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Genetic Variation and Character Association Studies for Seed Yield and its Attributes in Diverse Panel of Mungbean Genotypes [*Vigna radiata* (L.) Wilczek]

Navreet Kaur Rai[1], Ravika[1], Rajesh Yadav[1], Amit[1], Kavita[1], Pawan Kumar[1], Rahul Dhaniya[1] 10.18805/LR-5481

ABSTRACT

Background: Mungbean [*Vigna radiata* (L.) Wilczek] is one among the most important and oldest cultivated pulse crop of the world grown in different seasons. The present investigation was carried out to access variability, correlation, path coefficients and cluster analysis for better understanding of genetic architecture of seed yield and its attributes in mungbean.

Methods: The experimental material consisted of 142 diverse mungbean genotypes including released varieties from different agro-climatic zones of India and advanced genotypes developed at CCS HAU, Hisar. These genotypes were evaluated at Pulses Research Area, CCS HAU, Hisar during *kharif* 2021 and 2022 in randomized block design with two replications. Each genotype was planted in three rows, each of 4 m length with spacing of 45 cm between the rows and 10 cm between plants.

Result: The narrow differences between PCV and GCV indicated that the observed variation primarily stemmed from genetic factors, thereby suggesting ample opportunities for selection. Most of the characters exhibited high heritability with high, moderate or low genetic advance indicating presence of both additive and non-additive gene action, therefore, recombinant breeding in early generations will be beneficial. The correlation and path analysis suggested that selection for traits such as seeds per pod, number of pods per plant and 100-seed weight would prove effective in enhancing mungbean seed yield. The hierarchical cluster analysis grouped the genotypes into eight diverse clusters. Cluster IV was found to have better performing genotypes in terms of yield as well as yield related traits. Overall, genotypes MH 1468, MH 1871, MH 1762, IPM 604-16 and IPM 205-7 were found significantly early in maturity along with high mean values of seed yield and its related traits. As a result, these genotypes can be further used in breeding programmes for mungbean improvement.

Key words: Correlation, Diversity, GAM, GCV, Heritability, Path coefficient analysis, PCV.

INTRODUCTION

The growing global population, diminishing biodiversity, limited agricultural resources, poverty and the formidable climatic conditions have significant impact on worldwide food and nutritional security. Pulses play a crucial role in sustainability of agriculture and can provide effective solution to address these concerns as they contribute significantly to environmental, economic and social aspects of farming systems (Singh, 2017). Mungbean [*Vigna radiata* (L.) Wilczek], is one of the oldest cultivated and most important pulse crops. It is a diploid (2n= 2x =22), belongs to family Leguminosae; subfamily papilionoideae and tribe Fabeae and it is believed to be originated in the Indian subcontinent, with evidence of its cultivation dating back over 4,000 years. It was an important crop in ancient India and spread to Southeast Asia and other regions through trade and agricultural expansion (Partap *et al.,* 2021). Mungbean being a pulse crop plays a key role in crop rotation by interrupting the conventional sequence of cereal crops (Rice-Wheat) and can be utilized as a green manure also (Sharma *et al.,* 2023). It is highly valued for its nutritional quality as it is rich in protein (25.10%), carbohydrates (59-65%), fiber (13.40%), vitamin A (83 mg/100 g), thiamine (0.72 mg/100 g) and riboflavin (0.15 mg/100 g) (Vairam *et al.,* 2016). Therefore, enhancing mungbean production and productivity is imperative to meet the escalating global demand for vegan protein-rich diets, address food security challenges and optimize resource use in sustainable agriculture.

Mungbean breeding faces significant bottlenecks due to limited genetic diversity, low harvest index and the complex interplay of biotic and abiotic stress, which hinders the development of robust, high-yielding cultivars. Consequently, to develop mungbean cultivars that are both locally adapted and high-yielding, breeding programs must incorporate a diverse array of genotypes. This approach is essential for integrating various traits that address the

[1]Department of Genetics and Plant Breeding, CCS Haryana Agricultural University, Hisar-125 004, Haryana, India.

Corresponding Author: Ravika, Department of Genetics and Plant Breeding, CCS Haryana Agricultural University, Hisar-125 004, Haryana, India. Email: ravika.sheoran@hau.ac.in

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needs of farmers and end consumers (Neupane *et al.,* 2021). Genetic diversity among the genotypes serves as a crucial resource for breeding programs, aiding in the development of innovative farming systems, enhancing production diversity and generating new high-quality products (Jing *et al.,* 2010). As yield is the most important agronomic and economic feature in crops which is a outcome of numerous interacting component characteristics that have relatively low heritability and are influenced by multiple loci with mostly uncertain genetic foundations, hence, to develop a plant genotype with an appropriate blend of attributes, complete information on the relationship of these traits with yield, as well as detailed *a priori* knowledge of the genetic mechanism governing these traits, are required for any successful breeding program. Furthermore, insights into the genetic relationships between yield and its characteristics will assist in defining selection criteria and pinpointing beneficial secondary traits. This will ultimately lead to improved yields and will broaden the potential for success in breeding programs (Evans and Fischer, 1999). In addition, as for two traits, correlation doesn't exist among them but it involves complicated pathways including many other traits also. As a result, selection for seed yield will be more effective when path coefficient partitioning the relationship into direct and indirect effects, which demonstrates the relative relevance of each of the causal components (Dewey and Lu, 1959), are computed. Hence, the current investigation was undertaken to estimate the genetic variability, trait associations and diversity among 142 mungbean genotypes for seed yield and its allied traits.

MATERIAL S AND METHODS

The experimental material consisted of 142 diverse mungbean genotypes including released varieties from different agro-climatic zones of India and advanced genotypes developed at CCS HAU, Hisar. These genotypes were evaluated during *kharif* 2021 and 2022 in randomized block design with two replications. Each genotype was planted in three rows, each of 4 m length with spacing of 45 cm between the rows and 10 cm between plants. The experiment was planted at Pulses Research Area, Department of Genetics and Plant Breeding, CCS Haryana Agricultural University, Hisar, Haryana. This site is geographically positioned at coordinates 29.15°N, 75.75°E and is characterized by a semi-arid climate with high temperatures in summer and low temperatures in winter. It is situated on the edge of the southwest monsoon region and has a tropical dry climate receiving about 350-400 mm average yearly rainfall. All suggested agronomic practices were implemented to raise a high-quality crop. The 142 mungbean genotypes were evaluated based on nine quantitative traits *viz.,* days to 50% flowering, days to maturity, plant height, number of branches per plant, number of pods per plant, number of seeds per pod, pod length, 100-seed weight and seed yield per plant. Genetic variability was assessed using genotypic coefficients of variation (GCV) and phenotypic coefficients of variation (PCV), as outlined by Burton and de Vane (1953). Heritability in the broad sense for each trait was calculated as per Singh and Chaudhary (1985), while the expected genetic advance at a 5% selection intensity was calculated as per Johnson *et al.* (1955). The city block (Manhattan) distance was employed to construct a dendrogram through hierarchical clustering of genotypes, using the Unweighted Pair-Group Method with Arithmetic Averages (UPGMA). Statistical analysis was conducted using R Studio version 2023.06.2+561. The list of genotypes and their pedigree used in the study are described in Table 1.

RESULTS AND DISCUSSION

Analysis of variance and yield performance of genotypes

The pooled mean squares for each of the nine traits under study were highly significant (P<0.01) for genotypes, indicating a substantial amount of variability in the experimental material. All through analysis of means, coefficient of variation and critical differences (CD) further revealed significant difference among the genotypes for all traits, confirming the presence of considerable genetic variability (Table 2). The box plot distribution in Fig 1 illustrates the mean performance of 142 mungbean genotypes pertaining to seed yield and its attributes. Seed yield per plant showed significant variation among genotypes, ranging from 4.21 (g) to 18.37 (g). Out of the 142 genotypes, 69 genotypes displayed seed yields above the mean (10.46 g) and highest seed yield per plant was observed in MH 1762 (18.37 g) followed by MH 1871 (17.08 g), MH 1703 (16.66 g) and IPM 604-16 (16.16 g), while the lowest yield was recorded in genotype VGG 16-036 (4.21 g). Similar reports were found in the investigations of Govardhan *et al.* (2017); Muthuswamy *et al.* (2019); Talukdar *et al.* (2020); Afroz *et al.* (2022); Samita *et al.* (2022); Thonta *et al.* (2023) and Kumar *et al.* (2024). The wide spectrum of variation observed for studied traits among these genotypes provides plant breeders with ample opportunities to select superior and desired genotypes for crop improvement programmes.

Genetic variability parameters

The estimates of characteristics revealed that the phenotypic coefficients of variance (PCV) for almost all the qualitative characters was marginally higher than their corresponding genotypic coefficient of variance (GCV), indicating that the expression of the trait was significantly influenced by genetic factors rather than environmental variables (Fig 2). The genotypic coefficients of variation (GCV) and phenotypic coefficients of variation were categorized as low (<20%), moderate (20-30%) and high (>30%) as suggested by Sivasubramanian and Menon (1973). Among all the traits studied, seed yield per plant, number of branches per plant and plant height expressed high GCV and PCV, while moderate genotypic and

Table 1: List of genotypes used in the experiment.

S. no.	Name	Pedigree	S. no.	Name	Pedigree
1	PM 1801	PM 5 × PU 31	49	IPM 1103-1	IPM 06-5 × IPM 409-4
2	JLPM 707-27	SML 668 × Naval local	50	TBMB 17-2	TARM-1 × Kopergoan
3	ML 818	5145/87 × ML 267	51	Pusa BM 16	Mutant of Pusa Vishal 30 Kr gamm rays
4	RMG-1148	RMG-62 × PDM-219	52	PM 1605	PM 5 × PU 31
5	IPM 02-3	IPM 99-125 × Pusa bold 2	53	IPMD 101-2	IPM99-125 × (IPM03-1 x SPS-5)
6	IPM 1604-1	PDM 139 × EC 369223	54	MML 2568	Mutant of TMB 37
7	MH 1468	MH 318 × AKM 9904	55	Pusa M 2132	KM 12-28 × Pusa M 1333
8	Pusa M 22-32	MH 318 × Pusa ratna	56	MHBC 20-7	Muskan × BDYR 2
9	KM 2419	KM 2355 × KM 2328	57	PM 504-20-27	Vaibhav × Pusa 9531
10	BCM 20-6	IPM 494-4 × IPM 2-3	58	PM 1624	PM 5 × PM 6
11	MML 2577	Mutant of TMB 37 (50 KR)	59	MH 1830	KM 2241 × MH 521
12	SVM 55	SVM 88 × IPM 205-7	60	IPM 1610-1	EC 391178 × IPM 99-125
13	IPM 410-3	IPM 03-1 × NM 1	61	RMG 1132	RMG 62 × PDM 219
14	PMD-14	Pusa Vishal × PMD-3	62	RMG 1166	IPM 2-3 × COGG 912
15	SVM 98	SVM 55 × IPM 410-3	63	OBGG 105	NM 94 × ML 1628
16	IPM 1704-14	MH 318 × EC 369223	64	MH 1890	MH 805 × MH 318
17	PMS-12	Pusa vishal × MH-318	65	ANDGG 1301	Meha × GM 4
18	TMB 230	TMB 24 × Samrat	66	MML 2576	Mutant of TMB 37
19	IPM 604-16	Sona mung × IPM 99-125	67	PMD-8	Pusa Vishal × PMD-3
20	MH 1871	IPM 409-4 × MH 318	68	Pusa M 2141	MH 318 × IPM 02-14
21	IPM 205-7	IPM 02-1 × EC 398889	69	OBGG 106	NM 94 × ML 1628
22	Pusa BM 9	Mutant of Pusa Vishal 14Kr gamma rays	70	PMD-7	Pusa Vishal × MH 565
23	VGG 18-002	EC 496839 × IPM 406-4	71	MH 1801	IPM 02-17 × MH 521
24	MH 421	Muskan × BDYR 2	72	PMD-9	Pusa Vishal × PM-5
25	IPMD 604-1-7	Sona mung × IPM 99-125	73	SKNM 1911	Pusa Vishal × COGG 912
26	MML 2575	Mutant of TMB 37 (600 Gy)	74	VGG 17-036	Vamban 3 × Pusa 14-01
27	SKNM 1801	GM 4 × Meha	75	BDYR-1	Not known
28	SML 832	SML 302 × Pusa bold 1	76	COGG-8	COGG 923 × VC 6040
29	DGGV 91	DGG 1 × AKM 9904	77	Pusa 1072	Pusa Vishal × IPM 99-125
30	VGG 16-047	VBN (Gg) 2 × SM 47	78	COGG 11-02	COGG 912 × IPM 02-3
31	MH 1762	IPM 02-3 × MH 318	79	EC 30400	Exotic collection
32	SML 1932	SML 668 × Mash 1008	80	EC 251552	Exotic collection
33	OBGG 108	NM 94 × Harsha	81	EC 399223	Exotic collection
34	VGG 17-043	VBN (Gg) 2 × IPM 99-125	82	EC 393410	Exotic collection
35	PM 1602	PM 5 × PU 31	83	EC 470090	Exotic collection
36	Pant M 5	Sel. From VC 6368	85	IPM 512-1	IPM 99-125 × Co 5
37	SML 1933	SML 668 × Mash 1008	86	Ganga-8	K 851 × Pusa 105
38	Pusa M 19111	Pusa 105 × Pusa vishal	87	HUM 16	Pusa Vishal × HUM 8
39	MH 1703	IPM 02-17 × MH 521	88	IC 15276	International collection
40	MML 2560	Mutant of SML 668 (600 Gy)	89	IC 1031096	International collection
41	Pusa M 1971	Pusa 105 × Pusa vishal	90	IPM 99-3	Not known
42	PM 1601	PM 5 × PU 31	100	COGG 13-19	Co 6 × COGG 912
43	PM 1520	PM 5 × Pusa 871	101	ML 194	Not known
44	TCADM 20-5	HUM16 × Samrat	102	ML 778	MUG 262 × Pant M-3 32
45	IPMD 1604	IPM 2-23 × DMG 1045	103	COGG 13-14	COGG 912 × Kopergaon
46	IPM 1603-1	MH 03-18 × EC 369223	104	NVL 638	NVL 605 × NVL 585
47	TBMB 117-5	Samrat × Kopergaon	105	NDMZ-13-11	NDM 1 × PDM 54
48	Pusa M 2131	IPM 02-3 × Pusa vishal	106	NDMZ-15-2	NDM 1 × HUM 1

Table 1: Continue...

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107	NDMZ 215-1	NDM 1 × HUM 1	125	VGG 16-036	IPM 03-01 × SPS 5
108	NBPGR 150	Selection from IC 39289	126	TMB 37	Kopergaon × TARM-2
109	OUM 11-5	Mutant of Dhauli	127	VGG 18-021	VBN(Gg) 2 × MH 421
110	PBM-14	Not known	128	IPM 1205-2	IPM 02-3 × VBG 04-003
111	PDM 96-262	Not known	129	VMK 18-02	GAM 5 × BMS 13-12
112	PLM 24	Not known	130	KM 2421	KM 2328 × K 851
113	Pusa 105	(Taiwan-1 × ML6) × (EGMG 16 × ML3)	131	MHBC 20-14	Sel. from MH 560 (Asha × BDYR 1)
114	Pusa 0871	IPM 99-125 × Pusa Vishal	132	RMG 1169	IPM 02-3 × COGG 912
115	T-44	T-1/T-49	133	MH 18-181	IPM 2-17 × MH 318
116	RMG 991	RMG 268 × UPM 98	134	Pusa M 41	MH 318 × Pusa vishal
117	SML 1455	SML 690 × SML 475	135	MHBC 20-8	MH 98-1 × PDM 96-262
118	SMH 95-1	Not known	136	MML 2579	Mutant of TMB 37 (50 KR)
119	SMH 99-1	Not known	137	SKNM 2006	ML 1451 × GM 4
120	Sona Mung-1	Landrace selection from West Bengal	138	IPMD 1202-1	IPM 99-125 × VBG 04-008
			139	Pusa M 42	ML 1451 × Pusa 1332
121	SVM 6111	SML 668 × Pusa 9531	140	MGG 499	MGG 347 × SM 131
122	TRCM 2014-2	SPS 5 × IPM 99-125	141	MH 18-189	MH 805 × MH 318
123	VGG ru-2	Not known	142	VGG 17-106	CO 8 × Cinna mung
124	WBM-031	Selection from Sunderban area			

Table 2: Analysis of variance (ANOVA) for various quantitative characters of mungbean (2021 and 2022 pooled).

Source	df	Mean square								
		DF	DM	PH	NBP	NPP	NSP	PL	HSW	SYP
Replication	1	72.004	65.127	243.553	0.001	5.111	0.857	0.310	0.016	0.312
Genotype	141	24.18**	47.02**	202.00**	0.79**	25.90**	2.81**	1.34**	1.87**	21.44**
Error	141	0.316	0.588	1.227	0.047	0.674	0.158	0.097	0.034	0.116
C.D. at 5%		1.112	1.517	2.192	0.430	2.67	0.786	0.617	0.364	0.675
C.V. (%)		1.398	1.181	2.228	7.586	6.011	4.737	4.578	4.412	3.264

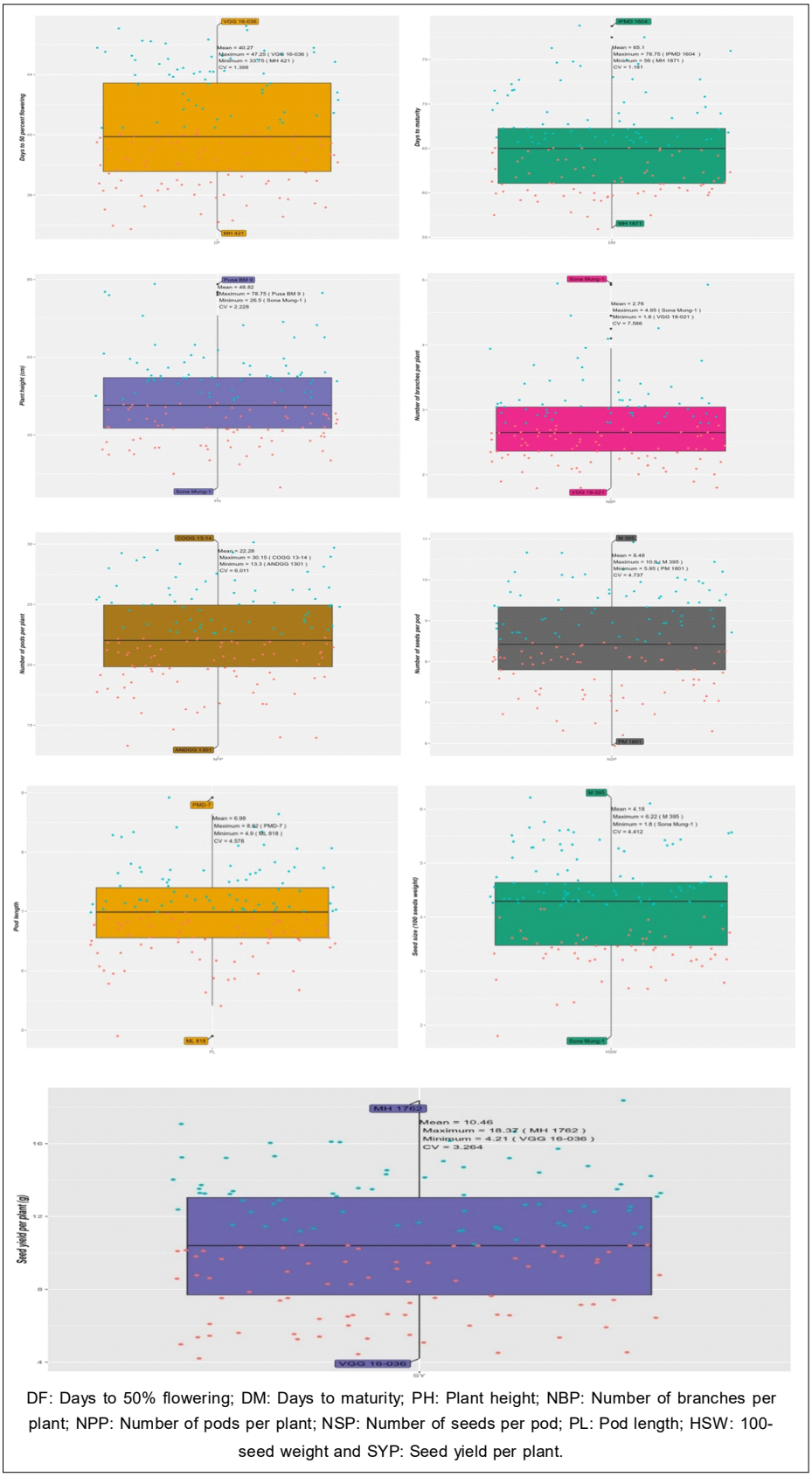
DF: Days to 50% flowering; DM: Days to maturity; PH: Plant height, NBP: Number of branches per plant; NPP: Number of pods per plant; NSP: Number of seeds per pod; PL: Pod length; HSW: 100-seed weight and SYP: Seed yield per plant.

phenotypic coefficient of variation were observed for 100-seed weight, number of pods per plant, number of seeds per pod and pod length. Low estimates of GCV and PCV were recorded in days to 50% flowering and days to maturity. Our findings are in accordance to the studies of Hemavathy *et al.* (2015); Nalajala *et al*. (2022) and Sofia *et al*. (2023).

According to Johnson *et al.* (1955), heritability and the anticipated genetic advance as a percentage of the mean are directly linked to the extent of additive gene effects. Consequently, straightforward selection would prove effective for traits exhibiting high heritability and high genetic advance. High heritability (>60%) estimates were recorded for all the traits *viz.,* 100-seed weight, number of branches per plant, days to 50% flowering, days to maturity, pod length, seed yield per plant, plant height, number of pods per plant and number of seeds per pod. In the present investigation, high magnitude of genetic advance as per cent mean (>20%) along with high heritability was recorded for seed yield per plant and number of branches per plant. Earlier studies of Nalajala *et al.* (2022) for seed yield per plant while that of Yoseph *et al.* (2022) for days to maturity and days to 50% flowering are also in agreement with the findings of the present study. The remaining traits exhibited high heritability (>60%) with moderate (10-20%) or low (<10%) genetic advance revealing control of non-additive gene action and high influence of environment on all these characters and therefore, intermating in early generations of the hybridization programme can be helpful. Talukdar *et al.* (2020); Harini *et al.* (2022) and Sofia *et al.* (2023) recorded similar results for number of branches per plant and number of pods per plant.

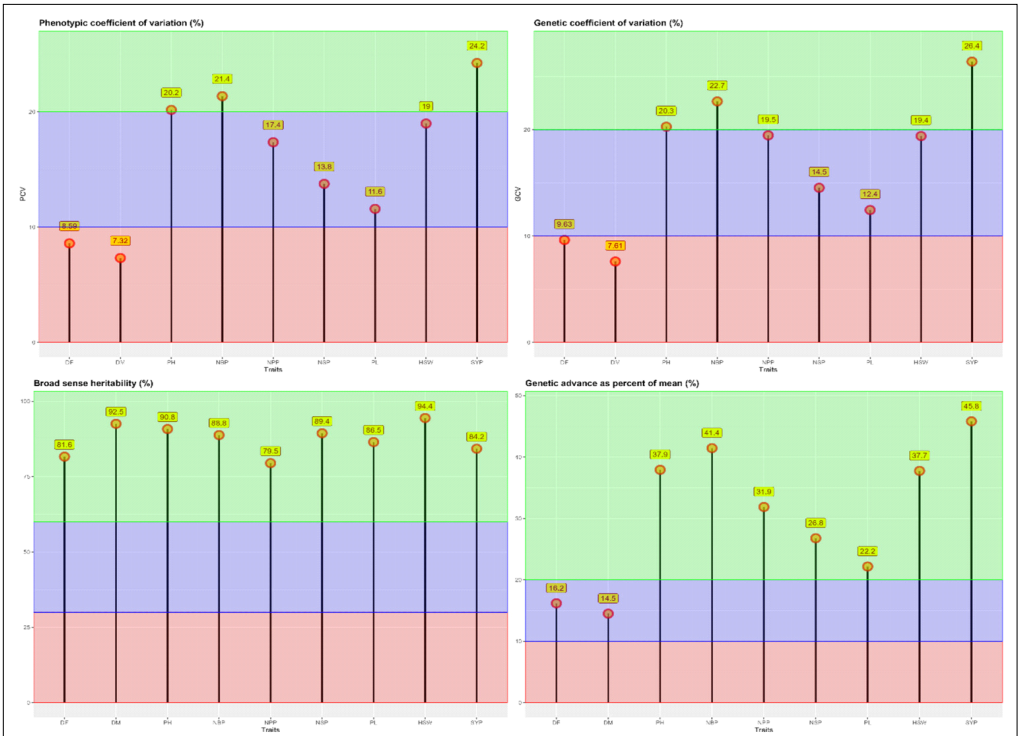
Association among seed yield contributing traits

Since seed yield is complex trait influenced by many factors and have a low genetic inheritance, therefore, relying solely on heritability and genetic advance for this trait selection could lead to suboptimal choices, whereas incorporating both of these along with association of yield with other



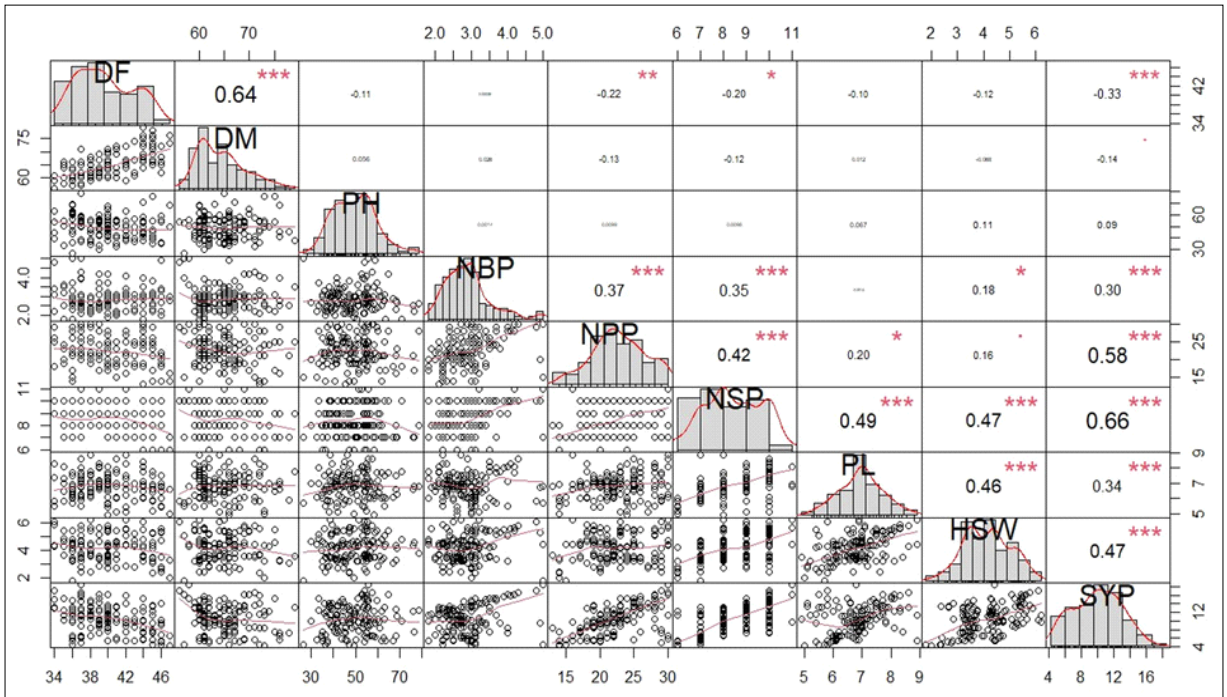
DF: Days to 50% flowering; DM: Days to maturity; PH: Plant height; NBP: Number of branches per plant; NPP: Number of pods per plant; NSP: Number of seeds per pod; PL: Pod length; HSW: 100-seed weight and SYP: Seed yield per plant.

Fig 1: Box plot presentation of different mungbean genotypes for various characters.



DF: Days to 50% flowering; DM: Days to maturity; PH: Plant height; NBP: Number of branches per plant; NPP: Number of pods per plant; NSP: Number of seeds per pod; PL: Pod length; HSW: 100-seed weight and SYP: Seed yield per plant.

Fig 2: Line graph representation of genetic variablity parameters for various quantitative traits.



DF: Days to 50% flowering, DM: Days to maturity, PH: Plant height, NBP: Number of branches per plant, NPP: Number of pods per plant, NSP: Number of seeds per pod, PL: Pod length, HSW: 100-seed weight and SYP: Seed yield per plant.

Fig 3: Scatter plot diagram representing correlation between different nine morphological traits in mungbean.

traits may offer greater benefits. So, inferential understanding of the association between yield and its related causal factors is crucial for developing effective plant selection guidelines. A thorough critical perusal of the scatter plot (Fig 3) revealed significant phenotypic correlation coefficients between the traits. In the present investigation number of seeds per pod, number of pods per plant, hundred seed weight, pod length and number of branches per plant exhibited positive significant association with seed yield per plant. Furthermore, correlation coefficients among different yield related traits were assessed in mungbean and results are presented in Table 3. Hence, opting for these traits for selection could lead to a noteworthy increase in yield. To determine yield related characters affecting seed yield directly or indirectly, analysis of path coefficient is helpful. Path coefficient usually lies between -1 and +1, where values closer to -1 represent strong negative effect and those closer to +1 indicate strong positive effect. The highest positive direct effect on seed yield per plant was exhibited by number of seeds per pod (0.4645) followed by number of pods per plant (0.3920), 100-seed weight (0.2245), days to maturity (0.0743) and plant height (0.0360), while number of branches per plant (-0.0636), pod length (-0.1114) and days to 50% flowering (-0.1886) exhibited negative direct effect on seed yield per plant (Table 4). In order to enhance the seed yield, the characters that have high direct effects on seed yield per plant are considered as the most important traits for selection. These results of correlation and path were in accordance with the findings of Dhunde *et al.* (2021); Parsaniya *et al.* (2022); Rahevar *et al.* (2023); Aravinth *et al.* (2023) and Srivastava *et al.* (2024).

Cluster analysis

Hierarchical cluster analysis using Unweighted Pair Group Method using Arithmetic Averages (UPGMA) method was used to classify the 142 mungbean genotypes on the basis of nine yield related quantitative traits. The 142 genotypes of mungbean were grouped into eight clusters and maximum genotypes were grouped in cluster V (29) followed by cluster II (27), cluster I (22), cluster III (17), cluster VI and VII (16 each), cluster VIII (10) and cluster IV (5) (Fig 4). Cluster analysis by Abna *et al.* (2012) resulted in three major clusters in 20 greengram genotypes. Similarily, Gokulakrishnan *et al.* (2012); Rahangdale *et al.* (2023) and Chauhan *et al.* (2024) also assessed genetic divergence in mungbean and reported four, seven and nine clusters, respectively.

Maximum intra-cluster distance was observed in cluster I while minimum was recorded in cluster IV, close relatedness among the genotypes of cluster IV. Maximum inter-cluster distance was observed between cluster II and cluster V followed by cluster I and cluster V and cluster I and cluster II whereas, minimum inter-cluster distance was recorded in cluster III and cluster VII (Table 5). This suggested that genotypes from the most distant clusters can be used as parents to obtain more heterotic combinations in hybridization programme. Similar findings

Table 3: Type of correlations among different quantitative traits of 142 mungbean genotypes.

Traits	Positive correlation	Negative correlation
Days to 50% flowering	Days to maturity	Number of pods per plant, number of seeds per pod, plant height, seed yield per plant
Days to maturity	Days to 50% flowering	Seed yield per plant
Plant height (cm)	None	Days to 50% flowering
Number of branches per plant	Number of seeds per pod, number of pods per plant, 100-seed weight, plant height, seed yield per plant	None
Number of pods per plant	Number of seeds per pod, number of branches per plant, pod length, 100-seed weight, seed yield per plant	Days to 50% flowering
Number of seeds per pod	Pod length, 100-seed weight, number of pods per plant, number of branches per plant seed yield per plant	Days to 50% flowering
Pod length (cm)	Number of seeds per pod, 100-seed weight, number of pods per plant, seed yield per plant	None
Hundred seed weight (g)	Number of seeds per pod, pod length, number of branches per plant, number of pods per plant, seed yield per plant	Days to 50% flowering
Seed yield per plant (g)	Number of pods per plant, number of seeds per pod, number of branches per plant, pod length, 100-seed weight	Days to 50% flowering, Days to maturity

were reported by Rahangdale *et al.* (2023) and Chauhan *et al.* (2024).

The cluster IV consisted of genotypes that had maximum mean values for almost all the yield contributing traits *viz.,* number of branches per plant, number of pods per plant, number of seeds per pod and seed yield per plant. Cluster VI showed highest mean value for 100-seed weight whereas cluster VII exhibited highest mean value for pod length. Early flowering and maturing genotypes were observed in cluster IV, cluster VII and cluster II (Table 6). Largely, better performing genotypes with high values of seed yield and yield influencing traits from cluster IV and

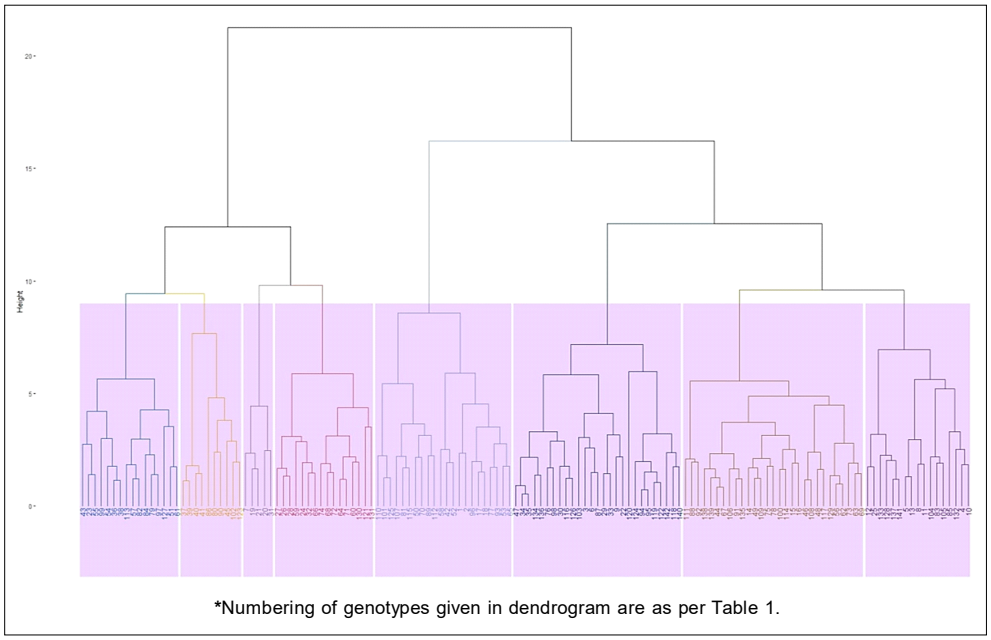
Table 4: Path coefficient (pooled) for various quantitative traits indicating direct effect (diagonal and bold) and indirect effect (above and below diagonal) on seed yield in 142 mungbean genotypes.

	DF	DM	PH	NBP	NPP	NSP	PL	HSW	R^2
DF	-0.1886	0.0492	-0.0055	-0.0003	-0.0869	-0.0757	0.0125	-0.0269	-0.322**
DM	-0.1248	0.0743	-0.0006	-0.0008	-0.0454	-0.0299	-0.0031	-0.0153	-0.146*
PH	0.0286	-0.0012	0.0360	-0.0076	-0.0219	-0.0137	-0.0042	0.0093	0.025
NBP	-0.0008	0.0009	0.0043	-0.0636	0.1415	0.1823	-0.0031	0.0479	0.309**
NPP	0.0418	-0.0086	-0.0020	-0.0229	0.3920	0.1996	-0.0315	0.0340	0.602**
NSP	0.0307	-0.0048	-0.0011	-0.0250	0.1684	0.4645	-0.0656	0.1145	0.682**
PL	0.0212	0.0021	0.0014	-0.0018	0.1109	0.2738	-0.1114	0.1098	0.406**
HSW	0.0226	-0.0051	0.0015	-0.0136	0.0593	0.2369	-0.0545	0.2245	0.472**
					RESIDUAL: 0.119				

DF: Days to 50% flowering; DM: Days to maturity; PH: Plant height, NBP: Number of branches per plant; NPP: Number of pods per plant, NSP: Number of seeds per pod; PL: Pod length; HSW: 100-seed weight and SYP: Seed yield per plant.

Table 5: Intra cluster (Diagonal) and Inter cluster distances in mungbean.

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII
Cluster I	44.45							
Cluster II	48.87	32.56						
Cluster III	44.59	45.22	26.16					
Cluster IV	36.16	30.28	30.99	12.62				
Cluster V	49.58	49.92	31.12	33.96	21.50			
Cluster VI	41.96	46.46	37.41	36.88	41.85	35.83		
Cluster VII	47.45	46.86	27.90	29.81	32.01	39.38	26.29	
Cluster VIII	40.53	47.51	32.26	32.48	37.60	36.01	32.05	29.13



*Numbering of genotypes given in dendrogram are as per Table 1.

Fig 4: Dendrogram depicting distribution of 142 mungbean genotypes into eight distinct clusters.

Table 6: Cluster means for different quantitative characters in mungbean.

	DF	DM	PH	NBP	NPP	NSP	PL	HSW	SYP
Cluster I	44.32	70.36	49.14	2.58	19.00	6.95	6.24	3.47	7.34
Cluster II	37.48	62.74	60.04	2.80	20.63	7.81	6.59	3.74	8.26
Cluster III	40.24	63.65	44.59	2.98	27.06	8.39	6.32	3.29	11.68
Cluster IV	35.40	57.80	55.40	4.10	27.20	10.02	5.88	4.82	16.02
Cluster V	38.86	62.62	41.69	2.57	21.48	8.24	6.69	4.38	10.24
Cluster VI	42.63	67.94	52.44	2.84	20.75	9.33	7.24	5.07	11.69
Cluster VII	37.94	61.00	48.44	2.87	24.94	9.44	7.92	5.00	13.58
Cluster VIII	42.50	70.90	51.50	4.05	26.70	9.86	7.86	4.65	12.00

DF - Days to 50% flowering; DM - Days to maturity; PH - Plant height; NBP - Number of branches per plant; NPP - Number of pods per plant; NSP - Number of seeds per pod; PL - Pod length; HSW - 100-seed weight; SYP - Seed yield per plant.

cluster VIII could be used in the breeding programmes to combine yield contributing traits. Genotypes MH 1468, MH 1871, MH 1762, IPM 604-16 and IPM 205-7 were found early maturing along with high mean values of yield related characters such as number of seeds per pod, number of pods per plant, 100-seed weight and seed yield per plant. These genotypes can further be used in breeding programmes for mungbean improvement.

CONCLUSION

The understanding of variability present among the genotypes of a crop species is of utmost importance for their genetic improvement to produce high yielding cultivars. In this study, high magnitude of variability was observed for number of seed yield per plant followed by number of branches per plant, plant height and 100-seed weight implying adequate scope for selection. Significant association and positive direct effect of number of seeds per pod, number of pods per plant and 100-seed weight on seed yield suggested that for yield improvement in mungbean, selection for these traits would be beneficial. Broad range of diversity among the genotypes was also observed through cluster analysis which categorized the mungbean genotypes into eight distinct clusters. The diversity studies suggested hybridizing genotypes from Cluster II and Cluster V to produce superior transgressive segregants. Overall, genotypes MH 1468, MH 1871, MH 1762, IPM 604-16 and IPM 205-7 were found superior regarding early maturity and yield related characters, therefore, these can further used be in breeding programmes for mungbean improvement. The findings of this study will aid in identifying heterotic clusters and superior parent lines, which are crucial for designing effective breeding strategies to develop enhanced mungbean cultivars.

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Data availability statement

All the data associated with the manuscript is mentioned in the text of the manuscript

Conflict of Interest

The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

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