, blistering of the interveinal regions, and deformation of the leaves. As a result of shorter internodes and petioles, young plants infected with ChiLCV have elongated basal leaves, which are crowded and exhibit stunted development (Sran *et al.* 2023). There were fewer blossoms and fruits on the diseased plants, and those that did form had significantly smaller petals and

curled tips (Mishra *et al.* 1963). When *C. annuum* was surveyed at the Indian Agricultural Research Institute, two different symptom kinds were noted (Dhanraj *et al.* 1968). The first type's symptoms matched those previously documented (Mishra *et al.* 1963). A different set of symptoms included the afflicted plants growing upright and bushy with dark green foliage. The tips of the leaves were curled downward, and instead of the upward rolling of the margins that were observed in the first type, the leaves form changed from oval to round, with significant puckering and leatheriness (Thakur *et al.* 2018).

Numerous outside factors have an impact on the disease's incidence and severity in natural conditions. Environmental elements including the age of the plant, the host's genetic composition, the microclimate around it, and the fertility of the soil can all have an impact on symptoms (Matthews 1991) other than virus strain. The presence of homologous betasatellites molecules has also been linked to an increase in the severity of symptoms related to the ChiLCV (Kumar *et al.* 2016). Although the viral genomic DNA-A and -B include open reading frames (ORFs) known to produce infection, betasatellites were discovered to be necessary for the development of severe leaf curl symptoms in *Capsicum* spp. (Chattopadhyay *et al.* 2008; Ruhel and Chakraborty 2019). Only when the viral genome and satellite DNA was present the typical symptoms of the chilli leaf curl virus have been seen (Chattopadhyay *et al.* 2008). Additional proof of the involvement of betasatellite molecules in the production of the leaf curl symptom in *C. frutescens* was presented by Kumar *et al.* (2011). The typical ChiLCV symptoms, such as stunting and leaf curling, appeared when *C. frutescens* plants were agro-inoculated with infectious clones containing both the partial tandem repeats (1.9-mer) and betasatellite (1.7-mer) of the viral genome. However, no leaf curling symptoms showed up when the viral genome was used alone (Nalla *et al.* 2023).

Vector and virus transmission

Whiteflies multiply easily on host plants in warm weather, and their numbers rise quickly even when they have natural adversaries. Approximately 15–25% of chilli plants were first found to exhibit the characteristic leaf curl symptoms in the field, and whiteflies quickly spread the virus, resulting in a

50–100% infection rate (Senanayake *et al.* 2007). The virus may spread even by a single whitefly, but if eight or more are present on a plant, there may be a 100% likelihood of transmission (Senanayake *et al.* 2012). There exists a direct correlation between the incidence of chilli LCVD and the population of whiteflies. *B. tabaci* is polyphagous by nature, it can reproduce quickly and widely, which makes it easier for it to co-exist in huge populations across a variety of agro-ecological zones. According to recent reports, whiteflies' wide range of host range may be caused by the presence of the gene *BtPMT1*, which is derived from plants and allows them to neutralise phenolic glucosides, a toxin that plants release as a defence mechanism (Xia *et al.* 2021). Additionally, as they are sucking pests, their feeding also harms the plant directly and may cause a decrease in photosynthetic potential. Also, the honeydew excreted by their feeding nymphs encourages the growth of sooty mould, which hinders plants' ability to photosynthesize.

During the acquisition access period (AAP), whiteflies ingest the virus by their stylets while feeding on the phloem of infected plants, and during the inoculation access period (IAP), they transmit the virus through their saliva in the phloem of other plants (Sinisterra *et al.* 2005; Wei *et al.* 2014). The vector contains an array of proteins that aid in the effective transmission of viruses. The viral genome is transferred into the host cell nucleus by the vector, which probably transmits the virus to the plant in uncoated form during the infection phase. Because the viral genome only encodes a small number of proteins, it is mostly dependent on the cellular DNA replication proteins to replicate its DNA. Whiteflies spread virus in persistent manner and require incubation period of hours to days. In a study Czosnek *et al.* (1993) reported the whiteflies need to be fed for at least 90 minutes after acquiring the virus and 120 minutes after being inoculated in order to spread begomoviruses in tomatoes. The proliferation of polyphagous whitefly B-biotype, which can reproduce twice as quickly as non-B biotype, has been linked to the rapid spread of begomoviruses that infect chillies (Wang *et al.* 2023). Plant viruses have the ability to alter the life cycle and behaviour of their insect vectors by direct and plant-mediated indirect impacts (Moreno-Delafuente *et al.*

2013). In plants infected with the tomato leaf curl china virus (*TYLCCNV*), the B-biotype has been shown to have higher fecundity (Luan *et al.* 2013). According to several studies, begomoviruses linked to certain crops, such as tomatoes or chillies, can spread to other host species by way of whitefly vectors (Senanayake *et al.* 2012; Kushwaha *et al.* 2015). On the other hand, begomoviruses appear to exhibit some degree of host selectivity. Tomato yellow leaf curl virus (*TYLCV*) has been shown to infect and reproduce in sweet peppers and chillies. Nevertheless, when different strains and inoculation methods are employed, chillies usually show no symptoms or just mild ones (Nalla *et al.* 2023).

Disease Management

Controlling viral diseases involves cultural and mechanical measures that reduce the rate of infection, transmission, and severity. The primary approach to managing begomoviruses has been the use of pesticides targeted at the whitefly vector. However, it has been shown that using pesticides is expensive for farmers, only partially successful, and dangerous for consumers, farmers, and the environment (Borah and Das 2012). Because the virus spreads during the vector's probing of the plant surface, prior to ingesting, and before the insecticides have a chance to act, managing the vector with pesticides is frequently ineffective (Kenyon *et al.* 2014). Like Begomovirus, whiteflies can develop tolerance to widely used pesticides and frequently evolve into novel biotypes (Naveen *et al.* 2017). More than 40 active components in pesticides have been demonstrated to cause resistance in whiteflies (Whalon *et al.* 2013). The unexpected appearance of the whitefly as a viral vector has caused confusion and perturbation for researchers worldwide due to its prevalence and unpredictable presence on various hosts in specific regions. As a result of these qualities, managing and controlling *B. tabaci* is difficult. ChiLCV management focuses on controlling vector transmission, restricting the viral outbreak, and minimising the disease's devastating impact on crop productivity.

Development/Identification of resistant material

Resistance breeding is the most effective method for developing chilli LCVD resistance in chilli genotypes. Resistance breeding is based on the detection of robust resistant sources that are free of

disease signs by screening under native field conditions, followed by resistance confirmation by artificial inoculation. Identifying novel sources of resistance to the ever-changing begomovirus in chilli is vital for breeding efforts to provide long-lasting host plant resistance. Disease resistance screening for LCVD began in the late 1960s, mostly in open field conditions (Mishra *et al.* 1963) (Figure 1). The resistance breeding in chilli includes breeding methods like backcross method, pedigree selection, single-seed descent method, mass selection, recurrent selection and hybridization. In addition, from the before mentioned methods backcross method is mostly utilize to transfer the resistance from resistant backgrounds to the agronomically suitable chilli cultivars. For utilization of these breeding methods there is a great need to understand the fore lying genetic mechanisms of the chilli LCVD resistance. Disease resistance comes from two genetic mechanisms: monogenic (qualitative) and polygenic (quantitative). The former relies on a single gene, while polygenic resistance involves many genes. Monogenic inheritance occurs when a gene interacts with the pathogen's genes, resulting in total resistance to the infection. Quantitative resistance delays disease progression by increasing latency duration and other epidemic-related characteristics while exhibiting no evident genetic interaction with the virus. Research on resistance breeding in chilli is rapidly expanding and will play a crucial role in developing chilli LCVD resistance strategies. This includes the exploration of wild sources of *Capsicum* to utilize untapped reservoir of chilli LCVD resistance. In one such experiment Kumar *et al.* (2006) examined 307 genotypes of five *Capsicum sp.* for chilli LCVD and found three without symptoms: BS-35, EC-497636, and GKC-29. The same symptomless genotypes were tested further by grafting and alternating grafting with Pusa Jwala, and the findings verified the resistance responses. As a result, these three genotypes demonstrated features of potential chilli LCVD resistance donors. GKC-29 and BS-35 are *C. frutescens* landraces from the North-East area of India, whilst EC-497636 originated from Hungary. Except for the hybrid CH-27, public sector researchers seldom ever create cultivars resistant to the chilli leaf curl virus (Dhaliwal *et al.* 2015). The private sector released the majority of the tolerant or partially resistant cultivars that are currently available on the

Resistant Sources (ChiLCVD)



Fig. 1 Germplasm and chilli lines showing resistance to chilli leaf curl virus disease (ChiLCVD)

market. Despite ongoing scientific endeavours, a critical need remains for methodical screening to pinpoint the origins of the constantly changing begomovirus species and create novel, resistant cultivars endowed with favourable horticultural characteristics. Also, the use of biotechnological tools assists the transfer of desirable resistant genes into

agronomically favourable genotypes as traditional breeding techniques like backcross breeding without marker assisted selection reduce the accuracy especially in case of recessive resistance control and it is also take more time as compare to the other advance genetic approaches.

Advanced genetic approaches

There are two main techniques for managing LCVD in chilli using non-conventional methods: direct strategies and indirect strategies involving virus-vector control (Shingote *et al.* 2022). The development of whitefly resistance in plants falls under the indirect strategy, whereas the direct control approach comprises pathogen-derived resistance (PDR), RNA interference (RNAi), and genome editing techniques.

Pathogen derived resistance (PDR)

The conventional method for the management of chilli LCVD is time taking and less efficient. With the advancement of the genetics and biotechnological methods such as PDR provide effective and rapid approach for the development of resistance against plant viruses in different crops. This technique was first validated in tobacco by the creation of tobacco plants expressing the coat protein gene of tobacco mosaic virus (TMV) (Abel *et al.* 1986). The PDR method depends on the post-transcriptional gene silencing (PTGS) process to effectively employ genes derived from viruses to eradicate viruses. One of the most effective methods for inducing resistance to viral infections among PTGS is RNAi. RNAi is a natural defence antiviral mechanism that breaks down sequence-specific viral RNA by using double-stranded RNA (dsRNA). The viral RNA is interfered by the dsRNA, which is processed into short 21–24 nt RNAs by dicer-like proteins. In the experiment by Sharma *et al.* (2015) an effort was made to show how RNA silencing techniques may restrict ChiLCV infection. Over-expression of dsRNA specific to *AC1/AC2/ C1* was found to be effective in targeting different species of ChiLCV. Using computational techniques, Mishra *et al.* (2020) discovered chilli miRNAs exclusive to ChiLCV critical genes. Chili-encoded miRNAs that target the CP (V1) and Rep (C1) genes have been predicted; these miRNAs may be utilised to silence the ChiLCV virus. The ability to tolerate extreme viral loads and natural field conditions, rapidly evolving ChiLCV variants that eluded sequence-specific recognition in RNAi mechanism, and uncertainties surrounding the release of genetically modified (GM) crops are just a few of the challenges that the RNAi method will need to overcome. Singh *et al.* (2022) recently tried a unique

method of applying a cocktail of dsRNAs in *Nicotiana benthamiana* to suppress ChiLCV infection by RNA interference.

Transgenic approach

Due to their enormous recombination potential, geminiviruses have evolved to be able to take advantage of a wide range of host cellular functions. As a result, there has been some discussion of the processes relating to limiting viral accumulation inside host cells, preventing virus migration within plant cells, and activating plant defence systems. The CRISPR/Cas system, which consists of CRISPR-associated proteins and clustered regularly interspaced short palindromic repeats, has effectively emerged as one of the most accurate and promising genome-editing techniques in the last ten years (Kale *et al.* 2021). According to a study, the tomato yellow leaf curl virus (TYLCV) genome was effectively interfered with by *CP* or *Rep* specific sgRNA in both the transgenic tomato and *N. benthamiana* lines (Tashkandi *et al.* 2018). Remarkably, Ali *et al.* (2016) found that sgRNAs specific to the stem loop were more effective in inhibiting the growth of many begomoviruses, including TYLCV, Merremia mosaic virus, and Cotton leaf curl Kokhran virus, than were sgRNAs that targeted the *CP* and *Rep* sections of the viral genome. According to Chandrasekaran *et al.* (2016), cucumbers with *eIF4E* knockout by CRISPR/Cas9 showed total resistance to viruses causing diseases including papaya ringspot, zucchini yellow mosaic, and cucumber vein yellowing. Plant DNA virus resistance is being more often reported as a result of recent developments in CRISPR/Cas9 technology. For instance, resistance to TYLCV was created by this CRISPR/Cas9 technique that targeted the *MP* or *CP* region (Tashkandi *et al.* 2018). Multiplexed sgRNA targeting the ChiLCV genome was created by Roy *et al.* (2019), and their strategy was successful in eliminating the ChiLCV genome. Consequently, the CRISPR/Cas system emerges as a potent instrument for plant defence against viruses and opens new possibilities for genetically modifying chilli to prevent the deadly chilli LCVD.

Conclusion

In summary, the global output of chillies is seriously threatened by the disease caused by the chilli

leaf curl virus and the begomoviruses that are linked to it. It is essential to design long-lasting and efficient control strategies to lessen yield losses brought on by LCD. There are essentially two strategies to manage this disease one is to generate varieties resistant to begomovirus and the other is to breed for vector-resistant cultivars. Ultimately, the best course of action is to combine the two resistance-building techniques. Advance molecular breeding holds the key to these, which helps in efficient and effective identification of resistant sources and its introgression into elite genotypes. Other than this, RNA interference (RNAi) against a number of ChiLCV transcripts showed promise as a quick and efficient method of developing

resistance to a variety of plant viruses. In addition, genome editing employing the CRISPR-Cas system has provided a novel approach to cultivate resistance to ChiLCV by modifying host susceptibility variables. Several non-essential host susceptibility characteristics may prove to be more effective targets for the CRISPR-Cas system in order to achieve broad range resistance against plant viruses. Although, transgenic techniques against ChiLCV appeared to be quite promising but the dissemination of transgenic types is hampered by uncertainty over government regulations and public acceptance in India.

Conflict of interest: Authors declare no competing interest.

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