











REVIEW ARTICLE

Strategies for the control of Cotton leaf curl virus (CLCuV): Unveiling molecular mechanisms, overcoming challenges, and pursuing sustainable solutions

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Abstract

Cotton leaf curl virus (CLCuV) represents a critical threat to cotton cultivation, significantly impacting the agricultural sector through its influence on host-pathogen dynamics. This review delves into the nature of CLCuV, outlining the molecular mechanisms underlying the virus-host interactions and its broader implications on crop yield and quality. Recent advancements in sustainable disease management are explored, highlighting the integration of genetic engineering techniques such as CRISPR-Cas9 and advancements in remote sensing technologies, which offer promising pathways for developing disease-resistant cotton varieties. The manuscript provides a comprehensive analysis of current strategies and innovations in combating CLCuV, including the role of genetically modified cotton and integrated pest management in enhancing crop resilience. Furthermore, it discusses the potential of molecular biology and genetic engineering to usher in a new era of sustainable agriculture. Looking ahead, this work underscores the importance of continued research and collaboration in developing eco-friendly and efficient disease management strategies. Ultimately, this review contributes to the existing body of knowledge by offering new insights into the molecular basis of CLCuV resistance, paving the way for innovative approaches to safeguard global cotton production.

KEYWORDS: Cotton leaf curl virus (CLCuV), sustainable agriculture, integrated pest management, genetically modified cotton, CRISPR-Cas technology, disease resistance breeding

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1. INTRODUCTION

The majority of the world's clothing, fuel, food, and animal feed is made from cotton which is why its cultivation is so common. Regarding oilseed and fiber crops, it is at the top of the world rankings. Worldwide, more than 60 countries produce cotton, the most common species being *Gossypium hirsutum*. However, several bad illnesses can affect cotton crops. These include bacterial blight, angular leaf spot, fusarium wilt, and cotton leaf curl virus (CLCuV). The CLCuV virus is continually transmitted by the whitefly (*Bemisia tabaci*) (Atiq *et al.*, 2023).

A major contributor to Pakistan's GDP comes from its cotton exports; the country ranks fourth in the world for cotton production. Producing a large amount of cotton goods, Pakistan accounts for about 0.6% of GDP and adds 2.4% to the total value added in the agricultural sector. However, biotic factors, such as insect pests and diseases, reduced the anticipated spread of cotton farming by 6.8% in 2021-22 (M Afzal, Saeed, Riaz, Ishtiaq, & Rahman, 2023).

Crop loss in Pakistan is caused by the cotton crop and other susceptible alternative hosts infected with the cotton leaf curl disease (CLCuD) (J. Farooq *et al.*, 2014). The illness first appeared in 1967 (Akhtar, Hussain, Khan, Haq, & Iqbal, 2004), but nobody paid any attention to it. All cultivars of cotton, resistant to the CLCuV Burewala strain before 2001 became susceptible to CLCuD when its resistance was broken (A. Farooq *et al.*, 2011). A yearly loss of \$10 million resulted from it (Muhammad Afzal, Saeed, Riaz, Ishtiaq, & Habib ur Rahman, 2023).

To come up with efficient methods for managing cotton leaf curl disease, it is crucial to identify the cryptic species of whiteflies and the plants that serve as hosts for begomoviruses. Worldwide, 40 diseases in vegetable and fiber crops have been caused by *B. tabaci*, a vector for many begomoviruses (Thesnim, Jangra, Kumar, & Ghosh, 2023).

China, India, the United States, Brazil, and Pakistan are among the 80+ nations that grow cotton. Yet, owing to changes in the weather, increased pressure from insect pests, and new diseases, cotton production has remained flat. The geminivirus, which is carried by whiteflies, causes CLCuD, which is a serious problem for the yield of cotton crops in Northern India and Pakistan. Damage to fiber quality and yield losses of up to 90% are possible outcomes of CLCuD. The growth and harvest of early cotton are stunted because the crop is more vulnerable to viral attacks. Annual yield loss in Pakistan due to CLCuV is around 30%; the extent to which this happens depends on factors such as the time of infection, the cultivar, the kind of infection, the population of whiteflies, and the weather (Hassan, Hussain, Mushtaq, Ali, & Chaudary, 2023). Maximum losses in seed cotton and fiber length are observed in the disease's negative effects on yield and fiber quality. The arthropod community is directly impacted by insect pests, which are responsible for the fall in productivity. Certain lepidopterous species can be efficiently controlled by transgenic cotton cultivars that contain poisonous proteins; however, these kinds are unable to manage sucking insect pests. Sucking insect pest populations may rise due to the decrease in insecticide use in *Bt* cotton, elevating their status as a major component of the insect pest complex (Chauhan *et al.*, 2023). The widespread use of conventional pesticides to eliminate sucking pests has major consequences, including the development of pest resistance, the return of previously eradicated pests, the introduction of secondary pests, pollution, health risks, and ecological degradation (Zharkov, Nizamutdinov, Dubovikoff, Abakumov, & Pospelova, 2023).

Insect pests such as cotton thrips, cotton leafhoppers, and tobacco whiteflies have kept Pakistan's cotton production flat for the past 20 years. The most infamous pest is the whitefly, which feeds on cell sap, cuts boll output in half and produces honeydews that sooty mold loves. In 1993, CLCuV caused a 38.7 percent average reduction in Pakistani yields (Hussain, Ali, & Khan, 2014).

Another polyphagous that reduces cotton output by 4.45 per cent is jassid, which feeds on cell sap and injects harmful substances into leaves. Thrips inflict extensive harm and inhibit the growth of cotton seedlings. To influence food security and keep the world's cotton supply stable, CLCuV control is crucial. To effectively control and prevent CLCuV outbreaks, there must be collaboration among researchers, agricultural extension services, lawmakers, and farmers. Sustainable agricultural techniques, including integrated pest management, crop rotation, and the adoption of resistant crop types, are promoted by measures to control CLCuV (Shahbaz *et al.*, 2023).

China, India, the United States, Brazil, and Pakistan are among the 80+ nations that farm cotton as a crop (Vaddula & Singh, 2023). Climate change, insect pests, and illnesses like CLCuD are affecting cotton productivity, though. Significant production losses and a decline in fiber quality can be caused by CLCuD, a geminivirus that is carried by whiteflies. The early phases of cotton growth are the most vulnerable to the illness (Reddy *et al.*, 2023).

Annually, CLCuD reduces Pakistan's harvest by over 30 percent. There is a wide range of disease susceptibility across cotton cultivars; some are more tolerant than others. Cotton fiber quality is impacted by CLCuD as well, with a decrease in micronaire value, strength, and length. The disease has caused Pakistan's cotton harvest to fall short of expectations (Aqueel *et al.*, 2023).

Cotton crops are susceptible to several insect pests, including CLCuD, thrips, jassids, and whiteflies. Genetically modified cotton (*Bt* cotton) has reduced bollworm populations but increased populations of sucking insect pests. Chemical control methods are relied upon by Pakistani farmers, yet this practice has resulted in health risks, environmental damage, and the evolution of insect resistance (M. F. Khan, Umar, Alrefaei, & Rao, 2023).

Farmers, academics, extension agents, and legislators must work together to CLCuD and other cotton diseases. Additionally, it promotes environmentally friendly farming methods

including resistant crop types, crop rotation, and integrated pest management. The field of agricultural science and technology benefits from these endeavors (Sain, Brown, & Monga, 2023).

There are limits to the current techniques of cotton disease control, which include agronomic measures, chemical control, and resistant cultivars. The overuse of chemicals poses risks to human and environmental health and may cause bacteria to develop resistance. There is a risk that the creation of disease-resistant cultivars will fall behind the rate at which new pathogen strains evolve due to the lengthy procedure involved (Mohamed, 2023). The global cotton industry is in dire need of long-term, eco-friendly solutions to the problems of cotton disease control and crop stability and production.

The introduction of GM cotton varieties and integrated pest management techniques have played a significant role in reducing the impact of the CLCuV. Whiteflies are carriers of CLCuV and have been the target of control efforts that have included the use of insecticides, biological control agents, and cultural practices (Divya, Zhai, Makesh Kumar, Moriones, & Pappu, 2023). A greater emphasis on crop rotation and variety has been advocated as a means to disrupt the viral life cycle. Education and awareness campaigns are examples of community-based initiatives that have been implemented to provide farmers with the information they need to control CLCuV. Recent advances in molecular biology have revealed promising new possibilities for the possible creation of cotton cultivars that are resistant to CLCuV. Thanks to advancements in remote sensing technology, CLCuV epidemics may now be monitored and diagnosed early on, allowing for targeted interventions and timely reactions. To manage and halt the development of CLCuV, many strategies have been implemented by regulatory bodies and governments. Some examples of these measures include quarantine protocols and limitations on the use of pesticides and genetically modified crops. Governments, agricultural groups, and scientific institutions must work together to spread knowledge about CLCuV and create appropriate management measures because the

virus is spreading globally (Jain, Chahal, Singh, Sain, & Siwach, 2023).

The primary aim of this manuscript is to thoroughly investigate and elucidate the molecular mechanisms underpinning Cotton Leaf Curl Virus (CLCuV) infection and its impact on cotton crops. By exploring the complex interactions between the virus and its host, this study seeks to identify sustainable management strategies that can mitigate the economic and agronomic devastations caused by CLCuV. In doing so, we aim to bridge current knowledge gaps through innovative research, ultimately contributing to the development of more resilient cotton varieties and improved disease management practices. This work aspires to offer significant insights into the sustainable cultivation of cotton, thereby enhancing global cotton production and protecting the livelihoods of farmers worldwide.

2. Understanding CLCuV for Targeted Control

2.1 Classification and Genome Organization of CLCuV

The Geminiviridae family is the most extensive family of plant viruses, comprising more than 300 officially recognized species (Fuji *et al.*, 2022). The group is composed of nine different genera, namely Becurtovirus, Begomovirus, Capulavirus, Curtovirus, Eragrovirus, Grablovirus, Mastrevirus, Topocovirus, and Turncurtovirus. The International Committee on Taxonomy of Viruses (ICTV) has put up a distinctive set of criteria for categorizing and designating novel geminiviruses. According to the new rule, if the full-length nucleotide sequence identity of a newly identified geminivirus is less than 89% using the cluster V method, it will be classified as a new species. Conversely, if the sequence identity is greater than 89%, it will be classified as a member of the same species (Sain *et al.*, 2023).

Begomoviruses are transmitted by *B. tabaci*, which has a genomic size ranging from 2.7 to 3.0 kilobases. The DNA-A of bipartite begomoviruses consists of six fragmented open reading frames

(ORFs) that encode a range of proteins, including AC1/Rep, AC2/TrAP, AC3/REn, AV2, AV1/CP, and AC4 proteins. DNA-B has two open reading frames (ORFs) that encode nuclear shuttle proteins (NSPs) and movement proteins (MPs) on the sense strand and complementary strands, respectively (Arif *et al.*, 2022).

The genome of bipartite begomoviruses comprises two components, DNA A and B. DNA A is responsible for encoding various essential proteins including replication, coat protein, transcriptional activator protein, replication boosting protein, and a protein involved in viral movement as shown in Fig 1. DNA-B contains the genetic information for the production of both the movement protein and the nuclear shutter protein. Monopartite begomoviruses possess a solitary genomic component consisting of DNA-A (Yaqoob *et al.*, 2020).

2.2 Host-pathogen Interactions for Targeted Approaches

Whiteflies serve as the main carrier for begomoviruses, leading to significant economic damage through direct feeding and transmission to various crops. Monopartite and bipartite viruses both possess a shared area that functions as the replication origin and facilitates bidirectional transcription (V Pandey *et al.*, 2023).

RNA silencing is an essential defense mechanism in plants and other eukaryotes. It plays a vital role in controlling gene expression and safeguarding against intrusive nucleic acids, such as viruses (P. Kumar, 2023; Niu *et al.*, 2021). Plant viruses, like the CLCuV, have developed strategies to inhibit RNA silencing as a means to overcome the host's immune response against viral infections (N. Gupta, Reddy, Bhattacharyya, & Chakraborty, 2021). The utilization of RNA interference technology has facilitated the specific suppression of genes in pathogens, offering a new and innovative strategy for enhancing resistance against diseases. The proteins derived from DNA-A and DNA-B are linked to several processes such as viral DNA replication, vector transmission, encapsidation, as well as the movement of viral particles between

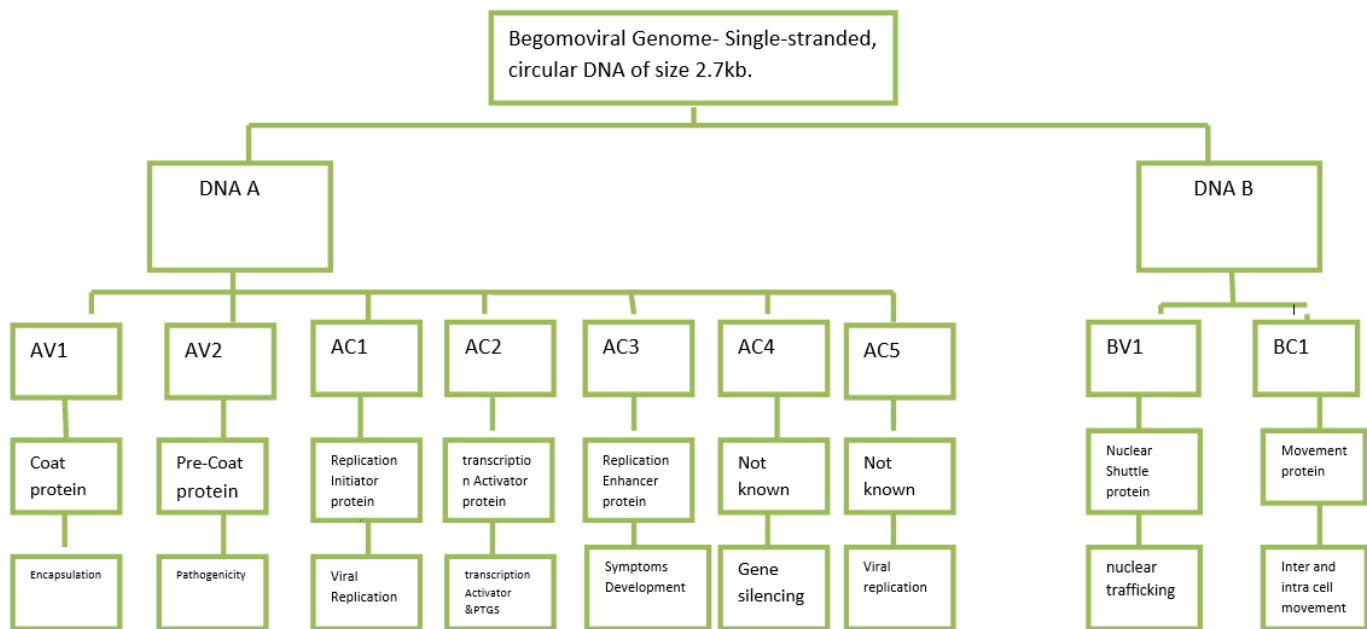


Figure 1. Begomovirus genomic organization displaying different ORFs (genes): satellites and DNA segments linked with different ORF-encoded proteins.

cells and inside cells (Lacomme, Pogue, Wilson, & Santa Cruz, 2023).

Begomoviruses are classified into two categories: New World (NW) and Old World (OW) begomoviruses (Vineeta Pandey, Srivastava, & Gaur, 2021). Betasatellites referred to as DNA b, possess a solitary open reading frame (ORF) called bC1, which inhibits the suppression of host gene silencing and amplifies the pathogenicity of the associated begomovirus (Shafiq *et al.*, 2020). Alphasatellites, sometimes referred to as DNA 1, are self-replicating nano virus-like satellites that are frequently associated with begomoviruses and their betasatellite complexes. Three types of alpha satellites have been discovered. Type one enhances symptoms when there is a co-infection, while types two and three are linked to bipartite begomoviruses in the New World (Nogueira *et al.*, 2021).

The genome of the begomovirus contains viral suppressors of RNA silencing (VSRs), such as V2 and C4. The source of V2 is cotton leaf curl (Siviya, 2022). The Multan virus efficiently combats TGS by interacting with Argonaute 4 and suppressing RNA-dependent DNA Methylation. The C4 protein derived from TYLCV V2 hinders the action of the

SAM synthetase enzyme and interacts with AGO4, resulting in a decrease in methylation of the viral

DNA. C4 disrupts the transmission of RNA silencing signals, host defense mediated by kinases, and hormone signaling. The protein-protein interaction network of bipartite begomoviruses, known as NSP-MP-host, has two prominent hubs that are highly enriched with proteins associated with auxin response and regulators of auxin signaling. These hubs are believed to specifically target the auxin signaling pathway (Gouveia-Mageste *et al.*, 2020).

2.3 Vector-Mediated Transmission and Control Implications

Begomoviruses can multiply and build up in whitefly salivary glands, which causes behavioural changes and higher transmission rates. The virus is transmitted more easily by infected whiteflies because they feed and probe plants more frequently (Czosnek, Gorovits, & Ghanim, 2021; Sarwar, 2020). Longer feeding durations are associated with begomovirus infection in whiteflies, which in turn increases the rates of virus acquisition and transmission. Virus infection, population density,

and the presence of infected plants can all impact whitefly behaviour. Disease management and control could benefit from a better understanding of the variables that regulate these altered behaviours and the impacts of various plant characteristics. The predominant vector for viral transmission and a pest to many plant and agricultural species is the whitefly species *B. tabaci*. The intricacy of *B. tabaci* and its host-parasite connection has been shown by genetic investigations. It is known that whiteflies acquire the virus and then transmit it to healthy plants through their salivary glands; however, the specific mechanism by which *B. tabaci* transmits the virus is still unclear (Cicero & Brown, 2011; Giorgini, Formisano, García-García, Bernat-Ponce, & Beitia, 2023; Wei *et al.*, 2014). The virus and *B. tabaci* interact on a molecular and cellular level, which could cause the whitefly to activate its innate immune system and genes that respond to stress. The transmission of begomoviruses by *B. tabaci* involves certain proteins that are connected to endosymbionts (I. Singh, Kaur, Kumar, Singh, & Sharma, 2021).

The implementation of various strategic measures holds paramount importance in the management of the CLCuV. These measures encompass exerting control over the whitefly vector, cultivating cotton varieties that exhibit resistance against the virus, practicing crop rotation, embracing integrated pest management techniques, conducting regular monitoring activities, and enforcing stringent quarantine measures. These strategies are designed to diminish whitefly populations, curtail the transmission of viruses, impede the life cycle of whiteflies, and prevent the dissemination of CLCuV to previously unaffected regions (D. P. Singh, 2023).

3. Genetic Approaches in Controlling CLCuV

3.1 Development of Resistant Cotton Varieties

Understanding the genetic factors responsible for resistance to CLCuD is essential for the development of breeding techniques aimed at producing cotton genotypes that are resistant to the virus. The resistance to CLCuD is governed by a dominant gene, along with the involvement of many

modifier genes. Reciprocal crosses demonstrate that only nuclear heredity is associated with the transmission of resistance, while other factors, such as cytoplasmic genes, do not contribute to this inheritance (Ahuja, Monga, & Dhayal, 2007).

Studies have demonstrated that the utilization of both genetically modified and naturally occurring sources of resistance can enhance disease resistance, Ginning Outturn (GOT), and fiber quality. Two quantitative trait loci (QTLs) have been identified as being associated with resistance to CLCuD through the screening of 2400 Simple Sequence Repeat markers (SSRs) on a plant population that was created by crossing parents with different levels of resistance (Sattar *et al.*, 2023). QTLs have been identified as being associated with resistance to CLCuD in various genotypes over two consecutive years. (Pathak & Rathore, 2023).

Gossypium hirsutum does not possess resistance to CLCuV and exhibits limited genetic variety. Conversely, wild diploid species of *Gossypium* can exhibit tolerance to different stressors, including CLCuV. (Sodha, Verma, Chhokar, & Paul, 2022). Interspecific hybridization encounters obstacles such as insufficient boll formation, ovule malfunction, and embryo termination. The use of exogenous hormones has been proven to be useful in preventing premature boll shedding. It has been observed that screening of CLCuV -resistant lines imported from the US can transfer the resistant genes to other commonly produced cotton varieties (Sodha *et al.*, 2022).

3.2 Genetic Engineering for Enhanced Resistance

Traditional plant breeding techniques have been used to develop virus-resistant cotton varieties, but these methods have limited genetic diversity and have been constrained by the Burewala strain (Aslam, Khan, Ahmed, & Dandekar, 2020). Genetic engineering techniques have emerged as a vital tool for long-term resistance against CLCuD. Genetically modified transgenic cotton plants have been developed using *Agrobacterium* and particle bombardment methods, followed by plant

regeneration through somatic embryogenesis or organogenesis. The viral CP gene has been the most often used gene to confer PDR against plant viruses. Various viral genes have been exploited, including coat protein, mobility protein, replicase gene, antisense RNA, satellite RNA, and faulty interfering genes. Artificial microRNA technology has been used to create transgenic tobacco resistant to CLCuBV. Regeneration and genetic modification with a focus on insect resistance, herbicide tolerance, and fiber quality have been documented in earlier reviews of cotton biotechnology. Agrobacterium-mediated transformation is one of the most established methods for developing transgenic cotton, utilizing the natural ability of the bacterium to transfer its DNA into plant cells (Krishnamurthy, Krishnaraju, & Ningaraju, 2023).

The field of biotechnology has made significant progress in the development of genome editing tools such as CRISPR/Cas9. These techniques enable accurate and focused adjustments to be made to the genetic material of plants (El-Mounadi, Morales-Floriano, & Garcia-Ruiz, 2020; Vats *et al.*, 2019). These techniques can improve disease resistance by deactivating genes that make an organism susceptible to diseases or by introducing advantageous mutations. Transcription activator-like effector nucleases (TALENs) are an alternative potent instrument, akin to CRISPR/Cas9, however employing a distinct molecular mechanism. RNA interference (RNAi) is a groundbreaking technology employed in plant biotechnology to suppress particular genes, preventing their conversion into protein. These strategies are at the forefront of plant biotechnology and hold great potential for effectively managing diseases in cotton in a sustainable manner (M. A. Abdullah *et al.*, 2023).

3.3 Challenges and Opportunities in Genetic Strategies

Systemic acquired resistance (SAR) is a technique used to manage several infections. However, there has been limited research on managing Geminiviruses, specifically against CLCuV (N. Gupta *et al.*, 2021). The systemic acquired

resistance (SAR) mechanism in cotton plants against CLCuV by administering various SAR-inducing chemicals. Systemic Acquired Resistance (SAR) is a cascade of metabolic events that plays a pivotal part in the plant's immune response to pathogens. Plants react to the flow of salicylic acid-dependent signaling, leading to the widespread and enduring expression of disease resistance (Jan *et al.*, 2021). This defense system generates pathogenesis-related proteins and phytoalexins to combat various pathogen infections. Benzothiadiazole (BTH) can stimulate the systemic acquired resistance (SAR) pathway, which occurs after the signaling of salicylic acid (SA). This stimulation leads to the production of pathogenesis-related proteins, phenolic compounds, and antioxidants that can inhibit the multiplication of viruses. BTH has proven to be efficacious in eliciting resistance against many pathogens in crops, including geminivirus. The objective of the study was to augment the resistance of tolerant and susceptible types by administering elicitors at various concentrations and combinations in a controlled environment (M. F. Khan *et al.*, 2023).

The CRISPR/Cas system, which utilizes RNA-guided endonucleases (RGENs), has been identified as an adaptive immune system in bacteria and archaea. Compared to ZFNs and TALENs, this method is the most straightforward and effortless to create and replicate (Khalil, 2020). The CRISPR/Cas9 system functions as the RNA-based adaptive immune system in bacteria and archaea. The indigenous CRISPR system confers viral resistance by incorporating multiple copies of viral DNA into the bacterial genome. The CRISPR/Cas9 system can be replicated in mammalian cells by employing three fundamental elements: Cas9, a CRISPR RNA (crRNA) that determines specificity, and an auxiliary trans-activating RNA (tracrRNA) (D. Gupta *et al.*, 2019). The fusion of the crRNA and tracrRNA duplexes can result in the creation of a chimeric sgRNA. The broad utilization of CRISPR/Cas9 is attributed to its cost efficiency and simplicity in the process of designing and cloning. It can inhibit polygenic characteristics in plants,

such as the synthesis of gossypol in cotton. Investigating gene function and modifying the regulatory network linked to genes is a potent strategy that will be enhanced by the utilization of developing site-specific genome editing tools (Siva, Shanmugapriya, & Santhoshinii, 2023).

The CRISPR/Cas9 system is engineered to selectively identify and bind to particular regions within the host genome. The non-target sequences are identified based on the length of the sgRNA, which ranges from 20 to 23 nucleotides (Akram *et al.*, 2023). The target DNA sequence is antiparallel to the initial 20 nucleotides of the sgRNA, succeeded by a sequence referred to as the PAM, which typically consists of the nucleotides "NGG". Nevertheless, there is a possibility of unintended cutting of DNA sequences that have three to five base pair differences in the region of the sgRNA-guiding sequence that is away from the PAM site. There are multiple CRISPR/Cas variations and kinds that have varied PAM requirements, which can improve the accuracy of targeting. Different configurations of guide RNA can impact the cutting of desired and undesired sites (Manghwar *et al.*, 2020). To minimize unintended effects, several approaches have been suggested, including reducing the amount and duration of active Cas9 protein within cells or altering the half-life of Cas9. To address the issue of off-target effects in genome editing, it is necessary to conduct in-silico studies and develop gene editing tools. Advanced artificial intelligence techniques, such as deep learning and machine learning, can be utilized to assess the susceptibility of the genome to off-target effects (R. Khan, Ghayas, Khalid, & Amjad, 2023).

Abiotic stressors, such as elevated temperature, water scarcity, and excessive salinity, are unfavourable environmental factors that disturb an organism's internal balance, impacting its overall health and development. The occurrence of these pressures is affected by several genes, transcription factors, and metabolic pathways, which ultimately result in the adaptation to abiotic stress. Gaining insight into the molecular foundation and mechanisms of tolerance towards non-living

environmental stimuli is essential for the advancement of genetically modified plants (Nawaz *et al.*, 2023).

Various transcription factors can be employed to augment cotton's resistance to drought-induced stress. The upregulation of these genes has been observed to play a role in enhancing drought and salinity resistance in both Arabidopsis and cotton. RNA interference (RNAi) has been documented as an effective method for suppressing the activity of cotton *PHYA1* genes, resulting in enhanced tolerance to drought, heat, and salt stress (Z. Khan *et al.*, 2023).

Gene editing techniques can be employed to selectively modify numerous members of gene families at the level of gene expression. To investigate the effects of drought stress on cotton plants, researchers created SIMAOK3 mutants using CRISPR/Cas9 technology. The introduction of mutations in the *OsDST* gene of rice using CRISPR-Cas9 resulted in enhanced salt and drought tolerance. This was achieved by widening the leaves and decreasing the density of stomata (Manimurugan, Zanwar, & Sujatha, 2023).

The resistance to abiotic stress is governed by numerous genes and regulatory networks, encompassing signal transduction and the modulation of metabolite production in both positive and negative directions. CRISPR-Cas9 technologies can be used to specifically target these genes, aiming to enhance stress tolerance and improve crops in the face of rapidly changing climate conditions. Advanced techniques involve the use of HDR-mediated gene targeting to simultaneously combine and integrate several genes (Wimberger, 2023).

Molecular breeding techniques provide several benefits to the breeding community, especially in the domain of cotton. The benefits encompass precision, acceleration, increased genetic variety, greater trait enhancement, resilience to diseases and pests, tolerance to stress, improved quality of fibers, and the promotion of sustainable agriculture. Molecular breeding techniques provide precise

genetic alterations, enabling breeders to selectively target specific genes linked to desired traits. Additionally, they enable the investigation and use of genetic variation in cotton, enabling breeders to obtain and incorporate advantageous characteristics from other germplasm sources (Alagarsamy, 2023).

These methods also facilitate the creation of cotton cultivars with inherent resistance to pests and diseases, hence decreasing dependence on chemical pesticides. Additionally, they facilitate the advancement of cotton cultivars with enhanced resilience to abiotic pressures, hence guaranteeing superior agricultural output and consistency. Molecular breeding approaches additionally enhance fiber quality, allowing breeders to discern and choose plants with exceptional fiber characteristics (Manimurugan *et al.*, 2023).

Nevertheless, cotton molecular breeding methods have certain constraints. Obstacles like as regulatory hurdles, unintended impacts on non-target organisms, the intricate nature of genetics, scarcity of genetic resources, and the demanding technology and resource needs can impede their extensive implementation. The regulatory frameworks differ among countries and regions, and the process of obtaining regulatory permission for genetically modified crops can be intricate and time-consuming. Furthermore, the effectiveness of molecular breeding is dependent on the presence and thorough understanding of a wide range of germplasm resources, which may not be easily obtained or accessible to all breeding programs (Brown & Khan, 2022).

4. Vector Control Measures

4.1 Understanding and Targeting Whitefly Vectors

Begomoviruses can elicit cellular and molecular reactions in their insect vectors, which can impact their ability to transmit the virus. *B. tabaci* is the most geographically widespread among whiteflies, with more than 44 physically similar species (Ishfaq, Shafiq, Ali, & Haider, 2023). These insects inflict direct damage by eating on plants and also

transmit plant pathogenic viruses. More than 90% of the transmitted virus types are the most detrimental. The efficiency of begomovirus transmission is determined by the intricate interactions between the virus, vector, and host plant. Various aspects, including the acquisition of the virus by the vector, the vector's landing and probing behaviour, and its feeding habits, all contribute to the transmission process (Naveed *et al.*, 2023).

Whiteflies spread persistent viruses through a sequential process that involves the intake, attachment, entrance, translocation, circulation, retention, and release of the virus. The viral particles that have been obtained enter the midgut and esophagus and then proceed to enter and move across the cell through the basal membrane. After being acquired, replicated, and dispersed, they enter the hemolymph and eventually settle in the major salivary glands. The viruses are discharged into the plant's phloem by the saliva of the vectors, originating from the salivary glands. Following the introduction of the virus into the plant through saliva, the virus undergoes replication within the plant cells and subsequently disseminates to other plant regions, resulting in symptoms such as leaf yellowing, restricted growth, and reduced crop productivity (Nalla, Schafleitner, Pappu, & Barchenger, 2023).

B. tabaci is a significant agricultural pest and a carrier of plant viruses due to factors such as chemical resistance, reduction in natural predators, and the widespread adoption of monoculture. Confirmation of the molecular divergence among worldwide *B. tabaci* species has been achieved through demographic and molecular investigations (Health, 2013). Whitefly inflicts harm by transmitting several strains of viruses, such as single-stranded DNA viruses belonging to the Begomovirus genus, to various crops, leading to diminished agricultural yield and quality (A. Kumar & Kumar; Morales, 2006). *B. tabaci* is highly harmful due to its capacity to spread numerous plant viruses, such as Crinivirus, Carlavirus, Toradovirus, Ipomovirus, and the largest cluster of Begomovirus viruses (A. Kumar & Kumar, 2022).

B. tabaci, a versatile insect that feeds on a wide range of plants, can be found on all types of cotton. However, the level of infection may vary depending on the insect's feeding habits. The management of whitefly is affected by temperature, relative humidity, and environmental conditions (Ahmed *et al.*, 2020; Aregbesola, Legg, Sigsgaard, Lund, & Rapisarda, 2019). Whiteflies inflict harm by transmitting many types of viruses, such as single-stranded DNA viruses belonging to the Begomovirus genera, to various crops, leading to diminished agricultural yield and quality (Vineeta Pandey *et al.*, 2021).

Whiteflies have been engaging with geminiviruses for thousands of years and consistently spread begomoviruses after a period of incubation lasting from hours to days. The swift dissemination of begomoviruses that infect chilli plants has been linked to the proliferation of the polyphagous whitefly B-biotype, which has a reproductive rate twice as fast as non-B biotypes. Plant viruses can alter their insect vectors, hence affecting their life cycle and behaviour (Naveed *et al.*, 2023).

The global dissemination and expanded host spectrum of begomoviruses are ascribed to the co-evolutionary dynamics between the viral capsid protein and whiteflies. Several studies have documented the transmission of begomoviruses, which are linked to certain crops, to different host species via whitefly vectors. Nevertheless, there appears to be a certain degree of host selectivity exhibited by begomoviruses (Czosnek & Ghanim, 2012; Naveed *et al.*, 2023; Rosen *et al.*, 2015; Seal, VandenBosch, & Jeger, 2006).

Relying solely on symptoms for the diagnosis of CLCuV is not conclusive or dependable, as the presence of numerous species of begomoviruses and other viruses, particularly from the genera Potyvirus and Cucumovirus, can complicate the accuracy of the diagnosis (Hema & Konakalla, 2021). Field-based diagnostics can utilize laboratory tests that employ molecular detection techniques, such as polymerase chain reaction (PCR) and species-

specific primers. Recombinase polymerase amplification (RPA) and loop-mediated isothermal amplification (LAMP) are widely used diagnostic assays that operate at a constant temperature and are suitable for use in field settings (Naveen & Bhat, 2020).

4.2 Biological Control Agents for Whitefly Management

Ladybugs, mini pirate bugs, lacewings, hoverflies, parasitoid wasps, entomopathogenic fungi, nematodes, microbial insecticides, inundative releases, botanical extracts, companion planting, and Integrated Pest Management (IPM) are all viable strategies for whitefly management (Токарева, Мещкова, & Пузрина, 2022). Ladybugs are highly predatory insects that consume nymphs and eggs, whereas Mini Pirate Bugs primarily feed on nymphs, thrips, and mites. Whiteflies are infected and killed by entomopathogenic fungi, such as *Beauveria bassiana* and *Isaria fumosorosea*. *Steinernema feltiae* and *Heterorhabditis bacteriophora*, which are types of nematodes, invade and eliminate whitefly larvae and pupae residing in the soil (Bara & Laing, 2020; Glare, McKinnon, Gwynn, & Brownbridge, 2019). Organic farming utilizes microbial pesticides such as *Bacillus thuringiensis* and Spinosad (Costa, Guiné, Costa, Correia, & Nave, 2023). Whitefly infestation can be mitigated through the implementation of inundative releases of predators and parasitoids, the utilization of botanical extracts such as neem oil and azadirachtin, and the practice of partner planting with trap crops like marigolds (as shown in table 1).

5. Integrated Pest Management (IPM) Strategies

5.1 Holistic Approaches in CLCuV Control

An all-encompassing method of pest control, integrated pest management (IPM) makes use of a variety of techniques. We are becoming better at understanding and controlling agricultural pests and diseases thanks to emerging technologies like bioinformatics, precision agriculture tools, and

Table 1. Biological control agents for whitefly management.

Biological control agents	Target	Mode of action	Reference
<i>Burkholderia</i> sp. (S ₁ HL ₄)	CLCuV	The host's ISR may be triggered by bacteria. Plants that have the potential to develop defense mechanisms in the future offer long-lasting protection against CLCuV.	(dos Santos & Franco, 2023)
<i>Bacillus cereus</i>	Whitefly	<i>Bacillus cereus</i> produces chitinase, which can break down the exoskeleton of whiteflies.	(dos Santos & Franco, 2023)
<i>Beauveria bassiana</i>	Whitefly	Whitefly infections are caused by <i>Beauveria bassiana</i> through direct cuticle penetration.	(dos Santos & Franco, 2023)
<i>Eretmocerus</i> spp	Whitefly	The parasite <i>Eretmocerus eremicus</i> exists. It deposits its eggs beneath the nymphs of whiteflies, where they hatch and start eating the whitefly.	(dos Santos & Franco, 2023)
<i>Encarsia</i> and <i>Eretmocerus</i> parasitoids	Whitefly	These are parasitoids, these insects. After becoming parasites, their larvae destroy their host.	(dos Santos & Franco, 2023)
Ladybugs	Whitefly	Predatory beetles that consume whiteflies, aphids, and other pests at various life stages.	(Mishra, Omkar, Kumar, & Pandey, 2012)
Mini Pirate Bugs	Whitefly	Small predatory bugs that feed on whitefly eggs and nymphs.	(Mollá, Biondi, Alonso-Valiente, & Urbaneja, 2014)
Lacewings	Whitefly	Larvae are voracious predators of whitefly nymphs and eggs.	(Sengonca, Al-Zyoud, & Blaeser, 2005)
Hoverflies	Whitefly	Larvae predate on whitefly populations. Adults are important pollinators.	(Jiang, Li, He, & Wu, 2022)
Parasitoid Wasps	Whitefly	Tiny wasps lay eggs in or on whitefly nymphs. The hatching larvae consume the nymph from the inside.	(Perring, Stansly, Liu, Smith, & Andreason, 2018)
Entomopathogenic Fungi	Whitefly	Fungi that infect and kill whiteflies, such as <i>Beauveria bassiana</i> and <i>Metarhizium anisopliae</i> .	(Gebremariam, Chekol, & Assefa, 2022)

Nematodes	Whitefly	Soil-dwelling microscopic worms that can infect and kill whitefly pupae in the soil.	(Gajjar & Patel)
Microbial Insecticides	Whitefly	Products based on microorganisms (e.g., <i>Bacillus thuringiensis</i>) that are toxic to whiteflies.	(de Maagd, 2015)
Inundative Releases	Whitefly	Releasing large numbers of natural enemies to overwhelm whitefly populations.	(Aregbesola et al., 2019)
Botanical Extracts	Whitefly	Natural plant-derived substances (e.g., neem oil, pyrethrin) that repel or kill whiteflies.	(Dubey, Ravindra Shukla, Ashok Kumar, Priyanka Singh, & Bhanu Prakash, 2011)
Companion Planting	Whitefly	Growing certain plants that repel whiteflies or attract their natural enemies next to crops.	(Inbar & Gerling, 2008)
Integrated Pest Management (IPM)	Whitefly	A holistic approach combining multiple strategies to manage pests sustainably.	(Karlsson Green, Stenberg, & Lankinen, 2020)

genomic approaches. To maximize output from inputs, precision agriculture makes use of cutting-edge technology. By gathering information without physically touching crops, remote sensing technology helps farmers spot disease and pest infestations in their early stages (A. Abdullah & Umer, 2004). Using drones for crop monitoring allows for early detection of symptoms of biotic stress and provides high-resolution images. Pest and disease patterns can be better understood with the use of satellite imagery and Geographic Information Systems (GIS), which in turn helps with treatment application and overall crop management (Kurdekar, Ahirwar, Kumar, MR, & Sreekumar, 2020).

The goal of cultural control is to reduce the availability, attractiveness, and edibility of crops to different pests and diseases. Everything from land management to soil sterilization to irrigation to fertilizer to sanitation to disease-free seed and plants to trap crops to the optimal times to sow and harvest are all part of this system (El-Zik & Frisbie, 2018; N. Kumar et al., 2023). The earliest evidence of

cultural control dates back to 1500 BC, when farmers began using practices like crop rotation, sanitation, and planting dates to control pests and diseases that affected important crops (D. P. Singh, 2023).

The successful eradication of citrus canker in Florida in 1913, crop rotation, and sanitation practices are examples of methods that are utilized in cultural control (M. Abbas et al., 2022). Disease severity is greatly affected by crop nutrients; however, pests such as red rot, wilt, smut, bunt, root-knot, white beetle grubs, moth and fly pupae, and lepidopterous pests can be effectively controlled through crop rotation (M. Abbas et al., 2022; D. P. Singh, 2023). Weed management is essential in lowering the prevalence of mealybugs, cotton leaf CLCuV, and bollworm, and trap crops are utilized to capture pests in particular planted areas where they are easily hit.

In Florida, thrips, aphids, and whiteflies can all be effectively controlled with different colored

mulches. For example, silver mulch works wonders for pepper and tomato thrips (M. Abbas *et al.*, 2022).

To improve harvest yields, chemical control has been more used in the past half-century. The Romans initially recorded using Sulphur as a pesticide around 2000 B.C., then arsenic in 900, and finally DDT in 1873. An overabundance of pesticides can decimate ecosystems that support life on Earth, including those of humans and other animals. These chemicals are the basis for around a third of agricultural products. The economy should only be subjected to pesticides when required, with fungicides and insecticides used selectively to reduce damage (D. P. Singh, 2023).

5.2 Synergies Between Genetic and Environmental Management

Although traditional phenotypic-based methods have been useful in the past for developing new cotton varieties, these methods are becoming increasingly inappropriate as a result of environmental changes and climate change. Genomic-assisted selection shows promise as a solution to these problems. Precise and accurate monitoring and measurement of various traits associated with adaptation, growth and yield are made possible by high throughput phenotyping (HTP) platforms that employ digitalizing systems and next-generation molecular markers such as SNPs and QTLs (Amudha, Balasubramani, Malathi, Monga, & Kranthi, 2011).

Several methods have been devised to document the morpho-physiological, nutritional needs, and pathological parameters of cotton plants. These methods include thermal, spectral, fluorescence, and three-dimensional imaging systems. By utilizing these technologies, complex traits can be quickly phenotyped, and crop health can be improved in a variety of environmental settings. Researchers can analyse a large number of SNP markers with high precision and repeatability using high-throughput genotyping platforms like the Cotton SNP63K array (D'Agostino *et al.*, 2023; Velioglu, 2020).

There are more than 29 significant traits or QTLs linked to cotton DNA markers, demonstrating the genome's complexity. Nevertheless, these methods rely on a gel electrophoresis system, are labor-intensive, and are expensive per data point. Cotton's complicated genome has been deciphered with the help of next-generation sequencing and high-throughput marker-assisted selection. As a result of the accuracy and precision they provide, single nucleotide polymorphism (SNP) markers have found widespread use in breeding programs (A. Abbas & Muqaddasi, 2021; Sabev, Valkova, & Todorovska, 2020; Waghmare, 2022).

Combining genotyping with phenotyping, envirotyping sorts environments into categories to assess how well they reflect target populations in specific settings. The Cotton SNP63K array, which measures genetic diversity within *G. hirsutum* from different world origins with minor allele frequencies out of 38,822 SNPs, is one of the most innovative high-throughput genotyping systems developed in recent years (Ali, Maryam, Saddique, & Ikram, 2023).

5.3 Success Stories in IPM Implementation

Integrated pest management (IPM) is a globally acknowledged approach aimed at mitigating the environmental and public health hazards associated with artificial insecticides. The integrated pest management (IPM) strategy for *B. tabaci* involves employing biocontrol, physical, and mechanical methods, while also utilizing a restricted number of specific pesticides. According to Abubakar *et al.* 2022, the combination of neem oil and *B. bassiana*-mediated biocontrol increased the death rate of *B. tabaci* larvae on aborigine leaves (Abubakar, Koul, Chandrashekar, Raut, & Yadav, 2022). The synergistic effect of various concentrations of neem (1.0%) and *B. bassiana* on *B. tabaci* resulted in a mortality rate of 92.3% for the nymphs. The synergistic effects of combining biologicals and chemicals in integrated pest management (IPM) have a significant potential (73%) for effectively controlling whitefly-transmitted viruses, surpassing the effectiveness of individual methods.

Researchers examined the effectiveness of synthetic pesticides, phytochemicals, and microbes in controlling whitefly populations. They found that spiromesifen resulted in the most significant reduction in whitefly counts, with a reduction of 82.27% (Abubakar *et al.*, 2022).

6. Advanced Diagnostics for Early Detection

6.1. Molecular Diagnostics and Their Role

Early detection of viruses during the initial stages of plant infection and identification of vectors responsible for disease transmission are essential for efficient management and the prevention of crop damage and economic loss. PCR-based diagnostic techniques can be used to detect CLCuV (Chavhan *et al.*, 2023; Gawande *et al.*, 2022). However, their effectiveness is restricted because of the rapid evolution of single-stranded viral genomes. Loop-mediated isothermal amplification (LAMP) is an innovative technique that overcomes these restrictions by providing fast, highly sensitive, specific, simple, and relatively inexpensive amplification at a constant temperature (Chaouch, 2021). The LAMP technique has been employed for the detection of various plant viruses, including tobacco streak virus, cucumber mosaic virus, potato leaf roll virus, Chinese wheat mosaic virus, barley yellow dwarf viruses, Cucurbit chlorotic yellows virus, potato virus Y, and tomato yellow leaf curl virus (Gawande *et al.*, 2022). Researchers have developed and standardized rapid and highly sensitive diagnostic assays, known as Loop Mediated Isothermal Amplification (LAMP) and Rolling Circle amplification actuated LAMP assays, for the detection of CLCuV in Cotton leaves and its transmitting vector whitefly (Gawande *et al.*, 2022; Sharma *et al.*, 2017).

6.2 Remote Sensing Technologies for Surveillance

To develop virus-resistant cotton, it is necessary to identify and screen cotton lines that possess resistance. The utilization of serological and molecular virus detecting techniques (MVDT) is essential in verifying the virus species and strains,

enabling breeders to strategize crosses and breeding schemes (Ashraf, Brown, Iqbal, & Yu, 2023; Binyameen *et al.*, 2021; Hasan *et al.*, 2019). High-throughput sequencing (HTS) enables the identification of all viral species in a plant, including previously unknown ones. Knowledge of the virome is crucial for breeding and molecular breeding programs to comprehend the presence and characteristics of viral-resistant genes required for the integration of elite genetic lines (Kaur *et al.*, 2023). The process of developing a new resistant elite variety can be expedited if there is a known virus that causes symptoms and if there is access to resistant germplasm and molecular markers. Advanced virus detection methods, such as recombinase polymerase amplification (RPA), loop-mediated isothermal amplification (LAMP), and clustered regularly interspaced short palindromic repeats (CRISPR), have the potential to replace expensive qRT-PCR-based diagnostic testing systems. Point-of-care testing (POCT) tools such as CRISPR/Cas9-mediated lateral flow nucleic acid assay (CASLFA) and Editor-Linked Uniform Detection Assay (FELUDA) have the ability to expedite resistance selection and assist in the creation of molecular markers for molecular breeding strategies (Anwar, Kolachi, Baloch, & Soomro, 2022).

6.3 Remote Sensing Technologies for Surveillance

Artificial intelligence can be employed to cultivate virus-resistant strains in cotton, although erroneous input can result in catastrophic outcomes. The MVDT (Multivariate Decision Tree) algorithm can supply accurate input for AI training, whereas Deep Learning (DL) facilitates automated and hierarchical learning mechanisms. The use of molecular and biotechnological techniques can expedite the process of developing resistant cotton varieties by employing various integrated breeding strategies. These strategies include Marker Assisted Selection (MAS), Marker Assisted Introgression (MAI), Multi-parent Advanced Generation Inter-Cross populations (MAGIC), Genome-Wide Association Studies (GWAS), and Genomic

Selection (GS), in conjunction with DDAP and MVDT. Advanced breeding techniques, such as the CRISPR/Cas system, have the ability to create specific genetic changes, providing protection against eukaryotic viruses at a molecular level. Transgenic methods, such as the use of genetically modified (GM) plants that carry CLCuV genes, can confer resistance to CLCuD. Speed Breeding methods can expedite the implementation of cotton varieties that are resistant to viruses (Tarazi & Vaslin, 2022).

7. Emerging Technologies and Innovations

7.1 CRISPR-Cas and Its Potential in CLCuV Control

The identification of RNA interference (RNAi) brought about a significant transformation in the study of regulatory RNAs, specifically small RNAs. These small RNAs can selectively hinder the activity of genes that possess similar sequences when they are introduced into the organism *Caenorhabditis elegans* (Frolows & Ashe, 2021). Small RNAs are categorized into three main cell-autonomous pathways: PIWI-interacting (pi)RNAs, small interfering (si)RNAs, and genome-encoded microRNAs (miRNAs). The RNA interference (RNAi) pathway employs the dicer enzyme to cleave double-stranded RNA (dsRNA) into smaller fragments known as small interfering RNAs (siRNAs) (Wahba, Hansen, & Fire, 2021). CRISPR/Cas is a resilient immune mechanism that bacteria and archaea have developed to defend against invasive phages, viruses, and plasmids. CRISPR-Cas produces CRISPR-RNA (crRNA) by interacting with transactivating crRNA (tracrRNA). This gene drive possesses sufficient potency to disseminate modified genes across successive generations, ensuring their availability for reproductive purposes. CRISPR/Cas has extensive applications in bacteria, plants, animals, and medical science as a therapeutic and diagnostic tool. The recent identification of novel CRISPR-like systems in eukaryotes, including OMEGA and Fanzor, holds significant potential for enhancing the efficiency of gene editing in eukaryotic organisms

across a wide range of applications (Wang *et al.*, 2022).

The utilization of CRISPR/Cas presents a highly promising strategy for managing plant viruses and generating plants that are resistant to diseases, thus effectively tackling the issues of food security and hunger. The efficacy of multiplex genome editing in introducing accurate modifications in plant genomes has been proven, resulting in a decrease in the viral impact of begomoviruses on crop plants. CRISPR/Cas can potentially augment the activation of plant defense genes, thereby bolstering plants' resistance against viral infection (Bukhari, Saeed, & Briddon, 2021). CRISPR/Cas12 is a highly adaptable and potent genome editing tool for agricultural progress. It is guided by RNA and acts as a nuclease. The reduced dimensions of the virus facilitate effective transportation into plant cells and generate adhesive terminations, thereby streamlining the integration of modified DNA into the plant genome. CRISPR/Cas12a necessitates a PAM (protospacer adjacent motif) that is rich in T nucleotides, as this enhances its ability to target non-coding regions within the genome. It has been employed to modify genes associated with disease resistance, tolerance to abiotic stress, and enhanced yield (Alphonse, Marimuthu, & Murugan, 2021). A simple illustration is shown in Figure 2.

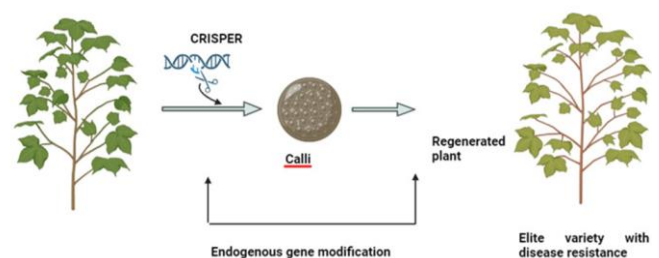


Figure 2. Utilization of CRISPR technology for improving disease resistance in cotton plant.

Accurate disease diagnosis is crucial for implementing effective control measures and management strategies. Cas proteins possess the ability to be programmed and exhibit a high level of specificity in their ability to bind and cleave nucleic acids. This characteristic makes them well-suited for nucleic acid detection. Advancements in research

have resulted in the creation of highly sensitive, portable, and affordable nucleic acid-based point-of-care (POC) testing devices. (Li *et al.*, 2023).

8. Conclusion

This paper has presented a thorough examination of the contribution of biotechnology in reducing cotton illnesses, covering the historical background and future prospects. The diverse array of cotton diseases poses substantial obstacles to both crop productivity and quality, which have traditionally been addressed through a range of treatments with differing effectiveness. Levels of achievement. Biotechnology, particularly transgenic approaches, provides a potent means to enhance disease resistance in cotton. The effective adoption of technologies such as Bt cotton and RNAi-based virus-resistant cotton has shown great promise in decreasing crop losses and enhancing the economic well-being of farmers. Nevertheless, these technologies are not exempt from constraints and obstacles. The intricate nature of genetic engineering, the possibility of gene dispersion, the emergence of pest resistance, and the financial implications of the technique all pose technological challenges. From what we know thus far, it's clear that transgenic methods can greatly improve cotton disease resistance. Benefits to farmers' bottom lines, reduced pesticide use, and greater crop yields are illustrated via illustrative case studies.

It is critical to meticulously plan and execute interventions, bearing in mind the many limitations and hurdles, as part of an all-encompassing approach to disease management. Maintaining a balance between biosafety and the possible benefits of these procedures requires regulatory frameworks to develop alongside evolving technologies. Furthermore, while there have been great strides in developing cotton plants with genetic modifications, there is still a lot of untapped potential in plant genomes that might be used to create traits that are resistant to diseases.

9. Recommendations for Possible Future Research Directions

We are really excited about the promising future of transgenic cotton research. Discovering new resistance genes, expanding our understanding of the cotton genome's uncharted regions, and developing new transgenic varieties through the application of cutting-edge biotechnological methods like synthetic biology and genome editing should be the top priorities for future research. Integrating transgenic strategies with other disease management methods is crucial. A holistic approach should be taken, one that includes digital agriculture technologies, biocontrol agents, and smart agricultural practices. Last but not least, it is critical to build and enhance regulatory frameworks that can adequately handle these innovations in biotechnology, guaranteeing safety while encouraging innovation, because of the field's fast evolution. In essence, there are substantial potential benefits to using transgenic techniques to control cotton diseases, although there are persistent hurdles in this area. We must devise a plan that integrates the development of new technologies with the careful consideration of their potential social, environmental, ethical, and regulatory impacts. We can maximize the benefits of new technology while minimizing its risks and downsides if we follow this plan.

Author Contributions

M Qureshi and A Raza conceptualized the study. M Qureshi, A Raza, A Tanveer, S Sabir, A Sharif, M Asif and M Hassan contributed to the literature review and preparation of the original draft. S Janiad and A Riaz reviewed and edited the manuscript and provided overall supervision. M Qureshi, A Raza, A Zeb and M Asif worked on graphics. All authors have read and agreed to the published version of the manuscript.

Data Availability Statement

All data is available and present in the publication.

Conflict of Interest

The authors declare no conflicts of interest.

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