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Dr. Manju Singh
ASPEE Shakilam
Biotechnology Institute,
Navsari Agricultural
University, Surat, Gujarat,
India

**Katariya Maheshkumar
Atubhai**
Department of Genetics and
Plant Breeding, N.M. College
of Agriculture, Navsari
Agricultural University,
Navsari, Gujarat, India

Chanchal Shakyawal
Department of Genetics and
Plant Breeding, N.M. College
of Agriculture, Navsari
Agricultural University,
Navsari, Gujarat, India

Rishabh Shukla
Department of Genetics and
Plant Breeding, N.M. College
of Agriculture, Navsari
Agricultural University,
Navsari, Gujarat, India

Simran Singh
Department of Genetics and
Plant Breeding, N.M. College
of Agriculture, Navsari
Agricultural University,
Navsari, Gujarat, India

Corresponding Author:
Chanchal Shakyawal
Department of Genetics and
Plant Breeding, N.M. College
of Agriculture, Navsari
Agricultural University,
Navsari, Gujarat, India

Exploitation of genetic variability and trait association for enhancing seed yield in mungbean (*Vigna radiata* L. Wilczek)

Manju Singh, Katariya Maheshkumar Atubhai, Chanchal Shakyawal, Rishabh Shukla and Simran Singh

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Abstract

Mungbean (*Vigna radiata*) a self-pollinated diploid legume is widely grown in tropical and subtropical regions due to its short duration and low input requirement. Nevertheless, improving yield remains challenging because genetic variation available for selection is often limited. In this study, genetic variability, trait associations and genetic divergence were assessed in 96 mungbean genotypes evaluated under summer 2021 conditions at N. M. College of Agriculture, Navsari Agricultural University. Genotypes were grown in an augmented block design with four standard checks and observations were recorded on flowering duration, days to maturity, plant height, primary branches, pods per cluster, pods per plant, pod length, seeds per pod, 100-seed weight, seed yield per plant and disease incidence of mungbean yellow mosaic virus (MYMV). Analysis of variance showed significant differences among genotypes for most traits with non-significant variation for primary branches per plant, pods per cluster and 100-seed weight indicating relatively narrower diversity for these characters. High genotypic and phenotypic coefficients of variation were detected for pods per plant and seed yield per plant, suggesting substantial exploitable variability. Broad-sense heritability estimates were high for key traits including days to 50% flowering, pods per plant, pod length, days to maturity and seed yield per plant. Coupled with high genetic advance as percent of mean these results indicated predominantly additive gene effects and strong potential for effective selection. Correlation analysis revealed predominantly positive associations between seed yield per plant and major yield components particularly pods per plant, plant height, pod length and seeds per pod. Path coefficient analysis further confirmed pods per plant as the largest contributor through direct effects on seed yield followed by plant height, seeds per pod and pod length. Overall, the findings identify yield-determining traits that can guide selection and parent choice to accelerate genetic improvement in mungbean.

Keywords: Genetic variability, heritability, genetic advance, character association, path coefficient analysis, genetic divergence, seed yield

Introduction

Mungbean (*Vigna radiata* (L.) Wilczek), commonly known as green gram, is an important self-pollinated diploid legume ($2n = 22$) belonging to the family *Fabaceae*, with a genome size of approximately 579 Mb (Kang *et al.*, 2014, Singh *et al.* 2026) ^[12, 36]. It is widely cultivated in tropical and subtropical regions owing to its short duration, wide adaptability and low input requirements. The crop thrives well under hot and semi-arid conditions and contributes significantly to sustainable agriculture through biological nitrogen fixation, enriching soil fertility and reducing nitrogen requirements for succeeding crops (Mbeyagala *et al.*, 2017) ^[18]. Mungbean is nutritionally rich, serving as an excellent source of protein and essential amino acids, particularly lysine which complements cereal-based diets (Majhi *et al.*, 2020) ^[16]. It is consumed in diverse forms such as whole grains, split daal and sprouts, making it a staple in many diets, especially in India the largest producer of green gram. Despite its importance, mungbean productivity remains low due to several constraints, including susceptibility to diseases such as Mungbean Yellow Mosaic Virus (MYMV), narrow genetic base and limited yield potential (Latha *et al.*, 2019) ^[15]. The highly self-pollinated nature of mungbean restricts natural genetic variability, posing challenges for effective selection and genetic improvement.

Therefore, the assessment of genetic variability, heritability and genetic advance is essential for identifying superior genotypes and designing efficient breeding strategies (Degefa *et al.*, 2014; Muthuswamy *et al.*, 2019) ^[6, 22]. In addition, correlation coefficient analysis helps in determining the degree of association among yield and its component traits while path coefficient analysis partitions these relationships into direct and indirect effects, thereby providing a clearer understanding of trait contributions to yield (Wright, 1921; Bhutia *et al.*, 2016; Shakyawal *et al.*, 2024) ^[40, 4, 31]. Furthermore, multivariate techniques such as cluster analysis enable the classification of genotypes into distinct groups based on genetic divergence, facilitating the selection of diverse parents for hybridization programmes and enhancing the scope for heterosis breeding (Shibli *et al.*, 2021) ^[32]. Therefore, the present investigation was undertaken to evaluate genetic variability, character associations and genetic divergence among mungbean genotypes to identify key traits and promising genotypes for yield improvement.

Materials and Methods

The experimental material for the present study includes 96 greengram genotypes. The experiment was carried out during the Summer 2021 season at the College Farm, N. M. College of Agriculture, Navsari Agricultural University, located in Navsari. The prevailing environmental conditions during the crop season were favourable for normal growth and development of the crop.

The experimental material comprised 96 derived genotypes of mungbean along with four standard checks including GM-4, GM-6, GM-7 and 40C in Augmented Block Design, where each and every check was replicated in four blocks. Each genotype was sown in a single row consisting of 20 plants, maintaining a spacing of 60 cm between rows and 15 cm between plants. All recommended agronomic practices were followed to ensure optimal crop growth. Observations were recorded on five randomly selected plants per genotype for various quantitative traits, including Days to 50% flowering, Days to maturity, Plant height (cm), Primary branches per plant, Pods per cluster, Pods per plant, Pod length (cm), Seeds per pod, 100 seed weight (g), Seed yield per plant (SYPP) (g) and Mungbean Yellow Mosaic Virus (MYMV) disease incidence (%).

Genotypic and phenotypic coefficients of variation were estimated following the method of Burton (1952) ^[5]. Heritability in the broad sense and genetic advance were calculated as per Hanson *et al.* (1956) ^[10]. Genotypic and phenotypic correlation coefficients were computed based on variance and covariance components. Path coefficient analysis was carried out according to the method proposed by Dewey and Lu (1959) ^[8] to partition the correlation coefficients into direct and indirect effects.

Results

Genetic Variability, Heritability and Genetic Advance

In the present investigation, analysis of variance revealed highly significant differences among genotypes for most of the characters studied (Table 1) indicating the presence of substantial genetic variability in the experimental material. However non-significant variation was observed for primary branches per plant, pods per cluster and 100 seed weight suggesting limited diversity for these traits among the studied genotypes. The mean performance and range

revealed considerable variation among genotypes for all traits. Days to 50% flowering ranged from 35.33 to 55.80 days with a mean of 43.19 days. Days to maturity varied from 64.00 to 81.00 days while plant height ranged from 33.50 cm to 84.20 cm reflecting wide diversity. Pods per plant exhibited a broad range from 6.00 to 38.30 and seed yield per plant ranged from 2.00 g to 12.80 g indicating substantial variability and scope for selection in yield improvement.

PCV values were higher than GCV for all traits indicating environmental influence on trait expression (Table 2). However, the differences between PCV and GCV were relatively low for most traits suggesting that environmental effects were minimal and that observed variation was largely due to genetic factors. High GCV and PCV values were observed for pods per plant (31.77% and 33.14%) followed by seed yield per plant (27.13% and 32.99%). Moderate GCV and PCV values were recorded for days to 50% flowering, plant height and seeds per pod. Low GCV and PCV values were observed for days to maturity. Heritability estimates in broad sense were high for most of the traits ranging from 67.63% to 96.59%. High heritability was recorded for days to 50% flowering, seeds per pod, pods per plant, pod length, days to maturity and seed yield per plant. Genetic advance as percent of mean (GAM) was highest for pods per plant (62.83%) followed by seed yield per plant (46.02%), plant height (27.15%), seeds per pod (25.87%) and days to 50% flowering (23.86%). Moderate genetic advance was observed for pod length while low genetic advance was recorded for days to maturity. The combination of high heritability and high genetic advance was observed for days to 50% flowering, plant height, pods per plant, seeds per pod and seed yield per plant.

Correlation and Path Coefficient Analysis

The correlation analysis revealed that genotypic correlation coefficients were generally higher than the corresponding phenotypic correlation coefficients (Table 3). At the genotypic level, seed yield per plant exhibited strong and significant positive correlations with days to 50% flowering, days to maturity, plant height, primary branches per plant, pods per cluster, pods per plant, pod length, seeds per pod and 100 seed weight. Among these traits, pods per plant, plant height, seeds per pod and pod length showed particularly strong associations with yield. Days to 50% flowering showed a highly significant positive correlation with days to maturity but exhibited a negative and non-significant association with seed yield per plant. Plant height exhibited a strong positive and significant correlation with seed yield per plant as well as with pods per plant, pods per cluster, pod length and seeds per pod.

Primary branches per plant showed a significant positive association with pods per plant and seed yield per plant likewise, pods per cluster exhibited a strong positive correlation with pods per plant, seeds per pod and seed yield per plant. At the phenotypic level similar associations were observed although the magnitude of correlation coefficients was comparatively lower than genotypic correlations (Table 4). Path coefficient analysis revealed that pods per plant exerted the highest positive direct effect on seed yield per plant. This was followed by plant height, seeds per pod and pod length all of which also showed positive direct effects. Plant height and primary branches per plant influenced seed yield indirectly through pods per plant and other yield

components. Similarly, seeds per pod and pod length contributed indirectly *via* pods per plant. Days to 50% flowering and days to maturity showed relatively low or

negative direct effects on seed yield but contributed indirectly through other yield components. The residual effect was 0.64 (Fig. 1).

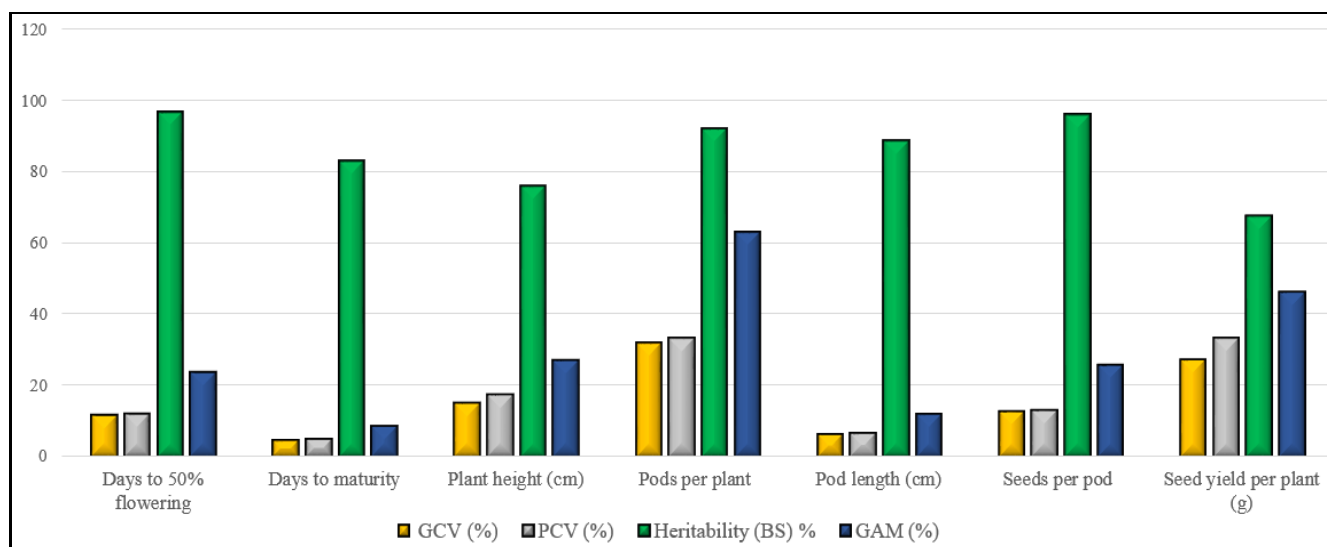


Fig 1: GCV, PCV, Heritability and GAM for quantitative character in mungbean

GCV	=	Genotypic coefficient of variation	PCV	=	Phenotypic coefficient of variation	σ_g^2	=	Genotypic variance
Heritability (BS)	=	Heritability (Broad sense)%	GAM	=	Genetic advance as percent of mean (%)	σ_p^2	=	Phenotypic variance

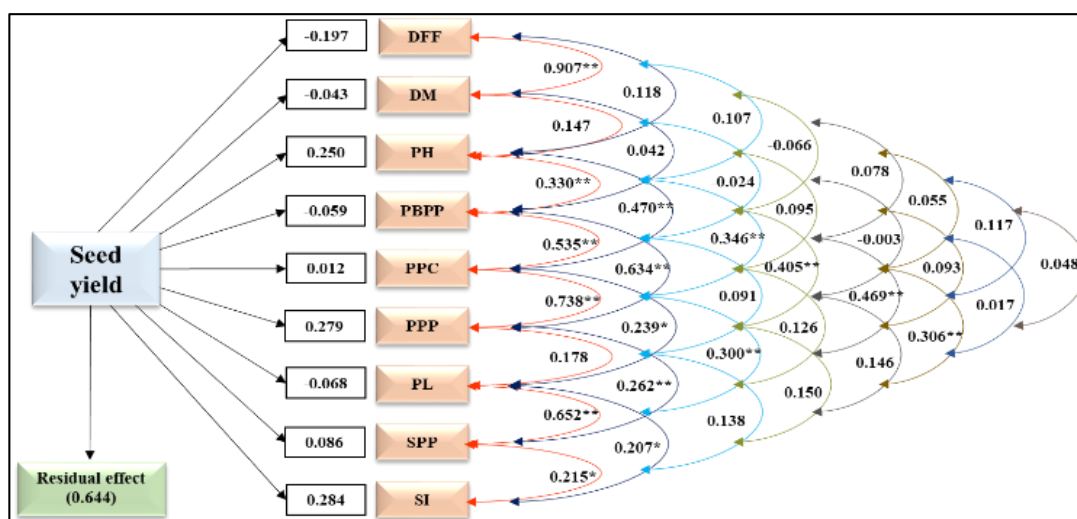


Fig 2: Phenotypic path diagram for seed yield per plant

Where,	DFF	=	Days to 50% flowering	DM	=	Days to maturity	PH	=	Plant height (cm)
	PBPP	=	Primary branches per plant	PPC	=	Pods per cluster	PPP	=	Pods per plant
	PL	=	Pod length (cm)	SPP	=	Seeds per pod	SI	=	100 Seed weight (g)
	SYPP	=	Seed yield per plant (g)						

Table 1: Analysis of variance for characters under study

Source	DF	DFF	DM	PH	PBPP	PPC	PPP	PL	SPP	SI	SYPP
Block	3	0.61 ^{ns}	2.42 ^{ns}	43.06 ^{ns}	0.02 ^{ns}	0.12 ^{ns}	2.51 ^{ns}	0.0027 ^{ns}	0.06 ^{ns}	0.05 ^{ns}	4.72 ^{ns}
Entries	99	31.96**	15.51**	97.36*	0.11*	0.54*	35.09**	0.25**	1.86**	0.27**	5.52*
Checks	3	14.13**	17.08**	69.47 ^{ns}	0.73**	3.2**	268.11**	0.24**	3.2**	1.06**	5.65 ^{ns}
Genotypes	95	26.75**	12.63**	96.02*	0.09 ^{ns}	0.46 ^{ns}	27.94**	0.2**	1.48**	0.13 ^{ns}	5.49*
Genotypes vs. Check	1	580.92**	285.05**	308.21**	0.26*	0.75 ^{ns}	15.48*	5.66**	33.97**	11.21**	8.2 ^{ns}
Residuals	9	0.91	2.14	23.02	0.03	0.18	2.26	0.02	0.06	0.05	1.78

* P <= 0.05; ** P <= 0.01

Where,	DFF	=	Days to 50% flowering	DM	=	Days to maturity	PH	=	Plant height (cm)
	PBPP	=	Primary branches per plant	PPC	=	Pods per cluster	PPP	=	Pods per plant
	PL	=	Pod length (cm)	SPP	=	Seeds per pod	SI	=	100 Seed weight (g)
	SYPP	=	Seed yield per plant (g)						

Table 2: Measure of variability parameters of all the characters

Trait	Mean	Range		σ_g^2	σ_p^2	GCV (%)	PCV (%)	h_{bs}^2 (%)	GA (%)	GAM (%)
		Min.	Max.							
Days to 50% flowering	43.19	35.33	55.80	25.83	26.75	11.77	11.98	96.59	10.31	23.86
Days to maturity	71.00	64.00	81.00	10.49	12.63	4.56	5.00	83.06	6.09	8.58
Plant height (cm)	56.60	33.50	84.20	73.01	96.02	15.10	17.31	76.03	15.37	27.15
Primary branches per plant	2.74	2.02	3.48	-	-	-	-	-	-	-
Pods per cluster	3.17	1.67	5.33	-	-	-	-	-	-	-
Pods per plant	15.95	6.00	38.30	25.68	27.94	31.77	33.14	91.92	10.02	62.83
Pod length (cm)	6.70	5.00	7.60	0.17	0.20	6.21	6.60	88.60	0.81	12.06
Seeds per pod	9.34	5.20	11.97	1.43	1.48	12.79	13.05	96.11	2.42	25.87
100 Seed weight	3.88	3.21	5.14	-	-	-	-	-	-	-
Seed yield per plant (g)	7.10	2.00	12.80	3.71	5.49	27.13	32.99	67.63	3.27	46.02

Table 3: Phenotypic correlation coefficients of seed yield per plant with other characters in derived genotypes of mungbean

Characters	DFE	DM	PH	PBPP	PPC	PPP	PL	SPP	SI	SYPP
Days to 50% flowering	1.000									
Days to maturity	0.907**	1.000								
Plant height (cm)	0.118 ^{NS}	0.147 ^{NS}	1.000							
Primary branches per plant	0.107 ^{NS}	0.042 ^{NS}	0.330**	1.000						
Pods per cluster	-0.066 ^{NS}	-0.024 ^{NS}	0.470**	0.535**	1.000					
Pods per plant	0.078 ^{NS}	0.095 ^{NS}	0.346**	0.634**	0.738**	1.000				
Pod length (cm)	0.055 ^{NS}	-0.003 ^{NS}	0.405**	0.091 ^{NS}	0.239*	0.178 ^{NS}	1.000			
Seeds per pod	0.117 ^{NS}	0.093 ^{NS}	0.469**	0.126 ^{NS}	0.300**	0.262**	0.652**	1.000		
100 Seed weight (g)	0.048 ^{NS}	0.017 ^{NS}	0.306**	0.146 ^{NS}	0.150 ^{NS}	0.138 ^{NS}	0.207*	0.215*	1.000	
Seed yield per plant (g)	-0.173 ^{NS}	-0.149 ^{NS}	0.404**	0.231*	0.371**	0.368**	0.184 ^{NS}	0.262**	0.387**	1.000

Table 4: Phenotypic path coefficients of seed yield per plant with other characters in derived genotypes of mungbean

Characters	DFE	DM	PH	PBPP	PPC	PPP	PL	SPP	SI	Correlation with seed yield per plant
Days to 50% flowering	-0.198	-0.040	0.029	-0.006	-0.001	0.022	-0.004	0.010	0.014	-0.173 ^{NS}
Days to maturity	-0.179	-0.044	0.037	-0.002	-0.000	0.027	0.000	0.008	0.005	-0.149 ^{NS}
Plant height (cm)	-0.023	-0.006	0.251	-0.019	0.006	0.097	-0.028	0.040	0.087	0.404**
Primary branches per plant	-0.021	-0.002	0.083	-0.059	0.007	0.177	-0.006	0.011	0.042	0.231*
Pods per cluster	0.013	0.001	0.118	-0.032	0.012	0.206	-0.016	0.026	0.043	0.371**
Pods per plant	-0.015	-0.004	0.087	-0.037	0.009	0.280	-0.012	0.023	0.039	0.368**
Pod length (cm)	-0.011	0.000	0.102	-0.005	0.003	0.050	-0.069	0.056	0.059	0.184 ^{NS}
Seeds per pod	-0.023	-0.004	0.118	-0.007	0.004	0.073	-0.045	0.086	0.061	0.262**
100 Seed weight	-0.009	-0.001	0.077	-0.009	0.002	0.039	-0.014	0.018	0.285	0.387**

***-Significant at 1% level of probability, *-Significant at 5.0% level of probability, Residual = 0.644, Bold diagonal figures are the direct effects

Discussion

The significant differences observed among genotypes for most of the traits indicate the presence of substantial genetic variability in the experimental material providing opportunities for effective selection and genetic improvement. Similar observations have been reported by Khajudparn and Tantasawat (2011) [13], Prasanna *et al.* (2013) [25], Degefa *et al.* (2014) [6], Muralidhara *et al.* (2015) [21], Ramakrishnan *et al.* (2018) [26], Muthuswamy *et al.* (2019) [22], Manivelan *et al.* (2019) [17], Wesly *et al.* (2020) [39], Salman *et al.* (2021) [29] and Sineka *et al.* (2021) [33].

The higher PCV values compared to GCV values for all traits suggest environmental influence on trait expression. However, the relatively narrow differences between PCV and GCV indicate that environmental effects were limited and that the observed variation was predominantly genetic in nature. High variability observed for pods per plant and seed yield per plant suggests greater scope for improvement through selection. Similar findings have been reported by several earlier workers. Moderate variability for days to 50% flowering, plant height and seeds per pod suggests comparatively lower response to selection while low variability for days to maturity indicates a narrow genetic base for this trait. The high heritability estimates observed

for most traits indicate that these characters are largely governed by genetic factors and that phenotypic selection would be effective. Similar results were reported by Asari *et al.* (2019) [2], Wesly *et al.* (2020) [39] and Singh *et al.* (2021) [35]. However, heritability alone does not provide complete information regarding expected selection response. Therefore, genetic advance was considered in conjunction with heritability. High heritability coupled with high genetic advance for days to 50% flowering, plant height, pods per plant, seeds per pod and seed yield per plant indicates the predominance of additive gene action with minimal environmental influence. Similar findings have been reported by Reddy *et al.* (2011) [28], Ramakrishnan *et al.* (2018) [26], Sandhiya and Saravanan (2018) [30], Anuradha *et al.* (2019) [11], Muthuswamy *et al.* (2019) [22] and Mohammed *et al.* (2021) [19]. These traits can therefore be effectively improved through direct phenotypic selection. In contrast, moderate genetic advance for pod length and low genetic advance for days to maturity suggest the involvement of non-additive gene effects, limiting the effectiveness of simple selection. Similar observations were reported by Desai *et al.* (2020) [7], Vadivel *et al.* (2020) [37], Jayaprada *et al.* (2021) [11], Mohammed *et al.* (2021) [19] and Singh *et al.* (2022) [34]. The higher magnitude of genotypic correlations

compared with phenotypic correlations indicates that the observed associations among traits were mainly governed by genetic factors rather than environmental influences. Seed yield per plant showed strong positive associations with several yield contributing traits particularly pods per plant, plant height, seeds per pod and pod length. Similar relationships have been reported by Garg *et al.* (2017)^[19], Mohan *et al.* (2019)^[20], Asari *et al.* (2019)^[2], Desai *et al.* (2020)^[7], Mohammed *et al.* (2021)^[19], Singh *et al.* (2022)^[34] and Kumar *et al.* (2022)^[14]. These findings suggest that simultaneous improvement of these characters may contribute to enhanced seed yield.

Path coefficient analysis further clarified the nature of these associations by partitioning correlations into direct and indirect effects. Pods per plant exhibited the highest positive direct effect on seed yield followed by plant height, seeds per pod and pod length indicating that these traits are major determinants of yield. Similar findings have been reported by Ramakrishnan *et al.* (2018)^[26], Wesly *et al.* (2020)^[39] and Singh *et al.* (2021)^[35]. Several traits also influenced yield indirectly through pods per plant demonstrating the complex interrelationships among yield components. Although days to 50% flowering and days to maturity showed low or negative direct effects their indirect contributions through other yield-related traits indicate their role in the overall yield architecture. The residual effect of 0.64 suggests that the traits included in the analysis accounted for a substantial proportion of the variability in seed yield and may therefore serve as useful selection criteria in mungbean breeding programmes.

Conclusion

This investigation demonstrated that the evaluated mungbean genotypes possess substantial genetic variability for yield-related traits with significant genetic differences evident for most characters under study. The combination of high genotypic and phenotypic variability, high broad-sense heritability and high genetic advance for pods per plant and seed yield per plant supports the predominance of additive genetic control and indicates that phenotypic selection for these traits should be efficient. Character association and path analyses consistently identified pods per plant as the most important yield-contributing trait through the strongest direct effect on seed yield per plant. Additionally, plant height, seeds per pod and pod length contributed positively and directly, making them reliable secondary targets for selection. Therefore, breeding strategies aimed at improving mungbean yield should prioritize genotypes with superior pods per plant along with favorable expression of plant height, seeds per pod and pod length thereby enabling more accurate and faster genetic gains in subsequent selection and hybridization programs.

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