



REVIEW ARTICLE

Viral diseases in *Vigna* species - Impacts, management opportunities and future perspectives: A review

Godwin P¹, Shoba D^{1*}, Arumugam Pillai M¹, Saravanan S², Sheela J³, Kavitha Pushpam A⁴, Arumugachamy S¹ & Juliet Hepziba¹

¹Department of Genetics and Plant Breeding, V.O. Chidambaram Agricultural College and Research Institute, Tamil Nadu Agricultural University, Killikulam 628 252, Tamil Nadu, India

²Rice Research Station, Tamil Nadu Agricultural University, Ambasamudram 627 401, Tamil Nadu, India

³Department of Plant Pathology, V.O. Chidambaram Agricultural College and Research Institute, Tamil Nadu Agricultural University, Killikulam 628 252, Tamil Nadu, India

⁴Department of Crop Physiology and Biochemistry, V.O. Chidambaram Agricultural College and Research Institute, Tamil Nadu Agricultural University, Killikulam 628 252, Tamil Nadu, India

*Email: shoba.d@tnau.ac.in



OPEN ACCESS

ARTICLE HISTORY

Received: 21 August 2024

Accepted: 20 September 2024

Available online

Version 1.0 : 12 December 2024

Version 2.0 : 01 January 2025

Version 3.0 : 16 January 2025



Additional information

Peer review: Publisher thanks Sectional Editor and the other anonymous reviewers for their contribution to the peer review of this work.

Reprints & permissions information is available at https://horizonepublishing.com/journals/index.php/PST/open_access_policy

Publisher's Note: Horizon e-Publishing Group remains neutral with regard to jurisdictional claims in published maps and institutional affiliations.

Indexing: Plant Science Today, published by Horizon e-Publishing Group, is covered by Scopus, Web of Science, BIOSIS Previews, Clarivate Analytics, NAAS, UGC Care, etc See https://horizonepublishing.com/journals/index.php/PST/indexing_abstracting

Copyright: © The Author(s). This is an open-access article distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution and reproduction in any medium, provided the original author and source are credited (<https://creativecommons.org/licenses/by/4.0/>)

CITE THIS ARTICLE

Godwin P, Shoba D, Arumugam P M, Saravanan S, Sheela J, Kavitha P A, Arumugachamy S, Hepziba J. Viral diseases in *Vigna* species - Impacts, management opportunities and future perspectives: A review. Plant Science Today. 2025; 12(1): 1-12. <https://doi.org/10.14719/pst.4756>

Abstract

Pulses are the second-largest class of food crops worldwide, with around 1.58 million hectares under cultivation. represent. They are also excellent sources of protein. The major cultivated *Vigna* species in India include Blackgram [*Vigna mungo* (L.) Hepper], Greengram [*Vigna radiata* (L.) Wilczek], Cowpea [*Vigna unguiculata* (L.) Walp.], Moth bean [*Vigna aconitifolia* (Jacq.) Maréchal] and Adzuki bean [*Vigna angularis* (Willd.) Ohwi & H. Ohashi]. However, the yield of these crops is significantly reduced by viral diseases caused by a diverse range of viral strains. Notable viral diseases affecting *Vigna* species include yellow mosaic, cowpea severe mosaic, cowpea yellow mosaic, cowpea aphid-borne mosaic, cowpea golden yellow mosaic, bean common mosaic, leaf crinkle and leaf curl. The primary challenge in managing these viral diseases lies in effectively integrating the substantial knowledge accumulated, which is essential for developing genotypes with durable resistance to viral infections. Molecular markers and QTL (Quantitative Trait Locus) mapping are valuable tools for identifying genomic regions associated with viral disease resistance, aiding future breeding programs. This abstract provides an overview of each *Vigna* species, the viral diseases affecting them, and recent advancements in developing resistant genotypes. It also highlights systematic screening efforts within *Vigna* germplasm to identify various sources of viral resistance in *Vigna* species.

Keywords

management; molecular breeding approaches; transgenic breeding approaches; *Vigna* species; viral diseases

Introduction

Pulses are the world's second-largest class of food crops, grown on approximately 1.58 million hectares and producing 23.4 million tonnes of protein annually. India is among the leading producers and consumers of pulses, contributing 0.23 million tonnes from 0.66 million hectares (1). Within the Papilionaceae family, *Vigna* is one of the most significant genera, comprising up to 150 species primarily found in Africa and Asia (2). In India, the key *Vigna* species cultivated include black gram (*Vigna mungo* [L.] Hepper), green gram (*Vigna radiata* [L.] Wilczek), cowpea (*Vigna unguiculata* [L.] Walp.), moth bean (*Vigna aconitifolia* [Jacq.] Maréchal) and adzuki bean (*Vigna angularis* [Willd.] Ohwi & H. Ohashi).

In India, black gram is cultivated on 4.63 million hectares, yielding 600 kg/ha and producing 2.78 million tonnes (3). Asia contributes to 90% of the world's mung bean production (4), a crop known for its high protein content (25g/100g) (5). Green gram (mung bean), native to India, is grown on approximately 4.03 million hectares with a production of 3.01 million tonnes and a productivity of 783 kg/ha. It contains around 20-50% protein (5). Cowpea, primarily cultivated as a *kharif* crop, can also be grown as a *rabi* crop in peninsular India, with a protein content of 22-24% (5). Moth bean thrives in warm, dry climates, particularly in India's semi-arid and desert regions. It is widely found across India, from the north-eastern Himalayan foothills to Saurashtra in the west and from the north-western Himalayas down to Karnataka in the south (6). Adzuki bean, with a protein content ranging from 16.33% to 29.2% (7), is primarily grown in China, Korea,

Japan and India, with an annual cultivation area of about 0.70 million hectares (8). These *Vigna* species are essential to the Indian diet.

India exported 775,024.48 metric tonnes of pulses globally, valued at USD 672.31 million during the 2022-23 fiscal year (9). Viral diseases are a significant biotic factor contributing to both production and economic losses (10). Table 1 lists notable viral diseases affecting *Vigna* species, including their genus, family and genome structure. Although various disease management strategies have been developed and implemented, complete resistance has not yet been achieved. Researchers must focus on advanced breeding techniques to improve resistance and yields against these viral diseases. This review highlights potential management strategies for viral diseases in different *Vigna* species, encouraging further research (Fig. 1).

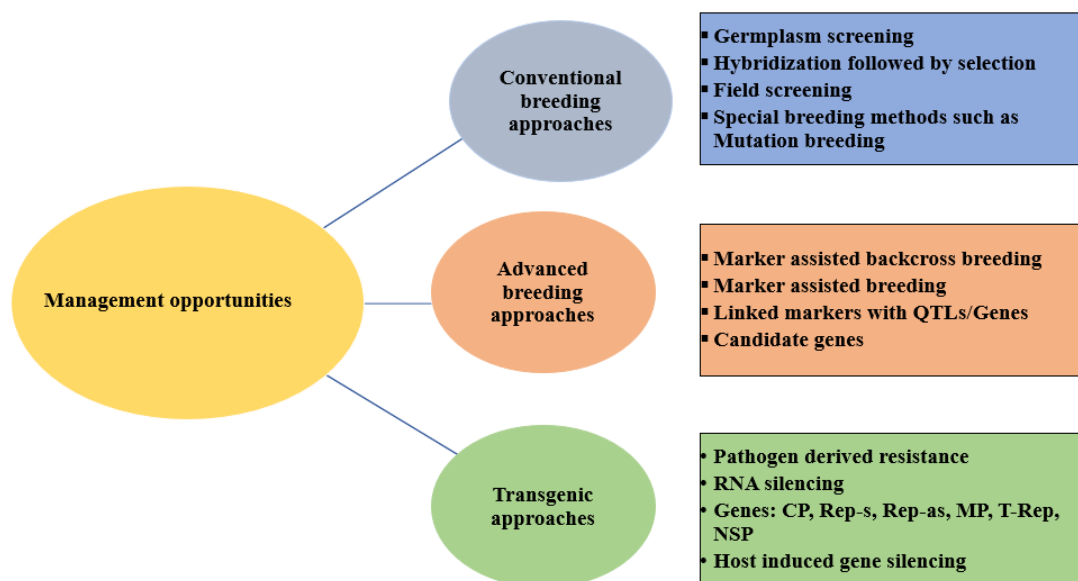


Fig. 1. Outline of management opportunities against viral diseases in *Vigna* species.

(CP-Coat Protein, Rep- Replication Protein, NSP-Nuclear Shuttle Protein, MP-Movement Protein, QTL-Quantitative Trait Loci)

Table 1. Genus, family and genome structure of notable viral diseases of *Vigna* species

Crop	Viral Diseases	Viral species	Genus and Family	Genome	Reference
Blackgram and Green gram	Mung bean yellow mosaic	Mung bean yellow mosaic virus (MYMV)	Begomovirus, Geminiviridae	ssDNA	(82)
		Mung bean yellow mosaic India virus (MYMIV)	Begomovirus, Geminiviridae	ssDNA and β -satellite	
	Leaf crinkle	Urdbean leaf crinkle virus (ULCV)	Begomovirus, Geminiviridae	ssDNA	
	Leaf curl	Groundnut bud necrosis virus (GBNV)	Begomovirus, Geminiviridae	ssDNA	
Cowpea	Cowpea mosaic	Cowpea mosaic virus (CPMV)	Comovirus, Secoviridae	ssRNA	
		Cowpea severe mosaic virus (CPSMV)		ssRNA	
		Cowpea aphid borne mosaic virus (CABMV)	Potyvirus, Potyviridae	ssRNA	
		Cowpea golden yellow mosaic virus (CGYMV)	Begomovirus, Geminiviridae	ssDNA	
Moth bean	Yellow Mosaic	Mung bean yellow mosaic virus (MYMV)	Begomovirus, Geminiviridae	ssDNA	
Adzuki bean	Mosaic	Bean common mosaic virus (BCMV)	Potyvirus, Potyviridae	ssRNA	

Occurrence of yellow mosaic virus diseases in black gram, green gram and moth bean

In 1960, yellow mosaic disease was first identified in mungbean and the virus responsible was named mungbean yellow mosaic virus (MYMV) (11). Losses due to the MYMV strain range from 60% to 100% in Northern India, while MYMV has caused significant yield reductions in Southern India. MYMV and MYMIV strains are distinguishable based on nucleotide sequence identity (12) and in India, MYMV is readily transmitted by *Bemisia tabaci* (13). MYMIV also infects moth bean, initially discovered in Pakistan (14).

Genetics of yellow mosaic virus resistance and various resistance sources in black gram, green gram and moth bean

The main challenges in the genetic improvement of black gram include limited genetic variability, the absence of an ideal genotype suited for diverse cropping systems, susceptibility to biotic stresses and a shortage of high-quality improved seeds (15). Since the 1970s, plant breeders and virologists have worked on breeding for resistance to yellow mosaic virus (YMV) through host resistance. However, reports differ on the inheritance pattern of yellow mosaic disease (YMD) resistance. In black gram, YMV resistance has been described as monogenic dominant (16), governed by complementary recessive genes (17), monogenic recessive (18) and digenic recessive (19). To improve YMD resistance in blackgram and greengram, it is important to research and use the available genetic diversity (20). Resistant genotypes identified for various mosaic diseases in black gram and green gram are listed in Table 2.

Mutation breeding for yellow mosaic virus disease resistance in black gram and green gram

Mutations serve as a valuable tool for introducing variability and aiding in selecting mutants with desirable traits, including YMD resistance in crop plants, which can be achieved through mutation breeding (21). In the M3 generation, five green gram mutants (M5, M18, M26, M70 and M71) were identified as resistant to YMD (22). Prasad, Sarla and Vamban 2 are three mutant black gram varieties derived from the popular variety T9, known for their resistance to mung bean yellow mosaic disease (MYMD) (Table 3).

Molecular breeding approaches for YMV resistance in *Vigna* species

Marker-assisted selection is a vital tool in breeding programs, especially for traits that are difficult to evaluate phenotypically. The effectiveness of breeding programs that provide resistance to MYMV has significantly increased through studies on germplasm diversity, identification of markers associated with resistant genes and development of QTL maps using molecular markers (23). Simple Sequence Repeat (SSR) markers, known for their effectiveness in identifying varieties, hold substantial potential in genetic and breeding studies (24). Various SSR markers linked to YMV resistance, as identified in previous studies, include CEDG180 (25), CEDG141 (26), CEDG228, CEDG044, Vrd1 and STSbr1 (27) for MYMIV and CEDG185 (28) for MYMV. Additionally, SCAR markers such as CM 815, CM 9 (29), ISSR 8111357, YMV1 FR (30) and MYMVR-583 (31) are associated with MYMV resistance.

Table 2. Resistant genotypes identified in black gram, green gram and moth bean for various mosaic diseases

S. No	Crop	Diseases	Resistant genotypes	References
1.	Black gram	MYMV	IC 27026, IC 06088, UL 2, HPU 4, HPU 188, UH 80-26, IP 99-127 and PLU 62	(83)
			Vamban 7, Ujala (OBG-17), Pant U-31, Ujala (OBG-17), Prasad (B 3-8-8), Pant U-40, Pant U 84, Vamban 2, Prasad (B 3-8-8) and UPU 2	(84)
			Pant U-84 and UPU-2	(19)
			VBN-6, VBN-8, VBN-9 and VBN-10	(85)
			KKB 05011 (KKM 1)	(86)
	MYMIV	NP 16, PLU 62, PLU 63, PLU 131, PLU 158, PLU 277, IPU12-19, IPU13-5, K 66-110, K 66-188, DPU 88-31, IPU13-6, NP 19, NP 21, NDU 88-8 and VMR 84	(87)	
2.	Green gram	MYMV	NM 94, ML 1628, CO-GG 930, CO-27, VPM 50, MH-565, VBN (Gg) 3, VBN (Gg) 4, Pusa Vishal, Bing Mung-2 and Bing Mung-1	(88)
		MYMIV	PDM 139, PDM 143, ML Nos. 131, 267, 337, NDM 88-14, PBM 14, PBM 27, IPM02-03, IPM410-9, IPM205-9, Pant M 4, MH 303, IPM409-4 and IPM205-7	(42)
3.	Moth bean	MYMV	PLMO 12, IC 36392, IC 129177, IC 129177, IC 129208, IC 36467, IC 129194, PLMO 30, IC 36096, IC 415152, IC 36573 and RMO 40	(89)

Table 3. Resistant mutant genotypes for MYMD in black gram and green gram

S. No	Crop	Diseases	Resistant genotypes	Reference
1.	Black gram	MYMD	Prasad and Sarla	(83)
			TU-94-2	
			Vamban 2	(90)
2.	Green gram	MYMV	Pant Moong 2, BM 4, Dhauri, ML 26-10-3, MUM-2	

CEL-I nuclease-based genotyping has been utilized to identify MYMV-associated SNPs on mungbean chromosomes 2, 5, 7, 9 and 10 (32). Mapping resources are limited, bulked segregant analysis (BSA) becomes a crucial tool for labelling genes that lack a linkage map (32). For example, the SSR marker VR9 effectively differentiated resistant and susceptible bulks in a black gram F₂ population from the T9 × LBG-759 cross (33). QTLs identified for MYMIV and MYMV resistance through composite interval mapping (CIM) and composite interval epistasis mapping (CIM-EPI) in black gram and green gram are detailed in Table 4.

QTL studies are critical in marker-assisted backcrossing (MABC), a precise method to introduce targeted genes into elite cultivars to enhance specific traits (34). Foreground selection helps confirm the transfer of desired QTLs, while background selection evaluates the recovery of the recipient parent genome. SSR markers showing polymorphism between parents are used at each backcross generation to calculate the recurrent parent genome (RPG) recovery percentage in the background selection (35). In black gram, foreground selection for MYMV resistance was conducted using six SSR markers from two key QTL regions found in linkage groups 2 (*qmymv2_60*) and 10 (*qmymv10_60*) (36).

Occurrence of urd bean leaf crinkle virus (ULCV) and urd bean leaf curl virus in black gram and green gram

Leaf crinkle disease, prevalent in Pakistan and India, can cause crop losses of up to 100%, depending on the season and variety affected (37). ULCV disease was first reported in Delhi in 1966 (38) and is transmitted by aphids (39). In India,

mung bean and urd bean leaf curl diseases were initially observed in 1968 in Pantnagar, Uttar Pradesh (40). According to Nene, mungbean leaf curl disease has historically caused significant yield losses, reaching up to 40% in 33 districts of Uttar Pradesh. In southern regions like Andhra Pradesh, the disease has already become a serious concern (41).

Resistance sources of ULCV and urd bean leaf curl virus in black gram and green gram

In India, resistant sources for leaf crinkle and leaf curl diseases are limited. However, black gram genotypes IUP 11-02 and IUP 110-26 show resistance to ULCV (42). In Tamil Nadu, varieties VBN (Bg) 9 and VBN (Bg) 10 are also highly resistant to ULCV (43). Two black gram varieties, Mash 391 and Mash 479, developed through the pedigree method, demonstrate high tolerance against multiple diseases, including leaf crinkle virus (LCV) (44). Among greengram varieties, MLT-GG R-16-007, RME-16-12, RME-16-3, MLT-GG R-16-009 and COGG 1319 are resistant to ULCV (45).

The black gram genotype PU-31 showed the lowest incidence of leaf curl, with GBG-1 following closely (46). In a study 500 seeds were collected from PBNV-GG (peanut bud necrosis virus-green gram) and PBNV-BG (peanut bud necrosis virus-black gram) infected green gram cv. K-851 and black gram cv. LBG-20 revealed no seed transmission of the leaf curl virus in these crops, as seedlings showed neither typical PBNV symptoms nor tested positive in DAC-ELISA tests (47). Additionally, black gram varieties VBN (Bg) 9, VBN (Bg) 10 and VBN (Bg) 11, released by the National Pulse Research Centre in Vamban, exhibit resistance to urd bean leaf curl virus (43).

Table 4. QTLs detected for MYMIV and MYMV resistance by composite interval mapping (CIM) and composite interval epistasis mapping (CIM-EPI) in blackgram and greengram

S.No	Resistance	Crop	Population	QTLs	LOD score	LG	Marker interval	PVE (%)	References
1.	MYMV	Black gram	F ₂	qMYMVD_60	4.56	10	CEDG180-CEDG116	21	(91)
				qMYMV4-1	6.07	4	VgSNP_04_32 - VgSNP_04_36	20.04	
2.	MYMV	Black gram x rice bean	F ₉ and RIL	qMYMV5-1	5.02	5	VgSNP_05_18 - VgSNP_05_19	15.02	(92)
				qMYMV6-1	3.32	6	VgSNP_06_32 - VgSNP_06_33	10.11	
				qMYMV10-1	3.48	10	VgSNP_10_02 - VgSNP_10_03	11.24	
3.	MYMV	Black gram	F _{2:3} and RIL	qmymv2_60	5.71	2	CEDAAG002-CEDG225-GMES4236	20.90	(93)
				qmymv10_60	6.98	10	cp05325-CEDG180-GMES4431	24.90	
4.	MYMIV	Green gram	F _{2:3}	qYMIV2.1	44.60	2	CEDG275-CEDG006	44.60	(94)
				qYMIV7.1	37.65	7	CEDG041-VES503	37.65	
5.	MYMIV	Green gram	F ₁₂	MYMIVr7_104	4.7	7	v02a7	0.23	(95)
				MYMIVr8_48.8	4.6	8	mg3pat423	0.22	
				MYMIVr9_6.4	8.2	9	m4pcc585	0.36	
				MYMIVr9_25	16.4	9	9DMB158	0.59	
				qYMIV1	2.62	2	CEDG100-cp02662	9.33	
				qYMIV2	2.54	4	DMB-SSR008-VR113	10.67	
6.	MYMIV	Green gram	F ₈ and RIL	qYMIV3	3.42	9A	CEDG166-CEDG304	12.55	(96)
				qYMIV4	10.00	2	CEDG100-cp02662	27.93	
				qYMIV5	2.55	6	CEDG121-CEDG191	6.24	
				qYMV2.1	7.44	2	CEDG020 - CEDG264	2.98	
				qYMV2.2	6.96	2	CEDG 264 - CEDG008	2.96	
7.	MYMV	Black gram	RIL	qYMV5.1	13.83	5	CEDG 264 - CEDG008	1.64	(97)
				qYMV8.1	10.56	8	CEDG 186 - CEDG271	1.63	
				qYMV9.1	10.30	9	CEDG 022 - CEDG166	1.51	

(LOD - Logarithm of the Odds, LG- Linkage Group, PVE- Phenotypic Variation Explained)

Occurrence of mosaic diseases in cowpea

Figure 2 shows a list of the most common viruses that reduce cowpea yield, as well as their vectors. Cowpea severe mosaic virus (CPSMV) possesses a single-stranded RNA genome. Distinguished from cowpea mosaic virus (CPMV) by (48) in 1964, CPSMV belongs to the family *Comoviridae*, genus *Comovirus* and is spread by chrysomelid beetles (*Cerotoma ruficornis* and *C. trifurcata*) (49). CPSMV is also seed-transmitted (50) and may cause up to 85% yield loss in seeds (51). Cowpea yellow mosaic virus, primarily an African virus, has occasionally been reported in the Americas (Suriname, U.S.A.) (52). An isolate from Suriname was identified as CPMV (48) but was previously known as cowpea yellow mosaic virus (CYMV) (53). CYMV, belonging to the family *Potyviridae*, genus *Potyvirus*, has a single-stranded RNA genome and is seed-borne at low levels (1-5%), easily transmitted by sap, with its primary vector being *Ootheca mutabilis* (52). CYMV can sometimes cause 5-10% yield losses (54).

Cowpea aphid-borne mosaic virus (CABMV), also from the family *Potyviridae*, genus *Potyvirus*, has a single-stranded RNA genome and is spread through the sap, seed (0-40%) and aphids (*Aphis craccivora*) (55). Cowpea aphid-borne mosaic virus can cause yield losses ranging from 13 to 87% in field settings (55). Cowpea golden yellow mosaic virus (CGMV) has a single-stranded DNA genome. Researchers have identified CGMV-like diseases in at least seven African countries (56). It remains unclear how similar diseases in Niger, Kenya, Tanzania, India and Pakistan relate to each other. Cowpea golden yellow mosaic disease (CGMD) is limited to northern India and is transmitted by whiteflies (57).

Genetics of mosaic resistance in cowpea and various resistance sources

CYMV resistance is controlled by a single dominant gene identified in *Dixielee Sel*, designated as the yellow mosaic resistance (YMR) genotype (58). Only when the resistance gene is homozygous recessive (*ymr ymr*) are tolerant and susceptible plants observed, as the dominant allele masks the effects of the three additive loci. CABMV resistance is managed by either a single dominant or recessive gene, with studies concluding that a single recessive gene confers CABMV resistance (59). In India, cowpea genotypes have shown resistance to CABMV under field conditions through sap inoculation, confirmed by DAS-ELISA testing (60). The resistant genotypes identified in cowpea for various mosaic diseases are listed in Table 5.

Molecular breeding approaches for mosaic disease resistance in cowpea

The current cowpea genetic map comprises 11 linkage groups (LGs) totalling 2,670 cM, with an average marker spacing of approximately 6 cM. This map contains 242 AFLP and 17 RFLP markers related to disease and pest resistance (61), as well as 133 RAPD, 39 RFLP and 25 AFLP markers from the original map (62). CPSMV resistance has been mapped to LG3 in cowpea (61). Identified QTLs linked to SSR markers AG1/AF48383 (AGB1), VM31 and VM1 show resistance to cowpea yellow mosaic virus (63). These three SSR loci are closely linked to a QTL on linkage group 2, with the VM31 locus associated with the QTL within a 95 % confidence interval covering 19 cM. CPMV resistance was found to be strongly correlated with six SNP markers (C35069548_1883, scaffold66293_6549,

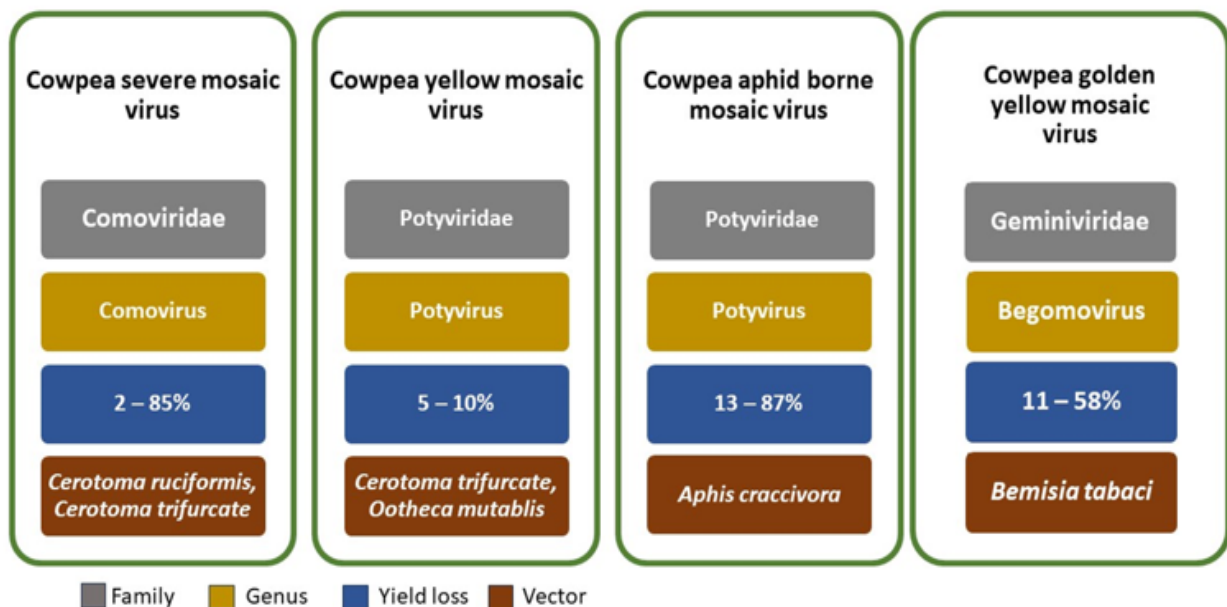


Fig. 2. Mosaic diseases and their vectors in cowpea.

Table 5. Resistant genotypes identified in cowpea for various mosaic diseases

Crop	Viral Diseases	Resistant genotypes	Reference
Cowpea	CYMV	TPTC 29, DC-15, JCPL-11, JCPL-18, JCPL-44, JCPL-45, JCPL-87, Pant Lobia 3, Pant Lobia 4, Pant Lobia 5, UPC 622, UPC 628, and KBC-9	(98)
	CABMV	IT86F-2014-1, IT86F-20895-1, TC1-6-10-1, CO6, IC521495, TC1-6-9-E, TC501-1-4, TC503, TC605, TCM418SDT, PGCP12, RC101 and TC99-1	(60)
	CGYMV	VRCP-4, VRCP-6	(99)

scaffold65342_6794, scaffold95805_2175, C35081948_540 and scaffold17319_4417). The first three markers are linked to immune response, while the remaining three are related to hypersensitive response (64). For CGMV resistance, the gene was linked to three AFLP markers: E.AAC/M.CCC515 at 4.3 cM, E.AAA/M.CAG352 at 16.8 cM and E.AGG/M.CTT280 at 14.2 cM, with LOD scores of 50.4, 24.4 and 28.7, respectively. Additionally, AFLP markers E.AAA/M.CAG352 and E.AAC/M.CCC515 were used to develop eight SCAR markers (65).

Occurrence of bean common mosaic virus (BCMV) in adzuki bean

Bean common mosaic virus (BCMV) was first reported in the United States in 1917 and the associated disease was initially referred to as bean mosaic. In 1934, it was renamed Bean Common Mosaic to differentiate it from Bean Yellow Mosaic, which was caused by the Bean Yellow Mosaic virus (BYMV) (66). BCMV consists of two serotypes, both of which were identified by (67). Reports have documented BCMV infections in *Vigna angularis* plants from China, Korea and India (68, 69). The virus has been shown to cause severe symptoms in adzuki beans, and even mild or symptomless infections can reduce crop yield by up to 50% (70). The absence of resistance sources and QTLs against BCMV in adzuki beans underscores the need for advanced breeding approaches.

Expression of RNA silencing genes against BCMV in adzuki bean

Plants utilize RNA silencing as a defense mechanism against viruses, with miRNAs playing a significant role in regulating target gene expression in response to various stresses (71). Essential for the biogenesis of miRNAs are regulatory proteins such as Argonaute (AGO), Dicer-like (DCL) and RNA-dependent RNA polymerase (RDR). DCL, an endoribonuclease -active member of the RNase III family, cleaves double-stranded RNAs (dsRNAs) into small RNA duplexes containing 21-24 nucleotides. Small RNAs guide AGOs to their targets, leading to the cleavage of target mRNA, chromatin modifications like histone and/or cytosine methylation, or heterochromatin formation (72). Initiating and amplifying the silencing signal requires the conserved RDR catalytic domain (73).

Additionally, the expression patterns of DCL, AGO and RDR genes under biotic (*Podosphaera xanthii* and BCMV infection) and abiotic (drought) stress were analyzed using quantitative real-time reverse transcription PCR (qRT-PCR) to investigate their role in post-transcriptional regulation of gene expression. In BCMV-infected plants, the genes VaDCL2a/2b/2d/4 and VaRDR1b/1c/2/3 were downregulated, while VaDCL2c was upregulated (74). The varying expression patterns of these genes in response to BCMV infection suggest that RNA silencing plays complex roles in regulating adzuki beans ability to withstand BCMV.

Candidate-resistant genes and gene silencing techniques against viral diseases in *Vigna* species

The traits' QTLs have been mapped to known genes using the candidate gene approach. Resistance gene analog (RGA) markers, specifically YR4 and CYR1, are fully associated with MYMIV resistance in *Vigna mungo* and *Vigna radiata*, suggesting that CYR1 may be a candidate gene for disease

resistance (75). In mungbean, CYR1 is found to be partially, but not completely, linked to MYMIV resistance, indicating that multiple loci, rather than a single gene, contribute to the transmission of resistance. Selected candidate differentially expressed genes (DEGs) associated with MYMV defense mechanisms-Vradi06g11500, Vradi09g06830, Vradi04g07450, Vradi08g04110, Vradi06g13520 and Vradi01g04820-were functionally validated through qRT-PCR analysis in green gram. The results revealed essentially identical expression patterns for each of the studied DEGs, consistent with the RNA-Seq findings and demonstrated that these DEGs were expressed in both susceptible and resistant genotypes (76).

Pathogenic derived resistance through transgenic approaches in *Vigna* species

Various transgenic approaches have been developed to confer virus resistance in crops, with pathogen-derived resistance (PDR) playing a crucial role in crop protection. Additionally, gene silencing technologies can be employed to express different functional or dysfunctional YMV genes in mung bean, such as coat protein (CP), protease, membrane protein (MP) and replicase (4). In one study, MYMIV clones were inoculated with a complementary-sense gene (AC1) encoding Rep (Replication) in mung bean plants, resulting in a 64% infection rate (77). However, the severity of symptoms and the percentage of infections decreased when co-inoculation was performed with the Anti-Rep construct. It was discovered that deletions of 75 and 150 amino acids at the N-terminal of the CP of MYMIV affect both pathogenicity and systemic spread (78). In mung bean, agro-inoculation of the CP hairpin construct (Cphp) has been shown to inhibit viral pathogenesis (79). An RNAi (hairpin) constructed under d35S, containing the coat protein gene of CABMV and the proteinase cofactor gene of CPSMV, was introduced via particle bombardment (80). In another study, researchers demonstrated that RNAi-derived resistance to MYMIV in cowpeas led to nearly complete resistance in plants where agro-infection of transgenic lines expressing AC2-hp and AC2+AC4-hp RNA was performed (81). Given the rapid advancements in biotechnology, PDR for managing YMD in *Vigna* holds great promise for the near future.

Prospects

The pursuit of resistance breeding and the use of modern breeding techniques to treat viral infections in *Vigna* are critical strategies for guaranteeing the sustainable and resilient production of these key plants. In addition to traditional resistance breeding, the use of advanced techniques such as Marker-Assisted Selection (MAS), Pathogen-Derived Resistance (PDR), Host-Induced Gene Silencing (HIGS) and Virus-Induced Gene Silencing (VIGS) has significantly accelerated the pace and precision of developing resistant genotypes within *Vigna* species. Furthermore, functional genomics has facilitated the identification of novel candidate genes that confer disease resistance, along with elucidating the molecular mechanisms underlying host plant resistance. In this era of rapid biotechnological advancement, PDR holds great potential for managing yellow mosaic diseases (YMD) in *Vigna* in days to come.

Conclusion

Climate change presents significant challenges to agroecosystems and global food security. To sustainably meet the growing demand for food, food production must be doubled. *Vigna* species represent an economically important group of crop plants, but the increasing incidence of various viral diseases is threatening their yield. Therefore, utilizing the genetic diversity within *Vigna* species is essential for developing resistance to these viral diseases. As technology advances and our understanding of plant-virus interactions deepen, gene silencing, gene editing and omics technologies are poised to play a pivotal role in shaping the future of crop protection and ensuring food security.

Acknowledgements

The authors wish to thank the Science and Engineering Research Board, Department of Science and Technology. Our heartfelt thanks to the Department of Plant Pathology and Department of Crop Physiology and Biochemistry, V.O.C Agricultural College and Research Institute, Killikulam.

Authors' Contributions

GP and SD conceived the concept and wrote the manuscript. SD and APM gave ideas for the design of the diagrams and tables. GP designed the diagrams and tables. SD, SJ, SS, KPA, AS and JH revised and finalized the manuscript. All authors read and approved the final manuscript.

Compliance with Ethical Standards

Conflict of interest: Authors do not have any conflict of interest to declare.

Ethical issues: None

References

- Crops and livestock products. Food and Agriculture Organization. FAO Statistical Database [Internet]. 2021. License: CC BY-NC-SA 3.0 IGO. [updated on 2024 Jul 25; cited on 2024 Jul 28]. <https://www.fao.org/faostat/en/#data/QCL>
- Datta S, Gupta S. Use of genomic resources in improvement of *Vigna* species. *Journal of Food Legumes*. 2009;22(1):1-10.
- Agricultural statistics at a glance. Department of agricultural statistics. Ministry of agriculture and farmers' welfare, government of India [Internet]. [updated 2024 Jul 30; cited 2024 Jul 31]. Available from: https://agriwelfare.gov.in/en/Agricultural_Statistics_at_a_Glance
- Karthikeyan A, Shobhana VG, Sudha M, Raveendran M, Senthil N, Pandiyan M, Nagarajan P. Mungbean Yellow Mosaic Virus (MYMV): A threat to green gram (*Vigna radiata*) production in Asia. *Int J Pest Manag*. 2014;60(4):314-24. <https://doi.org/10.1080/09670874.2014.982230>
- USDA. National nutrient database for standard reference. "Mungo beans, mature seeds, raw". US Department of Agriculture [Internet]. [updated 2024 Mar 1; cited 2024 Jul 12]. 2019. Available from: <https://fdc.nal.usda.gov/fdc-app.html#/food-details/174256/nutrients>
- Arora R. Diversity and collection of wild *Vigna* species in India. *FAO/IBPGR Plant Genet Resour Newslett*. 1985;63:26-33.
- Wang Y, Yao X, Shen H, Zhao R, Li Z, Shen X, et al. Nutritional composition, efficacy and processing of *Vigna angularis* (Adzuki bean) for the human diet: An overview. *Molecules*. 2022;27(18):6079. <https://doi.org/10.3390/molecules27186079>
- Pandiyan M, Sivakumar P, Krishnaveni A, Sivakumar C, Radhakrishnan V, Vaithiyalingam M, Tomooka N. Adzuki bean. In: Prataap A, Gupta S, editors. *The beans and the peas*. Cambridge: Woodhead Publishing. 2021;89-103. <https://doi.org/10.1016/B978-0-12-821450-3.00006-8>
- Agricultural and Processed Food Products Export Development Authority (APEDA) [Internet]. 2022-23 [cited on 2024 Jul 29]. Available from: https://apeda.gov.in/apedawebsite/SubHead_Products/Pulses.htm"https://apeda.gov.in/apedawebsite/SubHead_Products/Pulses.htm#
- Ilyas M, Qazi J, Mansoor S, Briddon RW. Molecular characterisation and infectivity of a "Legumovirus"(Genus *Begomovirus*: family Geminiviridae) infecting the leguminous weed *Rhynchosia minima* in Pakistan. *Virus Res*. 2009;145(2):279-84. <https://doi.org/10.1016/j.virusres.2009.07.018>
- Nene YL. A survey of viral diseases of pulse crops in Uttar Pradesh: Final technical report. 1972:191.
- Fauquet CM, Bisaro DM, Briddon RW, Brown JK, Harrison BD, Rybicki EP, et al. Revision of taxonomic criteria for species demarcation in the family Geminiviridae and an updated list of begomovirus species. *Arch Virol*. 2003;148(2):405-20. <http://doi.org/10.1007/s00705-002-0957-5>
- Bashir M, Zubair M. Identification of resistance in Urdbean (*Vigna mungo*) against two different viral diseases. *Pak J Bot*. 2002;34(1):49-51.
- Qazi J, Mansoor S, Amin I, Awan MY, Briddon RW, Zafar Y. First report of Mungbean Yellow Mosaic India Virus on mothbean in Pakistan. *Plant Pathol*. 2006;55(6):818. <http://doi.org/10.1111/j.1365-3059.2006.01475.x>
- Priya L, Arumugam PM, Shoba D, Kumari SMP, Aananthi N. Genetic variability and correlation studies in black-gram [*Vigna mungo* (L.) Hepper]. *Electron J Plant Breed*. 2018;9(4):1583-87. <http://doi.org/10.5958/0975-928X.2018.00197.7>
- Gupta S, Kumar S, Singh R, Chandra S. Identification of a single dominant gene for resistance to mungbean yellow mosaic virus in blackgram [*Vigna mungo* (L.) Hepper]. *SABRAO J Breed Genet*. 2005;37(2):85-89.
- Shukla GP, Pandya BP. Resistance to yellow mosaic in green gram. *SABRAO J Breed Genet*. 1985;17(2):165-71.
- Sandhiya V, Saravanan S. Genotypic analysis for retrieval of mymv resistant progenies from certain crosses of mungbean [*Vigna radiata* (L.) Wilczek]. *Indian J Agric Res*. 2020;54(4):511-15. <http://doi.org/10.18805/IJARE.A-5262>
- Verma RP, Singh DP. The allelic relationship of genes giving resistance to mungbean yellow mosaic virus in blackgram. *Theor Appl Genet*. 1986;72:737-38. <https://doi.org/10.1007/BF00266537>
- Chippy AK, Pillai MA, Shoba D. Genetic diversity analysis in blackgram [*Vigna mungo* (L.) Hepper]. *Electron. J Plant Breed*. 2021;12(1):37-45. <https://doi.org/10.37992/2021.1201.006>
- Priyadarshni S, Saravanan S, Elanchezyan K, Pushpam AK, Pillai MA. Efficiency and effectiveness of physical and chemical mutagens in cowpea [*Vigna unguiculata* (L.) Walp]. *Electron J Plant Breed*. 2020;11(03):803-08.
- Vairam N, Lavanya SA, Muthamilan M, Vanniarajan C. Screening of M3 mutants for yellow vein mosaic virus resistance in greengram [*Vigna radiata* (L.) Wilczek]. *Internet J Plant Sci*. 2016;11(2):265-69. <http://doi.org/10.15740/HAS/IJPS/11.2/265-269>
- Sudha M, Anusuya P, Mahadev NG, Karthikeyan A, Nagarajan P, Raveendran M. Molecular studies on mungbean [*Vigna radiata* (L.) Wilczek] and ricebean [*Vigna umbellata* (Thunb.)] interspecific

- hybridisation for mungbean yellow mosaic virus resistance and development of species-specific SCAR marker for rice bean. Arch Phytopathol Pflanzenschutz. 2013;46(5):503-17. <https://doi.org/10.1080/03235408.2012.745055>
24. Shoba D, Manivannan N, Vindhivarman P. Genetic diversity analysis of groundnut genotypes using SSR markers. Electron J Plant Breed. 2010;1(6):1420-25.
 25. Gupta S, Gupta DS, Anjum TK, Pratap A, Kumar J. Inheritance and molecular tagging of MYMIV resistance gene in blackgram [*Vigna mungo* (L.) Hepper]. Euphytica. 2013;193:27-37. <https://doi.org/10.1007/s10681-013-0884-4>
 26. Sathees N, Shoba D, Mani N, Saravanan S, Kumari MP, Pillai MA. Tagging of SSR markers associated to yellow mosaic virus resistance in black gram [*Vigna mungo* (L.) Hepper]. Euphytica. 2022;218(3):23. <https://doi.org/10.1007/s10681-022-02976-3>
 27. Singh N, Mallick J, Sagolsem D, Mandal N, Bhattacharyya S. Mapping of molecular markers linked with MYMIV and yield attributing traits in mungbean. Indian J Genet Pl Br. 2018;78(1): 118-26.
 28. Rambabu E, Anuradha C, Sridhar V, Reddy SS. Genetics of Mungbean Yellow Mosaic Virus (MYMV) resistance in black gram [*Vigna mungo* (L.) Hepper]. Int J Curr Microbiol App Sci. 2018;7(4):3869-72.
 29. Sai C, Natarajan P, Raveendran M, Rabindran R, Kannan Babu JR, Senthil N. Understanding the inheritance of mungbean yellow mosaic virus (MYMV) resistance in mungbean [*Vigna radiata* (L.) Wilczek]. Mol Breed. 2017;37:1-5. <https://doi.org/10.1007/s11032-017-0650-8>
 30. Tamilzharasi M, Vanniarajan C, Karthikeyan A, Soufmanien J, Pillai MA, Meenakshisundram P. Evaluation of urdbean (*Vigna mungo*) genotypes for mungbean yellow mosaic virus resistance through phenotypic reaction and genotypic analysis. Legume Res. 2020;43(5):728-34. <http://doi.org/10.18805/LR-4035>
 31. Dhole VJ, Reddy KS. Development of a SCAR marker linked with a MYMV resistance gene in mungbean [*Vigna radiata* L. Wilczek]. Plant Breed. 2013;132(1):127-32. <https://doi.org/10.1111/pbr.12006>
 32. Shoba D, Manivannan N, Vindhivarman P, Nigam SN. SSR markers associated for late leaf spot disease resistance by bulked segregant analysis in groundnut (*Arachis hypogaea* L.). Euphytica. 2012;188:265-72. <https://doi.org/10.1007/s10681-012-0718-9>
 33. Naik BJ, Anuradha C, Kumar PA, Sreedhar V, Chary SR. Identification of simple sequence repeats (SSR) markers linked to Yellow Mosaic Virus (YMV) resistance in blackgram [*Vigna mungo* (L.) Hepper]. Agric Update. 2017;12(TECHSEAR-3):812-19. [https://doi.org/10.15740/HAS/AU/12.TECHSEAR\(3\)2017/812-819](https://doi.org/10.15740/HAS/AU/12.TECHSEAR(3)2017/812-819)
 34. Ramalingam J, Raveendra C, Savitha P, Vidya V, Chaithra TL, Velprabakaran S. Gene pyramiding for achieving enhanced resistance to bacterial blight, blast and sheath blight diseases in rice. Front Plant Sci. 2020;11:591457 <https://doi.org/10.3389/fpls.2020.591457>
 35. Chandran S, Pukalenty B, Adhimoalam K, Manickam D, Sampathrajan V, Chocklingam V. Marker-assisted selection to pyramid the opaque-2 (o2) and β -carotene (crtRB1) genes in maize. Front Genet. 2019;10:859. <https://doi.org/10.3389/fgene.2019.00859>
 36. Subramaniyan R, Kulanthaivel V, Narayana M, Angamuthu M, Kothandaraman SV. Marker-assisted backcross breeding for enhancing Mungbean Yellow Mosaic Virus (MYMV) disease resistance in blackgram [*Vigna mungo* (L.) Hepper] cv MDU 1. Physiol Mol Plant Pathol. 2021;116:101732. <https://doi.org/10.1016/j.pmp.2021.101732>
 37. Biswas KK, Biswas KO, Malathi VG, Chattopadhyay CH. Evaluation of urdbean cultivars for identification of resistance to leaf crinkle disease by mechanical sap inoculation. Indian Phytopath. 2012;65(4):416-17.
 38. Williams FJ, Grewal JS, Amin KS. Serious and new diseases of pulse crops in India in 1966. Plant Dis Rep. 1968;52(4):300-04.
 39. Prasad M, Sarma B, Sangit Kumar SK, Prasad M. Transmission tests and varietal screening for urd leaf crinkle virus in blackgram [*Vigna mungo* (L.) Hepper]. Annals of Plant Protection Sciences. 1998;6(2):205-07.
 40. Singh G, Gurha SN, Ghosh A. Diseases of mungbean and urdbean and their management. In: Thind TS, editor. Diseases of field crops and their management. Ludhiana, India: National Agricultural Technology Information Centre; 1998:179-204.
 41. Rao R, Babu B, Sreekant M, Kumar V. ELISA and infectivity assay based survey for the detection of peanut bud necrosis virus in mungbean and urdbean in Andhra Pradesh. Indian J Plant Prot. 2003;31(1):26-28.
 42. ICAR-IIPR (Indian Institute of Pulses Research), Kanpur [Internet]. 2013. [updated on 2024 Jul 29; cited on 2024 Jul 30]. Available from: <https://iipr.icar.gov.in/variety/>
 43. Varieties released. NPRC (National Pulse Research Centre) – Vamban. [Internet] 2023. TNAU (Tamilnadu Agricultural University) [updated on 2024 Mar 23, cited on 2024 Jun 12]. Available from: <https://tnau.ac.in/site/prs-vamban/varieties-released/>
 44. Sandhu JS, Gill RK, Singh I, Singh S, Gupta SK. Urdbean variety Mash 391. Indian J Genet Pl Br. 2012;72(1):109-10.
 45. Sravika A, Kennedy JS, Rajabaskar D, Rajeswari E. Field screening of greengram [(*Vigna radiata* L.) Wilczek] genotypes for resistance against urdbean leaf crinkle virus. Indian J Agric Res. 2019;53(4):458-62. <https://doi.org/10.18805/IJARE.A-5184>
 46. Abdulrahimzai MR, Venkateswarlu N, Prasad KVH, Naidu GM. Evaluation of black gram genotypes for resistance against thrips and whitefly in relation to leaf curl and yellow mosaic virus. Andhra Pradesh J Agric Sci. 2019;5:173-80.
 47. Madhavi KJ. Seed transmission studies of Peanut Bud Necrosis Virus (PBNV) and Tobacco Streak Virus (TSV) isolates of blackgram and greengram of Telangana. J Pharmacogn Phytochem. 2021;10(5):330-32.
 48. Agrawal HO. Identification of cowpea mosaic virus isolates. Mededelingen Van De Landbouwhoogeschool te, Wageningen. 1964;64:1-53.
 49. De Jager CP. Cowpea severe Mosaic Virus, Kew, UK, CMI (Commonwealth Mycological Institute). CMI/AAB Descriptions of Plant Viruses. 1979;209.
 50. Walters HJ, Barnett Jr O. Bean leaf beetle transmission of arkansas cowpea mosaic virus. Phytopathol. 1964;54:911.
 51. Booker HM, Umaharan P, McDavid CR. Effect of cowpea severe mosaic virus on crop growth characteristics and yield of cowpea. Plant Dis. 2005;89(5):515-20. <https://doi.org/10.1094/PD-89-0515>
 52. Singh SR, Allen DJ. Cowpea pests and diseases [e-book]. Ibadan, Nigeria: International institute of tropical agriculture. Manual Series, No. 2. 1979 [cited on Jul 16 2024].113. Available from: https://pdf.usaid.gov/pdf_docs/PNAAV133.pdf.
 53. Chant SR. Viruses of cowpea, [*Vigna unguiculata* (L.) Walp.], in Nigeria. Ann Appl Biol. 1959;47(3):565-72. <https://doi.org/10.1111/j.1744-7348.1959.tb07288.x>
 54. Gilmer R, Whitney W, Williams R. Epidemiology and control of cowpea mosaic in western Nigeria. Proceedings First IITA Grain Legume Workshop, IITA. 1974. Ibadan, Nigeria.
 55. Bashir M. Serological and biological characterization of seed-borne isolates of blackeye cowpea mosaic and cowpea aphid-borne mosaic potyviruses in *Vigna unguiculata* (L.) Walp. Doctor of Philosophy [thesis]. Oregon State University; 1992.
 56. Thottappilly G, Rossel HW. Virus diseases of cowpea in tropical Africa. Int J Pest Manag. 1992;38(4):337-48. <https://doi.org/10.1080/09670879209371724>
 57. Varma A, Malathi VG. Emerging geminivirus problems: A serious threat to crop production. Ann Appl Biol. 2003;142(2):145-64. <https://doi.org/10.1111/j.1744-7348.2003.tb00240.x>

58. Bliss FA, Robertson DG. Genetics of host reaction in cowpea-to-cowpea yellow mosaic virus and cowpea mottle virus 1. *Crop Sci.* 1971;11(2):258-62. <https://doi.org/10.2135/cropsci1971.0011183X001100020027x>
59. Orawu M, Melis R, Laing M, Derera J. Genetic inheritance of resistance to cowpea aphid-borne mosaic virus in cowpea. *Euphytica.* 2013;189:191-201. <https://doi.org/10.1007/s10681-012-0756-3>
60. Dhanasekar P, Reddy K. Serological screening of cowpea genotypes for resistance against cowpea aphid borne mosaic virus using DAS-ELISA. *Asian J Plant Pathol.* 2015;9(2):83-90. <https://doi.org/10.3923/ajppaj.2015.83.90>
61. Ouédraogo JT, Gowda BS, Jean M, Close TJ, Ehlers JD, Hall AE. An improved genetic linkage map for cowpea [*Vigna unguiculata* L.) Walp] combining AFLP, RFLP, RAPD, biochemical markers and biological resistance traits. *Genome.* 2002;45(1): 175-88. <https://doi.org/10.1139/g01-102>
62. Menéndez CM, Hall AE, Gepts P. A genetic linkage map of cowpea (*Vigna unguiculata*) developed from a cross between two inbred, domesticated lines. *Theor Appl Genet.* 1997;95: 1210-17. <https://doi.org/10.1007/s001220050683>
63. Gioi TD, Boora KS, Chaudhary K. Identification and characterization of SSR markers linked to yellow mosaic virus resistance genes in cowpea (*Vigna unguiculata*). *Int J Plant Res.* 2012;2(1):1-8. <http://doi.org/10.5923/j.plant.20120201.01>
64. Bhattarai G, Shi A, Qin J, Weng Y, Bradley Morris BJ, Pinnow DL, et al. Association analysis of Cowpea Mosaic Virus (CPMV) resistance in the USDA cowpea germplasm collection. *Euphytica.* 2017;213:230. <https://doi.org/10.1007/s10681-017-2015-0>
65. Tizioto PC, Meirelles SL, Tullio R, Rosa AD, de Alencar MM, de Medeiros SR, et al. Candidate genes for production traits in Nelore beef cattle. *Genet Mol Res.* 2012;11(4):4138-44. <https://doi.org/10.4238/2012.September.19.1>
66. Jordan R, Hammond J. Bean common mosaic virus and bean common mosaic necrosis virus (genus Potyvirus; Potyviridae). In: Bamford DH, Zuckerman M, editors. *Encyclopedia of Virology.* Academic Press. 2021;184-91. <https://doi.org/10.1016/B978-0-12-809633-8.21293-4>
67. Wang WY, Mink GI, Silbernagel MJ, Davis WC. Production of hybridoma lines secreting specific antibodies to Bean Common Mosaic-Virus (bcmv) strains. In *Phytopathology.* 1984;74(9): 1142-42.
68. Jung HW, Jung HJ, Yun WS, Kim HJ, Hahm YI, Kim HJ. Characterization and partial nucleotide sequence analysis of Alfalfa mosaic Alfamoviruses isolated from potato and azuki bean in Korea. *Plant Pathol. J.* 2000;16(5):269-79.
69. Li YQ, Liu ZP, Yang K, Li YS, Zhao B, Fan ZF, Wan P. First report of bean common mosaic virus infecting Azuki bean (*Vigna angularis*) in China. *Plant Disease.* 2014;98(7):1017-17. <https://doi.org/10.1094/PDIS-01-14-0064-PDN>
70. Morales FJ. Common beans. In: Loebenstein G, Carr JP, editors. *Natural resistance mechanisms of plants to Viruses.* Dordrecht: Springer; 2006;367-82.
71. Chen X. Small RNAs and their roles in plant development. *Annu Rev Cell Dev Biol.* 2009;25(1):21-44. <https://doi.org/10.1146/annurev.cellbio.042308.113417>
72. Moazed D. Small RNAs in transcriptional gene silencing and genome defence. *Nature.* 2009;457(7228):413-20. <https://doi.org/10.1038/nature07756>
73. Sijen T, Fleenor J, Simmer F, Thijssen KL, Parrish S, Timmons L, et al. On the role of RNA amplification in dsRNA-triggered gene silencing. *Cell.* 2001;107(4):465-76. [https://doi.org/10.1016/S0092-8674\(01\)00576-1](https://doi.org/10.1016/S0092-8674(01)00576-1)
74. Li Y, Ma E, Yang K, Zhao B, Li Y, Wan P. Genome-wide analysis of key gene families in RNA silencing and their responses to biotic and drought stresses in adzuki bean. *BMC Genomics.* 2023;24(1): 195. <https://doi.org/10.1186/s12864-023-09274-9>
75. Anuragi H, Yadav R, Sheoran R. Gamma-rays and EMS induced resistance to mungbean yellow mosaic India virus in mungbean [*Vigna radiata* (L.) R. Wilczek] and its validation using linked molecular markers. *Int J Radiat Biol.* 2022;98(1):69-81. <https://doi.org/10.1080/09553002.2022.1998710>
76. Sudha M, Karthikeyan A, Madhumitha B, Veera Ranjani R, Kanimoli Mathivathana M, Dhasarathan M. Dynamic transcriptome profiling of mungbean genotypes unveil the genes respond to the infection of mungbean yellow mosaic virus. *Pathogens.* 2022;11(2):190. <https://doi.org/10.3390/pathogens11020190>
77. Haq QM, Jyothsna P, Ali A, Malathi VG. Coat protein deletion mutation of Mungbean Yellow Mosaic India Virus (MYMIV). *J Plant Biochem Biotechnol.* 2011;20:182-89. <https://doi.org/10.1007/s13562-011-0044-7>
78. Haq QM, Rouhibakhsh A, Ali A, Malathi VG. Infectivity analysis of a blackgram isolate of mungbean yellow mosaic virus and genetic assortment with MYMIV in selective hosts. *Virus Genes.* 2011;42:429-39. <https://doi.org/10.1007/s11262-011-0591-y>
79. Kumari A, Malathi VG. RNAi-mediated strategy to develop transgenic resistance in grain legumes targeting the Mungbean Yellow Mosaic India Virus coat protein gene. In: *Proceedings of the International Conference on Plant Biotechnology for Food Security: New Frontiers.* 2012;21-24.
80. Cruz AR, Aragão FJ. RNA i-based enhanced resistance to cowpea severe Mosaic virus and cowpea aphid-borne mosaic virus in transgenic cowpea. *Plant Pathol.* 2014;63(4):831-37. <https://doi.org/10.1111/ppa.12178>
81. Kumar S, Tanti B, Patil BL, Mukherjee SK, Sahoo L. RNAi-derived transgenic resistance to Mungbean Yellow Mosaic India Virus in cowpea. *PLoS One.* 2017;12(10). <https://doi.org/10.1371/journal.pone.0186786>
82. International Committee on Taxonomy of Viruses (ICTV). Taxonomy release history. Germany: ICTV; 2023. Available from: <https://ictv.global/taxonomy/history>
83. Gupta DS, Kumar J, Parihar AK, Gupta S. Breeding for high-yielding and disease-resistant urdbean cultivars. In: Gosal SS, Wani SH, editors. *Accelerated Plant Breeding.* Cham: Springer; 2020;173-91. https://doi.org/10.1007/978-3-030-47306-8_6
84. Singh DP, Singh BB, Pratap A. Genetic improvement of mungbean and urdbean and their role in enhancing pulse production in India. *Indian J Genet Plant Breed.* 2016;76(04): 550-67. <https://doi.org/10.5958/0975-6906.2016.00072.9>
85. Sala M, Yuvarani R, Saranya M, Nirubana V, Sridevi R, Gokulakannan K. Morphological screening of black gram genotypes with reference to mung bean yellow mosaic virus. *Int J Environ Clim Change.* 2022;12(12):1858-62. <https://doi.org/10.9734/JECC/2022/v12i121634>
86. Pillai MA, Shunmugavalli N, Selvi B, Muthuswamy A, Anand G, Shoba RP. Blackgram KKM 1 (KKB 05011), a rice fallow variety suited for Thimirabarani tracks of Tamil Nadu. *Electron J Plant Breed.* 2017;8(3):900-06. <https://doi.org/10.5958/0975-928X.2017.00149.1>
87. Gurha S, Misra D, Kamthan K. Studies on some aspects of yellow mosaic disease of blackgram [*Vigna mungo* (L.) Hepper]. *Madras Agric J.* 1982;69(7):435-38. <https://doi.org/10.29321/MAJ.10.A02739>
88. Nair RM, Götz M, Winter S, Giri RR, Boddepalli VN, Sirari A, et al. Identification of mungbean lines with tolerance or resistance to yellow mosaic in fields in India where different Begomovirus species and different *Bemisia tabaci* cryptic species predominate. *Eur J Plant Pathol.* 2017;149:349-65. <https://doi.org/10.1007/s10658-017-1187-8>
89. Meghwal R, Joshi U, Kumar S, Sharma R. Screening of moth bean (*Vigna aconitifolia*) core collection against yellow mosaic virus. *Indian J Agric Sci.* 2015;85:571-75. <https://doi.org/10.56093/ijas.v85i4.47948>
90. International Atomic Energy Agency (IAEA). Mutant variety database. IAEA; 2022. Available from: <https://nucleus.iaea.org/sites/>

[mvd/SitePages/Search.aspx](#)

91. Subramaniyan R, Narayana M, Krishnamoorthy I, Natarajan G, Gandhi K. Novel and stable QTL regions conferring resistance to MYMV disease and its inheritance in blackgram [*Vigna mungo* (L.) Hepper]. *J Genet.* 2022;101:18. <https://doi.org/10.1007/s12041-022-01359-w>
92. Mathivathana MK, Murukarthick J, Karthikeyan A, Jang W, Dhasarathan M, Jagadeeshselvam N. Detection of QTLs associated with Mungbean Yellow Mosaic Virus (MYMV) resistance using the interspecific cross of *Vigna radiata* x *Vigna umbellata*. *J Appl Genet.* 2019;60:255-68. <https://doi.org/10.1007/s13353-019-00506-x>
93. Vadivel K, Manivannan N, Mahalingam A, Satya VK, Vanniarajan C, Ragul S. Identification and validation of quantitative trait loci of mungbean yellow mosaic virus disease resistance in blackgram [*Vigna mungo* (L.) Hepper]. *Legume Res.* 2023;46(6):778-84. <http://doi.org/10.18805/LR-4459>
94. Alam AM, Somta P, Srinives P. Identification and confirmation of quantitative trait loci controlling resistance to mungbean yellow mosaic disease in mungbean [*Vigna radiata* (L.) Wilczek]. *Mol Breed.* 2014;34:1497-506. <https://doi.org/10.1007/s11032-014-0133-0>
95. Chen HM, Ku HM, Schafleitner R, Bains TS, George Kuo C, Liu CA. The major quantitative trait locus for Mungbean Yellow Mosaic Indian Virus resistance is tightly linked in repulsion phase to the major bruchid resistance locus in a cross between mungbean [*Vigna radiata* (L.) Wilczek] and its wild relative *Vigna radiata* ssp. *sublobata*. *Euphytica.* 2013;192:205-16. <https://doi.org/10.1007/s10681-012-0831-9>
96. Kitsanachandee R, Somta P, Chatchawankanphanich O, Akhtar KP, Shah TM, Nair RM. Detection of quantitative trait loci for Mungbean Yellow Mosaic India Virus (MYMIV) resistance in mungbean [*Vigna radiata* (L.) Wilczek] in India and Pakistan. *Breed Sci.* 2013;63(4):367-73. <https://doi.org/10.1270/jsbbs.63.367>
97. Narayanan M. Genetics of yellow mosaic virus resistance in blackgram [*Vigna mungo* (L.) Hepper] [thesis]. Department of Genetics and Plant Breeding, V.O.C AC and RI, Killikulam, Tamilnadu Agricultural University; 2021.
98. Kumar D, Golakia BA, Parakhia AM. Characterization and genetic diversity of cowpea [*Vigna unguiculata* (L.) Walp] genotypes linked to cowpea yellow mosaic virus. *Legume Res.* 2018;41(1):27-33. <https://doi.org/10.18805/lr.v0i0F.9101>
99. ICAR- IIPR, Kanpur. Project report, Arid Legumes, AINRP on Arid Legumes, Directorate of Pulse Development [Internet]. 2017. [cited on 2024 Jun 26]. Available from: <https://dpd.gov.in/7%20to%2012%20Arid%20Legumes%20Varieties.pdf>