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Review Article

UNDERSTANDING THE ORIGINS, IMPACTS, AND REMEDIES FOR MUNGBEAN YELLOW MOSAIC VIRUS

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ABSTRACT

Mungbean (*Vigna radiata*) is a crucial crop worldwide, especially in Asian countries, where it significantly contributes to agricultural yields. However, the Mungbean Yellow Mosaic Virus (MYMV), a begomovirus, causes substantial yield reductions. Despite ongoing efforts to identify resistant cultivars, most available varieties remain susceptible, potentially resulting in yield losses of up to 100%. In Pakistan, challenges such as inadequate irrigation, disease outbreaks, and poor-quality seed stocks exacerbate the impact of MYMV on mungbean production. Whiteflies (*Bemisia tabaci*) are the primary vectors for MYMV. Molecular characterization reveals that virus particles aggregate in the host nuclei, disrupting cell structure and leading to yield losses, with early infection stages resulting in more severe reductions. Efforts to manage MYMV include evaluating mungbean germplasm for resistance and emphasizing the importance of genetic resistance in disease control. Despite difficulties in developing resistant cultivars, ongoing research aims to reduce the impact of MYMV on mungbean production. This review explores the effect of MYMV on mungbean production, particularly in Pakistan, and examines the associated economic consequences. It also investigates the genetic susceptibility of mungbean cultivars, the influence of environmental conditions, and the dynamics of whitefly populations, which collectively contribute to MYMV incidence. The review highlights the correlation between whitefly populations and disease incidence and discusses strategies for managing MYMV and its vector. This paper provides a comprehensive overview of current approaches to develop sustainable and effective methods for mitigating MYMV-induced yield losses in mungbean cultivation.

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INTRODUCTION

Mungbean (*Vigna radiata* L.), is a prominent crop in the agriculture sector in Asian countries, contributing to approximately 90% of the worldwide yield (Sudha et al., 2013). Mungbean is considered the second most significant pulse crop after chickpea in Pakistan (Mukhtar et al., 2017, 2021). Its exceptional digestibility and nutrient content make it very desirable (Malik et al., 2014). The components of this substance consist of fat, fiber, vitamins, carbohydrates, and proteins. The food products under consideration exhibit a noteworthy level of nutritional worth and provide substantial content of protein (20-24%) and carbohydrates (60-65%).

According to Murakami et al. (1991), mungbean has a relatively short growing season of about 75-90 days, requires modest amounts of water, and integrates well into crop rotation systems with cereals. The mungbean production in Pakistan for the 2013-2014 period was approximately 92.9 thousand tons, cultivated across 130.9 thousand hectares (Government of Pakistan, 2014). Mungbean is grown in both the spring (February-March) and summer (June-July) seasons, with summer being the primary cultivation period. However, mungbean growth during the summer is often hindered by a significant infestation of whiteflies, which are vectors for the mungbean yellow mosaic virus (MYMV). Besides its seeds, mungbean foliage can also serve as a source of hay, fodder, and animal feed. Mungbean sprouts are highly valued in Asian cuisine for their high vitamin C and folate content (Nair et al., 2013). The root nodules of mungbean contain *Rhizobium* and *Bradyrhizobium* microorganisms that aid in fixing atmospheric nitrogen. Globally, mungbean is cultivated on over 7.0 million acres, producing approximately 3.5 million tons of grains. While most production occurs in Asia, other regions also cultivate mungbean (Nair et al., 2019). The mungbean genome is relatively small, with a size of 579 Mb and a diploid set of 22 chromosomes (2n) (Kang et al., 2014). Mungbean is considered an excellent source of easily digestible, high-quality protein (24%) and iron (40-70 ppm), making it beneficial for a balanced diet and reducing flatulence (Vairam et al., 2016). This pulse crop thrives in both spring and autumn and is resilient to adverse weather conditions (Ali et al., 2005).However, its production is significantly impacted by MYMV, which can cause substantial yield reductions (Parihar et al., 2017). Field trials have been conducted to evaluate mungbean germplasm for resistance to MYMV under field conditions. Employing genetic resistance is a crucial and environmentally sustainable method for managing MYMV. Currently, Pakistan lacks mungbean cultivars resistant to MYMV, making it essential to develop such resistance. To address this, the resistance of indigenous germplasm to mungbean yellow mosaic disease has been assessed using a severity-based scoring system, which has proven more effective than previous infection percentage-based methods (Akhtar et al., 2009).

Mungbean Yellow Mosaic Virus (MYMV)

Begomo viruses are prevalent in tropical and subtropical regions and have been observed infecting commonly cultivated plants, including mungbean. The Mungbean Yellow Mosaic Virus (MYMV) infects several other plant species, including blackgram, common bean, lima bean, and cowpea (Figure 1). Infected plants typically show symptoms such as a prominent golden or yellow mosaic, with relatively mild stunting, leaf curling, and distortion.

A longstanding hypothesis suggests that weeds may act as reservoirs for begomo viruses, potentially impacting crops negatively. However, most studies conducted to date have found that weeds are generally infected by viruses genetically distinct from those affecting crops (Rocha et al., 2013). Additionally, symptoms in weeds are often mild, lacking severe stunting and leaf distortion, which may indicate a co-evolutionary relationship between the virus and its host.

Recent research on begomo virus diversity in commonly cultivated bean plants suggests that weeds could serve as sources of genetic diversity for begomo viruses, potentially contributing to the emergence and evolution of crop-infecting strains. This hypothesis is supported by various studies, including research by Castillo-Urquiza et al. (2008). A distinct bipartite begomo virus associated with symptoms in mungbean has been identified as MYMV (Dhobale et al., 2023). MYMV significantly reduces the yield of various legume crops. The progression of the disease is influenced by factors such as vector population prevalence, favorable climatic conditions, and genetic susceptibility. The genetic variation among individuals affects their response to MYMV. Previous research indicates that mungbean resistance is controlled by a pair of recessive genes, while susceptibility is determined by a single recessive gene (Shukla and Pandya, 1985). Data suggests that susceptibility has a more pronounced impact than resistance.

The use of virus-resistant genotypes is crucial for effective disease control; however, the success of this approach has been limited. Symptoms of MYMV include yellow spots and streaks on leaves, stunted growth, reduced flowering, and dry, shriveled seeds. Most identified cultivars are susceptible to the disease, which can lead to significant damage and yield losses of up to 100% (Sudha et al., 2013; Mohan et al., 2014). The disease poses a serious threat to mungbean cultivation in various countries (Honda et al., 1983; Chenulu and Verma, 1988).

Distribution

According to the literature, the disease was first identified in India in 1940 on lima beans (Capoor and Varma, 1948), dolichos, and mungbeans (Capoor and Varma, 1950; Nariani, 1960). The average mungbean yield per hectare in Pakistan is considerably lower than in developed nations (Iqbal et al., 2011). The crop is grown on 220,000 hectares, yielding an annual production of 140,700 tons (GoP, 2015). Low yields in Pakistan may be due to insufficient irrigation, disease epidemics, or low-quality seed stock (Ahmad et al., 2017). The MYMV is the most prevalent and damaging virus affecting this crop in Pakistan, despite the presence of other viruses that also causes harm (John et al., 2008). Epidemic losses can vary up to 100%, depending on the crop variety and geographical location (Bashir et al., 2006). Iqbal et al. (2011) conducted a field experiment during the summer season to evaluate MYMV resistance in 100 different genotypes of mungbean germplasm at NARC Islamabad. The germplasm was classified into resistant and susceptible categories based on disease severity. Despite assessing the varied responses, no genotype showed observable resistance to MYMV. Eight genotypes exhibited moderate resistance, while thirty showed moderate susceptibility. Of the total accessions, 30 were found to be susceptible, and the remaining 43 were classified as highly susceptible. Habib (2012) conducted a screening for yellow mosaic disease (YMD) at the University of the Punjab in Lahore, Pakistan, under natural conditions. The low yield of mungbean varieties in Pakistan is significantly attributed to their lack of resistance to diseases and insect pests. YMD has been identified as a major factor contributing to the significant damage to mungbean crops in most agricultural areas of Pakistan during the summer (Kharif) season. Following an assessment of economic losses due to MYMV, a field experiment was carried out to examine the relationship between the virus and various climatic factors, aiming to develop a meteorological pest prediction model. Pakistan has increased mungbean production and area over the past two years, producing 132,700 tons on 186,700 acres (Government of Pakistan, 2014). Despite the reported area of 163,200 hectares in 2018-19, there remains considerable potential for improving varietal production and farmer yields. Reduced genetic diversity and several biotic and abiotic stress factors contribute to this shortfall (Nair et al., 2015; Saeed et al., 2018). Severe outbreaks of MYMV have occurred in Pakistan, Bangladesh, and India, though the disease has been documented on every continent except Australia (Varma et al., 2011). Mungbean is primarily produced in Asia and Australia (Alam et al., 2014). India is the leading global producer of mungbean, with a total yield of 2.17 million tons from approximately 4.32 million hectares. According to a 2018 project report, the average yield of mungbean in India is relatively low (around 502 kg/ha) compared to other leguminous crops (Table 1).

Vector and transmission

The MYMV belongs to the Begomovirus genus and the Geminiviridae family. Its transmission is primarily facilitated by the insect vector known as whiteflies (*Bemisia tabaci*) (Selvi et al., 2006). The disease was first identified in 1942 in a chickpea field near Faisalabad, Pakistan (which was not yet an independent country) (Vasudeva, 1942). Based on sequence identity, the bipartite begomovirus isolates MYMV, MYMIV, and HgYMV are responsible for causing MYMV worldwide (Kang et al., 2005). Yellow mosaic disease, caused by yellow mosaic viruses (YMVs), significantly affects the growth and development of mungbean, particularly in South and Southeast Asia. MYMV is consistently transmitted through whiteflies rather than through seeds, soil, or human contact (Khan et al., 2012). There is a notable correlation between the frequency of whitefly occurrences and the onset of the disease (Bhagat et al., 2000). The incidence of the disease is expected to rise in tandem with the increase in whitefly populations (Parihar et al., 2017). Female whiteflies are more prolific than males (Qazi et al., 2007). The rise in whitefly populations is partly attributed to their evolving tolerance to insecticides, which has resulted from their overuse (Ahmad et al., 2017). The study demonstrates a significant positive correlation, supported by statistical evidence, between whitefly populations and two ecological factors: the highest temperature and the duration of abundant sunlight. Conversely, a statistically significant negative correlation was observed between whitefly populations and relative humidity and evening rainfall (Varma and Malathi, 2003).

Table 1. Historical perspectives of yellow mosaic virus and its potential impact on mungbean.

Distribution	Host Species	Impact of mungbean
India (Nariani, 1960)	Mung bean (*Vigna radiata*) (Binyamin et al., 2022)	Yellow-colored spots followed by yellow mosaic pattern speckled on young leaves
Pakistan (Ahmad, 1975)	Urdbean or black gram (*V. mungo*) (Archana et al. 2018: Sahni et al., 2023)	Gradually spots result in complete yellowing of leaves
Sri Lanka (Shivanathan, 1977)	Mothbean (*V. aconitifolia*) (Yaqoob et al., 2015)	The yellow leaves slowly dry and wither
Thailand (Thongmeearkom et al., 1981a)	Cowpea (*V. unguiculata*) (Malathi et al., 2005)	Few flowers and pods with immature and deformed seeds
Bangladesh (Jalaluddin and Shaikh, 1981)	Pigeon pea (*Cajanus cajan*) (Sivalingam et al., 2019)	Pods are reduced in size and turn yellow
Nepal (Shahid et al., 2012)	Soybean (*Glycine max*) (Usharani et al., 2004)	In severe cases, other plant parts become completely yellow
Taiwan (Karthikeyan et al., 2014)	Common bean (*Phaseolus vulgaris*) (Osei et al., 2022)	Photosynthetic rate decreases ultimately affecting the crop yield
Malaysia (Karthikeyan et al., 2014)	Lima bean (*P. lunatus*) (Shahid et al., 2012)	Early infection can also lead 10 100% yield loss
Philippines (Kulkarni et al., 2019)	*Dolichos lablab* (Capoor and Venna, 1950)	Over a broad geographic range, I 0% and 85% yield loss have been reported

Host-pathogen interaction

Several biochemical changes occur in plants in response to infection. When YMV disease develops, a compatible interaction between mungbean and YMV leads to systemic infection and the subsequent appearance of symptoms (Yang et al., 2007). Conversely, in an incompatible host-pathogen interaction, the activation of resistance (R) genes in response to avirulence (avr) proteins triggers a cascade of defense genes, including pathogenesis-related (PR) proteins, which ultimately leads to systemic acquired resistance (SAR) (Sels et al., 2008). These responses collectively hinder viral replication and impede YMV movement (Figure 1). Moreover, various reactive oxygen species (ROS) scavenging enzymes, such as superoxide dismutases (SOD), ascorbate peroxidases (APX), and catalases (CAT), play a crucial role in maintaining ROS homeostasis and thereby deactivating the pathogen (Torres, 2010; Oliveira et al., 2012).

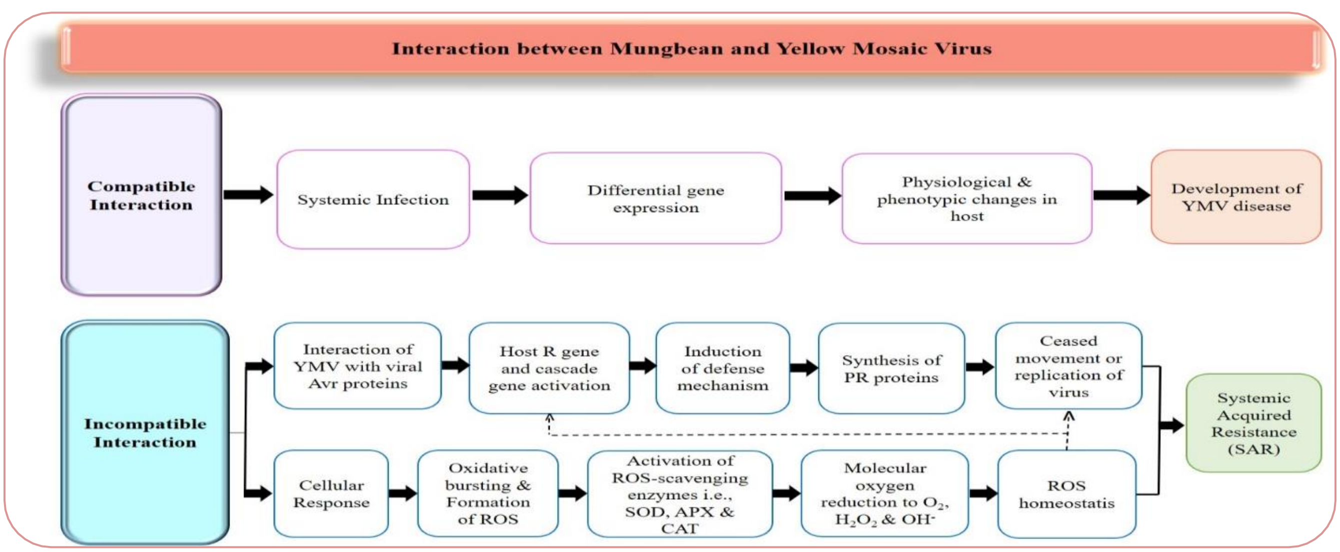

Figure 1. Interaction between mungbean and YMV.

Molecular characterization

The pathogen enters the phloem cells of the host organism through the proboscis of the whitefly. About two days before symptoms appear, viral aggregates become visible within the nucleus of the host cell (Thongmeearkom et al., 1981b). Initially, young leaves exhibit sporadic yellow spots, which evolve into a yellow mosaic pattern. Over time, the leaves turn completely yellow, dry out, and wither. This reduction in photosynthetic efficiency, due to smaller pods and yellowed leaves, leads to a significant decrease in production yield in the affected mungbean plants (Malathi and John, 2009). On mature leaves, MYMV causes asymmetrical green and yellow spots. According to Mohan et al. (2014), reduced production of pods, flowers, and seeds in infected plants is the primary contributor to the decline in yield.

MYMV is a highly destructive disease, particularly prevalent in Pakistan, where it leads to substantial annual losses in crop productivity (Bashir et al., 2005). The virus particles tend to aggregate into translucent clusters within the leaf cells and occasionally occupy the nuclear space of infected phloem cells. As early as two days before the disease becomes visible, hypertrophied nucleoli, viral aggregates, and fibrillar formations can be found in the nuclei of the phloem cells in mungbean. Infected phloem elements may also exhibit para-crystalline or double cylindrical accumulations of viral particles within vacuoles, although these particles are usually scattered randomly.

The timing of sowing significantly impacts the incidence of MYMV, influencing both crop development and yield (Sadeghipour, 2008). Early-stage infections lead to more substantial yield reductions compared to infections occurring later in the growing season (Kang et al., 2005). If the virus strikes three weeks after planting, a complete 100% yield loss can occur. However, infestations eight weeks post-planting result in minimal losses. Yield reductions ranging from 10% to 85% have been documented across a wide geographic range. Infected plants also exhibit delayed maturation and produce lower-quality grains (Singh et al., 2011). The reduced photosynthetic capacity of diseased plants is a key factor contributing to the decline in agricultural yield (Malathi and John, 2009).

Thongmeearkom et al. (1981b) examined symptoms in different lines of mungbean, finding that these symptoms could serve as good indicators of the stability or virulence of various viral isolates. The virus is transmitted to the host plant's phloem cells by whiteflies, where it multiplies. Within the leaf cells, virus particles tend to aggregate into translucent clusters and may even occupy the nuclear space of the infected phloem cells. As early as two days before visible symptoms appear, hypertrophied nucleoli, aggregates of virus particles, and fibrillar formations can be detected in the nuclei of phloem cells in mungbean. Infected sieve elements may also exhibit para-crystalline or double cylindrical accumulations of viral particles in their vacuoles, although virus particles are usually scattered randomly.

Malathi and John (2009) observed that young leaves develop random yellow spots, which progress into a yellow mosaic pattern. Over time, the spots enlarge until the entire leaf turns yellow. These yellowed leaves gradually deteriorate and dry out. Infected plants experience reduced yields, producing fewer flowers, pods, and some immature or malformed seeds. The pods of infected plants are smaller and yellowish in color. In severe cases, other parts of the plant may also turn completely yellow. Viral infection reduces photosynthetic efficiency, which negatively impacts crop production. The economic impact on crop yield is influenced by the timing of the MYMV infection, particularly in relation to the plant's developmental stage.

Management

The extent of crop damage is influenced by various factors, including the crop's developmental stage at the time of infection, the severity of disease symptoms on individual plants, and the proportion of plants affected (Figure 2). The widespread prevalence of MYMV infection has significantly reduced mungbean production, despite the substantial land dedicated to its cultivation (Archana et al., 2018; Ilyas et al., 2010). Although strategies such as vector control, management of alternative weed or viral hosts, use of immune or resistant crop cultivars, and cultural practices that slow disease progression have been employed to manage MYMV, these methods have proven largely ineffective. Consequently, there is an urgent need to enhance management techniques.

Given this context, the present investigation aimed to explore various aspects of integrated MYMV management through the use of a range of chemicals and neem-derived pesticides. One proposed crop management strategy includes preventing whitefly attacks or limiting cultivation to the spring season when whiteflies are absent. However, in Pakistan, spring cultivation is not commercially viable as it competes with wheat for land. Therefore, mungbean must be cultivated during the summer, making whitefly protection a crucial strategy. Chemical control of whiteflies typically involves extensive insecticide use, which is both costly and environmentally harmful. Thus, genetic resistance to MYMV remains the most reliable solution. Extensive research has been conducted to identify sources of resistance, but results have shown either the absence of such sources or the presence of only moderately resistant strains (Singh et al., 1996; Shad et al., 2006).

In a study by Jayappa et al. (2017), integrated MYMV management was tested in January and March 2016 using various insecticides and neem-based pesticides. They found that MYMV management (45.20%) and its vector were effectively controlled with the application of imidacloprid at a rate of 5 ml/kg of seeds, combined with two sprays of neemazal at 3 ml/l (3.7 per plant). Duraimurugan and Tyagi (2014) reported that the average avoidable loss due to the mungbean insect pest complex was 32.97%, with variations ranging from 27.03% to 38.06%. In cases of severe disease infection, potential yield losses could reach up to 85%. MYMV infection during the early growth stages can lead to substantial damage (Varma and Malathi, 2003).

Disease outbreaks are heavily influenced by environmental factors, as weather conditions play a crucial role in the emergence and spread of diseases. Bishnoi et al. (1996) found that environmental factors accounted for 81% of the variation in MYMV disease progression, necessitating a comprehensive assessment of these factors to develop an accurate disease forecasting system. High rainfall in July and low or no rainfall in August was identified as significant contributors to disease progression (Khan et al., 2018). Also, managing these diseases is challenging due to the complexity of pharmacotherapy, cultural practices, and the use of various botanical remedies. Developing mungbean cultivars resistant to MYMV and CLS is further complicated by the virus's diverse host range, differentiation, and quantitative inheritance. Aggregating resistant genotypes remains the most effective strategy for managing these diseases. Therefore, it is imperative for breeders and researchers to focus on developing mungbean genotypes with high resistance to the viruses responsible for Yellow Mosaic Disease (YMD) in these crops (Saeed et al., 2018).

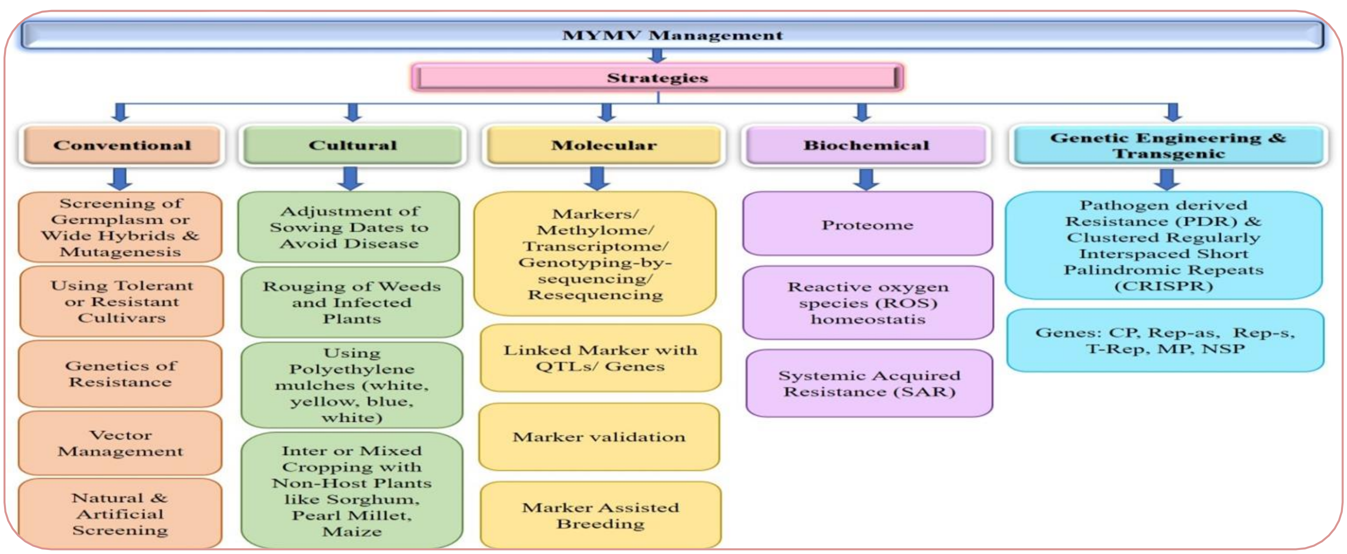

Figure 2. Management strategies used for mungbean yellow mosaic virus.

CONCLUSION AND FUTURE PERSPECTIVES

In conclusion, Mungbean Yellow Mosaic Virus (MYMV) poses a significant threat to mungbean cultivation, especially in regions like Pakistan, where the crop is of vital nutritional and economic importance. Transmitted by the whitefly vector, MYMV causes severe symptoms, including yellow mosaic patterns, stunted growth, and reduced yields, which have led to substantial annual losses due to the susceptibility of most mungbean cultivars. This situation underscores the urgent need for effective management strategies.

This review emphasizes the importance of genetic resistance as a sustainable approach to controlling MYMV. The assessment of mungbean germplasm for resistance, using a severity-based scoring system, is crucial for identifying resilient cultivars. However, the lack of resistant cultivars in Pakistan highlights the necessity for ongoing research and breeding programs focused on developing varieties with enduring resistance to MYMV. Future research should aim to deepen our understanding of the molecular mechanisms underlying MYMV infection, uncover the genetic basis of resistance, and explore biotechnological interventions.

Utilizing molecular tools for precise breeding and incorporating resistant genes can accelerate the development of MYMV-resistant mungbean varieties. Moreover, exploring alternative control measures, such as eco-friendly approaches or antiviral agents, could offer complementary strategies for integrated disease management. Given the global significance of mungbean, collaborative efforts among researchers, agricultural institutions, and policymakers are essential for a comprehensive response to MYMV. Implementing robust surveillance systems, educating farmers on disease management practices, and promoting sustainable agricultural practices can collectively reduce the impact of MYMV on mungbean crops.

Ultimately, a multidisciplinary approach that integrates genetics, agronomy, and virology is crucial for securing mungbean production and ensuring food security against viral threats like MYMV.

AUTHORS' CONTRIBUTIONS

RTB wrote, reviewed and edited the manuscript and prepared the figures; MM conceptualized the idea, collected and arranged the literature and wrote the original draft; TS, MIZ, and YI visualized, finalized, edited and reviewed the manuscript; QS supervised, validated and proofread the manuscript.

CONFLICT OF INTEREST

The authors declare no conflict of interest.

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