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Digambar Kalyankar
 Post Graduate Student,
 Department of Genetics and
 Plant Breeding, School of
 Agricultural Sciences, G H
 Raisoni University, Saikheda,
 Pandhurna, Madhya Pradesh,
 India

**Mukesh Rathod Pravin
 Gangasagar Deepak Sapkal**
 Research Guide & Assistant
 Professor, Department of
 Genetics and Plant Breeding,
 School of Agricultural Sciences,
 G H Raisoni University,
 Saikheda, Pandhurna, Madhya
 Pradesh, India

Corresponding Author:
Digambar Kalyankar
 Post Graduate Student,
 Department of Genetics and
 Plant Breeding, School of
 Agricultural Sciences, G H
 Raisoni University, Saikheda,
 Pandhurna, Madhya Pradesh,
 India

Assessment of Genetic Variability, Character Association, and Path Analysis in Mungbean (*Vigna radiata* L. Wilczek) Genotypes

Digambar Kalyankar and Mukesh Rathod Pravin Gangasagar Deepak Sapkal

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Abstract

The present investigation was carried out to evaluate genetic variability, character associations, and path coefficients for seed yield and its component traits among eight mungbean (*Vigna radiata* L. Wilczek) genotypes. The field experiment was conducted in a Randomized Block Design (RBD) with three replications during the Kharif 2025 season at the Research Farm of G H Raisoni University, Saikheda. Analysis of variance (ANOVA) indicated significant genetic differences ($P < 0.01$) among all genotypes for nine quantitative characters studied. High phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were recorded for seed yield per plant (31.30% & 31.05%), 1000-seed weight (25.34% & 25.25%), and number of primary branches per plant (19.67% & 18.31%). High broad-sense heritability coupled with high genetic advance as percentage of mean (GAM) was recorded for seed yield per plant (98.43%, 63.46%), 1000-seed weight (99.33%, 51.85%), number of pods per plant (99.34%, 55.62%), and number of seeds per pod (92.37%, 33.38%), demonstrating the predominance of additive gene action. Correlation analysis revealed that seed yield per plant exhibited a highly significant positive association with number of seeds per pod ($rg = 0.878$), primary branches per plant ($rg = 0.872$), pod length ($rg = 0.736$), leaves per plant ($rg = 0.697$), pods per plant ($rg = 0.658$), and 1000-seed weight ($rg = 0.541$). Path coefficient analysis demonstrated that number of seeds per pod (0.689), pods per plant (0.435), and leaves per plant (0.338) had maximum direct positive contributions toward seed yield. Genetic divergence analysis grouped the eight genotypes into four distinct clusters. High inter-cluster distance was recorded between G1 and G6 ($D2 = 1.288$), suggesting that crossing these entries could generate desirable recombinants in future breeding programs.

Keywords: Mungbean, Genetic Variability, Heritability, Genetic Advance, Correlation, Path Analysis, Genetic Divergence

Introduction

Mungbean [*Vigna radiata* (L.) Wilczek, $2n = 22$] is one of the most vital pulse crops grown in India. Belonging to the family Fabaceae, it is widely recognized for its high nutritional value, short growth duration (55–70 days), and ability to improve soil fertility through biological nitrogen fixation. Mungbean seeds contain approximately 24–27% protein, rich quantities of essential amino acids (specifically lysine), dietary fiber, and essential minerals such as iron and zinc. Because of its easy digestibility, it forms a major part of the vegetarian diet in South Asia. Despite its agronomic importance, average mungbean productivity remains low compared to its yield potential. Yield is a complex quantitative trait governed by polygenes and strongly influenced by environmental fluctuations. Direct selection for seed yield per se often yields poor results due to low direct heritability. Therefore, selection should be based on yield-contributing characters that demonstrate high genetic variability, high heritability, and positive correlations with yield. Estimation of genetic variability parameters—such as Phenotypic Coefficient of Variation (PCV), Genotypic Coefficient of Variation (GCV), Heritability (h^2_b), and Genetic Advance (GA)—provides essential insights into the nature of gene action governing various quantitative traits. Furthermore, correlation coefficient analysis helps plant breeders understand the strength and direction of associations among traits, while path coefficient analysis partitions correlation coefficients into direct and

indirect effects to identify true yield determinants. In addition, assessing genetic diversity through Mahalanobis D2 statistics and Principal Component Analysis (PCA) assists in identifying genetically divergent parents for hybridization. The objective of this study was to evaluate genetic parameters, trait associations, and genetic divergence among eight mungbean genotypes to provide recommendations for future breeding efforts.

Materials and Methods

Experimental Site and Plant Material

The present experiment was conducted during the Kharif season at the Research Farm of the Department of Genetics and Plant Breeding, School of Agricultural Sciences, G H Rasoni University, Saikheda, Pandhurna (M.P.), India (21.51' N latitude, 78.76' E longitude, 821.5 m ASL). The soil of the experimental site was clay loam in texture with uniform fertility. The experimental material comprised eight elite genotypes of mungbean obtained from the Agriculture Research Station, Badnapur: G1 (BPMR-145), G2 (BM-2003-2), G3 (BM-2002-1), G4 (BM-4), G5 (PM-707-5), G6 (KM 11-584), G7 (M-9339), and G8 (NMK-15-08).

Experimental Design and Layout

The trial was evaluated in a Randomized Block Design (RBD) with three replications. Each genotype was sown in rows spaced 30 cm apart with an intra-row plant spacing of 10 cm. Standard recommended agronomic practices and plant protection measures were adopted uniformly to ensure a healthy crop stand.

Data Collection

Observations were recorded on ten randomly chosen, competitive plants per genotype per replication for nine quantitative traits: Plant height (cm), Number of leaves per plant, Number of primary branches per plant, Number of pods per plant, Number of pod clusters per plant, Pod length (cm), Number of seeds per pod, 1000-seed weight (g), and Seed yield per plant (g).

Statistical Analysis

The collected data were subjected to Analysis of Variance (ANOVA) as per standard statistical procedures (Panse and Sukhatme, 1985) [10]. Genotypic and phenotypic coefficients of variation were estimated following Burton and DeVane (1953). Broad-sense heritability (h^2_b) and genetic advance as percentage of mean (GAM) were calculated according to Johnson *et al.* (1955) [7]. Genotypic and phenotypic correlation coefficients were computed per Al-Jibouri *et al.* (1958) [2], and path coefficient analysis was conducted following Dewey and Lu (1959) [5]. Genetic divergence was evaluated using Mahalanobis D2 statistic and Principal Component Analysis.

Results and Discussion

Analysis of Variance (ANOVA) and Mean Performance

The analysis of variance (ANOVA) indicated highly significant differences ($P < 0.01$) among all eight mungbean genotypes for the nine quantitative traits evaluated (Table 1). This confirms the presence of substantial genetic variability in the material, providing good scope for selection.

Table 1: Analysis of variance (ANOVA) for nine quantitative traits in mungbean genotypes

Character	Replication (df=2)	Genotype (df=7)	Error (df=14)	C.V. (%)
Plant height (cm)	0.214	73.131**	0.970	2.14
Number of leaves per plant	0.042	9.637**	0.133	3.24
Number of primary branches/plant	0.011	1.139**	0.056	7.19
Number of pods per plant	0.031	36.900**	0.082	2.22
Number of pod clusters/plant	0.082	1.094*	0.466	12.22
Pod length (cm)	0.012	4.815**	0.026	1.84
Number of seeds per pod	0.041	9.570**	0.256	4.84
1000-seed weight (g)	0.120	216.419**	0.485	2.07
Seed yield per plant (g)	0.008	5.500**	0.030	4.06

Genotype G4 exhibited the highest mean plant height (56.23 cm), while G6 recorded the maximum pod length (10.57 cm) and 1000-seed weight (51.67 g). The highest number of pods per plant was observed in G8 (18.53) followed by G7 (18.33).

Estimation of Genetic Variability Parameters

For all studied traits, the phenotypic variance (σ^2_p) and phenotypic coefficient of variation (PCV) were slightly higher than genotypic variance (σ^2_g) and genotypic coefficient of variation (GCV), indicating a low environmental influence on trait expression (Table 2).

Table 2: Estimates of genetic variability parameters for quantitative traits in mungbean

Character	Grand Mean	GCV (%)	PCV (%)	h^2_b (%)	GAM (%)
Plant height (cm)	46.04	10.65	10.86	96.07	21.42
Number of leaves per plant	11.08	15.93	16.26	95.98	31.95
Number of primary branches/plant	2.32	18.31	19.67	86.64	35.11
Number of pods per plant	12.87	27.09	27.18	99.34	55.62
Number of pod clusters/plant	3.74	8.62	12.22	49.72	12.52
Pod length (cm)	8.62	14.54	14.66	98.39	29.46
Number of seeds per pod	10.45	16.96	17.65	92.37	33.38
1000-seed weight (g)	33.56	25.25	25.34	99.33	51.85
Seed yield per plant (g)	4.25	31.05	31.30	98.43	63.46

High GCV and PCV values (>20%) were recorded for seed yield per plant (31.05% and 31.30%), number of pods per plant (27.09% and 27.18%), and 1000-seed weight (25.25% and 25.34%). High broad-sense heritability (>85%) combined with high genetic advance as percentage of mean (>30%) was observed for seed yield per plant (98.43%, 63.46%), number of pods per plant (99.34%, 55.62%), 1000-seed weight (99.33%, 51.85%), primary branches per plant (86.64%, 35.11%), seeds per pod (92.37%, 33.38%), and leaves per plant (95.98%, 31.95%). As per Johnson *et*

al. (1955) [7], traits showing high heritability accompanied by high genetic advance are controlled primarily by additive gene action, indicating that direct phenotypic selection will be effective.

Correlation Coefficient Analysis

Genotypic correlation coefficients (rg) were generally higher than phenotypic correlation coefficients (rp), confirming inherent genetic associations among characters (Table 3).

Table 3: Genotypic (rg) and phenotypic (rp) correlation coefficients between yield components and seed yield

Character	Genotypic Correlation (rg)	Phenotypic Correlation (rp)
Plant height (cm)	-0.116	-0.108
Number of leaves per plant	0.697**	0.662**
Number of primary branches/plant	0.872**	0.799**
Number of pods per plant	0.658**	0.653**
Number of pod clusters/plant	0.656**	0.405*
Pod length (cm)	0.736**	0.722**
Number of seeds per pod	0.878**	0.843**
1000-seed weight (g)	0.541**	0.537**

Seed yield per plant exhibited highly significant positive genotypic and phenotypic correlations with number of seeds per pod (rg = 0.878), primary branches per plant (rg = 0.872), pod length (rg = 0.736), number of leaves per plant (rg = 0.697), pods per plant (rg = 0.658), pod clusters per plant (rg = 0.656), and 1000-seed weight (rg = 0.541). This

indicates that selection for these traits will lead to simultaneous enhancement in seed yield.

Path Coefficient Analysis

Path coefficient analysis partitioned genotypic correlation coefficients into direct and indirect effects to evaluate the true contribution of each trait to seed yield (Table 4).

Table 4: Direct (bold) and indirect genotypic effects of quantitative traits on seed yield per plant

Character	Direct Effect	Indirect via Seeds/Pod	Indirect via Pods/Plant	Indirect via Leaves/Plant	Genotypic Correlation (rg)
Plant height (cm)	-0.084	-0.031	0.012	-0.013	-0.116
Number of leaves per plant	0.338	0.485	0.212	—	0.697**
Number of primary branches/plant	0.196	0.524	0.273	0.145	0.872**
Number of pods per plant	0.435	0.271	—	0.165	0.658**
Number of pod clusters/plant	-0.052	0.312	0.241	0.155	0.656**
Pod length (cm)	-0.331	0.488	0.331	0.252	0.736**
Number of seeds per pod	0.689	—	0.171	0.238	0.878**
1000-seed weight (g)	0.016	0.298	0.112	0.115	0.541**

The highest positive direct effect on seed yield was recorded for number of seeds per pod (0.689), followed by number of pods per plant (0.435), leaves per plant (0.338), and primary branches per plant (0.196). Pod length had a direct negative effect (-0.331) but maintained a high positive correlation with yield due to positive indirect contributions through seeds per pod (0.488) and pods per plant (0.331). The low residual effect (R = 0.106) confirms that the selected traits accounted for 89.4% of total variation in seed yield.

Genetic Divergence Analysis (D2 and PCA)

Mahalanobis D2 cluster analysis grouped the eight genotypes into four distinct clusters: Cluster I (G1, G2, G3, G4), Cluster II (G6, G7), Cluster III (G5), and Cluster IV (G8). The maximum inter-genotypic distance was observed between G1 and G6 (D2 = 1.288), followed by G2 and G6 (D2 = 1.270). Principal Component Analysis (PCA) revealed that the first four principal components contributed 89.82% of the cumulative genetic variance (PC1 = 57.45%, PC2 = 14.09%, PC3 = 10.03%, PC4 = 8.25%).

Conclusion

The current study demonstrates substantial genetic variability among the evaluated mungbean genotypes. High heritability coupled with high genetic advance as percentage of mean was observed for seed yield per plant, 1000-seed weight, number of pods per plant, and number of seeds per pod, indicating additive gene action. Character association and path analysis identified number of seeds per pod, number of pods per plant, and primary branches per plant as primary direct yield determinants. Therefore, direct phenotypic selection based on these component traits is recommended for yield improvement. Furthermore, hybridization between divergent genotypes from Cluster I (G1, G2) and Cluster II (G6, G7) is suggested to exploit heterosis and derive superior recombinants.

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Conflict of Interest

The authors declare no conflict of interest regarding the publication of this paper.

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