



# AGRI MAGAZINE

(International E-Magazine for Agricultural Articles)

Volume: 03, Issue: 05 (May, 2026)

Available online at <http://www.agrimagazine.in>

© Agri Magazine, ISSN: 3048-8656

## Yellow Mosaic Virus in Mungbean: Screening Techniques, Breeding and Genomic Strategies

\*Dr. P. Sharmela<sup>1</sup> and M. Arunkumar<sup>2</sup>

<sup>1</sup>Guest Faculty, The Gandhigram Rural Institute-Deemed to be University, Dindigul-624302, India

<sup>2</sup>Department of Genetics and Plant Breeding, CPBG, Tamil Nadu Agricultural University, Coimbatore-641003, India

\*Corresponding Author's email: [sharmeladpm@gmail.com](mailto:sharmeladpm@gmail.com)

The Mungbean (*Vigna radiata* L.), is an economically significant legume, indigenous to the Indian subcontinent. As a nutrient rich legume boosting significant levels of protein, fiber, and antioxidants, it plays a pivotal role in maintaining food and nutritional security. As the world's leading producer, India cultivates this crop across more than 4.32 million hectares. However, the productivity is severely constrained by Mungbean Yellow Mosaic Virus (MYMV), a member of the *Begomovirus* genus and this devastating condition is caused by two species of the Legumovirus family: MYMV and Mungbean Yellow Mosaic India Virus (MYMIV). These characterized begomoviruses genomes, consists of circular single-stranded DNA-A and DNA-B components, transmitted by whitefly (*Bemisia tabaci*) and produce a major yield constraint across South and Southeast Asia.

### Vector Dynamics and Symptoms

The transmission of MYMV is mediated by whitefly (*Bemisia tabaci*) in a persistent, circulative manner. During phloem-feeding, the vector inoculates the viral particles into the host's vascular bundle. The onset of infection is marked by the appearance of chlorotic spots on the trifoliate leaves, which progressively coalesce into a systemic yellow mosaic pattern. This leads to a significant reduction in total chlorophyll content and a concomitant decline in photosynthetic efficiency. The physiological losses are leaf senescence, stunted pod development, and yield losses reaching up to 85%, depending on the host genotype and the phenological stage at the time of infection. Under congenial conditions, the disease can cause up to 100% yield loss, with bright yellow mosaic patterns on foliage, reduced flowering, yellow-spotted pods, and the production of deformed immature seeds. The Yellow Mosaic Viruses (YMs) are typically phloem-limited and their status as a seed-borne disease remains a subject of debate. Some studies have detected viral DNA in healthy seedlings through PCR, and fail to demonstrate whitefly-mediated transmission, suggesting that the seedling's internal environment may inhibit visible symptom occurrence and further infection.

### Strategic Breeding and Genetic Integration for Viral Resistance

In addition to its agronomic significance, *V. radiata* serves as a premier model for pulse genomics due to its self-pollinating and diploid ( $2n = 22$ ) nature. Its relative compact genome of ~579 Mb provides a streamlined genetic framework that accelerates the mapping of quantitative trait loci (QTLs) and the characterization of resistance genes. Leveraging these genomic resources allows researchers to trace the evolutionary divergence of the Legumovirus family and refine marker-assisted selection (MAS) protocols. Such advancements are critical for developing high-yielding, resilient cultivars capable of mitigating the pathogenic stress that threaten food security across South and Southeast Asia.

To counter the persistent threat of viral pathogens, integrated strategy ranging from conventional plant protection to integrated biotechnological approaches has been adopted to develop resilient legume crops. As a primary strategy, plant breeding provides a highly sustainable framework for crop improvement, effectively reducing the environmental impact on pest and disease management. This approach prioritizes, the identification of resistant landraces, accessions, and breeding lines, providing a robust genetic defense and protects the harvest. A breakthrough was the discovery of natural resistance to MYMV in *Vigna radiata* var. *sublobata* the wild progenitor of the mungbean, *V. trilobata* and *V. umbellate*, by employing pre-breeding strategies, backcross breeding and advanced genomic tools, researchers have successfully introgressed these resistance genes from wild relatives into commercial cultivars. This allows the next-generation grain legumes to maintain high productivity while naturally neutralizing pathogenic stress.

The Extensive research also indicates, many mungbean lines exhibiting absolute resistance to YMD tend to be poor yielders, while high-yielding germplasm often remains susceptible. Significant progress in bridging this gap has been achieved through shuttle breeding programs, notably between the World Vegetable Centre (AVRDC) and NIAB, resulting in several YMD-resistant varieties. While most resistance sources are identified through field screening, specifically Indian genotypes such as IPM-02-03, PDM-139, Pusa 0672, and HUM16 have consistently demonstrated resistance across diverse environmental conditions and seasons.

### The Genetic Architecture of YMD Resistance

The most effective method to overcome Yellow Mosaic Disease (YMD) is the development of naturally resistant crop varieties, but the genetic background for this resistance is diverse. Based on research into the genetic architecture of *Vigna* species, the inheritance of resistance to MYMV is characterized by a high degree of complexity and variation across different genetic backgrounds. In some genetic backgrounds, resistance is governed by a single dominant gene, which represents a "gain-of-function" where the plant actively identifies and blocks the virus. Conversely, other varieties show recessive inheritance, suggesting the plant lacks a specific host protein that the virus requires for replication and movement.

The interaction between genes governing resistance in mungbean is not uniform; it fluctuates depending on the specific parental lines and the viral strains involved. In complex cases, such as interspecific crosses, researchers have observed the interaction of multiple genes, including dominant and recessive epistasis, where one gene masks the effect of another. The YMD resistance is frequently reported as digenic (controlled by two genes). These genes often exhibit epistasis, where the effect of one gene is dependent on the presence of another. This includes both dominant and recessive epistasis, particularly in interspecific crosses.

### Mechanisms of Gene Action

The way these genes interact dictates the plants physiological response to the virus:

1. **Restriction of Movement:** Certain gene interactions prevent the virus from moving cell-to-cell through the plasmodesmata or via the phloem (long-distance movement).
2. **Inhibition of Replication:** Resistance genes may interfere with the virus's ability to hijack the plant's cellular machinery to create copies of itself.
3. **Vector-Host Interaction:** Some resistance observed in the field is actually directed at the whitefly vector rather than the virus itself, preventing the virus from ever entering the plant.

Nowadays breeders are moving from simple morphological selection to recombination breeding and delayed selection methods. These strategies allow scientists to better stabilize the resistance while maintaining high yields. The recessive traits are mostly hidden and the use of MAS can quickly identify resistant plants in the lab without waiting for a field outbreak, significantly accelerating the development of the next generation.

## Screening Methods for YMD Resistance in *Vigna*

Screening for YMD resistance in mungbean and blackgram involves three primary approaches: Hot-Spot Screening, Viruliferous Whitefly Inoculation, and Agroinfection. Hot-spot screening is a field-based method utilizing the "infector-row technique," where susceptible "spreader" genotypes are planted among test genotypes to encourage natural infection (Fig.1). This method is highly dependent on environmental factors like temperature and humidity which influence whitefly populations. To gain more control, screening with viruliferous whiteflies is conducted in net houses by force-feeding whiteflies on infected plants before transferring them to healthy test plants, though disease severity does not always correlate linearly with the number of insects used. The most precise and uniform method is (agroinoculation), where *Agrobacterium tumefaciens* cultures containing viral DNA components are manually introduced into sprouted seeds through pricking; this laboratory technique bypasses insect-related variables, allows for the testing of specific viral strains, and often reveals that genotypes labeled "resistant" in the field may actually be susceptible when the virus is introduced directly, suggesting that some field resistance is actually vector-based rather than physiological.



**Fig.1** screening for MYMV resistance at National Pulses Research Centre, Vamban (Infector row technique)

## Genomic Insights into Viral Resistance

QTL mapping has emerged as a molecular approach for decoding the complex genetic architecture of viral disease resistance in grain legumes. By crossing two parents with contrasting traits, researchers can specify QTLs precisely on a chromosome with resistance genes. This technique helps in identifying the genetic markers needed in near future for developing resistant mungbean varieties. To uncover the MYMIV resistance, scientists developed a mapping population from a cross between the tolerant line *Vigna radiata* (NM92) and *V. radiata* ssp. *Sublobata* (TC1966). By screening these plants under field conditions with variety of molecular markers (such as RAPD, SCAR and SSR), they successfully identified four critical QTLs on linkage groups LG9 and LG8. In one of the interspecific crosses between the common mungbean (*Vigna radiata*) and its relative *V. umbellata*, researchers used SNP markers to isolate a major resistance locus, qMYMV4-1, on LG4. By locating these specific genomic regions, scientists will get a clear roadmap to quickly develop mungbean varieties that can naturally defend themselves against viral diseases.

## Mapping the Genetic Code

For decades, pulse farmers have battled the devastating Yellow Mosaic Disease (YMD), recent breakthroughs in genetic mapping are finally depicting its plant host resistance. By studying a unique cross between Mungbean and its hardy relative rice bean scientists have

founded précised gene tags. Through Genotyping-by-Sequencing (GBS), researchers identified five specific regions in the plant's DNA and they express plant defence mechanism. One QTL qMYMV4\_1, discovered on Chromosome 4, played major role in defense mechanism. The discovery suggests that resistance in Rice bean comes from a single recessive gene, the new mapping reveals a much more complex network of multiple genes working together.

This genetic map is not restricted to one area. Different studies have found "resistance markers" scattered across the plant's genome:

- Chromosome 3: Linked to the reliable CM9 marker.
- Chromosomes 2, 5, 7, 9, and 10: Various (SNPs) that signal a plant's ability to withstand the virus. In both blackgram (*Vigna mungo*) and mungbean (*Vigna radiata*), these genes are the primary candidates for shielding the plant from viral infection. The key Genetic Markers that scientists have identified are two crucial Resistance Gene Analog (RGA) markers YR4 and CYR1 that acts for resistance. In some studies, these markers are perfectly aligned with the plant's ability to resist the virus. This also validates, that CYR1 might actually be a functional part of the resistance gene itself. In other mungbean varieties, the link between the CYR1 marker and resistance is not perfect. This "partial" association is a major scientific clue: it tells us that resistance isn't always controlled by a single gene instead, multiple genetic locations are likely working together, and the genes responsible for resistance may vary from one variety to another.

### The Modern Toolkit for Virus-Resistance

To develop mungbean cultivars with robust resistance to the MYMV, researchers are moving beyond traditional methods and adopting a suite of cutting-edge "smart breeding" tools. Genomic selection allows breeders to predict a plant's viral resistance using computer models, skipping years of slow field testing by selecting the best lines based on their DNA profiles. To speed this up even further, rapid generation advancement (Speed breeding) uses controlled growth chambers to trick plants into flowering faster, potentially delivering new resistant varieties in record time. On the molecular front, next-generation sequencing has mapped the mungbean entire genetic code, helping scientists find specific "resistance blueprints" hidden in wild relatives. To understand how crops fight viruses, scientists are using a "multi-layered" approach called Omics. By combining different fields like genomics, transcriptomics, and metabolomics researchers mapping the complex networks that control plant immunity. When these insights are paired with traditional breeding tools like synthetic biology, they can exactly predict which genes provide resistance. Finally, CRISPR/Cas9 genome editing is being used as a precise tool to directly disable the virus's ability to replicate, as seen in recent successes targeting the MYMV coat and rep proteins. Together, these technologies are transforming mungbean breeding into a precise science, ensuring secured food supply

### Limitations in developing viral resistance

Improving the resistance with above said breeding and biotechnological tools, also have the obstacles to develop resistant lines. Traditional plant breeding is often a slow, labour-intensive process, and the genetic markers used to track resistance can sometimes be unreliable when moved between different plant populations. Furthermore, using tools like CRISPR can inadvertently put evolutionary pressure on viruses, potentially causing them to mutate into new, even more aggressive strains to survive. There is also the risk that disabling a plant susceptibility genes might accidentally stunt its growth, requiring even more precise "base editing" to fix. Finally, complex international regulations and public debate over the classification of genome-edited crops as GMOs create a final layer of uncertainty. To truly protect our harvests, researchers must continue to refine these tools shortening breeding cycles, improving DNA methods, and ensuring that new varieties are both safe and durable in the field.

## Conclusion

As our global population climbs toward 10 billion, the pressure to double food production, in an increasingly unpredictable climate has never been greater. For the mungbean, the "Yellow Menace" of the MYMV remains a formidable barrier to food security. However, by tapping into the vast genetic diversity of wild relatives and ancient landraces, we are discovering the natural blueprints for resilience. The future of farming lies in the seamless integration of nature and technology: using "Omics" to map out viral resistance, AI-driven genomic selection to predict the strongest crops, and precision tools like CRISPR to disable viral threats at the molecular level. By combining these advanced biotechnologies with traditional breeding, we can move away from chemical dependency and toward a new era of climate-smart legumes ensuring that the mungbean remains a sustainable, virus-resistant powerhouse for generations to come.

## References

1. Mishra GP, Dikshit HK, S. V. R, Tripathi K, Kumar RR, Aski M, Singh A, Roy A, Priti, Kumari N, Dasgupta U, Kumar A, Praveen S and Nair RM (2020) Yellow Mosaic Disease (YMD) of Mungbean (*Vigna radiata* (L.) Wilczek): Current Status and Management Opportunities. *Frontiers in Plant Science*. 11:918. doi: 10.3389/fpls.2020.00918
2. Kang, Y. J., Kim, S. K., Kim, M. Y., Lestari, P., Kim, K. H., Ha, B. K., et al. (2014). Genome sequence of mungbean and insights into evolution within *Vigna* species. *Nature Communication*. 5, 5443. doi: 10.1038/ncomms6443
3. Naimuddin, Akram, M., and Aditya, P. (2011a). First report of natural infection of mungbean yellow mosaic India virus in two wild species of *Vigna*. *New Dis. Rep.* 23, 21–22. doi: 10.5197/j.2044-0588.2011.023.021
4. Naimuddin, K., Akram, M., and Singh, N. P. (2016). Yellow mosaic of mungbean and urdbean: current status and future strategies. *Journal of Food Legumes* 29 (2), 77–93.
5. Mathivathana, M. K., Murukarthick, J., Karthikeyan, A., Jang, W., Dhasarathan, M., Jagadeeshselvam, N., et al. (2019). Detection of QTLs associated with mungbean yellow mosaic virus (MYMV) resistance using the interspecific cross of *Vigna radiata* × *Vigna umbellata*. *Journal of Applied Genetics* 60, 255–268. doi: 10.1007/s13353-019-00506-x
6. Jha UC, Nayyar H, Chattopadhyay A, Beena R, Lone AA, Naik YD, Thudi M, Prasad PVV, Gupta S, Dixit GP and Siddique KHM (2023) Major viral diseases in grain legumes: designing disease resistant legumes from plant breeding and OMICS integration. *Frontiers in Plant Science* 14:1183505.