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Genetic variability and character association studies in mungbean (*Vigna radiata* L. Wilczek)

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Abstract

The investigation titled “Genetic Variability and Character Association studies in Mungbean (*Vigna radiata* L. Wilczek)” was conducted during Kharif 2024 at Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola, evaluating 35 genotypes including a standard check using a randomized block design with two replications. Ten traits were assessed, and analysis of variance revealed significant genetic differences across all genotypes. Phenotypic coefficient of variation (PCV) exceeded genotypic coefficient of variation (GCV) for every trait, with the greatest variability seen in seed yield per plant, followed by pods per plant, pod length, primary branches per plant, 100-seed weight, plant height, seeds per pod, days to flowering, protein content, and days to maturity. Traits showing both high heritability and genetic advance as a percent of the mean included seed yield, pod length, pods per plant, primary branches, 100-seed weight, protein content, plant height, seeds per pod, days to maturity, and flowering. Seed yield per plant was significantly and positively correlated with pods per plant, 100-seed weight, seeds per pod, pod length, primary branches, and plant height, while non-significant correlations were observed with protein content and phenological traits. Path coefficient analysis confirmed strong direct effects of these yield components, emphasizing their importance in selection indices for breeding. Among the genotypes, GMU-2020-19, GMU-2020-11, GMU-2020-8, and GMU-2020-24 surpassed the check variety PKV-Green Gold in seed yield and yield-related traits, making them promising candidates for future mungbean varietal improvement programs.

Keywords: Mungbean, genetic variability, heritability, correlation, path analysis

Introduction

Pulses are the primary source of protein for India’s largely vegetarian population and also serve as valuable fodder and cattle concentrates. Their role in symbiotic nitrogen fixation is especially important in light of rising nitrogen fertilizer costs, contributing significantly to soil fertility and reducing erosion due to their deep root systems. Despite these benefits, pulse production has lagged behind cereal gains following the Green Revolution, leading to less area expansion and productivity, and causing price increases. Green gram (*Vigna radiata* L.), a legume cultivated for edible seeds and sprouts across Asia, belongs to the Fabaceae (Papilionaceae) family with a diploid chromosome number of $2n = 24$. India, considered its center of domestication, harbors diverse cultivated and wild subspecies.

Green gram accounts for roughly 16 % of India’s pulse-growing area and contributes 10 % of national pulse output. The seeds are nutritionally rich with approximately 20-28 % protein, 1.0-1.5 % fat, 3.5-4.5 % fiber, and 55-65 % carbohydrates, alongside essential minerals like calcium, phosphorus, iron, zinc, and bioactive flavonoids such as vitexin and isovitexin. Their protein is highly digestible and complements cereal-based diets; mung dal khichadi is commonly recommended for its nutritional completeness and ease of digestion. Health benefits extend to cardiovascular support in women, bone fortification due to phosphorus and calcium, cognitive enhancement via manganese, and skin protection through zinc content, which is also utilized in topical preparations in Ayurvedic practice.

Materials and Methods

The study titled “Genetic Variability and Character Association Studies in Mungbean (*Vigna radiata* L. Wilczek)” was conducted during Kharif-2023-24 at the Pulse Research Unit, Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola.

Thirty-five mungbean genotypes (34 experimental + 1 check) sourced from the Germplasm Management Unit, IIPR, Kanpur, were evaluated in a randomized block design with two replications. Sowing occurred on 30 July 2024 using dibbling at 45 × 10 cm spacing Standard agricultural practices, including land preparation, gap filling after 7-8 days, and plant protection, were employed.

Observations were taken on five randomly selected plants per genotype in each replication and means were used for analysis. Recorded traits included days to 50% flowering and maturity, plant height, number of primary branches per plant, pods per plant, seeds per pod, pod length, 100-seed weight, seed yield per plant and Protein content (%). Protein content (%) was estimated using micro-Kjeldahl method (digestion-distillation-titration) with a nitrogen-to-protein conversion factor of 6.25, following AOAC protocols.

Results and Discussion

The analysis of variance (ANOVA) for ten key traits (Table 1.) including days to 50% flowering, maturity, plant height, primary branches, pods per plant, seeds per pod, pod length, 100-seed weight, seed yield, and protein content was conducted on data from five randomly selected plants per genotype per replication under a randomized block design with two replicates. The treatment mean sum of squares for all these traits were highly significant ($p < 0.01$), indicating substantial genetic variability among the 35 mungbean genotypes, consistent with the findings of similar studies on mungbean germplasm.

Mean performance varied widely across genotypes (Table 2.). Days to 50% flowering ranged from 35 to 43 days (mean = 39.47), maturity from 65.5 to 73.5 days (mean = 69.34), plant height from 38.92 to 64.40 cm (mean = 52.89), primary branches from 2.80 to 5.00 (mean = 3.79), pods per plant from 11.5 to 26.7 (mean = 17.26), seeds per pod from 7.9 to 12.4 (mean = 10.66), pod length from 7.40 to 12.66 cm (mean = 9.02), 100-seed weight from 2.92 g to 5.55 g (mean = 3.86 g), seed yield per plant from 3.48 g to 13.30 g (mean = 7.27 g), and protein content from 19.52% to 23.85% (mean = 21.71%). Notably, genotypes GMU-2020-19, GMU-2020-11, and GMU-2020-8 consistently exhibited superior performance for yield components and yield per plant, highlighting their potential for breeding programs aimed at yield enhancement.

All traits showed higher phenotypic coefficient of variation (PCV) than genotypic coefficient of variation (GCV) (Table 2.), indicating environmental influence on trait expression. High GCV and PCV (>20%) were observed for seed yield per plant and pods per plant, consistent with Rao *et al.* (2006), Prasanna *et al.* (2013) [13], and Muzibul *et al.* (2014) [10]. Traits such as primary branches, pod length, and 100-seed weight exhibited moderate variability (10-20%), aligning with Rao *et al.* (2006). In contrast, seeds per pod and plant height had low GCV (<10%) but moderate PCV, echoing findings by Rao *et al.* (2006), Muzibul *et al.* (2014) [10], and Asari *et al.* (2019) [1], while days to flowering, maturity, and protein content showed low variability in both GCV and PCV, in agreement with Rao *et al.* (2006), Prasanna *et al.* (2013) [13], Muzibul *et al.* (2014) [10], Kate *et al.* (2017) [8], and Asari *et al.* (2019) [1]. Variability classification followed the Shivasubramanian and Menon (1973) scale: low (0-10%), moderate (10-20%), high (>20%).

The present investigation found high broad-sense heritability (Table 2.) for seed yield per plant, pod length, number of pods per plant, primary branches per plant, protein content, 100-seed weight, seeds per pod, and both phenological traits (days to 50% flowering and maturity), indicating predominant additive gene effects suitable for selection—a result consistent with Rao *et al.* (2006), Prasanna *et al.* (2013) [13], Katiyar *et al.* (2015) [7], Yadav *et al.* (2017) [19], and Asari *et al.* (2019) [1]. Conversely, plant height and seeds per pod exhibited lower heritability, implying non-additive gene influence as noted by Muzibul *et al.* (2014) [10] and Nagrale *et al.* (2018) [11]. Traits such as pods per plant demonstrated high heritability coupled with high genetic advance, mirroring findings by Rao *et al.* (2006), Bains *et al.* (2007) [3], and Tabasum *et al.* (2010) [17], while seed yield per plant and pod length showed high heritability with moderate genetic advance, aligning with Rao *et al.* (2006). The classification of heritability and genetic advance followed Robinson *et al.* (1951) and Johnson *et al.* (1955) [6], respectively, facilitating the identification of traits most responsive to selection.

In the present study, genotypic correlation coefficients exceeded phenotypic ones for all traits (Table 3. And Table 4.), indicating minimal environmental influence on seed yield which aligns with findings from Prasanna *et al.* (2013) [13] and Kate *et al.* (2017) [8]. Seed yield per plant displayed strong positive and significant correlations at both levels with number of pods per plant, 100-seed weight, seeds per pod, pod length, primary branches per plant, and plant height, supporting results from Parameswarappa (2005) [12], Das *et al.* (2014), and Bains *et al.* (2007) [3]. Associations with protein content and days to 50% flowering were positive but non-significant, similar to Das *et al.* (2014); seed yield also had a non-significant negative genotypic correlation with days to maturity, confirming Katiyar *et al.* (2015) [7]. Phenological traits days to flowering and maturity were highly correlated with each other genotypically and phenotypically and positively associated with seeds per pod, in line with Tripathy *et al.* (2016) [18] and Bhanu *et al.* (2017) [2]. Plant height correlated positively with pods per plant, seeds per pod, primary branches, 100-seed weight, and pod length, echoing Parameswarappa (2005) [12], Kate *et al.* (2017) [8], and Nagrale *et al.* (2018) [11]. Additionally, primary branches showed strong positive associations with seeds per pod, 100-seed weight, pods per plant, seed yield, and pod length (Nagrale *et al.*, 2018) [11], while pods per plant had strong ties with seed yield, 100-seed weight, seeds per pod, and pod length (Tabasum *et al.*, 2010 [17]; Yadav *et al.*, 2017) [19]. Pod length correlated positively with 100-seed weight, seed yield, and seeds per pod (Yadav *et al.*, 2017 [19]; Nagrale *et al.*, 2018) [11], and both seeds per pod and 100-seed weight exhibited significant positive correlations with seed yield at genotypic and phenotypic levels (Kate *et al.*, 2017 [8]; Nagrale *et al.*, 2018) [11].

Path coefficient analysis at the genotypic level partitioned the correlations with seed yield into direct and indirect effects (Table 5.), revealing that the number of pods per plant exerted the highest positive direct influence, followed by number of seeds per pod, 100-seed weight, plant height, and primary branches per plant findings in agreement with Parameswarappa (2005) [12], Rao *et al*. (2006), Tabasum *et al*. (2010) [17], Prasanna *et al*. (2013) [13], Muzibul *et al*. (2014) [10], Kate *et al*. (2017) [8]. Conversely, days to maturity, days to 50% flowering, and pod length manifested negative direct effects, corroborating reports by Muzibul *et al*. (2014) [10], Asari *et al*. (2019) [1], and Bhanu *et al*. (2017) [2]. All positively contributing traits also exhibited favorable indirect effects on yield. These results highlight pods per plant, 100-seed weight, seeds per pod, plant height, and primary branches as key yield components for selection in mungbean breeding.

Table 1: Analysis of variance for various characters

Sr. No.	**Characters**	**Mean sum of Squares**		
		Replication	**Treatment**	**Error**
	Degree of freedom	1	34	34
1	Days to 50% flowering	0.7	11.35**	2.67
2	Days to maturity	0.06	9.61**	1.79
3	Plant height (cm)	1.01	75.50**	25.68
4	Number of primary branches per plant	0.39	0.52**	0.14
5	Number of pods per plant	0.02	27.16**	3.14
6	Pod length (cm)	0.20	4.31**	0.27
7	Number of seed per pod	1.81	2.09**	0.88
8	100 seed weight (g)	0.07	0.44**	0.13
9	Seed yield per plant (g)	0.17	11.66**	0.46
10	Protein content (%)	0.93	1.84**	0.52

* Significant at 5 percent level **significant at 1 percent level

Table 2: Estimates of genetic parameters in mungbean

Sr. No.	**Characters**	**Range**	**Mean**	**GCV%**	**PCV%**	**Heritability (%)**	**Genetic Advance (GA)**	**GAM (%)**
1	Days to 50% plants flowering	35-43	39.47	5.28	6.71	61.91	3.38	8.56
2	No. of days to maturity	65.5-73.5	69.34	2.85	3.44	68.56	3.37	4.86
3	Plant height (cm)	38.92-64.4	52.89	9.44	13.45	49.24	13.64	23.13
4	No. of primary branches per plant	2.8-5	3.79	11.58	15.17	58.30	0.69	18.22
5	No. of pods per plant	11.5-26.7	17.26	20.08	22.55	79.26	6.36	36.82
6	Number of Seeds per Pod	7.9-12.4	10.66	7.28	11.43	40.55	1.02	9.55
7	Pod length (cm)	7.4-12.66	9.02	15.76	16.77	88.25	2.75	30.49
8	100 Seed weight(gm)	2.92-5.55	3.86	10.35	13.92	55.30	0.61	15.86
9	Seed yield per plant (gm)	3.48-13.3	7.27	32.55	33.86	92.41	4.69	64.46
10	Protein content (%)	19.52-23.85	21.71	3.75	5.01	55.99	1.25	5.78

Table 3: Estimation of genotypic correlation coefficient (r) of different characters in mungbean

Characters	**Days to 50% Flowering**	**Days to Maturity**	**Plant Height (cm)**	**Number of primary Branches /Plant**	**Number of Pods/Plant**	**pod length (cm)**	**Number of Seeds/Pod**	**100 Seed weight(gm)**	**Protein content (%)**	**Seed yield per plant (gm)**
Days to 50% flowering	1	0.744**	0.221	-0.148	0.178	-0.064**	0.389**	-0.247**	0.188	0.140
Days to maturity		1	-0.156	-0.132	-0.020	-0.007**	0.364**	-0.138**	0.038	-0.011
Plant height(cm)			1	0.412**	0.483**	0.304**	0.425**	0.377**	0.203	0.457**
No. of primary branches per plant				1	0.528**	0.496**	0.567**	0.530**	0.106	0.517**
No. of pods per plant					1	0.423**	0.504**	0.544**	0.203	0.817**
Pod length(cm)						1	0.352**	0.652**	-0.197	0.548**
No. of seed per pod							1	0.534**	0.018	0.613**
100 seed weight(gm)								1	-0.156	0.713**
Protein content (%)									1	0.217
Seed yield/plant(gm)										1

Table 4: Estimation of phenotypic correlation coefficient (r) of different characters in mungbean

Characters	Days to 50% Flowering	Days to Maturity	Plant Height (cm)	Number of primary Branches /Plant	Number of Pods/Plant	pod length (cm)	Number of Seeds/Pod	100 Seed weight(gm)	Protein content (%)	Seed yield per plant (gm)
Days to 50% flowering	1	0.618**	0.169	-0.111	0.135	-0.051	0.282	0.176	0.119	0.100
Days to maturity		1	-0.126	-0.098	-0.022	-0.011	0.266	-0.090	0.048	-0.010
Plant height(cm)			1	0.302**	0.352**	0.212**	0.286	0.257	0.126	0.314**
No. of primary branches per plant				1	0.387**	0373**	0.415**	0.396**	0.045	0.382**
No. of pods per plant					1	0.304**	0.360*	0.405**	0.147	0.652**
Pod length(cm)						1	0.237	0.487**	-0.124	0.406**
No. of seed per pod							1	0.386*	0.011	0.437**
100 seed weight(gm)								1	-0.060	0.564**
Protein content (%)									1	0.148
Seed yield/plant(gm)										1

Table 5: Path Coefficient Analysis showing direct (Diagonal values) and indirect effects of various characters in Mungbean

Characters	Days to 50% Flowering	Days to Maturity	Plant Height (cm)	No of primary Branches/Plant	No of Pods/Plant	Pod length (cm)	No of Seeds/Pod	100 Seed weight (gm)	Protien content (%)	Seed yield per plant (gm)
Days to 50% flowering	-0.074	-0.023	0.0007	-0.001	0.090	0.081	0.177	-0.125	0.008	0.140
Days to maturity	-0.036	-0.030	-0.003	-0.003	-0.048	0.078	0.217	-0.188	0.002	-0.011
Plant height (cm)	-0.007	0.001	0.055	0.029	0.210	-0.054	0.112	0.102	0.003	0.457**
No. of primary branches per plant	0.002	0.003	0.026	0.062	0.303	-0.090	0.100	0.106	0.005	0.517**
No. of pods per plant	-0.041	0.003	0.029	0.051	0.579	-0.055	0.120	0.122	0.009	0.817**
Pod length(cm)	0.013	0.008	0.024	0.029	0.222	-0.069	0.105	0.225	-0.009	0.548**
No. of seed per pod	-0.031	-0.018	0.024	0.026	0.330	-0.042	0.193	0.130	0.001	0.613**
100 seed weight (gm)	0.020	0.016	0.013	0.026	0.266	-0.052	0.071	0.363	-0.010	0.713**
Protien content (%)	0.030	-0.005	-0.013	0.012	0.161	-0.020	0.004	0.004	0.044	0.217

Conclusion

In a Kharif 2024 trial at the Pulses Research Unit (Dr. PDKV, Akola), 35 mungbean genotypes (including PKV-Green Gold as check) were evaluated in an RBD with two replications. Observing ten traits, ANOVA revealed significant genetic differences and wide variability. Genotype GMU-2020-19 led in yield (13.30 g), plant height (64.40 cm), branches (5), pods (26.70), pod length (12.66 cm), seeds/pod (12.40), and 100-seed weight (5.55 g), followed by GMU-2020-11, GMU-2020-8, and GMU-2020-24 all outperforming the check. GMU-2020-1 was earliest to flowering (35 days) and maturity (65.5 days), matched by GMU-2020-11 and GMU-2020-24. High GCV/PCV for yield components and strong heritability suggested good selection potential. Positive correlations and path analysis confirmed that pods, seed weight, seeds per pod, branches, and plant height directly boosted yield, while delayed flowering and maturity had negative effects. Thus, GMU-2020-19, GMU-2020-11, GMU-2020-8, and GMU-2020-24 are recommended for future mungbean breeding.

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