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Overview of integrated strategies and molecular advances in managing okra yellow vein mosaic virus

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Okra yellow vein mosaic virus (OYVMV) is recognized as a key threat to okra crops in tropical and subtropical regions. This review has critically studied epidemiology, molecular mechanisms, and management strategies related to OYVMV. The complicated interactions between the virus, its vector (*Bemisia tabaci*), and the okra plants have been discussed. It demonstrated that these interactions collectively influence disease severity and spread of OYVMV. Traditional control measures, including cultural practices, chemical applications, and biological control, alongside emerging molecular approaches such as CRISPR/Cas9 gene editing, RNA interference, and marker-assisted breeding, have an important influence on the study and management of OYVMV. Challenges posed by evolving viral strains, insecticide resistance, and environmental factors analysis integrated with conventional management practices with advanced biotechnological interventions provide a comprehensive framework to guide future research and to achieve sustainable control of OYVMV in okra.

Keywords: OYVMV, transmission, epidemiology, molecular characterization, management.

INTRODUCTION

Begomoviruses are members of the Geminiviridae family, and these are among the most economically destructive viruses infecting plants, especially in tropical and subtropical areas (Iftikhar et al., 2021). These viruses are named based on their twin (geminate) particle morphology and belong to the Begomovirus genus. The begomoviruses spread with the help of the whitefly (*Bemisia tabaci*) and their adaptability and effective vector transmission make them significant threats to crops (Azeem et al., 2022; Idrees et al., 2024). Generally, begomoviruses possess a circular, single-stranded DNA genome, which can be possibly a monopartite in some or geminate twin particle DNA genome (Fiallo-Olivé & Navas-Castillo, 2020). The twin particles' genome includes DNA-A, responsible for virus replication and host interactions, while DNA-B is necessary for viral movement within the host tissues (Mandal et al., 2022). Monopartite which Have one genome particle only, begomoviruses often depend on different beta satellites and alpha satellites particles to improve their infectivity, expanding host range and overpower host defenses (Kumar et al., 2021). Their genetic diversity caused by mutation, recombination and pseudo recombination permits these viruses to fit to various hosts and environmental conditions. The whitefly is important and play a significant role in the epidemiology of begomoviruses spread them in persistent circulative manner (Idrees et al., 2024). Once the virus has been acquired by whitefly, the virus circulates in the hemolymph of insect and moves to the salivary glands which allowing transmission of virus to healthy plants during next feeding. Whitefly population dynamics are affected by environmental factors with warm or moderately wet climates assisting their proliferation and enhancing virus transmission rates (Lobin et al., 2022). Begomoviruses cause huge losses in different crops such as

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tomatoes, cotton, legumes, chilies, and cucurbits. Few examples are below:

1. ***Tomato Yellow Leaf Curl Virus (TYLCV):*** Tomato infecting virus globally, it causes symptoms like curling, yellowing and stunted growth, while yield losses can reach 100% in epidemics (El-Sappah et al., 2022).
2. ***Cotton Leaf Curl Virus (CLCuV)*****:** Destructive to the production of cotton in South Asia, it produce symptoms like leaf curling and vein thickening, downgrading fiber quality and produce.
3. ***Chili Leaf Curl Virus (ChiLCV)*****:** Infect chili peppers, it produces leaf curling and stunting which reduce yield and quality (Ali et al., 2012; Shingote et al., 2022).
4. ***Mungbean Yellow Mosaic Virus (MYMV*****):** This virus disturbs legumes like mungbean and urdbean and cause yellow mosaic symptoms and important yield losses (Balasubramaniam et al., 2024).
5. ***Squash Leaf Curl Virus (SLCV)*****:** This virus cause symptoms like leaf curling and stunted growth, hampering production in cucurbits like squash and watermelon (Venkataravanappa et al., 2021)

Begomoviruses exercise several strategies to bypass the plant defenses system. The replication-associated protein called (Rep) facilitate viral replication, Coat protein (CP) supports in encapsulation and whitefly-mediated transmission (Ali et al., 2012; Shakir et al., 2023). Transcriptional activator protein (TrAP) overpowers RNA silencing, a crucial plant resistance response (He et al., 2024). Beta satellites connected with monopartite begomoviruses encode βC1 protein which intensifies symptoms and dominates host defenses. Managing begomoviruses is challenging owing to their adaptability so developing resistant crops provides short-term solution. Viral evolution often makes these efforts ineffective that's why whitefly control via insecticides is imperfect by resistance development and environmental concerns. Integrated pest management (IPM) is the most sustainable strategy (Varman et al., 2025). OYVMV significantly effects okra (Abelmoschus esculentus) causes serious losses. OYVMV was reported for the first time in India by Kulkarni in 1924 and later it got spread across Asia and Africa. OYVMV produces symptoms like vein yellowing, mosaic and stunted growth which cause yield losses ranging from 50% to 94% depending on severity (Fig. 1) (Jamir et al., 2020).

Transmission and epidemiology of OYVMV**:** OYVMV is transmitted with the help the whitefly vector as of other begomoviruses which is a highly efficient vector assisting its rapid spread in okra-growing areas (Figure 2) (Adzim, 2023). The OYVMV is spread persistently in a circulative manner, progressing from the whitefly's digestive system to hemolymph and salivary glands. This permit the whitely vectors to cause multiple plant infections throughout their lifespan (Kumar & Vashisth, 2024). This mechanism along with the nature of vector is the cause of the epidemics.

Figure 1. Symptoms of Okra Yellow Vein Mosaic Virus (OYVMV) infection. Infected okra plants exhibit vein yellowing, mosaic patterns, leaf curling, and stunted growth, leading to severe yield losses.

The epidemiology of OYVMV is strongly linked with the population dynamics of insect vector which flourishes in warm and humid climates mostly. Environmental factors such as temperature rainfall or humidity significantly effect whitefly populations and ultimately the prevalence of OYVMV (Yadav et al., 2022). Optimal environmental conditions such as high temperatures and moderate rainfall enhance vector proliferation and virus transmission rates which frequently results in seasonal disease outbreaks (Jitu et al., 2021). Human agricultural practices sometime help OYVMV to get more serious and transmission increases from normal (Jitu et al., 2021). The cultivation of susceptible okra cultivars or infected planting material along with monocropping give constant reservoirs for the OYVMV inoculum and its vector (Zeshan et al., 2019). The transfer of infected plants with disease and vector between regions accelerates the geographic spread of the disease and needs quarantine laws to manage (Dubey et al., 2021). The timing of infection causes varied severity on host plant by OYVMV. Early infections can create severe symptoms like vein yellowing, thickening of veins, stunted growth of plant and reduced fruit quality and losses can reach up to 94% in severity (Ali et al., 2012). The ability of OYVMV to infect alternative hosts complicates control efforts by maintaining a viral inoculum all the time (Elena & García-Arenal, 2023). In Pakistan, disease incidences have been reported from 50% to 100%, with severity fluctuating across regions. For example, a study in Sindh province reported disease incidences of 71.67% in Hyderabad and 88.33% in Tando Allahyar having severity scores of 4.98 and 5.20 respectively (Ali et al., 2012). In Bangladesh, surveys conducted in 2018 across three districts, Rajshahi, Natore and Naogaon showed altering disease incidences and severity highlighting the widespread nature of OYVMV in the region (Hossain et al., 2023). The severity of OYVMV adversely affects okra yield and quality (Hossain et al., 2021). Infected plants show symptoms such as yellow vein clearing, chlorosis, leaf curling and stunting which cause economic losses to the crop. The severity of these symptoms correlates with disease incidence and environmental factors. The virus acquisition and transmission cycle involve ingestion from feeding by insect then endocytosis and passage across insect tissues likes gut, secretion in saliva and inoculation of virus into plants upon next feeding (Davis & Thompson, 2024). Compatibilities between vector's coat proteins or midgut proteins and plant factors control virus replication and spread through plant tissues.

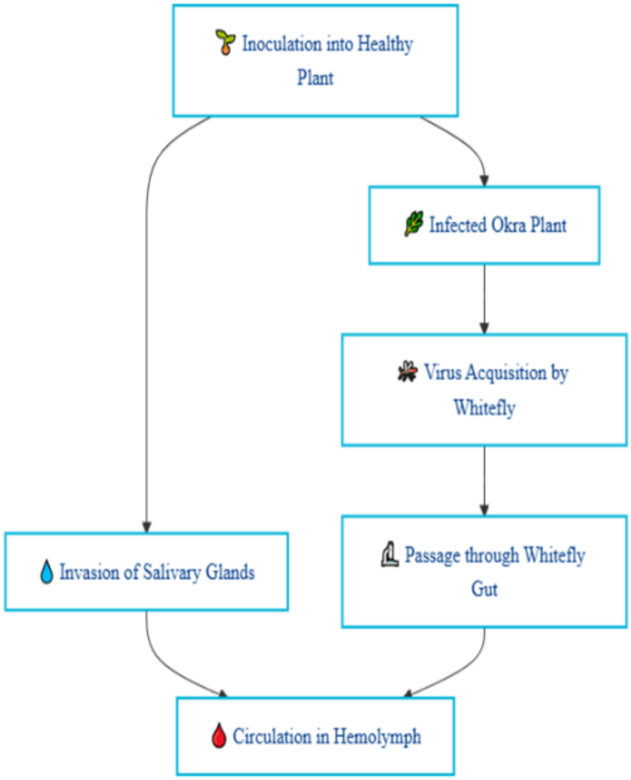

Figure 2. Transmission cycle of OYVMV. The virus is transmitted in a circulative, persistent manner by the *Bemisia tabaci*. The diagram illustrates the acquisition, retention, and inoculation process, highlighting the role of whiteflies in disease spread.

Environmental or meteorological factors such as temperature, humidity and rainfall effect disease severity. For example, higher disease incidences have been observed during the rainy season affecting significantly to disease severity (Yadav et al., 2022). Effective management of OYVMV requires an integrated strategy targeting both the disease and its insect vector. These integrated methods include development of resistant varieties, crop rotation along with field sanitation and chemical use to control whitefly (Varma & Malathi, 2003). Varieties like Arka Anamika showed high resistance to OYVMV while others like Arka Abhag and Parbhani Kranti exhibit moderate resistance (Ali et al., 2012). Biological control agents e.g. parasitoids and predators of whiteflies are famous as environment friendly control methods (Soumia et al., 2021). A multidisciplinary approach combining plant pathology, entomology and agroecology etc. are critical to handle the complex interactions between OYVMV, its vector and environmental variables (Jones, 2009).

***Impact of OYVMV on okra yield and production*:** The yield and economic losses caused by OYVMV in okra vary between 50%-94% depending on the disease severity and the growth stage of the crop when getting infected . The most severe losses in yield occur when the plants gets infected in early stages of its lifecycle (Zeshan et al., 2019). Plants exhibit different symptoms like stunted growth, reduced leaf surface area and malformation in fruits etc. while early infections can cause immature and malformed fruit (Zeshan et al., 2019) and OYVMV infection also negatively affects the quality of okra produce. Fruits/pods harvested from infected okra plants are mostly smaller in size, malformed and discolored which makes them less appealing to buyers in markets (Kumari et al., 2021). The characteristic symptoms of OYVMV infection include yellowing of leaves and vein clearing on okra which is often combined by mosaic patterns. These symptoms affects the photosynthetic efficiency of okra, reducing overall growth and productivity (Khaskheli et al., 2017) . Systemic nature of OYVMV ensures that if a plant is infected, disease symptoms appear in all parts of the plant (Kumar & Vashisth, 2024). This systemic infection prevents recovery of the plant from disease and damage throughout the lifecycle of the plant (Appiah et al., 2020). Yield losses due to OYVMV show significant variations in different regions due to environmental factors of area, farming practices, and type of cultivated okra variety (Kumar et al., 2017). The environmental conditions help in the proliferation of Bemisia tabaci and increase virus transmission rates during warm temperatures with moderate to high humidity (Zeshan et al., 2019). Areas with less hot and humid conditions or efficient vector control measures can minimize disease effects and losses of the disease (Dhole et al., 2023). In South Asia, especially in India and Pakistan, OYVMV has caused severe epidemics in the last few decades (Kuor, 2023). Widespread cultivation of susceptible okra varieties with inadequate pest and disease management measures intensifies the disease (Appiah et al., 2020). Similarly, in some regions of Africa, OYVMV has emerged as a new threat to the okra cultivation fields (Venkataravanappa et al., 2022). The economic impact of OYVMV extends to beyond direct losses of yield because it also results in deformed fruit and low fruit quality lower market prices and lower the profits of farmers (Zeshan et al., 2019). These losses could be devastating to the agriculture farms relying heavily on okra cultivation. The expenses cost for the management of OYVMV such as the cost of purchasing pesticides to manage whiteflies or the cost of purchasing resistant varieties add to the economic load of the farmers (Varman et al., 2025). Okra farming is entirely dropped by some farmers where OYVMV is prevalent in high levels which effect on the supply of okra crop in local markets. This situation is not only having impacr on the incomes but also negatively contribute to food security since okra is a vital source of dietary fiber, minerals and vitamins in most parts (Harris et al., 2019). One of the serious challenges of OYVMV management is resistance development in *Bemisia tabaci* to a large number of insecticides which reduces chemical control efficacy (Horowitz et al., 2020). This highlights the need and move towards integrated pest management (IPM) approaches. Resistant okra varieties development has been beneficial for managing the influence of OYVMV on okra. Issues of resistance durability in the varieties are still a concern since OYVMV will experience high mutation and recombination that may make him overcome the resistance and defense mechanism of the okra. Constant monitoring and breeding are necessary to prevent the losing leverage of the resistance in IPM. Other cultural practices like the rotation of crops, elimination of diseased plant residues, and use of physical barriers such as insect-proof nets or mulches are useful in controlling OYVMV (Yadav et al., 2022).

However, the limitation to this strategy is that the farmers have limited resources and often do not have any awareness at all (Hossain et al., 2023). The transmission and timing of infection of OYVMV are often influenced by epidemiological factors and contribute ultimately to the Yield impacts. Early-season infections coupled with high whitefly populations have a severe impact compared to late-season diseases (Ali et al., 2012; Jitu et al., 2021). Additionally, mixed infections with other begomoviruses or secondary infections from bacteria and fungi or opportunistic pathogens can intensify the symptoms and damage to the plants (Davis & Thompson, 2024). The characteristics symptoms and losses caused by OYVMVD emphasize on the importance of coordinated research and integrated pest management strategies (Davis & Thompson, 2024). Advancements in the molecular and biotechnology fields provide opportunities to combat the OYVMVD (Tiwari et al., 2023). Different Tools like RNA interference (RNAi) are helpful to silence viral infectivity-related genes, and genome editing methods can help develop virus-resistant varieties are getting importance now days (Voloudakis et al., 2022). Using biological control agents to manage the *Bemisia tabaci* offers a better eco-friendly alternative to chemical insecticides (Ali et al., 2024; Kheirodin et al., 2020). Awareness can be spread using Public campaigns and extension services which will help encourage the adoption of IPM strategies and resistant varieties by farmers (Varman et al., 2025). Although OYVMV has proved to be a significant danger to okra production, its management can teach us how to combat other begomovirus diseases as well in other economically important crops (Davis & Thompson, 2024). In conclusion, the devastating impacts of the okra yellow vein mosaic virus on the quality and production of okra point out the need for integrated management practices for better control and management.

Molecular biology of OYVMV: Genome organization, replication, and recombination: Molecular biology knowledge of OYVMV is essential to figure out its pathogenesis, virus-host interactions and strategies for effective disease management (Kanyika, 2022). The genome of OYVMV consists of a bipartite, single-stranded DNA genome particle. It consists of twin particles called particle A and B which have approximately 2.7–2.8 kb each (Shuja et al., 2022). This genome has bidirectionally arranged overlapping open reading frames and consists of 2 distinct groups: virion-sense and complementary-sense strand genes (Hossain et al., 2023). In the virion-sense strand of OYVMV, there are the coat protein (CP) genes that are required for viral DNA replication and encapsulation and interaction with the *Bemisia tabaci* (Levy et al., 2022). These genes code for protein such as V2 which facilitates cell-to-cell movement of virion and inhibits RNA silencing in the host (Davis & Thompson, 2024). The complementary-sense strand has some crucial genes, such as replication-associated protein (Rep or C1), that trigger and control the replication (Mandal et al., 2022). The transcriptional activator protein (TrAP or C2) initiates late gene transcription and assists in suppressing host defense (Guerrero et al., 2020). The replication enhancer protein (REn or C3) improve the replication efficiency and the C4 protein aids in symptom expression by interfering with host signal transduction pathways (Davis & Thompson, 2024). The intergenic region is the center for the virus replication process and has a stem-loop structure with a conserved non-nucleotide sequence. The sequence is crucial for rolling-circle replication and contains binding sites for viral and host proteins (Davis & Thompson, 2024). OYVMV replicates with the help of a rolling-circle mechanism based on the coordinated activity of viral proteins and host cellular machinery (Singh et al., 2020). The replication process starts with the Rep protein, which recognizes the origin of replication and introduces a nick in the virion-sense strand at the conserved sequence, and this generates a 3' hydroxyl group to initiate DNA synthesis (Shuja et al., 2022). Host DNA polymerases expand the 3' end and synthesize a complementary strand while displace the original strand . Rep slices the displaced strand, circularizes it and ligates the ends to form a new single-stranded DNA (Kumar 2023). The displaced strand now also perform as a template for double-stranded DNA synthesis using host polymerases and this process also produce intermediates for further replication and transcription of genome (Gupta et al., 2021). This replication model guarantees rapid viral genome increase and ultimately leading to high concentrations of virus in infected plants (Shuja et al., 2022). Recombination plays an important role in the genetic diversity of OYVMV and its adaptability to different environment and hosts. The compact genome along with overlapping genes promote recurrent recombination events due to which new novel strains to the emerge having changed virulence, host range and other capabilities (Shahriar et al., 2021). OYVMV exchange genetic material with other begomoviruses or associated satellite DNAs or any other mutation, it adapts to new host species and dodges immune responses of the plants (Hossain et al., 2023). The high recombination potential of OYVMV create the challenges for breeders and their efforts to create resistant varieties as new strains of virus can arise rapidly and overcome the resistance (Umar et al., 2023). OYVMV has evolved different strategies to interact effectively with its host and insect vector. Proteins such as TrAP and V2 suppress the host RNA silencing mechanisms which is normally a powerful antiviral defense mechanism in the plants (Zhai et al., 2022). The virus use host cellular machinery for its DNA replication and transcription ensuring its effective dissemination (Ncube Kanyika, 2022). C4 protein interrupt auxin signaling pathways in host and cause vein clearing and the characteristic yellow mosaic symptoms in infected okra plants (Kumar & Dasgupta, 2023). Research focused on genome organization, replication and recombination is essential for developing solutions to mitigate the impact of OYVMV and protect okra cultivation (Adzim, 2023).

***Previous studies on the genetic diversity of OYVMV*:** Researchers have shown considerable interest in the genetic diversity of OYVMV as it plays a crucial role in adaptation, virulence, host range and resistance to management practices (Kumar et al., 2016). OYVMV show significant variability due to high mutation rates, recombination events and interactions (Hossain et al., 2023). This genetic diversity not only complicates disease management but also create challenge for breeders who are constantly developing resistant okra varieties (Ganesh et al., 2022). OYVMV has a high mutation rate during its replication as a single-stranded DNA virus (Venkataravanappa et al., 2015). The (Rep) protein which is Replication associated protein and it facilitates rolling-circle replication in OYVMV does not have proofreading capabilities so this can lead to frequent base substitution mutations (Shuja et al., 2022). Previous studies reported that variability in the coding regions of coat protein (CP) and movement protein (V2) genes (He et al., 2024) has the effect on the efficiency of virion packaging and movement from cell to cell in host which ultimately influencing the host range and pathogenicity of virus (Jeyaseelan et al., 2018). The mutation mostly occurs in the origin of replication and transcription regulatory elements which containing the intergenic region (IR) (Venkataravanappa et al., 2015). Any Change in these regions has impact on replication efficiency and gene expression on virus which ultimately contribute to strain differentiation. Recombination is a very prominent characteristic of these begomoviruses including OYVMV and reported as mainly responsible for the genetic diversity (Venkataravanappa et al., 2015). Recombination primarily happens when two or more begomoviruses infect a single host and during the replication process can generate new strains with possibly different abilities (Srivastava et al., 2022). Recombination between OYVMV and other related begomoviruses like Bhendi yellow vein mosaic virus (BYVMV) can produce new strains possessing different disease dynamics has also been reported (Venkataravanappa et al., 2015). Recombination and mutation might have impact on the resistance breeding programs since OYVMV tends to recombine and form new strains with other virulence factors such as host RNA silencing suppressors which enhance disease symptoms (Jeyaseelan et al., 2021). OYVMV exhibits remarkable genetic diversity in various geographical locations and host plants (Singh et al., 2014). Molecular studies of various isolates from South Asia, the Middle East and Africa have indicated unique clusters that are geographically separated and adapted to local environmental conditions (Hossain et al., 2023). Strains of OYVMV obtained from other host crops like cotton and hibiscus possess distinctive genetic footprints as against strains infecting the okra plant (Zhou et al., 1998).

Molecular markers like restriction fragment length polymorphism (RFLP) and simple sequence repeats (SSRs) have been extensively employed to study the genetic diversity of OYVMV. RFLP tests have revealed important polymorphisms in the genome of OYVMV, specifically in the CP and IR regions (Wasala et al., 2019). Phylogenetic analysis based on SSR markers has classified OYVMV into separate clades, which outline their evolutionary connections with geographical positions (Wang et al., 2021). Though OYVMV exhibits huge genetic variability and whitefly vectors (*Bemisia tabaci*), transmission commonly encounters many problems in their propagation. Such a problem could reduce the genetic variability of the infection cycle (LaTourrette & Garcia-Ruiz, 2022). However, subsequent mutations and recombination processes regenerate diversity once more, allowing the virus to survive in new environmental situations and avoid host resistance (Venkataravanappa et al., 2015). The genetic diversity of OYVMV is difficult for disease control and resistant varieties schemes (Ganesh et al., 2022). Varieties having resistance genes for old strains are susceptible to new recombination strains following mutation (Shwetha et al., 2024). Excessive variability in genomic areas may lead to false negative results which have wide spectrum and sophisticated detection mechanisms (Kim et al., 2019). Recent studies of OYVMV have clarified its evolutionary past and significance in devastating epidemics (Ali et al., 2012). Phylogeographic analyses of isolates obtained from India, Pakistan and Bangladesh have unveiled extensive genetic variation which indicate several introductions and localized evolution of OYVMV (Hossain et al., 2023). Some parts of the genome such as the IR and CP have been identified as base of evolution while mutations and recombination happen more often there to produce diverse strain (Fiallo-Olivé & Navas-Castillo, 2023). The wide genetic variability of OYVMV supports its success as a pathogen allow it to modify to various host plants, geography and environmental situations. By knowing the genetic variability of OYVMV scientists can make better predictions about the evolutionary pattern of OYVMV and plan more efficient disease management approaches.

Approaches for disease management and resistance breeding: Management of OYVMD becomes crucial for improved production of okra in regions where this disease prevails (Bilqees et al., 2020). This OYVMV severely reduces crop quantity and quality, resulting in huge economic losses to farmers. The high degree of genetic diversity in the virus, coupled with frequent recombination, make conventional management efforts useless (Siddiqui et al., 2023). Integrated management practices that mix disease management methods to ensure efficient control. Various methods of disease management that comprise cultural practices, chemical control, biological methods, molecular and breeding strategies for breeding defend okra varieties (Kumar et al., 2017). Integrated disease management (IDM) form a complete approach by integrating various approaches to minimize the OYVMV infection on okra crops. Non-host crop rotation decreases virus and manages the vector availability (Hossain et al., 2023). Intercropping with barrier plants may reduce the vector population and form a barrier in transmission of the disease. Early detection of disease and removal of infected plants minimize the infection spread for healthy crops. Proper spacing and pruning improve air circulation, lowers the humidity and decrease the whitefly infestations which are a primary vector of OYVMV. Controlling the whitefly population is necessary step while trying to manage OYVMV. Systemic insecticides targeting whiteflies can be effective but their unnecessary use may cause resistance against insecticides and emphasize on alternative eco-friendly approaches (Ghongade & Sangha, 2021). Biological control agents such as Encarsia formosa and Eretmocerus eremicus has shown good results in reducing whitefly populations (Ivezić et al., 2025). Reflective mulches like silver-colored polyethylene disturb whitefly population makes it harder for them to locate host plants. Advancements in molecular biology and biotechnology propose new possibilities for managing OYVMV (Shwetha et al., 2024). Accurate diagnostic techniques like polymerase chain reaction (PCR) and loop-mediated isothermal amplification (LAMP) enable the early diagnosis of OYVMV (Crego-Vicente et al., 2024). They also enable precise tracking of virus and their genetic diversity (Wu et al., 2024). Gene editing tools like CRISPR/Cas9 can be used to target particular genes in okra for improved resistance against the OYVMV (Faizal et al., 2024).

RNA interference (RNAi) is capable of silencing critical genes and provide a superior way to shield okra plants against infection (Sharma et al., 2024). Resistance breeding continues to be among the most potent and long-term management

Table 1. Characteristics comparison of different management strategies.

Management strategy	Key Features	Advantages	Limitations	Examples/References
Cultural Practices	Adjusting planting dates, crop rotation, use of mulches, removal of infected plants, sanitation practices	Low cost; eco-friendly; sustainable	Requires careful planning; may not fully prevent virus spread	(Jitu et al., 2021)
Chemical Controls	Application of insecticides (e.g., imidacloprid) targeting the whitefly vector	Rapid reduction in vector populations; immediate effects	Development of insecticide resistance; environmental hazards; residue concerns	(Ali et al., 2012)
Biological Controls	Use of natural enemies (parasitoids, predators) and biopesticides (e.g., neem extracts)	Environmentally friendly; sustainable; low chemical residues	Efficacy can vary with environmental conditions; requires conservation of beneficial organisms	(Ganesh et al., 2022)
Molecular Approaches	Techniques such as CRISPR/Cas9 gene editing, RNA interference (RNAi), marker-assisted breeding, and transgenic development	Specific targeting; potential for durable, broad-spectrum resistance; reduced reliance on chemicals	Regulatory and transformation challenges; potential off-target effects; technology still emerging in okra	(Ganesh et al., 2022; Sharma et al., 2024)
Integrated Pest Management (IPM)	Combining cultural, chemical, biological, and molecular strategies to manage both the vector and the virus	Synergistic effect; reduced overall pesticide use; sustainable long-term management	Complex implementation; requires accurate, timely information and strong extension support	(Varman et al., 2025)

techniques in IPM (Vinay et al., 2024). Still there is high genetic diversity and recombination capability of OYVMV and it presents a major risk which requires improvement in methods for detection and utilization of resistance factors in okra genotypes (Vinay *et al.,* 2024). Natural sources of resistance genes have also been discovered in okra varieties and wild relatives like Abelmoschus caillei (Ahmed & Ladan, 2022). Marker assisted selection (MAS) allows researchers to locate resistance genes on the molecular level (Ganesh et al., 2022). Recent research has discovered quantitative trait loci (QTLs) associated with resistance to begomoviruses that can be transferred into resistant okra varieties. Future management of OYVMV is expected to involve a mix of integrated pest management, molecular-based methods and resistance breeding. With advancing research and technology, innovative techniques like synthetic antiviral molecules might become alternative solutions. Climate smart agricultural methods that minimize environmental stressors impacting the crop might also supplement conventional practices assist in restricting the spread and influence of OYVMV with changing climatic conditions (Table 1).

***Conclusion*:** Okra Yellow Vein Mosaic Virus (OYVMV) remains a significant constraint to okra cultivation worldwide, particularly in tropical and subtropical regions. Its efficient transmission by whitefly vectors, high genetic diversity, and ability to adapt to changing environments make its management challenging. Traditional control strategies, including cultural practices, insecticide applications, and biological control, have shown limited success due to evolving viral strains and insecticide resistance in whiteflies. Therefore, a more integrated and sustainable approach is necessary to combat this devastating disease. Advancements in molecular biology and biotechnology offer promising solutions for managing OYVMV. Gene-editing techniques such as CRISPR/Cas9 and RNA interference (RNAi) hold great potential for developing virus-resistant okra varieties. Additionally, marker-assisted breeding (MAB) and genome-wide association studies (GWAS) can facilitate the identification and incorporation of resistance genes into elite cultivars. These modern tools, when combined with conventional breeding approaches, can enhance the durability of resistance against emerging OYVMV strains.

Future research should focus on understanding the molecular interactions between OYVMV, its vector, and the host plant to identify novel targets for genetic resistance. Additionally, exploring the role of endophytes and other biocontrol agents could lead to environmentally friendly and sustainable disease management strategies. Improved early detection methods, such as loop-mediated isothermal amplification (LAMP) and high-throughput sequencing, can aid in rapid and precise disease diagnosis, enabling timely intervention. The implementation of integrated disease management (IDM) strategies, combining host resistance, vector control, and agronomic practices, remains the most viable long-term solution. Strengthening extension services and farmer awareness programs will be crucial to ensuring the adoption of these strategies in the field. Policymakers should also emphasize quarantine regulations and breeding programs to mitigate the spread of OYVMV across different regions. In conclusion, while OYVMV poses a persistent threat to okra production, recent advancements in molecular biology, plant breeding, and integrated pest management provide promising avenues for its control. A multidisciplinary approach involving genetic resistance, vector management, and sustainable agricultural practices will be key to reducing the impact of OYVMV and securing global okra production.

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***SDGs addressed*:** Zero Hunger, Good Health and Well-being, Industry, Innovation, and Infrastructure.

***Policy referred*:** Integrated Pest Management (IPM) Policy; Biotechnology and GMO Policy; Plant Quarantine and Phytosanitary Policies.

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