



Dissecting Genetic Variability of Yield-associated Traits and MYMV Resistance in Segregating F₂ Populations of Green Gram (*Vigna radiata* L.)

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ABSTRACT

Background: Green gram [*Vigna radiata* (L.) Wilczek] is an important edible legume crop cultivated almost all over India and it is the third most important pulse crop after chickpea and pigeon pea. With a view to search for more variability among the parents and their F₂ generations for ten morphological traits and MYMV (Mungbean Yellow Mosaic Virus) incidence, the present study was undertaken to elucidate information on variation of different characters contributing towards seed yield of segregating populations of green gram.

Methods: The present experiment comprised four diverse parents viz., KM-22-24, GM-6, HUM-27 and GM-8 and their F₂ populations of the crosses viz., cross-I (KM-22-24 × GM-6) and cross-II (HUM-27 × GM-8) to elucidate information on variation of different characters contributing towards seed yield of segregating populations of green gram. The disease MYMV incidence (%) was also recorded in parents and F₂ generation. The experiment was carried out in summer-2023 (crossing), *kharif*-2023 (selfing) and summer-2024 (evaluation) at Navsari Agricultural University, Navsari, Gujarat.

Result: The segregating populations manifested increased mean values over the parental means in the cross-I for days to maturity, plant height, branches per plant and pod length while in cross-II for the traits viz., branches per plant and pods per plant. In cross-I, the traits viz., branches per plant, seeds per pod and seed yield per plant showed moderate value of GCV and higher value of PCV while in the cross-II, the traits like branches per plant and seeds per pod showed higher value of GCV and PCV. This higher value indicated the greater scope of improving this character by applying the selection in an appropriate direction. Higher heritability coupled with high genetic advance as per cent mean was observed for days to flowering, days to maturity, plant height and pod length in cross-I. Similarly, in cross-II days to flowering, plant height, branches per plant, seeds per pod and seed yield per plant show the same result. Hence, priority should be given to these traits in formulating selection strategies to obtain desirable genetic gain by selection.

Key words: GCV, Genetic advance, Genetic variability, Green gram, Heritability, PCV.

INTRODUCTION

Green gram [*Vigna radiata* (L.) Wilczek] 2n = 2x = 22 is an important edible legume crop cultivated almost all over India and it is the third most important pulse crop after chickpea and pigeon pea. It is believed to originate from the Indian Subcontinent, according to De Candolle (1885), Piper and Morse (1914), Vavilov (1926) and Zuckovskij (1962). Green gram thrives well in a wide range of environments, including high temperate zones. It grows well on sandy loam soils and in dry conditions. It enriches soil fertility through biological nitrogen fixation with the help of Rhizobium bacteria in nodules and checks soil erosion as a cover crop (Murakami *et al.*, 1991). Green gram contains about 24 per cent of protein and because of its easy digestibility and low production of flatulence it is favoured for children and the elderly people (Haytowitz and Matthews, 1986; Adsule *et al.*, 1986).

Genotypic variation is important for any crop improvement programme as it is only variation which transmits to next generation. Heritability refers to the ratio of genotypic variance to the total phenotypic variance or total variance, for the trait. It is a good index for transmission of characters

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from parents to their offspring. It aids plant breeder in selection of good genotypes from diverse populations. Genetic advance is the improvement of progeny of selected

plants over parental populations. Heritability estimates along with genetic advance are generally more useful in predicting the gain under selection instead of using heritability alone (Falconer, 1981). With this in mind, the current study aimed to assess the variation in yield and yield-related traits in the F₂ generation of green gram by analyzing genetic parameters such as phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability and genetic advance. These insights are expected to guide the formulation of effective selection indices for crop improvement, focusing on enhancing yield potential and quality traits.

MATERIALS AND METHODS

The experimental material comprised hundred F₂ progenies derived from the crosses KM-22-24 × GM-6 and HUM-27 × GM-8 which were maintained at Pulses and Castor Research Station, Navsari Agricultural University, Navsari for evaluation in a non-replicated manner. Mean, range, genotypic coefficient of variation, phenotypic coefficient of variation, heritability and genetic advance as per cent of mean were studied for ten quantitative traits viz., days to flowering, days to maturity, plant height (cm), branches per plant, pods per plant, pod length (cm), seeds per pod, 100 seed weight (g), harvest index (%) and seed yield per plant (g) in F₂ progenies of green gram. The data recorded for the different characters excluding MYMV incidence were subjected to analysis of variance. Different parameters of the genetic variability were computed by standard statistical procedures.

The analysis of variance was conducted following the method proposed by Panse and Sukhatme (1957). The variability parameters, including phenotypic and genotypic coefficients of variation (PCV and GCV), were calculated using the approach outlined by Burton and DeVane (1953). Additionally, heritability and genetic advance were classified into low, medium and high categories in accordance with the criteria established by Johnson *et al.* (1955).

RESULTS AND DISCUSSION

Analysis of mean, range and variance

The 100 selected F₂ progenies of two crosses KM-22-24 × GM-6 and HUM-27 × GM-8 showed a wide range of variation, which might be due to the inclusion of diverse parents, segregation and recombination (Table 1 and 2). Mean values for all observed characters in the segregating population ranged between the mean values of parents. Additionally, the population manifested increased mean values over the parents for days to maturity, plant height, branches per plant, pod length, 100 seed weight and seed yield per plant for cross KM-22-24 × GM-6 and branches per plant and pods per plant for cross HUM-27 × GM-8. However, the characters days to flowering, pods per plant, seeds per pod and harvest index exhibited low mean value over parents for cross KM-22-24 × GM-6 and days to flowering, days to maturity, plant height, pod length, seeds

Table 1: Mean, range and variance values for ten morphological characters in parents and F₂ generation of cross-I (KM-22-24 × GM-6).

Characters	Mean ± Standard error			Range			Variance		
	KM-22-24	GM-6	F ₂	KM-22-24	GM-6	F ₂	KM-22-24	GM-6	F ₂
Days to flowering	39.50±0.240	46.30±0.367	36.35±0.549	38-48	44-47	28-48	2.28	1.34	30.11
Days to maturity	51.20±0.072	61.70±1.184	62.71±0.752	49-54	55-64	46-79	3.51	14.01	52.61
Plant height (cm)	34.90±0.615	33.10±0.433	35.00±0.674	28-40	32-35	21-48	13.21	0.88	37.01
Branches per plant	3.50±0.454	2.30±0.213	3.67±0.114	3-5	1-3	2-5	0.72	0.46	0.83
Pods per plant	24.20±0.250	24.30±0.517	22.77±0.498	22-26	22-26	20-29	1.51	2.68	3.73
Pod length (cm)	6.50±0.370	6.24±0.064	6.85 ± 0.175	5.00-8.00	6.00-6.50	4.00-9.00	0.89	0.04	0.79
Seeds per pod	9.00±0.416	9.50±0.453	8.50 ± 0.206	7-11	7-12	4-13	1.56	2.06	4.23
100 Seed weight (g)	5.98±0.160	5.98±0.118	5.95 ± 0.058	5.10-6.20	5.10-6.20	5.10-7.40	0.14	0.14	0.34
Seed yield per plant (g)	12.57±0.292	12.22±0.391	8.08 ± 0.173	11.0-14.5	10.1-13.8	5.40-13.8	1.07	1.53	2.99
Harvest index (%)	19.38±0.334	21.26±0.743	19.07±0.238	17.0-22.0	18.0-26.0	15.0-27.0	2.17	5.52	5.67

per pod, 100 seed weight and seed yield per plant for cross HUM-27 × GM-8. The increase in mean value as a result of hybridization indicates scope for further improvement in traits in subsequent generations.

Components of variation

The values of PCV were observed slightly higher than GCV for all ten characters indicating minor influence of environmental factors. Estimates of genetic parameter are presented in Table 3 and 4. The graph showing high, moderate, low GCV and PCV is presented in Fig 1 and 2. Additionally, the differences between values of GCV and PCV for all the traits were very low indicating the influence of environment to be the minimum. Therefore, these traits could be easily exploited through selection. Branches per plant, pod length seeds per pod and seed yield per plant exhibited higher values of GCV and PCV for both the crosses indicating the greater scope of improving this character by applying the selection in an appropriate direction. The similar result for high GCV and PCV is in accordance with Asari *et al.* (2019); Gadakh *et al.* (2013); Joseph *et al.* (2020) and Singh *et al.* (2022).

Moderate GCV and PCV values were observed for the traits viz., days to flowering, days to maturity, plant height and harvest index. This indicated that the extent of response of these traits for selection would be less. The present result of moderate GCV and PCV showed resemblance with findings of Gayacharan *et al.* (2020); Yoseph *et al.* (2022); Prithviraj *et al.* (2020) and Sabatina *et al.* (2021).

However, pods per plant and 100 seed weight were reported with low GCV and PCV values indicating a narrow range of variability for these traits and restricting the scope of selection for these traits. The present result of low GCV and low PCV showed resemblance with findings of Dutt *et al.* (2020) and Joseph *et al.* (2020).

Heritability and genetic advance

High heritability indicating that the characters are least influenced by the environmental effect and the selection for improvement of such characters may not be useful since because broad sense heritability is based on total variance which include both fixable (additive) and nonfixable (dominance and epistatic) variance. Heritability estimates are shown in Fig 3 and 4. High genetic advance as per cent of mean indicate that the characters are governed by additive gene action and selection is effective. Heritability estimates along with genetic advance are more useful than heritability alone in predicting the resultant effect on selecting best individuals.

Higher heritability coupled with high genetic advance, as percent mean, is observed for days to flowering, plant height, branches per plant, pods per plant, seeds per pod and seed yield per plant. This confirmed higher additive gene action; thus, the improvement could be brought by direct phenotypic selection over the genotypes. Similar kind of results for high heritability and high genetic advance as a per cent of the mean are in favour of the outcome of Degefa *et al.* (2014); Yoseph *et al.* (2022); Asari *et al.* (2019); and Gadakh *et al.* (2013).

Table 2: Mean, range and variance values for ten morphological characters in Parents and F₂ generation of cross-II (HUM-27 × GM-8).

Characters	Mean ± Standard Error			Range		Variance		
	HUM-27	GM-8	F ₂	HUM-27	GM-8	F ₂	HUM-27	GM-8
Days to flowering	40.50±0.453	41.70±0.473	37.85±0.554	38-48	40-45	28-48	2.06	2.23
Days to maturity	67.20±0.359	72.20±0.786	65.92±0.446	66-69	65-75	57-79	1.29	6.18
Plant height (cm)	47.20±0.696	36.70±0.578	30.69±0.463	28-50	35-39	20-43	4.84	3.34
Branches per plant	2.50±0.167	2.50±0.167	3.46±0.102	2-3	2-3	1-6	0.28	0.28
Pods per plant	8.90±0.348	14.10±0.348	22.55±0.641	7-10	13-16	20-30	1.21	1.21
Pod length (cm)	6.43±0.256	8.50±0.401	7.46±0.152	5.50-7.20	7.0-10.0	4.5-11	0.66	1.61
Seeds per pod	9.90±0.504	8.30±0.396	7.64±0.253	8-12	7-10	2-15	2.54	1.57
100 seed weight (g)	5.31±0.048	6.28±0.042	5.90±0.056	5.1-5.5	6.1-6.4	5.1-7.2	0.02	0.02
Seed yield per plant (g)	8.87±0.228	8.10±0.181	7.87±0.153	8.0-10.1	7.5-9.0	5.8-13.9	0.52	0.33
Harvest index (%)	18.26±0.764	19.09±0.564	18.71±0.253	14.5-22.0	16.8-21.5	14.5-27.1	5.83	3.18
								6.42

Higher heritability with medium genetic advance as percent is observed in days to maturity and hundred seed weight indicating the effect of non-additive gene action. The same result of high heritability and medium genetic advance as a per cent of the mean were found by Azam *et al.* (2018) and Alom *et al.* (2014). Medium heritability and high genetic advance as per cent are observed for seeds per pod and

seed yield per plant in cross-I. The high genetic advance suggests that additive gene action predominantly controls the character. The same result of moderate heritability and high genetic advance as a per cent of the mean was found by Mohan *et al.* (2014) and Azam *et al.* (2018). Moderate heritability indicates that the environment also plays a role in the expression of the character, though genetics still

Table 3: Estimate of genetic variability parameters for ten quantitative characters in the F₂ population of cross-I (KM-22-24 × GM-6).

Characters	Mean	σ_p^2	σ_e^2	σ_g^2	GCV %	PCV %	h_{bs}^2 %	GA	GAM %
Days to flowering	36.35	30.11	1.81	28.30	14.65	15.10	94.19	10.65	29.29
Days to maturity	62.71	52.61	8.76	43.85	10.77	11.57	86.67	12.95	20.65
Plant height (cm)	35	37.01	7.54	29.47	16.17	17.38	86.54	10.85	30.99
Branches per plant	3.67	0.83	0.59	0.24	13.78	24.82	30.84	0.58	15.77
Pods per plant	22.77	3.73	2.03	1.70	5.80	8.49	46.74	1.86	8.17
Pod length (cm)	6.85	0.79	0.46	0.32	11.29	12.96	75.94	1.39	20.27
Seeds per pod	8.50	4.23	1.81	2.43	18.39	24.20	57.75	2.45	28.79
100 Seed weight (g)	5.95	0.34	0.14	0.20	7.53	9.80	59.01	0.71	11.92
Seed yield per plant (g)	8.08	2.99	1.30	1.69	16.19	21.41	57.22	2.04	25.24
Harvest index (%)	19.07	5.67	3.84	1.83	7.80	12.49	39.04	1.92	10.04

GCV = Genotypic coefficient of variation (%); PCV = Phenotypic coefficient of variation (%); GAM = Genetic advance as per cent of mean (%), σ_g^2 = Genotypic variance; σ_p^2 = Phenotypic variance; GA = Genetic advance (%); h_{bs}^2 % = Heritability (Broad sense).

Table 4: Estimate of genetic variability parameters for ten quantitative characters in the F₂ population of cross-II (HUM-27 × GM-8).

Characters	Mean	σ_p^2	σ_e^2	σ_g^2	GCV %	PCV %	h_{bs}^2 %	GA	GAM %
Days to flowering	37.85	30.65	2.14	28.51	14.11	14.63	93.01	10.61	28.03
Days to maturity	65.92	19.89	3.73	16.16	6.27	6.77	85.21	7.88	11.96
Plant height (cm)	30.69	21.45	4.10	17.35	13.60	15.09	81.23	7.75	25.25
Branches per plant	3.46	1.04	0.28	0.76	25.21	29.46	73.26	1.54	44.45
Pods per plant	22.25	2.86	1.21	1.64	5.69	7.49	57.60	2.01	8.89
Pod length (cm)	7.46	2.31	1.13	1.18	15.21	20.40	55.58	1.74	23.36
Seeds per pod	7.64	6.39	2.06	4.34	27.45	33.10	68.78	3.58	46.89
100 Seed weight (g)	5.90	0.31	0.02	0.29	9.14	9.45	93.54	1.07	18.21
Seed yield per plant (g)	7.87	2.33	0.42	1.91	17.61	19.40	82.37	2.59	32.93
Harvest index (%)	18.71	6.42	4.51	1.91	7.76	13.54	32.84	1.71	9.16

GCV= Genotypic coefficient of variation (%); PCV= Phenotypic coefficient of variation (%); GAM = Genetic advance as per cent of mean (%), σ_g^2 = Genotypic variance; σ_p^2 = Phenotypic variance; GA = Genetic advance (%); h_{bs}^2 % = Heritability (Broad sense).

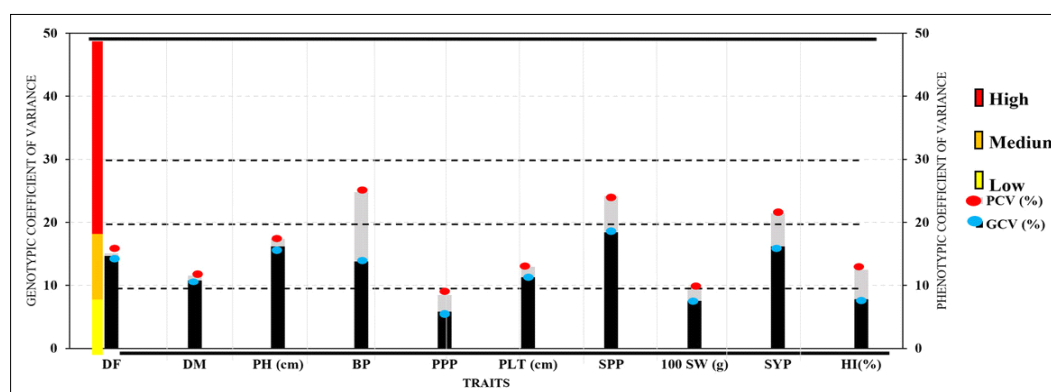


Fig 1: GCV(%) and PCV(%) of cross-I (KM-22-24 X GM-6) in F₂ population for ten different characters.

have a meaningful influence. In this context, selection based on phenotypic performance will be effective, but environmental conditions must be considered.

Mung bean yellow mosaic virus (MYMV) incidence (%)

Mung bean yellow mosaic disease caused by whitefly transmitted begomoviruses is the most limiting factor in improving the productivity of green gram (Malathi *et al.*, 2017). The typical symptoms of disease are bright yellow mosaic of leaves, stunted growth, reduction in leaf lamina and pods

number and highly misshapen shrivelled seeds. MYMV incidence was recorded in all F₂ progenies of crosses *i.e.* cross-I KM-22-24 × GM-6 and cross-II HUM-27 × GM-8 and the score was given from 0 (highly resistant) to 9 (highly susceptible). Mean scores of MYMV incidence exhibited by F₂ progenies of a green gram are depicted in Fig 5 and disease rating grade scale given by IIPR, Kanpur (U.P.) shown in Table 5.

The distribution of plants across different disease reaction classes in the two segregating populations

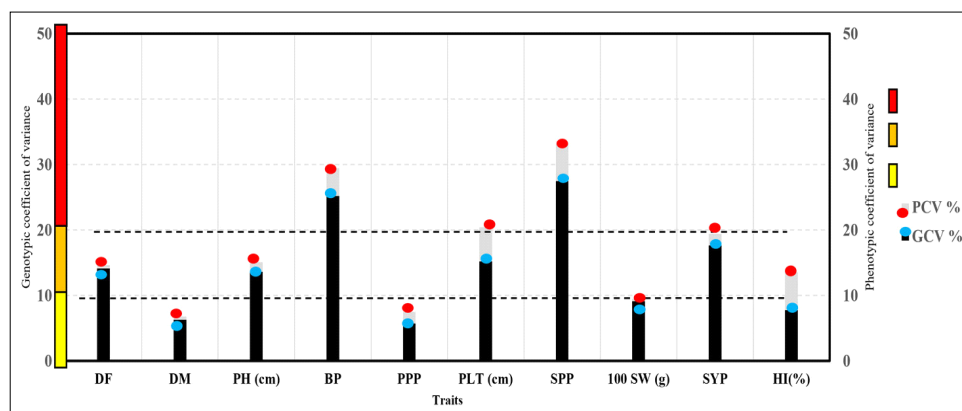


Fig 2: GCV(%) and PCV(%) of cross-II (HUM-27 × GM-8) in F₂ population for ten different characters.

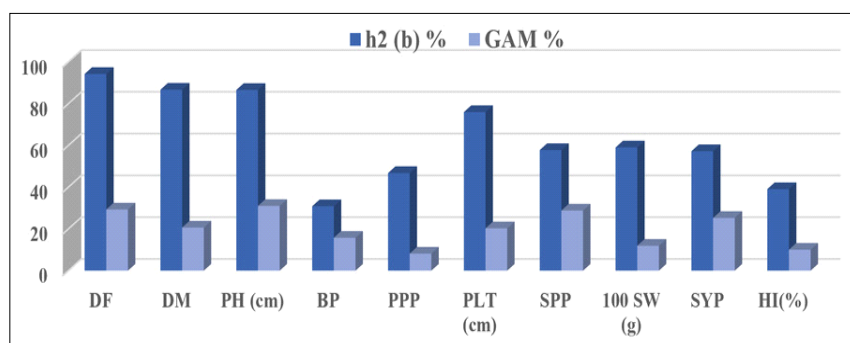


Fig 3: Heritability (bs) % and GAM % of cross-I (KM-22-24 × GM-6).

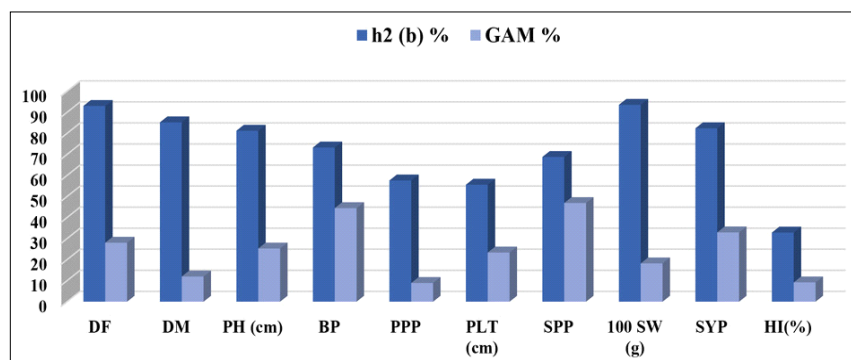


Fig 4: Heritability (bs)% and GAM % of cross-II (HUM-27 × GM-8).

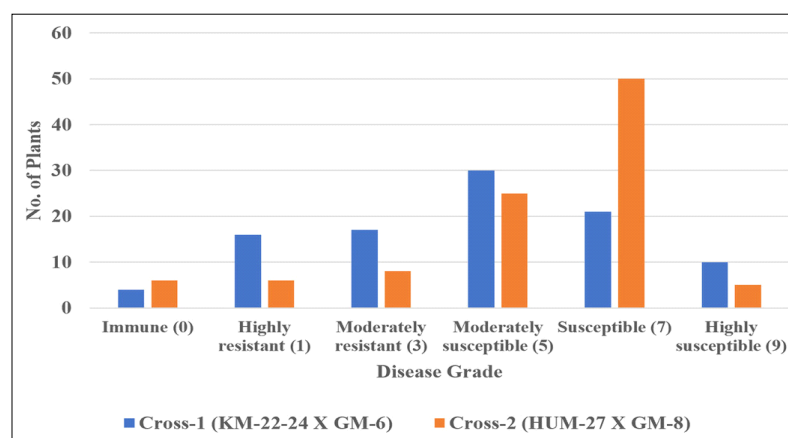


Fig 5: Disease severity comparison among two populations.

Table 5: Disease rating grade for MYMV in green gram (0-9 grade).

Scale	Description	Reaction	Designation
0	No visible symptoms on leaves	Free	I
1	1-10% leaf area covered with symptoms	Resistant	R
3	1-20% leaf area covered with symptoms	Moderately resistant	MR
5	20-30% leaf area covered with symptoms	Moderately susceptible	MS
7	30-50% leaf area covered with symptoms	Susceptible	S
9	>50% leaf area covered with symptoms	Highly susceptible	HS

revealed clear differences in their response to disease pressure. In Cross-1 (KM-22-24 × GM-6), plants were distributed across all resistance categories, with 4 plants classified as immune (grade 0), 16 as highly resistant (grade 1), 17 as moderately resistant (grade 3), 30 as moderately susceptible (grade 5), 21 as susceptible (grade 7) and 10 as highly susceptible (grade 9). This population exhibited a relatively higher frequency of plants in the resistant and moderately resistant classes, indicating wider genetic variability for disease resistance. In contrast, Cross-2 (HUM-27 × GM-8) showed a skewed distribution towards susceptibility, with only 6 immune, 6 highly resistant and 8 moderately resistant plants, whereas a large proportion of the population was categorized as moderately susceptible (25 plants) and susceptible (50 plants), along with 5 highly susceptible plants. The predominance of susceptible individuals in Cross-2 reflects limited resistance potential in this population.

Overall, Cross-1 demonstrated a more balanced segregation pattern with a higher proportion of resistant classes, suggesting its suitability for genetic studies on disease resistance and for selection of superior recombinants in breeding programmes.

CONCLUSION

It can be concluded from the present research work that variability in F₂ generations was found with wide range of variation among segregating population due to contrasting parents traits used in the crossing program. The higher value of GCV and PCV for the traits viz., branches per plant

and seeds per pod indicates that there is a greater scope for improving these traits by applying selection in the subsequent generations. The F₂ segregating generations of both the cross-I (KM-22-24 × GM-6) and cross-II (HUM-27 × GM-8) could be subjected for the selection of improvement of the seed yield as they showed high GCV and PCV heritability and genetic advance as per cent mean for few yield attributing traits. Higher heritability coupled with high genetic advance as per cent mean was observed for days to flowering and plant height in both the crosses, while in cross-I, days to flowering, days to maturity, plant height and pod length showed high heritability coupled with high genetic advance per cent mean. Similarly, in cross-II days to flowering, plant height, branches per plant, seeds per pod and seed yield per plant showed the same result. Hence, priority should be given to these traits in formulating selection strategies to obtain desirable genetic gain by selection.

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Disclaimers

The views and conclusions expressed in this article are solely those of the authors and do not necessarily represent the views of their affiliated institutions. The authors are responsible for the accuracy and completeness of the

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Conflict of interest

The authors declare that there are no conflicts of interest regarding the publication of this article. No funding or sponsorship influenced the design of the study, data collection, analysis, decision to publish, or preparation of the manuscript.

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