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Genetic Variability Analysis and Characterization for MYMV Resistance in Mungbean

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Abstract: A set of twenty-five advanced breeding lines including five released varieties were evaluated for genetic variability, heritability, and genetic advance for yield and related traits. The total of ten traits were studied including resistance to mungbean yellow mosaic virus disease (MYMV). Seed yield per plant has shown a high phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) indicating greater scope for improvement of this trait. Plant height and 100 seed weight showed moderate PCV and GCV whereas days to 50 percent flowering, seed per pod, and pod length showed low PCV and GCV. High heritability estimates coupled with high genetic advance were observed for 100 seed weight and seed yield per plant revealing the presence of less environmental influence and prevalence of additive gene action which suggest that selection would be rewarding for these traits. Screening for MYMV disease under natural conditions showed seven genotypes were resistant and nine genotypes were moderately resistant. This study revealed that 65C was high-yielding and resistant to MYMV disease. Moreover, 59C(10) yielded more than 65C but it was moderately susceptible to MYMV so both of these genotypes can be improved for their respective flaws and can be incorporated in the future breeding pipelines for their further development as a variety.

Keywords: Environmental influence, Genetic advance, Genetic variability, Heritability, MYMV

Pulses are leguminous crops having an annual life cycle with the seed of variable size, shape, and color within a pod. Mungbean [*Vigna radiata* (L.) Wilczek] is a well-known pulse crop with 2n=2x=22 chromosomes and a genome size of 579 Mb (Kang et al 2014). It belongs to the Fabaceae family. Along with this, it is the third most important food legume among the thirteen food legumes grown in India (Ramakrishnan et al 2018). The presence of a high number of proteins, vitamins, minerals, enzymes, and fibers makes it a nutritionally rich crop. Its protein is a rich source of lysine but poor in methionine. However, methionine deficiency can be completed by cereal-based protein. Moreover, it also possesses a good amount of calcium, phosphorus, and iron (Tiwari and Shivhare 2016). A part from its nutritional benefit, mungbean also has an important role in cropping systems due to its short life cycle and nitrogen fixation ability in soil. Its cultivation can improve soil fertility by adding about 30-40 kg N/ha after the harvest of the crop reducing the nitrogen requirement of the succeeding crop by 25 % (Mbeyagala et al 2017). Due to its self-pollinating nature, it shows low natural variability for target traits, making selection ineffective. Knowledge of genotypic variation present in the crop for target traits is necessary for choosing a suitable selection method. Genotypic and phenotypic coefficient of variation, heritability, and genetic advance are important parameters for improving target traits and also for maximizing genetic gain through selection. High heritability along with high genetic advance indicates the presence of additive gene action. Prevalence of additive gene action is always desirable as it is the only gene action that can be fixed by selection. Therefore, this study was conducted to assess genetic variability, heritability, and genetic advance in advanced generations of green gram.

Mungbean yellow mosaic virus (MYMV) is a deadly disease, causing yield losses in green gram for years. Its damage to the production of mungbean cannot be avoided as sometimes it can lead to 75-100% yield loss (Reshami et al 2020). This virus comes under the genus *Begomovirus* which belongs to the *Geminiviridae* family. It is transmitted by the whitefly (*Bemisia tabaci*) which serves as a vector to cause the widespread of this disease (Mishra et al 2020). Using insecticides as a measure of chemical control to impede the infestation of white flies can be a useful approach (Younas et al 2021) But is not always desirable due to its high cost and less eco-friendly nature. Developing varieties having resistance to MYMV disease is a feasible and affordable approach. Identifying new sources of resistance is very important to aid the development of new resistant varieties.

After the identification of new sources, the responsible genes can be transferred from the same to develop new superior breeding lines. The lines used in this study have been screened for MYMV resistance to ascertain their response to the disease. The resistant lines than are identified can be incorporated into breeding pipeline for their further improvement.

MATERIAL AND METHODS

The study was conducted during the summer, of 2018 at Navsari Agricultural University, Navsari. Experimental material comprised 20 genotypes (Table 1) alongwith 5 checks viz., GM-4, GAM-5, GM-6, GM-7, and Meha. These genotypes were laid out in randomized block design along with respective checks in three replications. GM-4 was kept as infector row for establishing suitable inoculum and to identify resistant genotypes. It was planted after two consecutive rows of genotypes. Each row is comprised of 20 plants with 60 cm x 15 cm inter and intra row spacing. Each progeny row consisted of 20 plants and observations were recorded from 10 randomly selected plants. The ten characters analyzed were days to 50 percent flowering, plant height, primary branches per plant, pods per cluster, pods per plant, pod length, seed per pod, 100 seed weight, harvest index, and seed yield per plant. Genetic variability analysis of each quantitative trait was carried out using different variability parameters. The data analysis was done using Rstudio with version 2021.9.1.372. Phenotypic, genotypic, and environmental variances were estimated according to the methods suggested by Federer and Searle (1976). Estimation of Phenotypic and genotypic coefficient of variation was done according to the methods suggested by Burton and Vane (1953), whereas estimation of heritability and expected genetic advance were done according to Lush (1940) and Johnson et al (1955), respectively. Estimates of GCV, PCV, heritability, and genetic advance as percent mean were categorized as low, moderate, and high by following Sivasubramaniam and Menon (1973), Robinson et al (1951) and Johnson et al (1955), respectively. Disease scoring for mungbean yellow mosaic virus (MYMV) was done as suggested by Sekar et al 2017 and the plant was categorized to various classes accordingly.

RESULTS AND DISCUSSION

The genotypic differences were significant for most of the characters except for primary branches per plant and pods per plant, indicating a considerable amount of genetic variability among the studied genotypes for various traits (Table 2). There is a sufficient amount of variability present in genotypes that will respond to the selection (Table 3).

Mean performance of genotypes: Most of the characters have shown remarkable variation as (Table 3). Days to 50 percent flowering have depicted sufficient variability.GM-4 was the earliest in flowering whereas 64A and 65C were the last to express 50 percent flowering. The highest plant height was in 95B followed by 47D and Meha whereas, 62A was the shortest among all. Subsequently, 19C and 34A were having the highest number of primary branches per plant but, GM-6 has shown to bear the lowest number of primary branches per plant. Genotype 95B recorded highest number of pods per plant but it was with low number of pods per cluster and such type of results were also obtained by Sandhiya and Shanmugavel (2018). Besides this lowest number of pods per plant in 13A and was also with low pods per cluster. The

Table 1. Genotypes subjected to genetic variability analysis

Sr. no.	Genotype	Pedigree	Sr. no	Genotype	Pedigree
1.	13A	Meha × Pusa vishal	14.	56C	Meha × GM-4
2.	34A	Meha × Pusa vishal	15.	59C (10)	Meha × GM-4
3.	34A (7)	Meha × Pusa vishal	16.	59C (5)	Meha × GM-4
4.	42A	Meha × Pusa vishal	17.	65C	Meha × GM-4
5.	62A	Meha × Pusa vishal	18.	79C	Meha × GM-4
6.	64A	Meha × Pusa vishal	19.	37D	Meha × GJM-1008
7.	48B	Meha × GJM-1006	20.	47D	Meha × GJM-1008
8.	65B	Meha × GJM-1006	21.	Meha	Check variety
9.	94B	Meha × GJM-1006	22.	GAM-5	Check variety
10.	95B	Meha × GJM-1006	23.	GM-6	Check variety
11.	18C	Meha × GM-4	24.	GM-7	Check variety
12.	19C	Meha × GM-4	25.	GM-4	Check variety
13.	40C	Meha × GM-4			

highest pod length was observed for GM-7 which was also accompanied by higher seeds per pod. Such type of results was also observed earlier by Sushmitha and Jayamani (2018). Moreover, 42A was having shortest pods which were obviously accompanied by low seeds per pod. The highest seed yield per plant was observed for 59C (10) followed by 65C. Furthermore, 13A was having lowest seed yield and was also having lower pods per plant and such type of results were also reported by Jayaprada et al (2021). The highest 100 seed weight (g) was observed for GM-6 followed by GAM-5 whereas 79C was possessing the lowest 100 seed weight. Subsequently, 37D was having highest harvest index

Table 2. Analysis of variance (mean sum of square values) for various traits in green gram

Source of variation	DF	DTF	PH (cm)	PB	PPC	PPP	PL (cm)	SPP	SYP (g)	100 SW (g)	HI (%)
Replications	2	5.45	202.34	0.89	0.29	21.21	0.12	1.43	1.79	0.02	45.31
Genotypes	24	11.28**	86.88**	0.35	0.36*	64.13	0.68*	0.79*	2.56**	0.63**	46.59**
Error	48	1.87	22.55	0.24	0.17	43.85	0.33	0.37	0.28	0.01	12.17

DTF = Days to 50 per cent flowering PH = Plant height PB = Primary branches per plant
PPC = Pods per cluster PPP = Pods per plant PL = Pod length
SPP = Seed per pod SYP = Seed yield per plant 100 SW = 100 seed weight
HI = Harvest index

Table 3. Mean performance of green gram genotypes for various quantitative traits

Genotypes	Days to 50% flowering	Plant height (cm)	Primary branches per plant	Pods per cluster	Pods per plant	Pod length (cm)	Seeds per pod	Seed yield per plant (gm)	100 seed weight (g)	Harvest Index (%)
13A	47.33	39.83	2.53	2.77	11.50	6.75	9.25	2.33	4.00	19.09
34A	50.67	43.11	3.27	3.15	16.74	6.91	9.44	2.74	4.07	14.94
34A(7)	48.33	46.11	2.46	3.23	14.80	6.70	9.30	4.05	4.13	20.39
42A	50.33	42.51	2.63	3.04	14.70	5.90	9.19	2.97	3.92	16.22
62A	48.67	36.19	2.81	3.03	22.53	6.38	8.87	3.54	4.10	22.36
64A	51.33	44.87	2.87	3.54	25.29	6.63	9.69	2.73	4.10	6.36
48B	49.67	43.35	2.67	3.53	17.87	7.15	9.90	3.75	4.13	20.61
65B	47.33	38.50	2.17	3.17	13.30	6.24	9.48	3.51	4.43	16.62
94B	47.33	40.50	2.60	3.10	13.47	7.65	10.43	3.04	4.20	22.27
95B	50.67	57.35	3.01	2.76	28.93	6.87	9.84	3.37	4.00	20.52
18C	47.00	44.80	2.19	3.01	16.84	6.75	9.23	4.68	3.83	16.09
19C	50.67	49.67	3.48	3.57	27.13	6.43	9.74	4.56	3.97	20.86
40C	50.00	51.63	2.89	3.54	16.27	6.87	9.57	4.60	4.13	18.49
56C	50.00	47.67	3.13	2.98	18.70	7.03	9.61	3.90	3.97	16.41
59C(10)	50.33	47.91	2.84	3.81	23.49	7.04	9.86	5.88	3.70	20.25
59C(5)	46.33	42.29	2.70	4.03	18.77	6.44	9.10	4.14	3.67	17.94
65C	51.33	53.05	2.70	3.44	21.33	6.94	9.13	5.19	3.67	18.01
79C	48.67	42.66	2.77	3.53	18.20	6.83	9.63	4.57	3.40	20.95
37D	48.00	40.65	2.43	3.60	15.83	6.81	10.33	2.71	3.87	25.53
47D	48.67	53.55	2.81	3.05	17.73	6.83	9.13	4.80	4.00	25.24
MEHA	49.00	53.55	3.01	3.79	25.68	6.90	9.08	4.17	4.28	14.29
GAM-5	50.67	38.79	2.35	3.47	13.40	6.88	9.15	4.18	5.18	14.01
GM-6	48.00	45.76	2.01	2.96	16.38	7.75	9.84	4.56	5.21	18.73
GM-7	48.33	47.06	2.75	3.80	17.18	8.03	11.18	5.11	4.90	17.70
GM-4	42.67	45.38	2.50	3.33	20.08	7.61	9.60	5.13	4.91	16.58
Mean	48.85	45.47	2.70	3.33	18.65	6.89	9.58	4.01	4.15	18.42

followed by 47D and 62A whereas 64A was reported to have the lowest harvest index. The genotypes 59C(10) (5.88 g) and 65C (5.19 g) have significantly outyielded Meha and GAM-5 check varieties but not GM-4, GM-6, and GM- 7 (Fig. 1).

PCV and GCV estimates: The 25 genotypes exhibit an ample amount of phenotypic variability for different characters and it ranges from 4.58 to 38.15 % (Table 4). The phenotypic coefficient of variation (PCV) was highest for pods per plant (38.15 %) and lowest for days to 50 percent flowering (4.58 %). The highest genotypic coefficient of variation (GCV) was obtained for seed yield per plant (21.75 %) whereas days to 50 percent flowering possessed the lowest GCV (3.63%). Days to 50 percent flowering, seed yield per plant, and 100 seed weight showed a narrow difference between PCV and GCV indicating the low or negligible environmental influence on the expression of these traits hence, selection would be effective for these traits. Similar results were also obtained by Hemavathy et al (2015) and Sineka et al (2021). High PCV and GCV were exhibited by seed yield per plant showing an ample amount of variability for this trait. Plant height and 100-seed weight showed moderate PCV and GCV values and similar results were also obtained by Jangra and Yadav (2015) and Vir and Singh (2016). Low estimates of PCV and GCV values were seen for days to 50 percent flowering, pod length, and seeds per pod and these results are following Sahu et al (2014) and Jayaprada et al (2021). Primary branches per plant, pods per cluster, pods per plant, and harvest index showed low to moderate estimates for PCV and GCV showing low variability

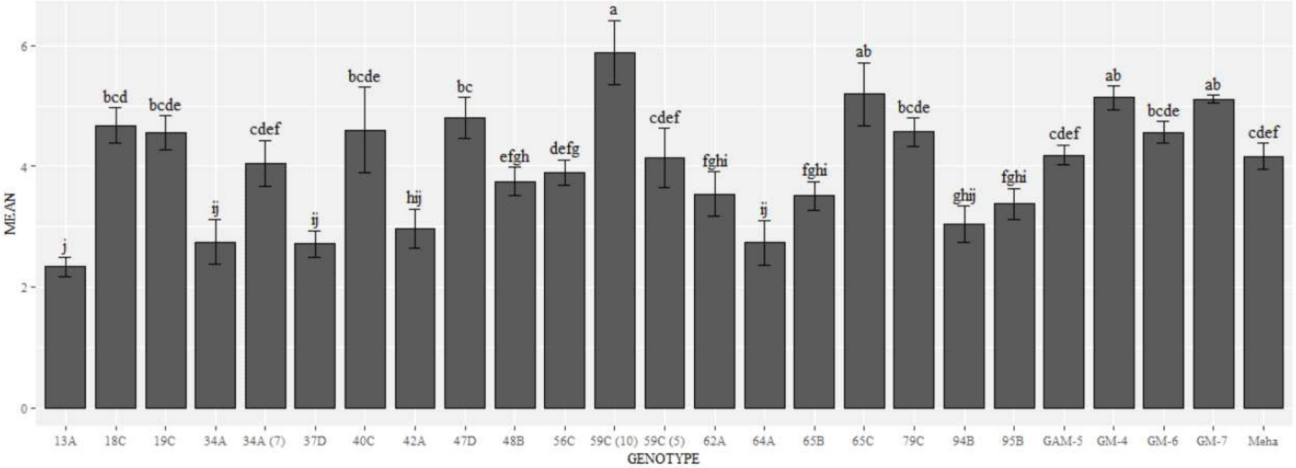

Fig. 1. Comparison of different genotypes for seed yield per plant (g). Genotypes with different letter are significantly different from each other for seed yield per plant (g)

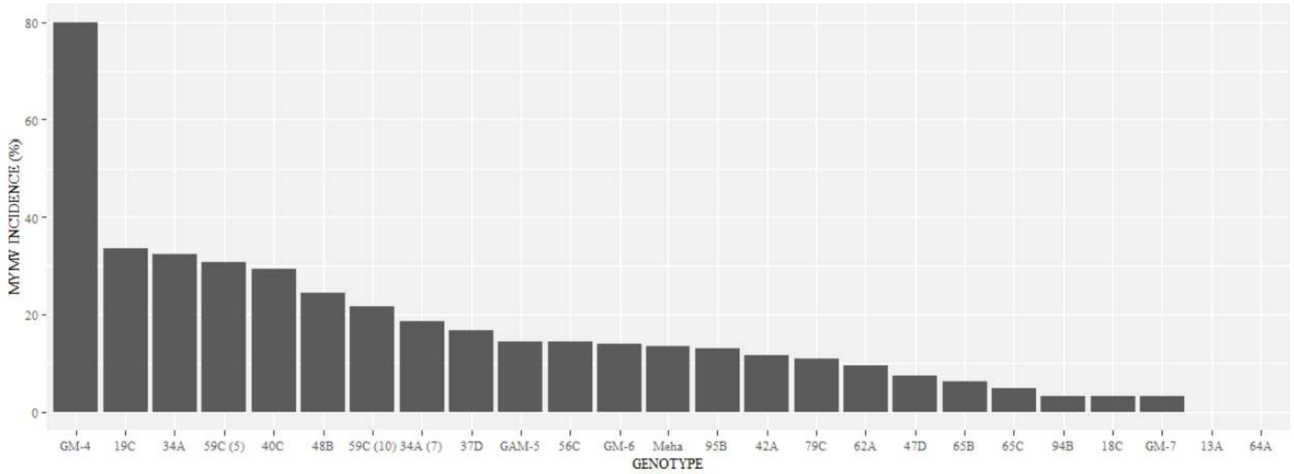

Fig. 2. Incidence of MYMV in green gram genotypes

Table 4. Estimates of genotypic coefficients of variation (GCV) and phenotypic coefficients of variation (PCV), heritability, genetic advance and genetic advance as per cent of mean for ten different characters of green gram

Characters	PCV (%)	GCV (%)	Heritability	Genetic advance (as % of mean)
Days to 50 per cent flowering	4.58	3.63	0.63	5.91
Plant height (cm)	14.59	10.18	0.49	14.65
Primary branches per plant	19.37	7.19	0.14	5.49
Pods per cluster	14.55	7.47	0.26	7.90
Pods per plant	38.15	13.94	0.13	10.50
Pod length (cm)	9.73	4.97	0.26	5.24
Seed per pod	7.42	3.90	0.28	4.22
Seed yield per plant (g)	25.43	21.75	0.73	38.31
100 seed weight (g)	11.23	10.93	0.95	21.92
Harvest index (%)	26.40	18.39	0.49	26.39

among these characters and indicating the limited scope of improvement of these characters through selection.

Heritability analysis: Broad sense heritability (%) is the proportion of phenotypic variability that is due to genetic reasons. The traits having higher heritability are largely governed by additive genes and selection could be rewarding for improvement of such yield attributes by individual plant selection. The heritability ranged from 13 to 95% (Table 4). The highest heritability was observed for 100 seed weight followed by seed yield per plant, indicating that these characteristics are less influenced by the environmental fluctuations. Such a trend for 100 seed weight was also observed by Hemavathy et al (2015) and Gayacharan et al (2020). High heritability estimates show the major role of the genetic constitution in the development of phenotype and such kind of traits are desirable in a breeding program of the crop. The moderate to low estimates of heritability were recorded for plant height, seeds per pod, pod length, pods per cluster, and primary branches per plant indicating more environmental influence on such traits. Similar trends for the characteristics like seed yield per plant and 100-seed weight were observed by Das et al (2010), Degefa et al (2014) and Usharani and Kumar (2016).

Genetic advance analysis: The values of genetic advance as percent of mean ranged from 4.22 (seeds per pod) to 38.31% (seed yield per plant). Seed yield per plant (38.31%), harvest index (26.39%) and 100 seed weight (21.92%) manifested high genetic advance as a percent of the mean. Moreover, these traits also possessed high heritability. High heritability coupled with high genetic advance indicates that these traits are governed by additive gene action and selection for these traits will be rewarding. Similar results were also obtained by Raselmiah et al (2016) and Sushmitha and Jayamani (2018). High heritability coupled with moderate genetic advance was seen for plant height and high heritability coupled with low genetic advance was seen for days to 50 percent flowering which clearly shows the character is governed by non-additive gene action and is highly influenced by environmental effects. Furthermore, selection for these traits will be less effective and will not yield any genetic gain. Moderate values of genetic advance as percent of mean were observed for pods per plant. These findings were similar to the results of Kumar et al (2013) and Kumar et al (2015). Low estimates of genetic advance were observed for seeds per pod, pod length, primary branches per plant, and pods per cluster suggesting that these characteristics are under high environmental influence and selection would be ineffective for these traits. Such kinds of results for seeds per pod were also obtained by Makeen et al (2007), Alom et al (2014) and Jangra and Yadav (2015).

Screening for MYMV in green gram genotypes : Among 25 genotypes studied, the variable response was observed for MYMV disease incidence as per Sekar et al (2017) (Figure 2). The 13A and 64A were highly resistant as they depicted no sign of MYMV incidence. Genotypes 47D, 62A, 65B, 94B, 18C, GM-7, and 65C were resistant where MYMV incidence was observed from 1 to 10 %. Likewise, 34A (7), 42A, 95B, 56C, 79C, 37D, GAM-5, Meha and GM-6 were categorized as moderately resistant (11 to 20%). Genotypes 48B, 40C, and 59C (10) were moderately susceptible (21 to 30%). The genotypes 34A, 19C, and 59(C)5 were susceptible (31-50%) and GM-4 was found highly susceptible (> 50%).

CONCLUSION

The present investigation revealed high heritability coupled with high genetic advance as a percent of the mean for the traits viz., seed yield per plant, and 100 seed weight.

This indicated that additive gene effects are operating for inheritance and mass selection or progeny selection would be worthwhile for further improvement of these traits. Plant height exhibited high heritability coupled with moderate genetic advance indicating environmental effects. Low heritability coupled with low genetic advance was observed for the character primary branches per plant, pods per cluster, pod length, and seeds per pod suggesting that these characteristics are under environmental influence and selection would be ineffective. Genotypes categorized as highly resistant and resistant against MYMV can be improved further by increasing yield. Genotypes 13A and 64A were highly resistant to MYMV but had low seed yield per plant and 59C(10) was high yielding but moderately susceptible to MYMV so further crossing programs can be designed for transferring genes for disease resistance and seed yield to develop high-yielding MYMV resistant genotypes.

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