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RESEARCH ARTICLE

Review of Cotton Leaf Curl Virus-genetic Studies

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ABSTRACT

CLCuV is a threat to cotton production worldwide. Cotton leaf curl disease is a risk to the cotton producing countries like China, Pakistan, India, the Philippines, and Thailand. This virus is responsible for the reduction in yield, as well as the decrease in the number of bolls and their weight, and the overall reduction in the size of the plants. CLCuD is caused by monopartite begomovirus along with alpha and beta satellites. There are many strains of CLCuV such as Cotton leaf curl Kokhran virus (CLCuKoV), Cotton leaf curl Alabad virus (CLCuAlV), Cotton leaf curl Rajasthan virus (CLCuRaV), Cotton leaf curl Multan virus (CLCuMuV), Cotton leaf curl Gezira virus. The whitefly, *Bemisia tabaci* is responsible for the transfer of CLCuD. Countless measurements can be taken to minimize the effect of virus on cotton plant, removal of alternate hosts, early sowing, use of proper fertilizers for healthy plant growth, pesticides for the eradication of pests' population (white fly). Some genetic and biotechnological approaches are also been devised to control and develop resistance against the virus. Further, resistance can be developed by producing transgenic varieties by pathogen derived resistance or gene editing by CRISPR-Cas technologies. In future, we will be able to produce new plant varieties with better resistance against disease and better yield. In this review the genetic component involved in CLCuV spread, its vector, transmission, affected areas, different strains, and management strategies are discussed.

Key words: CLCuV, Genetic component, Alpha-satellites, Beta satellites, *Bemisia tabaci*, Management

INTRODUCTION

Pakistan's most significant cash crop is cotton. Because of its capacity to bring in money for farmers, it is frequently described as "white gold" in the nation's farming community. Since cotton is Pakistan's primary source of foreign exchange revenues, which go directly toward the nation's GDP, cotton plays a crucial part in the country's economy (Ali et al., 2019; Razzaq et al., 2023). Pakistan ranks fourth among the world's cotton producers, behind the United States, China and India. The average cotton yield is approximately 570.99 kg/hm^2 in Pakistan. Cotton production is declining due to biotic stressors and climate change (Razzaq et al., 2021).

CLCuD or Cotton leaf curl disease, is currently rife. It was initially identified in the Punjab region, close to Multan, in 1985, though it was first observed there as early as 1967. CLCuD was the main factor by the early 1990s, limiting Pakistan's ability to produce cotton (Kamal et al., 2024a). It has since expanded into India and, more recently, into Pakistan's southwest and south-western provinces. (Briddon and Markham, 2000). The majority of Pakistan's cotton-growing regions saw the disease resurface in 1987 in an epidemic form. Pakistan's center and southern regions of Punjab were reported to be affected by the illness in 1992 (Fauquet and Nawaz-ul-Rehman, 2008).

Gossypium hirsutum L., or cotton, is a main crop used for the formation of fiber but numerous biotic and abiotic limitations affect cotton. The majority of these are caused by biotic causes, such as the cotton leaf curl virus (CLCuV) (Zafar et al., 2020). The carrier and vector of the infamous cotton disease CLCuV is the whitefly or *Bemisia tabaci*. CLCuV-infected plants may exhibit a variety of symptoms, including thickening of the veins, yellowing of the leaves, reduced growth, curling upward or downward and enation formation (Nadeem et al., 2024).

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Plant viruses have either an RNA or a DNA genome. There are two types of DNA viruses: (1) circular double-stranded DNA (dsDNA) containing viruses, such as caulimoviruses and badnaviruses, that use reverse transcription, for replication, from RNA; and (2) other circular single-stranded DNA (ssDNA) containing viruses, such as Gemini virus and nano viruses, which replicate by way of a dsDNA intermediate. Begomoviruses are a type of Gemini virus that are spread by whiteflies and infect a variety of commercially significant dicotyledonous crops, such as cotton, potatoes, tomatoes, cassava, and chilies. In cotton, begomoviruses produce leaf curl disease (Mahmood-ur-Rahman et al., 2021).

The monopartite begomovirus (family Geminiviridae) the disease-causing agent is carried by, whitefly (*Bemisia tabaci*), the vector. This illness has had two epidemic outbreaks in Pakistan in the last thirty years. Controlling viruses becomes challenging because of their higher rate of mutation and recombination, which results in the infection of many strains. The circumstances have been further enhanced by the availability of substitute host plants, agricultural methods, and ideal environmental circumstances (Sarwar et al., 2022).

The virus complex that causes CLCuD has a higher rate of recombination, which exacerbates the issue. The situation has been made worse because of the presence of substitute host crops like tomatoes and okra, or some other crops as well as the use of mixed-type agricultural methods, which have accelerated the emergence of new virus strains and vectors (Rahman et al., 2017a).

Depending on the helper virus species or strain, the causative agents of CLCuD comprise a helper begomovirus and one or more related alpha- and beta-satellites. It is widely known that there is a large degree of genetic variation in CLCuD-begomovirus species. Cotton leaf curl disease is mainly instigated by the four "fundamental" begomovirus species: Cotton leaf curl Alabad virus (CLCuAlV), Cotton leaf curl Gezira virus (CLCuGV), Cotton leaf curl Multan virus (CLCuMuV) and Cotton leaf curl Kokhran virus (CLCuKoV), (Sain et al., 2023).

The plant is more susceptible to CLCuV and creates virus-resistant cultivars by using whitefly-mediated transfer, grafting, and delayed sowing. The age of the plant and temperature are two abiotic factors that alter the epidemiology of the disease. By changing the composition of the main fiber components, including pectin, cellulose, and protein wax, this disease not only deteriorates fiber quality traits like, ginning out turn percentage, fiber fineness, fiber(staple) length, uniformity index of fiber, maturity ratio, and bundle strength of fiber but also affects yield (Kamal et al., 2024b).

The pathogen's capacity for evolution and the likelihood of viral recombination, which led to the evolution of new virus varieties, determine how quickly resistance breaks down. Due to viral mutation and a lack of long-lasting resistance, the immunity acquired against Multan-CLCuV became vulnerable to Burewala-CLCuV. The only method to effectively control CLCuD is to treat the seeds, which will purify the cotton crop safely during the first 40 to 50 days after sowing. Other methods of managing the disease include changing the dates of sowing, cultural practices, crop nutrition, buffer crops, systemic cotton seed poisoning, and vector control. Transcriptional gene silencing is another way of biotechnology that can help in this condition by regulating the genes. Wide-ranging resistance in the field can be established against all viruses with the use of biotechnological skills (Farooq et al., 2011).

The wax on leaves serves as a barrier to prevent infection by whiteflies and CLCuV. The resistance and susceptibility of *G. arboreum* and *G. hirsutum* types are also caused by several biochemical components found in leaf epicuticular wax, as well as by their quantity. (Majid et al., 2020).

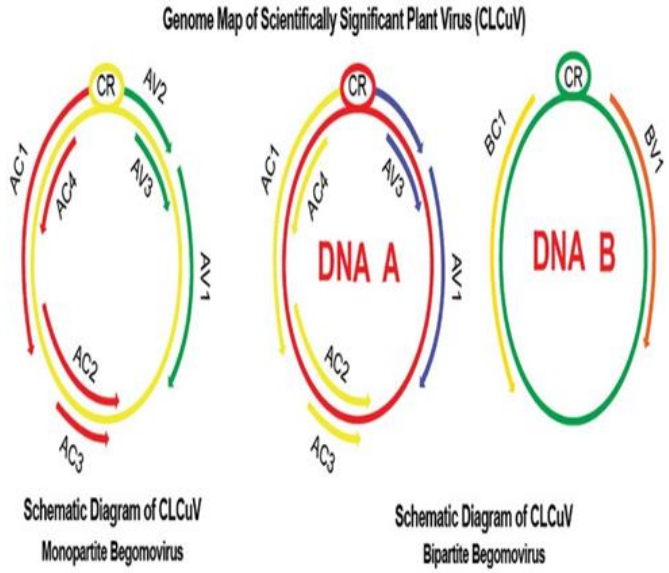
RNA-guided DNA nuclease cleaves the nucleic acid in a sequence-specific manner to produce the CRISPR/Cas system, which is derived from prokaryotic species and functions as an adaptive immune system to defend them against foreign DNA invaders like phages (Sorek et al., 2013). In recent times, the CRISPR/Cas system has arisen as the preferred instrument for genome editing purposes in many organisms, such as plants (Belhaj et al., 2015). Further, the best seed cotton yield can be obtained by regulating CLCuV through early planting with increased plant spacing and late planting with decreased plant spacing (Iqbal and Khan, 2010). The best pre-sowing fertilizer for managing CLCuD and whitefly was determined to be a mixture of all organic nutritional supplements; the best spray to control CLCuV incidence and whitefly infestation was a canola oil and bifenthrin (bifenthrin 10% EC) mixture (Humza et al., 2016).

Genome Organization of CLCuV

Begomoviruses produce CLCuD in conjunction with a non-essential alpha satellite (whose role is yet unknown) and the disease-specific satellite betasaellite [CLCuMB]) (Amrao et al., 2010). Most begomoviruses have two halves to their genomes, called DNA A and DNA B, (Fig. 1) which are both 2.5–2.8 kb in size. DNA A, the bipartite begomoviruses' component, can independently create copies and produce virions, but DNA B is needed for systemic infection. The intergenic region contains TAATATTAC sequence and the conserved stem-loop. DNA A and DNA B share around 200 sequence in base pairs, which is called as the common region (BY et al., 2005). All alpha-satellites have three features in common, a stem-loop structure with (TAGTATTAC) sequence, an open reading frame that codes for replication protein, a rich region of ~200nt (Siddiqui et al., 2016).

Isolate Identification

Multiple species of begomovirus were noticed in cotton during CLCuD outbreak in northwestern India and Pakistan, where six different species were



a) Begomo virus monopartite genome organization

b) DNA A, encodes for viral activities and coat protein

c) DNA B, encodes for NSP (nuclear shuttle protein) and movement protein)

Fig. 1: Begomo virus (Atiq et al., 2023)

identified. The cotton leaf curl viruses that were identified were Cotton leaf curl Kokhran (CLCuKoV), Cotton leaf curl Alabad (CLCuAlV), Cotton leaf curl Rajasthan (CLCuRaV), Cotton leaf curl Multan (CLCuMuV), Tomato leaf curl Bangalore virus (ToLCBaV) and Papaya leaf curl virus (PaLCuV). (It should be noted that name of Gemini viruses are on the basis of first host in which they are recognized; as a result, the names of viruses do not always indicate the preference of a given species or host range) (Kirthi et al., 2004).

Cotton Leaf Curl Gezira Virus

It is associated with okra leaf curl disease in Burkina Faso. Isolates of CLCuGV that were cloned and sequenced are twenty-three in number and they shared 95 to 99% of nucleotide sequence. Additionally, four alpha-satellite (DNA-1) and six beta-satellite molecules were described (Tiendrébéogo et al., 2010).

Cotton Leaf Curl Kokhran

Cotton leaf curl disease is caused by several plant virus diseases in Pakistan, including the cotton leaf curl Kokhran virus (CLCuKoV). The main causative virus linked to the CLCuD second outbreak in Pakistan was the CLCuKoV strain, also known as CLCuKoV-Bur, which first appeared in the area of Burewala, Pakistan. Six ORFs encode for four putative proteins that can be found in the 2.7 Kb monopartite ssDNA genome (Ashraf et al., 2023).

Cotton Leaf Curl Multan

Cotton leaf curl Multan virus (CLCuMuV) is a serious constraint on cotton output in South Asia and is currently spreading to Southern China (Wang et al., 2016). In 1967, the cotton leaf curl disease's first reports were seen in Multan, Pakistan. In 1987, the disease made a comeback in an epidemic fashion in most of Pakistan's cotton-growing regions. In 1992, the illness was reported in southern and central areas of Punjab, Pakistan (Fauquet et al., 2008).

Sequence Identity

The isolate, CLCuV-SG01, shows the most sequence similarity with the Leaf Curl virus of cotton from Rajasthan, while the other isolate, CLCuV-SG02, demonstrates the highest sequence identity with the Pakistan's Leaf Curl virus of cotton. There were 85% shared characteristics between the two isolates (Kumar et al., 2010). 40 CLCuMuV isolates share > 99 % nucleotide sequence identity with each other (Du et al., 2015). Also, Pakistani isolate HE599398 clustered together with KJ028212 and KC305093 Indian isolates and they share sequence identities of 68.4 and 69 percent to Pakistan isolate, respectively. The Indian isolate (AY704661) was clustered together with CLCuMuB isolate from the Philippines and one isolate (KF413619) exhibited 79.2 percent sequence similarity, whereas the Chinese isolate (JQ963630) remained closer to another isolate (KF413617)), sharing sequence homology of 96.9 percent with each other (Farooq et al., 2021).

Components of Cotton Leaf Curl Virus

Satellite-associated monopartite begomo virus mainly causes CLCuD. These satellites are named alpha-satellites and beta-satellites. Both satellites are encapsulated by the helper virus's coat protein and the helper virus is double in size than these components (Nawaz-ul-Rehman et al., 2021). DNA-A, that is a component of the helper virus genome, encodes both viral activities needed for replication and the coat protein, which is crucial for insect transmission. The second component produces two other products that are involved in locomotion between the tissues of the host cell (Briddon and Markham, 2000).

Alpha Satellite

Alpha satellites contain an alpha-Rep, that is a suppressor of the natural virus defense mechanism of host—gene silencing—and also responsible for the replication of alpha satellites. Alpha satellites are thought to have originated in the Nanoviridae family. It appears that the etiology of CLCuD is not significantly influenced by alpha satellites. Nonetheless, their comparatively high variety points to a significant evolutionary significance for them in the spread of illness (Nawaz-ul-Rehman et al., 2021).

Beta-satellite

The component of Cotton leaf curl Gemini viruses DNA A, cannot cause infection alone. It requires beta-satellites to produce specific pathogenic proteins to cause infection in the host.(Nawaz-ul-Rehman et al., 2021). CLCuV is a monopartite plant virus from the genus Begomovirus of Geminiviridae family, in conjunction with beta-satellite, a crucial disease-specific satellite from the recently formed family Tolecusatellitidae (genus Beta-satellite). It has a multifunctional single gene that encodes for protein βC1, a SCA satellite-conserved area and an adenine-rich region (Fig. 2). The CLCuMuB βC1 protein is essential for pathogenicity and symptom assessment. It also modifies several host cellular processes, including ubiquitination, and reduction of gene silencing, autophagy, promotion of CLCuD infectivity (Zubair et al., 2017).

Geographical Distribution

In 1967, in Multan Pakistan, the leaf curl disease was first observed in cotton. In 1987, in the active cotton-growing areas of Pakistan, the disease reappeared in its epidemic form. The disease was sensed all over the Punjab especially in the central and southern parts in Pakistan, in 1992. The disease was discovered in the border areas of India (Haryana, Punjab and Rajasthan) during 1997–98, connected to the south of Punjab, Pakistan. The most destructive virus known as Cotton Leaf Curl Virus (CLCuMV) causes a gigantic loss in the subcontinent (Fauquet and Nawaz-ul-Rehman, 2008).

At present, the virus with its satellites exists in five countries, including Pakistan, China, India, Thailand and the Philippines. From the 121 globally recognized isolates of CLCuMuV, they are distributed as Thailand (1), the Philippines (3), India (32), Pakistan (35), and China (50). Further, out of 447 isolates of CLCuMuB in world, 3 are from the Philippines, 49 from China, 65 isolates from India, and the mainstream of cotton-infecting CLCuMuB isolates, nearly 330 have been discovered from Pakistan (330) Notably no reports of satellites associated to CLCuMuV has been received from Thailand till now (Farooq et al., 2021).

Molecular Phylogenetics

CLCuMuV

The phylogenetic analysis of CLCuMuV sequences shows nine unique group formations. These groups of CLCuMuV populations are detected in five countries. They are named on the basis of the sort of host plants in which they cause infection. For example, a large number of Chinese CLCuMuV isolates almost thirty-nine, was known to be linked to hibiscus, four isolates to cotton, one to Passiflora and almost three to okra, while three isolates did not have any information of host (Farooq et al., 2021).

CLCuMuA

The 153 isolates of CLCuMuA from Pakistan are being divided into nine specific groups. It was discovered that out of 153, 113 isolates originate from cotton, four from okra, eleven from *Malus*, one isolate from Saccharum, one from Soybean and four from Spinach and one from *Bemisia tabaci*, whereas 18

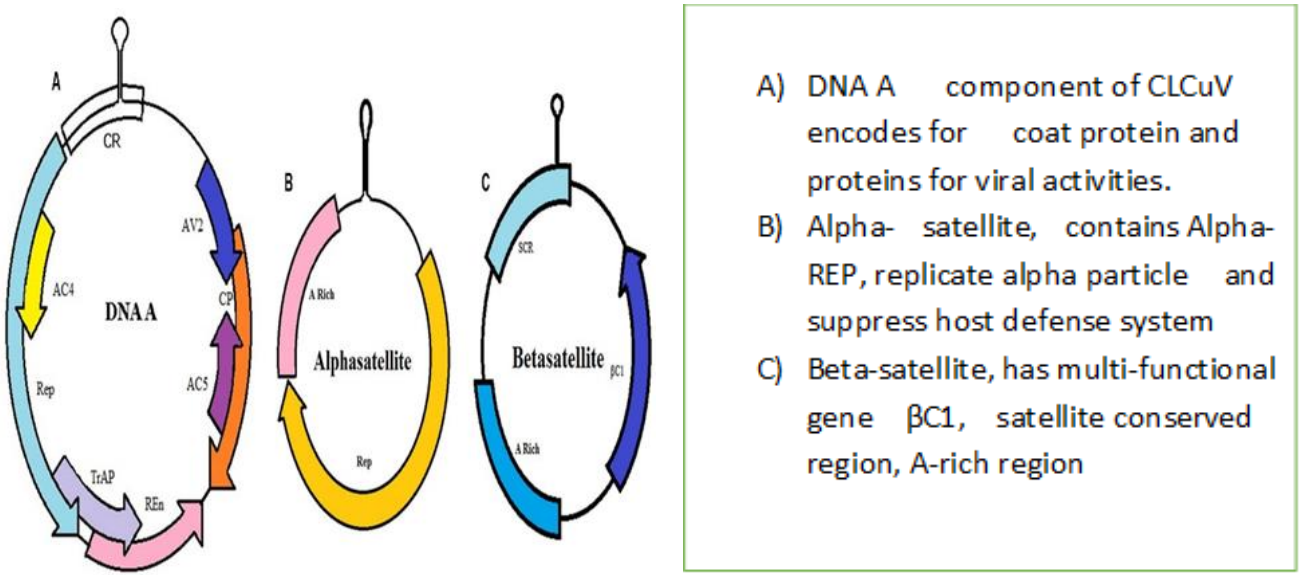


Fig. 2: Complex of CLCuV (Rahman et al., 2017b)

isolates didn't have any information of their host. Also, six isolates were associated with cotton, out of nine Indian CLCuMuA isolates. Further, their phylogenic analysis together with Pakistani isolates showed that isolate from Pakistan (LN829161) grouped with six of Indian CLCuMuA isolates (MF141732, MF141733, MF141734, MF141735, MF141740, and KY783480), whereas Pakistani isolate (MN922310) shared a clade with the isolate MG373554, sharing sequence of 68.4 percent (Farooq et al., 2021).

CLCuMuB

The analyses of beta-satellites population divide isolates from Pakistan into twelve separate groups. The largest one consists 266 isolates of cotton-infecting beta-satellites, second one is *B. tabaci* with 14 isolates, Jasmine contains 2, Spinacia(2), *L. esculentum* (7), chili (1), luffa (1), soybean (1), bean (1), *Nicotiana benthamiana*, *Nicotiana tabacum* (1), Malvacerum (1), while thirty three groups do not have any host information (Farooq et al., 2021).

Fig. 3: Upward curling of leaf (A, B), downward curling of leaf (C), thickening of veins (D, E)

Symptoms and Impact of CLCuV

The main symptoms of this virus is curling of leaves downward or upward, enation formation (a cup-like structure forms at the base of infected leaf), and inflamed veins of leaves (Fig. 3). There is two types of veins thickening on the plants of cotton; i) Minor thickening of veins ii) Major thickening of veins. Initially, the thickening is at the margins of leaves but with the increase in the intensity of the disease, it spreads inward and forms a thickened network of veins (Hina et al., 2012).

Tissues with deposited chloroplast get proliferated thus genotypes affected with CLCuV looks duskier than normal types. There are adverse effects of CLCuV on the cotton plants' growth and development. It causes a decrease in Boll weight (33.8 percent), number of bolls (72.5 percent) per plant, plant height (40.6 percent)and ginning outturn (3.9 percent) of Cotton (Mahmood et al., 2003).

Transmission and Vector

The whitefly, Bemisia tabaci causes great damage in many regions having agricultural importance, not only by its efficient transmission of many Gemini viruses, but also by direct feeding as a pest. It is main reason of several epidemics in the world (Gilbertson et al., 2015). It's possible that different whitefly species can transmit different begomoviruses at varying degrees of effectiveness, also some whitefly species can only transmit specific viruses (Polston et al., 2014). The curl leaf disease that affects cotton is been linked to eleven different viruses. All Asia II 7, MEAM1 and MED of *B. tabaci* can get CLCuMuV and CLCuMuB, but only Asia II 7 has the ability to transmit CLCuMuV and CLCuMuB (Pan et al., 2018).

B. tabaci is a genetically diverse specie that not only spreads viruses but also directly stunts the growth of cotton plants (Inbar and Gerling, 2008). Several hundred plant species can become infested by the polyphagous whitefly (Williams, 2012). It is a vector of almost 200 plant viruses, the whitefly also stops the development of the infected plant by drawing their sap of phloem (Stewart et al., 2013). 24 biotypes of *B. tabaci* complex are recognized by defining their biological and molecular characteristics.(De Barro et al., 2011).

How CLCuV Spread

It is a complex molecule consists of a monopartite begomovirus DNA A, alpha-satellite and beta-satellite, and is causing the disease. 2.8kb is the genomic size of the begomovirus. It consists of many genes that encodes for coat protein, replication-associated protein (Rep), transcriptional activator protein (TrAP), replication enhancer protein (REn), proteins for pathogenicity determination, proteins for virus movement (AV2) and viral genome replication (AC5), a suppressor gene (AC4) for RNA silencing (Amrao et al., 2010).

There exists symbiotic relationship between these molecules. They form a complex by the interacting their proteins. Alpha-satellites have single-stranded DNA molecules that do not display any important sequence uniqueness with the genome of helper virus but they do have the ability to replicate themselves (Saunders et al., 2000). On the other hand, Beta-satellites are also single stranded molecules of DNA of the size 1.4 kb. They require a monopartite begomovirus for its encapsidation and replication. These molecules structures are highly conserve, and

contain, satellite conserved region (SCR), βC1 (single coding gene) and Adenine-rich region. The βC1 gene control the symptoms of the disease (Iqbal et al., 2016). There are abilities in these molecules to interact with the helper viruses and causes infection in a many species of plants along with cotton (Xie, 2010).

Detection of CLCuV

PCR with degenerate or specific primer is used for the amplification of this virus. Another method named as "Rolling circle amplification" is also used to amplify helper virus and its recombinants (Haible et al., 2006). But assays for manageable identification have not yet been developed. As genome sequencing technologies progress, it will be feasible to create assays that will be useable in the field for identification and detection of the entire complex, including the vector and virus complex, and to track the blowout of abundant crop species (Saleem et al., 2016).

Disease Management

CLCuD is a danger to cotton crop in all countries where whitefly is a minor or major pest. Many short and long-term strategies are used to reduce the impact and to manage this disease.

Short-term Strategies

Following the disease's widespread development in Pakistan, several temporary measures to lower the disease's vector population in the area were devised. The initial steps taken to control this disease included, for instance, treating seeds to prevent the early establishment of whitefly populations, controlling whiteflies with pesticides on cotton crops, eliminating weeds (an alternative host for viruses), improving plant health by giving the plants the right amount of fertilizer, using biological agents, etc (Cook et al., 2011; Basit et al., 2013; Huseth et al., 2016; Follett, 2017).

Restricting the amount of the whitefly population on cotton crops in Pakistan is advised from the time of emergence until 70–90 days after sowing. Farmers always treat seed with insecticides in this regard because they offer protection against whitefly infestation for up to 45days, or up to 75 days, depending on reports (Singh et al., 2002).

There is no seed-borne transmission of CLCuD. It can also live on other plants like ageratum, hibiscus, tomato, and okra. Many herbaceous and woody species, such as okra, hibiscus, tobacco, cotton, sunflower, hemp and numerous weed plants, have been seen to exhibit symptoms resembling leaf curl in the field (Nour and Nour, 1964). Eliminating weeds from cotton crops generally decreases the likelihood that other hosts will be available, which minimizes the potential sources of inoculum (Knight et al., 2017).

The right amount of fertilizer can also be applied to reduce CLCuD damage. For instance, potassium supplementation may increase disease resistance because of its function in osmoregulation, molecular compound production, and energy gradient maintenance. By influencing metabolic activity, it also impacts the host-parasite compatibility connection and may aid in the regulation of CLCuD(Kafkafi et al., 2001).

Long Term Strategies

Resistance against CLCuD

Effective long-term management of the illness has been proposed to be achieved through breeding resistant types of cotton with adequate diversity in genetic (Rahman et al., 2012). It was previously believed that resistance against the viruses causing CLCuD was unstable due to the influence of numerous environmental conditions on the incidence and severity of the illness, such as light, temperature, plant age, relative humidity, etc (Rahman et al., 2005). In 2007, two genes causing resistance against the disease and viral causal agents was reported (Ahuja et al., 2007).

Using recombination breeding approaches a number of disease and virus-resistant varieties of cotton were established. By screening more than 1000 cotton accessions/ genotypes present in the gene pool of CCRI Multan under natural conditions in hot spots, resistant sources were identified. Three resistant-cotton genotypes ('Cedix', 'CP-15/2,' and 'LRA-5166,') were found (Rahman and Zafar, 2007; Arshad et al., 2009). This resistance was overcome within 5 years by the evolution of the Burewala strain. However, tolerant cotton genotypes have been identified which can control the disease, such as 'NN-3' and 'FH-142,' (Rahman et al., 2012), 'NIBGE-115'(Rahman and Zafar, 2007),

Pathogen Derived Resistance

The most effective method of managing the diseases has been thought to be the overview of a portion of the genome of a virus (whole gene or portion of it) that is typically preserved across multiple genomes of the same species (Goldbach et al., 2003). For example, the antisense RNA molecule silences the complementary target mRNA and prevents the target mRNA from being expressed. An investigation was carried out to target the virus's rep gene in transgenic cotton, which inhibited the invasion virus's ability to replicate (Amudha et al., 2011).

Interaction between the proteins of host and the viruses results in the suppression of the host protein gene or otherwise. It was verified that a pathogenicity determinant, satellite β DNA's βC1 protein gene (associated with CLCuMuV) work together with S1UBC3, Ubiquitin-conjugating (E2) enzyme of host (Eini et al., 2009).

CRISPR-Cas

The protein system that is associated with CRISPR, editing tool for genome, gives bacteria resistance to viruses, bacteria, and movable genetic elements. The CRISPR-Cas technology has drawn attention from researchers, primarily biologists, in a variety of domains

because it offers a higher specificity level, (Iqbal et al., 2016). In this method, CRISPR spacers cut the nucleic acid (DNA or RNA) of a archaea or virus (Kamal et al., 2024c). These sliced molecules are about 20 nt long. The genomes of 90% of archaea and 40% of bacteria contain them. CRISPR-Cas has the ability to subdue a number of complex creatures by the insertion of Cas9 protein and guide RNAs within plant cells (Rojas et al., 2018).

Modern gene editing methods like CRISPR/Cas have devised new chances of using plants to express biomolecules like AMPS (Antimicrobial peptides). They have a high potential to be used in obtaining molecules more rapidly and competently. Ther is a believe that within few years, the transgenic field for AMP formation will undergo a revolution credit to the editing tools of genes such as CRISPR/Cas (Santos et al., 2023).

Conclusion:

CLCuV is a threat to fiber producing countries, especially from cotton. This virus causes the loss of production, decreases the number and weight of bolls, and reduces the overall size of plants. It belongs to family of begomoviruses and causes infection in association with satellites. Beta-satellites consist of βC1 protein which play an important role in the infecting the host plant. It interacts with the host defense mechanism and hijack its machinery but the interaction between βC1 and vector White fly (*B. tabaci*) proteins is not completely understood. The infected plant shows the symptoms of CLCuV like leaves' upward or downward curling, enation (formation at extreme level of infection) and thickening of veins. Countless measurements can be taken to minimize the effect of virus on cotton plant, removal of alternate hosts, early sowing, use of proper fertilizers for healthy plant growth, pesticides for the eradication of pests' population (white fly). Some genetic and biotechnological approaches are also been devised to control and develop resistance against the virus, 'NN-3' ,'NIBGE-115' and 'FH-142' and are cotton varieties that contain resistance against CLCuD. Further, resistance can be developed by producing transgenic varieties by pathogen derived resistance or gene editing by CRISPR-Cas technologies. In future, we will be able to produce new plant varieties with better resistance against disease and better yield.

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