E-ISSN: 2618-0618
P-ISSN: 2618-060X

NAAS Rating (2026): 5.20
www.agronomyjournals.com
2026; 9(1): 202-207
Received: 17-11-2025
Accepted: 19-12-2025

K Dharani Sree
Department of Genetics and Plant Breeding, University of Agricultural Sciences, Dharwad, Karnataka, India

Sumangala Bhat
Department of Genetics and Plant Breeding, University of Agricultural Sciences, Dharwad, Karnataka, India

Suma Mogali
Department of Genetics and Plant Breeding, University of Agricultural Sciences, Dharwad, Karnataka, India

Gurupad Balol
Department of Genetics and Plant Breeding, University of Agricultural Sciences, Dharwad, Karnataka, India

Corresponding Author:
K Dharani Sree
Department of Genetics and Plant Breeding, University of Agricultural Sciences, Dharwad, Karnataka, India

Identification of mungbean genotypes with multiple disease resistance

K Dharani Sree, Sumangala Bhat, Suma Mogali and Gurupad Balol

DOI: https://www.doi.org/10.33545/2618060X.2026.v9.i1c.4606

Abstract
Mungbean is a high-protein legume and is widely cultivated in a variety of cropping systems. Foliar diseases like powdery mildew, anthracnose and mungbean yellow mosaic virus (MYMV) not only limit the productivity but also affect the physical quality of seeds rendering them unusable. In this study 130 advanced breeding lines were screened for multiple disease resistance using infector row method. Screening for powdery mildew and anthracnose was done during *kharif* 2021 and for MYMV during summer 2022 with two trials per season, each under protected and unprotected conditions to record the yield differences due to the diseases. Of the 130 advanced breeding lines screened, *Vigna trilobata* was found to show multiple disease resistance. The advanced breeding lines such as DGG-227, V-02-709, DGG-96, DGG-21 showed resistant reaction for anthracnose. GPM-19 was the only genotype which was found to be resistant to powdery mildew. During *summer* 2022, 18 genotypes showed resistant reaction towards MYMV.

Keywords: Advanced breeding lines, multiple disease resistance, mungbean, screening

Introduction
Mungbean is an important pulse crop in India and is believed to be originated from Indo Burma region. It is short duration legume crop grown mostly as a fallow crop in rotation with rice. Similar to the leguminous pulses, mungbean enriches soil nitrogen content. It is grown mostly in Asian region traditionally, while its cultivation has spread to Africa and America relatively in the recent times. India contributes more than 70% of world's mungbean production.

In the tropics, mungbean acts as a host for pathogens such as bacteria, viruses and fungi. Powdery mildew caused by *Erysiphe polygoni* is one of the prevalent fungal diseases causing severe yield losses in mungbean. The yield losses due to powdery mildew are estimated to be between 20% and 40% and 100% at seedling stage (Reddy *et al.*, 1994) [16]. In addition, numerous species of the fungus Colletotrichum are responsible for mungbean anthracnose but *C. truncatum* and *C. canescens* is the most prevalent pathogen in northern transistional tract of Karnataka (Mandal *et al.*, 2015) [9]. In India, it has been estimated that this disease reduces yield by 30% to 70% (Joshi and Tripathi, 2002) [5]. Mungbean yellow mosaic virus (MYMV) is one of the most destructive viral diseases of mungbean. MYMV is a member of family Geminiviridae and belongs to the genus Begomovirus and is transmitted by whitefly (*Bemesia tabaci)* as a vector. This disease can cause the yield losses upto 100% (Khattak *et al.*, 2000) [7].

The management of these diseases using chemicals is a costly affair and not environmentally safe. Hence deploying genetically resistant cultivars would be cost-effective, practically feasible, eco- and farmer-friendly and a viable alternative. With this prime concern, the advanced breeding lines of mungbean were screened for their response towards powdery mildew, anthracnose and MYMV to identify the genotypes with multiple disease resistance.

Materials and Methods
Experimental details
The disease reaction of one hundred and thirty advanced breeding lines including three suitable checks were screened for the above mentioned diseases under natural field conditions after ensuring enough load of inoculum using the infector rows. The experiment was conducted using

augmented design at E-block, Main Agricultural Research Station (MARS), College of Agriculture, Dharwad during the *kharif* 2021 and *summer* 2022. The advanced breeding lines of mungbean utilized in this investigation were obtained from AICRP on MULLaRP, UAS, Dharwad which included the stabilized lines derived from many crosses under the genetic background of diverse parental combinations, mutation *per se* and mutation breeding followed by recombination for some desirable traits. Apart from advanced breeding lines, the experimental material also included some of the varieties released by different stations across India and a few germplasm lines.

Screening for foliar diseases

During *kharif* 2021, the test genotypes and the checks were screened for fungal diseases *i.e.,* powdery mildew and anthracnose. One set of experiment was conducted with all the recommended cultivation and disease management practices. Another set of experiment was laid out during the same season in the vicinity of the first experimental plot under unprotected conditions. DGGV-2 was used as a susceptible check whereas TARM1 was used as a tolerant check. For disease reaction, percentage of leaf area covered by the disease was scored manually. The incidence of disease on the leaves of mungbean was scored by using standard scoring procedure given by Mayee and Datar (1986) [10]. The percentage was then converted to the disease score and the per cent disease index was calculated using the formula given by Wheeler (1969) [23]. Further the per cent yield reduction of each breeding line due to these diseases was calculated using the yield data from both protected and unprotected conditions.

$$\text{Per cent Disease Index (PDI)} = \frac{\text{Sum of numerical ratings}}{\text{Number of leaves observed x Maximum rating (9)}} \times 100$$

During *summer* 2022, the same set of 130 genotypes were screened for their reaction to MYMV since it has been discovered that the MYMV incidence is higher in summer than other seasons. In this season also two experiments (protected and unprotected conditions) were laid using augmented design. DGGV-2 was used as a susceptible check whereas IPM-2-14 was used as resistant check. The per cent disease incidence was calculated by using the formulae given by Bashir *et al*. (2006) [2] at 45 DAS, 60 DAS and physiological maturity. Based on the percent disease incidence, the genotypes were categorized into different groups based on the scale given by Bashir *et al.* (2006) [2]. Furthermore the per cent yield reduction of each breeding line was calculated.

$$\text{Per cent disease incidence} = \frac{\text{Total number of plants infected in a row}}{\text{Total number of plants in a row}} \times 100$$

The PDI of the diseases was further subjected to arc sine transformation and was then analysed using R software version 4.2.5 to know whether the breeding lines differed significantly for their reaction to these diseases.

Results and Discussion

The genotypes showed significant variation for reaction to all the three diseases (Table 1 and 2). Amongst all the breeding lines screened for powdery mildew, it has been found that only *Vigna trilobata* (wild relative) was immune and GPM-19 was resistant for this disease. The similar response of these two genotypes was previously reported by Sarkale (2015) [18] and Pooja and Bhat (2019) [15].

Table 1: Analysis of variance for foliar diseases screened during kharif 2021

Source of variation	Df	PDI (Anthracnose)	PDI (Powdery mildew)
Block (eliminating Check+Var.)	4	0.92	1.71
Entries (ignoring Blocks)	132	285.14 **	264.54 **
Checks	2	2414.87 **	3938.23 **
Varieties	129	248 **	204.91 **
Checks vs. Varieties	1	445.76 **	13.58 **
Error	8	1.15	1.05
Coefficient of variation		1.92	3.02
CD at 5% (Test Treatment and a Control Treatment)		2.99	2.85

df -degrees of freedom, CD-Critical difference, PDI-Per cent disease index

Table 2: Analysis of variance for foliar disease screened during summer 2022

Source of variation	d.f.	PDI (MYMV)
Block (eliminating Check+Var.)	5	1.65
Entries (ignoring Blocks)	132	201.56 **
Checks	2	3968.8 **
Varieties	129	144.27 **
Checks vs. Varieties	1	58.26 **
Error	10	1.58
Coefficient of variation		4.4
CD at 5% (Test Treatment and a Control Treatment)		3.5

df -degrees of freedom, CD-Critical difference, PDI-Per cent disease incidence

All the genotypes derived from the cross IPM-2-14 x IPM-2-17 (DGG-215-1, 2, 5, 6) except DGG-251 showed moderate resistance with lesser PDI than that of the parents in some cases. The reason behind this is that, both the parents involved in this cross are moderately resistant to powdery mildew which must have led to same level of resistance or rather increased levels of resistance with low PDI in the progeny. It was also observed that, in the crosses where the moderately resistant line DGG-1 was used as a female parent none of the breeding lines showed the resistance reaction but in the line DGG-216 (DGGV-2 x DGG-1) where DGG-1 was used as a male parent showed moderate resistance towards this disease. It can be reasoned that the pedigree method of breeding involving the parents DGGV-2 x DGG-1 has resulted in a genetic recombination conferring moderate resistance to powdery mildew. Since the pedigree to this segregant was not recorded, it is difficult to conclude about the genetic basis of this resistance (Table 3).

Some of the genotypes like DGG-10, DGG-19, DGG-12, DGG-95 derived from the crosses involving TARM-1, which was used as a tolerant check in this study showed moderate resistance. Some of the released varieties (COGG 912, Shikha, Vaibhav, Virat, AKM 8802) which were claimed as resistant in the corresponding locations showed similar reaction in Dharwad (Table 3). Two genotypes *viz.,* COGG 912 and Vaibhav showed similar response in the previous study conducted in the same location by Pooja and Bhat (2019) [15].

In the present investigation, the PDI of anthracnose ranged from 0.12 per cent to 91.56. The maximum PDI of 91.56 was recorded for the susceptible check, DGGV-2. For anthracnose most of the genotypes screened showed susceptibility except for some of the genotypes derived from mutants of Sonamung (DGG-191, DGG-227), the genotypes derived from the crosses involving TARM-1 and BGS-9 as parents (DGG-10, DGG-21) and the mutants of TARM-1 (DGG-95, DGG-96). This is because in the former case, the parent Sonamung is a photoperiod sensitive and the performance was poor in *kharif*. However, the mutants of this genotype performed well in *kharif* and were late maturing type, this might have aided the mutant genotypes to show resistance towards this disease resorting to the mechanism of disease escape. In the latter case, the mutations might have led to resistance in TARM-1 which is otherwise a susceptible variety. The germplasm lines like GPM-19, V-02-709 and *V. trilobata* showed resistance. One of the released variety, COGG-912 which was claimed to be resistant to foliar diseases was found to show similar reaction in this study. Some of the genotypes such as DGG-191, DGG-12, DGG-59 and DGG-122 screened previously in the same location showed consistently resistant response to anthracnose (Ashritha, 2021) [1].

In this study, the per cent disease incidence of MYMV ranged from 0 per cent to 85.57 per cent. Most of the breeding lines derived from resistant lines like IPM-2-14 (DGG-215-1, 2, 3, 5, 6, DGG-182-1,2, DGG-251) and IPM-2-03 which is moderately resistant (DGG-184,185, 186, 187, 71, 232) and the mutants of the resistant line LGG-460 (DGG-76, 73, 99) exhibited resistant to moderately resistant reaction. Interestingly some of the mutants of the susceptible line, Sonamung (DGG-190) and the recombinants involving mutant Sonamung (DGG-227,230) showed moderate resistance. The entry COGG 912 which was reported as highly resistant by Mahanta and Sao (2019) [8] was found to show resistant reaction in this study. The genotype, Samrat (PDM 139), which was reported as a resistant variety for use a parent in breeding programmes by Singh (1981) [19] and Paul *et al.* (2013) [14] has shown similar reaction in the current study.

Table 3: Disease response of advanced breeding lines of mungbean to foliar diseases

Pedigree	Advanced breeding lines	Anthracnose	PM	MYMV
Crosses involving DGG-1 (resistant to powdery mildew)				
GG-20-1	DGG-1	HS	MR	MS
DGG-1 X AKM-9904	DGG-178	S	MS	MS
DGG-1 X IPM 2-03 1-1	DGG-223	HS	HS	MS
DGG-1 X IPM-2-17	DGG-177	HS	MS	MR
DGG-1 X MH-2-15	DGG-180	HS	S	MR
DGG-1 X ML-1451	DGG-179	HS	HS	S
DGG-1 X Sonamung 57-2	DGG-224	HS	MS	MR
DGG-1 X Sonamung mutant 11-2	DGG-222	HS	HS	MR
DGG-1 × BWMCD-31	DGG-225	HS	S	HS
Crosses involving DGGV-2 (High yielding and susceptible to foliar diseases)				
Chinamung x TM-98-50	DGGV-2	HS	HS	HS
DGGV-2 X V-02-709	DGG-173	HS	S	S
	DGG-107	HS	HS	MR
	DGG-126	HS	HS	MR
DGGV-2 X WGG-42	DGG-203	HS	MS	MR
	DGG-205	S	S	MR
	DGG-197	HS	S	R
	DGG-199	HS	MR	MR
DGGV-2 X IPM 2-03	DGG-218	S	MS	R
	DGG-313	HS	S	MR
DGGV-2 X IPM 2-14	DGG-162	S	HS	MR
	DGG-100	HS	HS	MR
DGGV-2 X IPM-409-4	GBRD-9	HS	HS	MS
DGGV-2 x LGG-LGG (460)	DGG-250	S	MR	R
DGGV-2 X MH-421	DGG-124	HS	S	MR
DGGV-2 X SML1815	GG-K-21-5	HS	S	MR
	DGG-125	HS	MS	MR
	6 MBRD-118	HS	HS	S
	DGG-114-1	S	MS	MR
DGGV-2 X TM-96-2	DGG-119	HS	MR	HS
	8 BRD-9	S	MS	HS
DGGV-2 × SML-115	DGG-176	HS	S	MR
DGGV-2 X IPM-410-3	DGG-122	HS	S	S
DGGV-2 X RMG-1020	DGG-123	HS	MS	MR
DGGV-2 X GPM655460	Rpt – 8655460 T_1	HS	MS	R
DGGV-2 × Sonamung 57-2	DGG-219	HS	S	MS
DGGV-2 × SML66 × $VT_{11}7$	DGG-175	HS	S	MR
V-02-802 X DGGV-2	5 BRD – 3	HS	HS	MR
	DGG-113	HS	MR	S
	5 BRD 11	HS	MR	MR
	5 BRD 10	HS	S	MR
V-02-709 X DGGV-2	GG-K-21-1	HS	S	R
	GG-K-21-2	HS	S	MR

	7 BRD 12	HS	MR	HS
Crosses involving DGG-7 (Good yielder)				
Mutant of Selection 4	DGG-7	S	S	MR
DGG-7 X V-02-802	DGG-110	HS	S	R
	MBRD-56	HS	HS	S
	DGG -128	HS	MS	R
	5 MBRD-98	HS	MS	HS
	3 MBRD 58	S	HS	MS
	GG-K-21-3	S	S	MS
	DGG-109	HS	S	S
	4 MBRD -76	HS	MS	HS
V-02-802 X DGG-7	DGG-214	HS	S	MS
DGG-7 X V-02-803	GG-K-21-4	HS	HS	MS
DGG-7XV-02-709	DGG-116	MS	MS	R
	DGG -127	HS	MR	MS
	3 BRD-20	HS	MS	MR
	3 MBRD-36	HS	HS	HS
Mutant of DGG-7	DGG-59	HS	MS	S
Crosses involving IPM-2-14 (MYMV and leaf crinckle resistant)				
PDM 139 x EC 398884	IPM -2-14	HS	MR	R
IPM-2-14 X IPM 2-17	DGG-215-1	MS	MR	MR
	DGG-215-2	HS	MR	MR
	DGG-215-3	S	MS	R
	DGG-215-5	HS	MR	R
	DGG-215-6	HS	MR	S
	DGG-251	HS	HS	MR
	DGG-253	HS	MR	MS
IPM-2-14 X AKM-9904	DGG-182-1	HS	MS	MR
	DGG-182-2	HS	MS	MR
	DGG-182-3	HS	MS	S
Crosses involving Sonamung (premium quality, susceptible to MYMV, indeterminate growth)				
Mutants of Sonamung	DGG-188	HS	MS	MR
	DGG-190	HS	MS	R
	DGG-63	HS	S	MR
	DGG-65	HS	MR	MR
	DGG-64	HS	MR	MS
	DGG-62	HS	HS	MS
	DGG-75	HS	HS	MR
	DGG-191	MR	MS	MR
Sonamung mutant 11-2 × IPM 2-03 1-1	DGG-227	R	MR	MS
Sonamung mutant 11-2 × Sonamung 57-2	DGG-228	HS	HS	MR
Sonamung mutant 11-2 × BWMCD-31	DGG-229	HS	MS	HS
Sonamung mutant 11-2 × BPMR-145	DGG-230	HS	MS	MR
Crosses involving IPM-2-03 - large seeded, resistant to MYMV, relatively tolerant to major pests				
IPM 99-125 x Pusa bold 2	IPM-2-03	HS	MS	MR
Mutants of IPM-2-03	DGG-185	HS	MR	MR
	DGG-184	HS	MS	MR
	DGG-187	HS	S	MR
	DGG-71	S	S	MR
	DGG-186	HS	MS	MR
IPM 2-03 1-1 × BWMCD-31	DGG-232	S	S	MR
LGG-460 (Tolerant to MYMV)				
Mutant of LGG-460	DGG-76	HS	MS	R
	DGG-193	HS	MR	S
	DGG-99	S	MS	MR
	DGG-73	HS	MS	MR
Crosses involving TARM-1 (Tolerant to powdery mildew)				
Released from BARC, Trombay	TARM-1	S	MR	MR
TARM-1 X BGS-9	DGG-10	MR	MR	HS
BGS-9 X TARM-1 mutant no 44-3	DGG-19	S	MR	MS
BGS-9 X TARM-1	DGG-12	HS	MR	S
	DGG-20	HS	HS	S
	DGG-21	R	S	MS
Mutant of TARM-1	DGG-95	MR	MR	MS
	DGG-96	R	MS	S
	DGG-84	HS	HS	HS
Mutant of Vamban-2	DGG-80	S	MS	MR
	DGG-82	S	HS	MS
DGGV-2 X DGG-1	DGG-216	HS	MR	MS
	DGG 254	S	S	MS

GG-20-3	DGG-91	HS	HS	MR
TMB-37	DGG-213-1	HS	S	HS
Mutant no. 25-2 of VGG-2	DGG-252	HS	HS	S
-NA-	IPM- 2-17	MR	MR	MR
-NA-	IPM-14-10	HS	S	MR
GG-20-7	IPM-19-9	HS	HS	MR
PM 3 × APM 36	IPM 99 – 125	HS	HS	R
-NA-	IPM-3-02	HS	MS	S
DGG-17 × V-02-802	4BRB-1	HS	HS	S
Released varieties of mungbean				
PDM 139	Samrat	HS	MS	R
IPM 410 – 3	Shikha	HS	MR	R
KDM-1 x TARM 18 (Phule M-9339)	Vaibhav	HS	MR	MS
IPM 2-1 x EC398889 (IPM 205-7)	Virat	HS	MR	MS
Released by Dr.PDKV, Akola	AKM 8802	HS	MR	MS
GG-20-6, released by PAU, Ludhiana	TMB-37	HS	S	MR
Released by CVRC (Nirmal Seeds)	NUL-7	HS	S	MR
MGG 336 × COGG 902	COGG 912	MR	MR	R
Germplasm lines				
Germplasm	GPM-19	MR	R	R
Germplasm of mungbean	30 GPM-7	HS	MS	MR
AVRDC line	V-02-709	R	MS	S
Wild relative of mungbean	*V. trilobata*	R	I	HR
Landrace with good keeping quality	Karihesaru	HS	S	S

During *kharif* 2021, the per cent yield reduction ranged from 3.78 per cent to 86.06 per cent. The breeding line DGG-21 which recorded the least per cent yield reduction, was resistant to anthracnose but was susceptible to powdery mildew. Followed by DGG-227 which showed 7.41 per cent yield reduction and was resistant to anthracnose and moderately resistant to powdery mildew. The genotypes such as IPM-2-17, V-02-709, DGG-10, DGG-213-1, DGG-215-2, DGG-215-3, DGG-251 showed an yield reduction of less than 20 per cent. This yield reduction may be due to the confounding effect of powdery mildew and anthracnose during *kharif* 2021. Nonetheless, the powdery mildew symptoms were seen from 45 DAS to 60 DAS and disappeared in later stages due to the rains received during the cropping season whereas the anthracnose symptoms were severe till the end of the cropping season. Therefore it can be inferred that anthracnose had major contribution in the yield reduction in the present study. The similar results were obtained by Vandana *et al.* (2014) [21] who reported that yield losses due to anthracnose in their experimental material ranged from 24-67 per cent. During *summer* 2022, the advanced breeding lines such as DGG-21, DGG-186, DGG-203, DGG-251, IPB 3-02-0 2, DGG-59, DGG-187, DGG-215-3, 3 BRD-20, IPM 99-125, DGG-62, DGG-190, DGG-197, DGG-222, AKM 8802, *V.trilobata*, DGG-199, DGG-228, GPM-19, IPM-2-14 showed the yield reduction less than 10 per cent. All these genotypes showed resistance to moderately resistance reaction to MYMV with PDI ranging from 0 to 20 per cent.

Though the above-mentioned genotypes showed less per cent yield reduction most of them are inherently low yielding. The DGG-21 and DGG-215-2 were found to have high *per se* yield along with less yield reduction during both the seasons. On the other hand, the lines DGG-190, DGG-199 and IPM-2-14 performed well only in summer whereas the DGG-213-1 and IPM-2-17 only in *kharif* with high inherent yield and less yield reduction (Table 4).

Table 4: Seed yield (g/plant) of breeding lines under protected and unprotected conditions of the genotypes during both seasons.

	***Kharif* - 2021**			**Summer -2022**			**Disease reaction**		
	Protected	**Unprotected**	**% yield reduction**	**Protected**	**Unprotected**	**% yield reduction**	**anthracnose**	**powdery mildew**	**MYMV**
DGG-10	5.35	4.25	19.62	1.25	0.60	51.23	MR	MR	HS
DGG-21	6.82	6.61	3.78	5.55	5.22	5.92	R	S	MS
DGG-59	9.76	4.50	53.89	1.35	1.25	7.14	HS	MS	S
DGG-62	7.44	2.76	62.82	2.641	2.44	7.55	HS	HS	MS
DGG-186	3.25	1.45	55.17	3.72	3.61	2.78	HS	MS	MR
DGG-187	4.62	2.68	41.86	5.78	5.21	9.83	HS	S	MR
DGG-190	8.85	2.03	77.02	10.30	9.44	5.83	HS	MS	R
DGG-197	6.27	2.04	67.35	2.42	2.40	0.43	HS	S	R
DGG-199	5.28	1.80	65.79	6.87	6.51	5.19	HS	MR	MR
DGG-203	2.63	0.55	78.77	1.94	1.90	1.96	HS	MS	MR
DGG-213-1	11.40	9.88	13.25	6.44	3.73	42.03	HS	S	HS
DGG-215-2	7.78	6.56	15.57	6.02	5.26	12.50	HS	MR	MR
DGG-215-3	4.89	4.33	11.36	2.54	2.44	3.91	S	MS	R
DGG-222	4.64	2.31	50.18	2.58	2.48	3.85	HS	HS	MR
DGG-227	6.34	5.87	7.41	2.97	2.01	32.20	R	MR	MS
DGG-228	4.33	1.83	56.17	2.48	2.28	8.00	HS	HS	MR
DGG-251	2.91	2.38	17.87	1.60	1.48	7.19	HS	HS	MR
3 BRD-20	2.04	1.36	33.33	2.57	2.43	5.24	HS	MS	MR
IPM-2-14	5.56	2.12	62.05	5.98	5.44	9.00	HS	MR	R
IPM-2-17	10.60	9.87	6.85	6.32	4.07	35.48	MR	MR	MR
V-02-709	3.91	3.75	3.85	5.65	4.62	18.18	R	MS	S

The wild relative, *Vigna trilobata* which is considered as the secondary gene pool of this crop (Bisht *et al*., 2004) [3] has shown multiple disease resistance in the current study. There are two types of population of this species. One is beach population and the other is dry inland population. The beach population with small, thick and entire leaflets were screened in this study. Apart from disease resistance, it has also been observed that the seeds were bruchid resistant during the seed storage. The salt resistance screening experiment by Norihiko *et al.* (2010) [12] revealed that *V. trilobata* showed the highest level of resistance even in its seedling stage. Even though this species can serve as an excellent resistance source but the less crossability per cent of the interspecific cross between trilobata and radiata led to the limited research in this direction. The hybrid seed set is observed to be less due to flower drop after pollination and the hybrid lethality was also reported to be high in these crosses (Pandiyan *e al.*, 2012; Sarkale, 2015) [13, 18].

Further some of the advanced breeding lines, such as DGG-10 (MR to powdery mildew and anthracnose), COGG 912 (MR to powdery mildew and anthracnose; R to MYMV), GPM-19 (R to powdery mildew and MYMV; MR to anthracnose); DGG-227 (R to powdery mildew and anthracnose; MR to MYMV) showed tolerance to more than one disease. Some of the previous studies on mungbean for multiple disease resistance were conducted by Singh *et al.* (1988) [20]. Seventeen genotypes conferring multiple disease resistance were identified by Kaur (2006) [6]. There are instances in which it has been proven that this kind of resistance is governed by polygenes (Vanderplank, 1968) [22]. At the same time, some of the previous studies reported that the horizontal resistance is governed by single gene or oligo genes (Caldwell, 1968) [4]. Since the inheritance studies of the resistant lines identified in this study has not been done, the nature of resistance operating in these lines cannot be contemplated.

The resistant genotypes thus identified in the current study can be screened in multiple locations or multiple seasons/ years for identifying genotypes with stable resistance. And also the good yielding resistant genotypes identified can be further tested in different locations to check their suitability for release as varieties. They can also be used as parents in breeding programs. The wild relative *V. trilobata*, which was found to be resistant to all diseases, can be used as a donor parent in resistance breeding program by employing few simple procedures to overcome the crossability barriers.

Acknowledgement

The authors are indebted to the Department of Genetics and Plant Breeding, University of Agricultural Sciences, Dharwad, Karnataka, for providing support for undertaking this experiment and Indian Council of Agricultural Research for providing the financial assistance in the form of NTS fellowship.

Conflict of Interest: None

References

1. Ashritha. Genetic variability studies for yield, yield components and disease resistance in advanced breeding lines of mungbean. University of Agricultural Sciences, Dharwad, Karnataka, India; 2021.
2. Bashir M, Jamali AR, Ahmad Z. Genetic resistance in mungbean and mashbean germplasm against mungbean yellow mosaic Begomovirus. Mycopathology. 2006;4(2):1-4.
3. Bisht IS, Bhat KV, Lakhanpaul S, Latha M, Jayan PK, Biswas BK, *et al*. Diversity and genetic resources of wild Vigna species in India. Genet Resour Crop Evol. 2005;52(1):53-68.
4. Caldwell RM. Breeding for general and/or specific plant disease resistance. In: Proceedings of the Third International Wheat Genetics Symposium. Australian Academy of Sciences, Canberra, Australia; 1968. p.236-272.
5. Joshi D, Tripathi HS. Cultural, biological and chemical control of anthracnose of urdbean. J Mycol Plant Pathol. 2002;32(1):52-55.
6. Kaur L. Multiple disease resistant sources of mungbean. In: International Conference on Indigenous Vegetables and Legumes: Prospectus for Fighting Poverty, Hunger and Malnutrition. 2006. p.423-426.
7. Khattak GS, Haq MA, Ashraf M, Elahi T. Genetics of mungbean yellow mosaic virus (MYMV) in mungbean (*Vigna radiata* L. Wilczek). J Genet Breed. 2000;54(4):237-243.
8. Mahanta M, Sao A. Genetic association analysis for yield and its attributes in mungbean (*Vigna radiata* L.). Trends Biosci. 2019;12(13):1-4.
9. Mandal R, Narender S, Mehta SK, Khirbat SK. Influence of environmental conditions on the incidence of anthracnose of mungbean. Ann Agri-Bio Res. 2015;20(2):184-187.
10. Mayee CD, Datar VV. Phytopathometry. Technical Bulletin-I. MAU, Parbhani, Maharashtra, India; 1986. p.88-89.
11. Nair RM, Pandey AK, War AR, Hanumantharao B, Shwe T, Alam AK, *et al*. Biotic and abiotic constraints in mungbean production—progress in genetic improvement. Front Plant Sci. 2019;10:1340.
12. Norihiko T, Kaga A, Isemura T, Vaughan D, Srinives P, Somta P, *et al*. Vigna genetic resources. In: Proceedings of the 14th NIAS International Workshop on Genetic Resources: Genetic and Comparative Genomics of Legumes (Glycine and Vigna). 2010. p.11-21.
13. Pandiyan M, Senthil N, Suresh R, Chakravarthy N, Packiaraj D, Jagadeesh S. Interspecific hybridization of *Vigna radiata* × *Vigna trilobata*. Euphytica. 2012;35:1017-1022.
14. Paul PC, Biswas MK, Mandal DI, Pal PI. Studies on host resistance of mungbean against mungbean yellow mosaic virus in the agro-ecological condition of lateritic zone of West Bengal. Bioscan. 2013;8(2):583-587.
15. Pooja SK, Bhat S. Diversity among greengram germplasm to powdery mildew resistance caused by Erysiphe polygoni DC. Int J Curr Microbiol Appl Sci. 2019;8(7):2765-2771.
16. Reddy KS, Pawar SE, Bhatia CR. Inheritance of powdery mildew (*Erysiphe polygoni*) resistance in mungbean (*Vigna radiata* L. Wilczek). Theor Appl Genet. 1994;88(8):945-948.
17. Russel GE. Plant Breeding for Pest and Disease Resistance. London: Butterworths; 1978. p.485.
18. Sarkale AP. Validation of molecular markers associated with powdery mildew resistance in mungbean. M.Sc. Thesis, University of Agricultural Sciences, Dharwad, Karnataka, India; 2015.
19. Singh DP. Breeding for resistance to diseases in greengram and blackgram. Theor Appl Genet. 1981;59(1):1-10.
20. Singh G, Kapoor S, Singh K. Multiple disease resistance in mungbean with special emphasis on mungbean yellow mosaic virus. In: Proceedings of the Second International Symposium on Mungbean, AVRDC. 1988. p.290-296.
21. Vandana S, Sanghmitra B, Krishna M, Singh SK. Yield loss assessment in mungbean [*Vigna radiata* (L.) Wilczek] caused by anthracnose [*Colletotrichum truncatum* (Schw.) Andrus and Moore]. Bioscan. 2014;9(3):1233-1235.
22. Vanderplank JE. Disease Resistance in Plants. New York: Academic Press; 1968. p. 206.
23. Wheeler BEJ. An Introduction to Plant Diseases. London: John Wiley and Sons Ltd.; 1969. p. 301.