



Character Association Studies of Quantitative Characters in Summer Mung bean [*Vigna Radiata* (L.) Wilzek] Genotypes

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Abstract: The productivity of mung bean in India remains low due to a narrow genetic base for yield improvement, limited variability in yield-related traits, suboptimal ideotype of the mung bean plant, susceptibility to biotic and abiotic stresses, inadequate crop management, and weed infestation. The present study was conducted at the Agricultural Research Station, Ummedganj-Kota, Rajasthan, during summer 2024, to assess genetic variability and examine the relationships among quantitative traits in 26 mung bean genotypes of diverse origins. The analysis revealed highly significant mean squares for all morphological characters, indicating the presence of substantial variability. Traits such as the number of pods plant⁻¹, 100-seed weight, and plant height showed high heritability estimates and significant genetic advances, suggesting that additive gene effects predominantly influence these traits, with minimal environmental impact, and that simple phenotypic selection would be effective. The study also identified high direct effects of traits like harvest index, 100-seed weight, biological yield plant⁻¹, number of seeds pod⁻¹, number of pods plant⁻¹, and number of branches plant⁻¹ on yield. These findings suggest that targeted selection for these traits can effectively enhance grain yield in mung bean. Additionally, genotypes PMD-11, BCM 20-52, IPM 205-7, MH 1923, IPM 410-3, and SML 2159 were identified as promising donors for these traits in recombinant breeding programs aimed at yield improvement.

Key words: Genetic variability, correlation, path coefficient, mung bean genotypes.

Mung bean (*Vigna radiata* (L.) Wilczek) also known as green gram is one of the important pulse crops widely grown in arid and semi-arid regions of India. By virtue of its peculiarity of short duration, low water requirement and photo insensitiveness, it can be grown in various crop rotation practices (Singh *et al.*, 2015). It is tolerant to moisture stress and heat and low soil fertility. It is favored for consumption due to its high protein content, easy digestibility and low production of flatulence (Shil and Bandopadhyaya, 2007). The

protein is comparatively rich in the amino acid lysine which is predominantly deficient in cereal grains (Baskaran *et al.*, 2009). India is the largest producer of mung bean in the world and accounts for 65% acreage and 54% production (Pratap *et al.*, 2012). However, productivity of mung bean is very low (425 kg ha⁻¹) compared to its genetic potential (Anonymous, 2023-24). Therefore, there is a great scope for its improvement by developing high yielding, disease and pest resistance varieties with improved nutritional value.

Seed yield is a complex polygenic character, which is influenced by many independent characters. Direct selection would not be a reliable approach on account of being highly influenced by environmental factors. Studies on the correlation of characters and their relative direct and indirect effects on seed yield are important, as it is helpful in selection of desirable characters (Muthuswamy *et al.*, 2019). Organized and concerted efforts are required to enhance its productivity. Correlation provides information on the nature and magnitude of association of different component characters with seed yield. Path analysis permits a critical examination of specific forces acting to produce a given correlation and measure the relative importance of each factor. Thus, characters highly contributing to seed yield can be selected. Therefore, twelve traits and their correlations with seed yield were studied across 26 mung bean genotypes.

Materials and Methods

Twenty six genotypes of mung bean were evaluated in randomized block design with three replications during summer, 2024 at research farm of Agricultural Research Station, Ummedganj-Kota (Rajasthan). The seed of these mung bean genotypes were obtained from All India Coordinated Research Project on MULLaRP, ICAR-IIPR, Kanpur. Each genotype was raised in a six row plot of 4 m length with a spacing of 30 cm between rows and 10 cm between plants. All recommended agronomic practices were adopted to raise a healthy crop. Observations were recorded for twelve characters viz., days to 50% flowering, days to maturity, plant height (cm), number of branches plant⁻¹, number of clusters plant⁻¹, number of pods plant⁻¹, pod length (cm), number of seeds pod⁻¹, 100-seed weight (g), biological yield

plant⁻¹ (g), harvest index (%) and seed yield plant⁻¹ (g). Five plants were selected randomly from each plot for recording the observations for all the twelve characters except for days to 50% flowering and days to maturity, where, the observations were recorded on whole plot basis. Analysis of variance was estimated by the method suggested by Panse and Sukhatme (1985). The estimates of genotypic and phenotypic variance were calculated using the method suggested by Johanson *et al.* (1955). Genotypic and phenotypic coefficients of variation were worked out by the method advocated by Burton (1952). Broad sense heritability was calculated as per the method suggested by Lush (1940). The expected genetic advance for each character was calculated as per method given by Johanson *et al.* (1955). Genotypic and phenotypic correlations were determined according to Fisher (1954) and Al-Jibouri *et al.* (1958). The path analysis was done according to the method described by Dewey and Lu (1959). Statistical analysis of recorded phenotypic data was performed using OPSTAT software.

Results and Discussion

Analysis of variance

The analysis of variance exhibited significant differences among genotypes for all the twelve characters studied, indicating that material possessed adequate genetic variability required to the breeding programme for improving the seed yield of mung bean. Earlier Kumar (2023) and Shiv *et al.* (2017) also reported high variability for different traits in mung bean.

Variability and heritability parameters: A wide range of variability was exhibited by different characters namely; days to 50% flowering (36-57), days to maturity (61-78), plant height (35.33-71.67 cm), number of branches plant⁻¹ (1.67-4.5), number of clusters plant⁻¹ (3.33-11.67), number of pods plant⁻¹ (6.67-22.67), pod length (4.98-8.79 cm), number of seeds pod⁻¹ (5.1-8.5), 100-seed weight ((3.31-5.92 g)), biological yield plant⁻¹ (13.35-33.66 g), harvest index (7.2-44.14 %) and seed yield plant⁻¹ (1.89-8.97g). The highest GCV and PCV in mung bean genotypes were recorded for harvest index (%) followed by seed yield plant⁻¹ (g), number of pods plant⁻¹ and number of clusters plant⁻¹. It suggests a good potential for improvement in these characters, creating variability through

Table 1. List of mung bean genotypes used for present investigation

S. No.	Genotype	Parentage	Origin
1.	MH 1923	Vamban 2 × Sattya	CCSHAU, Hisar
2.	NVL 1337	NVL 825 × NVL 1130	NSPL, Pachora
3.	CGG 20008	CO 7 × IPM 205-7	TNAU, Coimbatore
4.	VGG 20-157	VBN (Gg) 2 × MASH 114	NPRC, Vamban
5.	IPM 410-3 (Check)	IPM 03-1 × NM 1	IIPR, Kanpur
6.	OBGG 103	LM 94 × ML 1628	OUAT, Berhampur
7.	Jawahar M6	PDM 11 × Kanika	JNKVV, Jabalpur
8.	BCM 20-74	IPM 02-14 × TMB 37	BCKV, Mohanpur
9.	MGG 519	TM 96-2 × SM 131	ARS, Madhira
10.	Pusa M 2441	KPS 3 × KM 15-66	IARI, New Delhi
11.	SML 2159	SML 668 × MH 421	PAU, Ludhiana
12.	Pusa 9531 (Check)	Sel. from NM 9374	IARI, New Delhi
13.	BRM-14	EC-319049 × PM5-1-1	BAU, Sabour
14.	SKNM 2210	GM 4 × LGG 460	SDAU, S.K. Nagar
15.	VGG 20-234	GM 4 × LGG 460	NPRC, Vamban
16.	COGG 22-03	CO 7 × LRB 576	TNAU, Coimbatore
17.	IPM 205-7 (Check)	IPM 02-1 × EC 398889	IIPR, Kanpur
18.	BCM 20-52	MH 318 × EC 369223	BCKV, Mohanpur
19.	SKNM 2107	GM 4 × Pusa 0672	SDAU, S.K. Nagar
20.	TAKM 140	TM 98-80 × SML 668	BARC, Mumbai
21.	BRM 15-1	LM-244 × P. Vishal-1	BAU, Sabour
22.	PMD-11	IPM 2-14 × MH 565	IARI, New Delhi
23.	Jawahar M5	TJM196 × PDM 139	JNKVV, Jabalpur
24.	OBGG 113	LM 94 × Harsha	OUAT, Berhampur
25.	DGG 96	TARM-1-28-1 (Mutant)	UAS, Dharwad
26.	MGG 389	Madhira mung × MI 267-6	ARS, Madhira

hybridization followed by selection. These are similar to results of Kumar *et al.* (2024) for seed yield plant⁻¹, number of pods plant⁻¹, harvest index and biological yield plant⁻¹ and Asari *et al.* (2019) observed for primary branches plant⁻¹, pods plant⁻¹, seed yield plant⁻¹ and clusters plant⁻¹. Perusal of the mean performance of various genotypes for different characters revealed that genotypes PMD-11, BCM 20-52, IPM 205-7, MH 1923, IPM 410-3 and SML 2159 were promising for seed yield plant⁻¹ and its important contributing characters.

GCV and PCV were moderate for plant height, biological yield plant⁻¹, number of branches plant⁻¹, 100-seed wt. and number of seeds pod⁻¹ which suggest that improvement in these characters might be gained to a reasonable extent. The response of selection depends on heritable portion of the variation in the population. A character having high GCV with high

heritability will be more rewardable in selection programme. High heritability estimates were observed for days to maturity, 100-seed wt, days to 50% flowering, plant height and number of pods plant⁻¹. Similar findings was also observed by Kumar *et al.*, 2024.

The genetic advance as per cent of mean provides an idea of the magnitude of progress that can be achieved by selection for a particular trait. High genetic advance as per cent of mean was estimated for number of harvest index, pods plant⁻¹, seed yield plant⁻¹, plant height, number of clusters plant⁻¹, biological yield plant⁻¹ and 100-seed wt. However, it was moderate for days to 50% flowering, number of seeds pod⁻¹, number of branches plant⁻¹, days to maturity and pod length. The heritability value coupled with genetic advance as per cent of mean would be more reliable and useful in predicting the gain under selection than the heritability estimates alone. The high estimate

Table 2. Analysis of variance for different characters of mung bean

Source of variation	d.f.	Days to 50% flowering	Days to maturity	Plant height (cm.)	No. of branches plant ⁻¹	No. of clusters plant ⁻¹	No. of pods plant ⁻¹	Pod length (cm)	No. of seeds pod ⁻¹	100- seed wt. (g)	Biological yield plant ⁻¹ (g)	Harvest index	Seed yield plant ⁻¹ (g)
Replications	2	0.46	4.50	49.42	0.03	0.26	5.43	0.48	0.85	0.02	0.20	28.12	1.38
Genotypes	25	49.63**	60.86**	230.51**	0.66**	4.81**	32.33**	1.22**	1.91	0.96**	44.99**	113.84**	3.34**
Error	50	0.86	0.35	7.29	0.22	0.75	1.44	0.22	0.17	0.02	4.22	14.82	0.82

*Significant at P=0.05, **Highly significant at P=0.01.

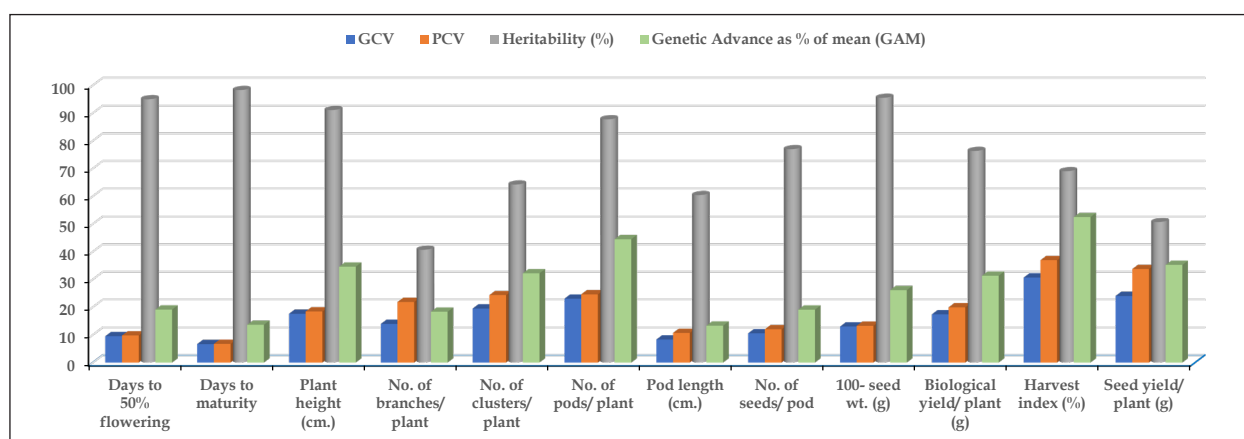


Fig. 1. Chart representation of variability parameters, heritability and genetic advance as per cent of mean.

of heritability coupled with the high estimate of genetic advance as per cent of mean was recorded for number of pods plant⁻¹, 100-seed wt. and plant height. These characters are governed by additive gene action and therefore may be improved by direct selection, which are akin to the results of Choudhary *et al.*, 2017 and Kumar *et al.*, 2024.

Correlation coefficient analysis: Seed yield is a complex polygenic character, which is influenced by many independent characters. Direct selection would not be a reliable approach on account

of being highly influenced by environmental factors. Selection for component characters would be helpful in selection of seed yield. In the present investigation, the values of genotypic correlation coefficients (r_g) were slightly higher than the corresponding phenotypic correlation coefficients (r_p) for most of the characters, indicating that the genetic relationship between the corresponding traits is stronger than the observable relationship. Earlier, Khatik *et al.*, 2022 also find the results of higher genotypic correlation coefficients than corresponding phenotypic correlation coefficients. Seed yield

Table 3. Estimates of genetic variability parameters for different characters of mung bean

Character	Range	Mean	GCV	PCV	Heritability (%)	Genetic advance	Genetic advance as % of mean (GAM)
Days to 50% flowering	36-57	42.31	9.53	9.78	94.97	8.09	19.13
Days to maturity	61-78	67.19	6.68	6.74	98.28	9.17	13.65
Plant height (cm)	35.33-71.67	49.00	17.61	18.45	91.08	16.96	34.61
No. of branches plant ⁻¹	1.67-4.50	2.75	13.96	21.88	40.68	0.51	18.34
No. of clusters plant ⁻¹	3.33-11.67	5.96	19.51	24.34	64.21	1.92	32.20
No. of pods plant ⁻¹	6.67-22.67	13.91	23.07	24.63	87.73	6.19	44.52
Pod length (cm.)	4.98-8.79	6.93	8.33	10.72	60.39	0.92	13.33
No. of seeds/pod	5.1-8.5	7.20	10.57	12.05	76.96	1.38	19.10
100-seed wt. (g)	3.31-5.92	4.33	12.99	13.29	95.48	1.13	26.15
Biological yield plant ⁻¹ (g)	13.35-33.66	21.18	17.41	19.93	76.30	6.63	31.33
Harvest index (%)	7.2-44.14	18.73	30.68	36.93	69.01	9.83	52.50
Seed yield plant ⁻¹ (g)	1.89-8.97	3.82	24.03	33.75	50.68	1.35	35.24

Table 4. Genotypic (rg) and phenotypic (rp) correlation coefficients between seed yield and its component characters in mung bean

Characters	r	Days to 50% flowering	Days to maturity	Plant height	No. of branches plant ⁻¹	No. of clusters plant ⁻¹	No. of pods plant ⁻¹	Pod length	No. of seeds pod ⁻¹	100- seed wt.	Biological yield plant ⁻¹	Harvest index	Seed yield plant ⁻¹
Days to 50% flowering	rg	1.000	0.856**	0.845**	-0.613**	-0.516**	-0.682**	-0.223*	-0.588	0.100 ^{NS}	0.471**	-0.823**	-0.845**
	rp	1.000	0.829**	0.791**	-0.406**	-0.407**	-0.610**	-0.152 ^{NS}	-0.496**	0.082 ^{NS}	0.397**	-0.690**	-0.604**
Days to maturity	rg		1.000	0.858**	-0.593**	-0.527**	-0.714**	-0.420**	-0.672**	0.017 ^{NS}	0.516**	-0.903**	-0.928**
	rp		1.000	0.812**	-0.394**	-0.435**	-0.670**	-0.345**	-0.584**	0.015 ^{NS}	0.438**	-0.750**	-0.668**
Plant height (cm)	rg			1.000	-0.787**	-0.572**	-0.755**	-0.410**	-0.652**	0.082 ^{NS}	0.475**	-0.882**	-0.911**
	rp			1.000	-0.437	-0.452	-0.668**	-0.252*	-0.513**	0.086 ^{NS}	0.425**	-0.698**	-0.596**
No. of branches/ plant	rg				1.000	0.860**	0.794**	0.029 ^{NS}	0.506**	-0.366**	0.095 ^{NS}	0.363**	0.583**
	rp				1.000	0.678**	0.585**	0.031 ^{NS}	0.300**	-0.222 ^{NS}	0.190 ^{NS}	0.332**	0.509**
No. of clusters/ plant	rg					1.000	0.753**	0.135 ^{NS}	0.518**	-0.262*	0.326**	0.341**	0.692**
	rp					1.000	0.691**	0.172 ^{NS}	0.382**	-0.205 ^{NS}	0.355**	0.297**	0.566**
No. of pods/ plant	rg						1.000	0.158 ^{NS}	0.704**	-0.466**	-0.134 ^{NS}	0.754**	0.943**
	rp						1.000	0.186 ^{NS}	0.603**	-0.442**	-0.035 ^{NS}	0.644**	0.756**
Pod length (cm)	rg							1.000	0.268*	0.623**	-0.124 ^{NS}	0.398**	0.542**
	rp							1.000	0.292**	0.497**	0.067 ^{NS}	0.269**	0.420**
No. of seeds/ pod	rg								1.000	-0.476**	-0.154 ^{NS}	0.736**	0.930**
	rp								1.000	-0.382**	-0.116 ^{NS}	0.576**	0.625**
100- seed wt. (g)	rg									1.000	-0.167 ^{NS}	-0.088 ^{NS}	-0.163 ^{NS}
	rp									1.000	-0.130 ^{NS}	-0.080 ^{NS}	-0.117 ^{NS}
Biological yield/ plant	rg										1.000	-0.769**	-0.378**
	rp										1.000	-0.536**	-0.055 ^{NS}
Harvest index	rg											1.000	0.873**
	rp											1.000	0.859**
Seed yield/ plant	rg												1.000
	rp												1.000

Genotypic correlation coefficients (rg) Phenotypic correlation coefficients (rp).

plant⁻¹ was positively correlated with number of pods plant⁻¹, number of seeds pod⁻¹, harvest index, number of clusters plant⁻¹, number of branches plant⁻¹ and pod length indicating that selection based on these characters may result in high seed yield. Dhole and Reddy (2018)

also reported positive correlation coefficients of seed yield with number of pods cluster⁻¹ and number of seeds pod⁻¹, Dadepeer *et al.* (2009); Rahim *et al.* (2010) and Prasanna *et al.* (2013) for number of primary branches plant⁻¹, number of cluster plant⁻¹, number of pods cluster⁻¹ and

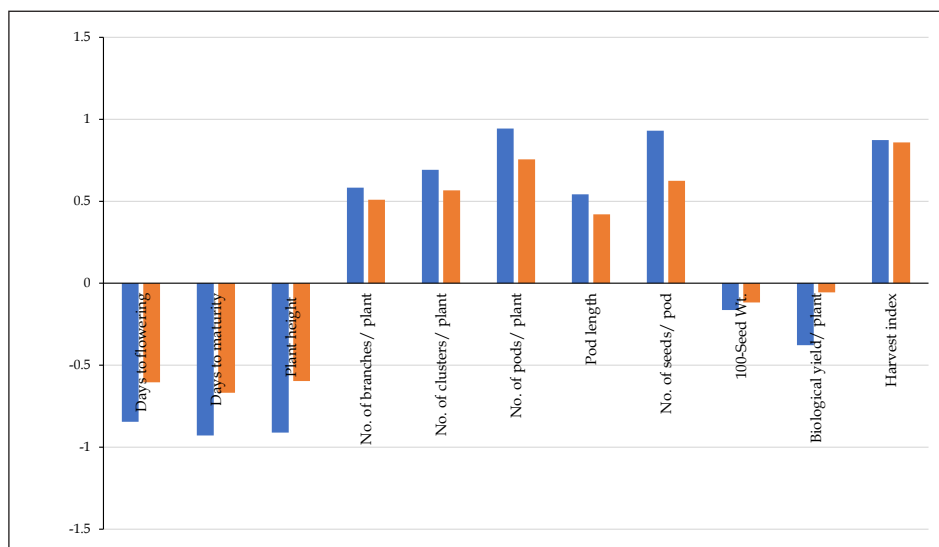


Fig. 2. Genotypic (rg) and phenotypic (rp) correlation of seed yield with its attributing characters.

Table 5. Direct (diagonal) and indirect effect of different characters towards seed yield per plant in mung bean genotypes

Character	Days to 50% flowering	Days to maturity	Plant height	No. of branches ⁻¹ plant	No. of clusters ⁻¹ plant	No. of pods ⁻¹ plant	Pod length	No. of seeds ⁻¹ pod	100-seed wt.	Biological yield ⁻¹ plant	Harvest index
Days to 50% flowering	-0.04	0.05	0.22	-0.22	0.30	-0.38	0.09	-0.36	0.08	0.37	-0.95
Days to maturity	-0.04	0.06	0.22	-0.21	0.30	-0.40	0.17	-0.41	0.01	0.41	-1.04
Plant height	-0.04	0.05	0.26	-0.28	0.33	-0.42	0.17	-0.40	0.07	0.38	-1.02
No. of branches/plant	0.03	-0.04	-0.20	0.36	-0.49	0.44	-0.01	0.31	-0.31	0.07	0.42
No. of clusters/plant	0.02	-0.03	-0.15	0.31	-0.57	0.42	-0.06	0.32	-0.22	0.26	0.39
No. of pods/plant	0.03	-0.04	-0.19	0.29	-0.43	0.55	-0.06	0.43	-0.39	-0.11	0.87
Pod length	0.01	-0.03	-0.10	0.01	-0.08	0.09	-0.41	0.17	0.52	-0.10	0.46
No. of seeds/pod	0.03	-0.04	-0.17	0.18	-0.30	0.39	-0.11	0.62	-0.40	-0.12	0.85
100- seed wt	0.00	0.00	0.02	-0.13	0.15	-0.26	-0.25	-0.29	0.84	-0.13	-0.10
Biological yield/plant	-0.02	0.03	0.12	0.03	-0.19	-0.07	0.05	-0.09	-0.14	0.79	-0.89
Harvest index	0.04	-0.05	-0.23	0.13	-0.20	0.42	-0.16	0.45	-0.07	-0.61	1.15

Residual effect-0.007

number of pods plant⁻¹, Kumar *et al.* (2005) for plant height and number of pods plant⁻¹. Significant correlations were also recorded among the above characters as well as seed yield which suggested that these characters may be considered for improvement of seed yield. Hence, it may be concluded that simultaneous selection for these characters would help for improvement of yield. Seed yield plant⁻¹ was negatively correlated with days to flowering, days to maturity and number of seeds pod⁻¹ indicating that these traits could be ineffective for increasing seed yield, which was in close agreement with findings of Muthuswamy *et al.* (2019) and Prasanna *et al.* (2013).

Path coefficient Analysis: Path analysis partitions the total correlation coefficient into direct and indirect effects and measures the relative importance of the causal factor individually" (Dewey and Lu, 1959). Seed yield is a dependent character. Maximum direct effect (Table 2 and Fig. 2) was exerted by the characters harvest index followed by 100-seed wt., biological yield plant⁻¹, number of seeds pod⁻¹, number of pods plant⁻¹ and number of branches plant⁻¹ indicating that there is always scope for enhancement of seed yield by selecting these characters. The low value of residual effect (-0.007) suggested that most of the characters which contribute to the seed yield had been taken into consideration. These characters exhibited positive correlation as well as had high direct effects on seed yield plant⁻¹, hence, selection should be practiced for these characters in order to isolate superior genotype having higher seed yield for mung bean improvement programme. The present

results are in close agreement with findings of Prasanna *et al.* (2013), Narasimhulu *et al.* (2013a) and Muthuswamy *et al.* (2019). The character viz., days to flowering, number of clusters plant⁻¹ and pod length had a negative influence on seed yield plant⁻¹. Therefore, selection of these characters could be ineffective for increasing seed yield.

Conclusions

The results of this study revealed that the morphological characters like seed yield plant⁻¹, harvest index, number of pods plant⁻¹, biological yield plant⁻¹ had high degree of genetic variability along with high heritability and high genetic advance as per cent of mean, which indicates that these characters were under control of additive gene action and therefore, providing opportunity of selection based on yield contributory traits in the mung bean improvement programme. The number of pods plant⁻¹, number of seeds pod⁻¹, harvest index, number of clusters plant⁻¹, number of branches plant⁻¹ and pod length had positive correlation with seed yield both at genotypic and phenotypic levels. Path analysis revealed harvest index, 100-seed wt., biological yield plant⁻¹, number of seeds pod⁻¹, number of pods plant⁻¹ and number of branches plant⁻¹ had positive and high direct effect towards seed yield plant⁻¹. Hence, these traits should be given more emphasis while selecting genotypes for yield improvement in mung bean.

Competing interests

Authors have declared that no competing interests exist.

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