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Genetic Basis of Yield Variation in Spring Mung Bean (*Vigna radiata* L.): A Correlation and Path Analysis Study

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ABSTRACT

The investigation was conducted in March to June, 2022 at CAU research farm Andro, Imphal East, Manipur, India to study the nature, magnitude and interrelationships of genetic variation present within various characters of mung bean. This study included 27 mung bean genotypes in a Randomized Block Design with three replications. Analysis of variance revealed significant genetic variation ($p<0.01$) for all studied traits. Phenotypic coefficient of variation (PCV) values was higher than genotypic coefficient of variation (GCV) values, indicating some environmental influence on trait expression. High heritability (>60%) was observed for plant height, number of clusters plant^{-1}, pod length, number of seeds plant^{-1}, 100-seed weight, protein%, and seed yield plant^{-1}. These traits also exhibited high genetic advance (>20%), suggesting a significant role of additive gene effects. Seed yield plant^{-1} displayed positive correlations with number of clusters plant^{-1}, number of pods plant^{-1}, pod length, number of seed pod^{-1} and 100-seed weight at both phenotypic and genotypic levels. Path analysis revealed that number of pods plant^{-1} and number of seeds pod^{-1} were the most significant contributors to seed yield. These findings suggest that selection for these traits, along with indirect selection for pod length, 100-seed weight, flowering time, and protein percentage, could be effective strategies for improving mung bean yield.

KEYWORDS: Mung bean, genetic variability, heritability, correlation, path analysis

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1. INTRODUCTION

Mung bean, scientifically known as *Vigna radiata* (L.) Wilczek. It is an indigenous crop from India commonly known as green gram, golden gram or moong. It is often referred to as a break crop or catch crop due to its short growing season and ability to improve soil health. Mung bean has high protein content (20–27%) and a composition that includes essential amino acids (9.59 mg 100 g^{-1}) (Degefa et al., 2013, Singh et al., 2022 and Chauhan et al., 2016). Proper nutrition can help prevent diseases and improve well-being (Bessada et al., 2019). For a healthier diet, experts suggest increasing your intake of plant-based proteins, with pulses being the top choice for protein content among all plants (Henchion et al., 2017 and Sahruzaini et al., 2020) and Pulses also contribute to better health as they reduce diabetes and cholesterolemia, Therefore, pulses could significantly increase the sustainability of our diets. (Magrini et al., 2018). It is cultivated worldwide and is a significant food (edible seeds and sprouts) crop across the South and Southeast Asian rice-based farming systems (Anonymous, 2020; Bohra et al., 2014). India is the world's leading producer of pulses, contributing a significant quarter to global production. This dominance is evident in both the quantity and diversity of pulses grown within the country (Pathak et al., 2017). Total pulses production during 2022–23 is estimated at 260.58 lakh tonnes which is higher by 14.02 lakh tonnes than the last five years' average pulses production of 246.56 lakh tonnes. India dominates the global pulse market, accounting for a quarter of worldwide production (25%), over a quarter of global consumption (27%) and a significant portion of imports (14%). Mung beans hold a significant share of the pulse market, representing 10% of total pulse production and occupying 16% of the area dedicated to pulse cultivation. Rajasthan leads in mung bean production, contributing 46% of the area and 45% of the yield (AICRPR's 2022–23 Kharif pulses report and Nalajala et al., 2023). According to the report of Directorate of Economics & Statistics, Government of India, Ministry of Agriculture & Farmer Welfare (DA & FW) mung bean covers an area of 0.005 lakh hectares in *kharif,* 2021–22 in Manipur and produces 0.005 lakh tonnes with a yield of 959 kg ha^{-1}. In regions where meat is scarce or vegetarian diets are prevalent, matured mung bean seeds are a valuable and easily digestible source of protein for human consumption (Anonymous, 2012). Several factors contribute to low green gram yields worldwide, including a significant portion of India's pulse cultivation, roughly 80%, is carried out using seeds saved by the farmers themselves (Ullah et al., 2020), growing on infertile soil, improper fertilizer application, inadequate crop management practices and a lack of better cultivars or hybrids (Aravinth et al., 2023; Ayerdi and Marraccini (2022). Selecting superior parents is a fundamental step in any effort to improve crop yields (Nalajala et al., 2022). A successful breeding program requires careful consideration of the genetic factors influencing multiple quantitative traits. This involves evaluating genetic parameters such as the phenotypic coefficient of variance (PCV), genotypic coefficient of variance (GCV), heritability, and genetic advance percentage of the mean (GAM) (Kumawat et al., 2018). Understanding the genetic variability within existing germplasm is crucial for developing new and improved high-yielding varieties. Selecting high-yield varieties based on their highly correlated characteristics becomes more accessible when the effect of different qualities on yield is ascertained using path coefficient analysis (Dewey et al., 1959). The current study primarily aimed to explore the nature, magnitude and interrelationships of genetic variation present within various characters of mung bean.

2. MATERIALS AND METHODS

The study was carried out at Central Agricultural University, Research Farm Andro, Imphal East, Manipur (795004), India during March to June, 2022, following Randomized Block Design (RBD) with three replications. The plot size was 3×1.5 m^2 with a spacing of 30×10 cm^2 between and within rows. The research farm is located at latitudes 25º4'5.45" N and longitudes and 94º8'42" E at an elevation of 790 meters above the MSL. The crop was sown in the month of May, 2023 and harvested in the month of July, 2023. During the cropping season the average maximum temperature was 30.73°C, average minimum temperature was 21.19°C and total rainfall was 41.95 mm. Standard agricultural practices were followed to promote optimal growth and development of the genotypes. Five plants were selected at random from each plot and each genotype in each replication for recording data. The different quantitative characters studied were plant height (cm), number of primary branches, days to 50% flowering, days to maturity, number of clusters plant^{-1}, number of pods plant^{-1}, pod length (cm), number of seeds pod^{-1}, 100 seed weight (g), protein percentage (%) and seed yield plant^{-1} (g). The phenotypic coefficients of variation (PCV) and genotypic coefficients of variation (GCV) were computed according to Burton and De Vane, 1953. The heritability percentage (H) was estimated as per the formula given by Allard, 1960. The genetic advance (GA) as percentage of mean was computed according to the formula suggested by (Johnson et al., 1955). The genotypic and phenotypic correlations were computed according to formula suggested by Falconer, 1967 and path analysis as suggested by (Dewey and Lu, 1959).

3. RESULTS AND DISCUSSION

Analysis of variance (ANOVA) was carried out for all the 11 characters under study by using R-studio

4.3.2. The statistical analysis (ANOVA) demonstrated significant differences among all the genotypes, highlighting the presence of genetic variability with a high level of significance (p<0.01) (Table 1). The estimate of variance components, broad-sense heritability and genetic advance for all the characters studied are presented in Table 2.

3.1. PCV and GCV

The highest PCV (19.33) was recorded for the character number of primary branches; high PCV and highest GCV were recorded for seed yield plant^{-1}. In the present study, the phenotypic coefficient of variation (PCV) values was higher than the genotypic coefficient of variation (GCV) values for all the 11 characters studied. The greater phenotypic coefficient of variation (PCV) compared to the genotypic coefficient of variation (GCV) suggests a notable influence of environmental factors on the expression of the observed characters however, less difference observed between GCV and PCV indicates that the characters are less affected by environmental variations and trait expression was governed by its own genotypes. Comparable findings were reported by Nalajala et al. (2022), Sabatina et al. (2021) and Kumar et al. (2017) in mung bean. Minimum PCV and GCV values were observed in days to maturity (3.56 and 2.55 respectively) and days to 50% flowering (5.86 and 4.85 respectively). Plant height, number of clusters plant^{-1}, 100 seed weight, protein percentage, seed yield plant^{-1} showed moderate values of GCV and PCV. Similar findings were reported by Nalajala et al. (2022), Sabatina et al. (2021), Kumar et al. (2017) Pathak et al. (2011).

Table 1: Analysis of variance of components in mung bean (*Vigna radiata* (L.)

Source	d. f.	Days to 50% flowering	Days to maturity	Plant height (cm)	Primary branches	No. of clusters Plant^{-1}	No. of pod Plant^{-1}	Pod length (cm)	No. of seed pod^{-1}	100 seed weight (g)	Protein percentage	Seed yield plant^{-1}
Replications	2	2.75	4.85	15.13	0.0079	0.43	2.37	0.03	0.16	0.026	1.05	0.029
Genotypes	26	26.21**	18.86**	194.06**	0.1013**	2.22**	7.5**	1.5**	3.4**	1.08**	46.15**	0.39**
Error	52	2.49	3.20	15.7	0.0099	0.15	1.07	0.03	0.07	0.022	0.58	0.017

*, ** significant at (p=0.05) and (p=0.01) respectively

Table 2 Genetic parameters used to differentiate 27 genotypes of mung bean

Sl. No.	Character	Mean	Coefficient of variation		Heritability (%) Broad sense	Genetic advance	Genetic advance as percentage of mean
			GCV	PCV			
1.	Plant height (cm)	41.9	15.59	18.12	74.11	11.86	27.66
2.	Number of primary branches	1.03	16.79	19.33	75.50	0.31	30.06
3.	Days to 50% flowering	47.56	4.85	5.86	68.69	4.02	8.29
4.	Days to maturity	72.6	2.55	3.56	51.49	2.74	3.78
5.	No. of clusters plant^{-1}	5.36	13.45	15.26	77.72	1.31	24.44
6.	N. of pods plant^{-1}	15.86	8.03	10.39	59.75	2.02	12.79
7.	Pod length (cm)	7.93	7.62	7.99	90.84	1.18	14.96
8.	100 seed weight (g)	10.82	13.04	13.61	91.85	1.00	25.76
9.	Number of seeds pod^{-1}	3.91	8.43	8.82	91.53	1.79	16.60
10.	Protein percentage	23.00	17.18	17.51	96.29	7.87	34.74
11.	Seed yield plant^{-1} (g)	1.77	17.34	18.82	84.98	0.58	32.94

3.2. Heritability and genetic advance

Heritability in broad sense (>60%) were recorded for characters *viz.*, protein percentage, 100 seed weight, number of seeds plant^{-1}, pod length, seed yield plant^{-1}, number of clusters plant^{-1}, plant height, number of primary branches and days to 50% flowering (Table 3). Comparable findings were reported by Marwiyah et al. (2020), Gayacharan et al. (2020) Raturi et al. (2015), Tabasum et al. (2010). The character's plant height, number of primary branches, number of clusters plant^{-1}, 100 seed weight, protein percentage and seed yield plant^{-1} had shown high heritability (>60%) coupled with high genetic advance as percent mean (>20%). Directly selecting for these characters could potentially lead to improved yields. Comparable findings

Table 3: Genotypic and Phenotypic correlation coefficient among yield and its attributing characters

Source	d. f.	Plant height (cm)	Days to 50% flowering	Days to maturity	No. of clusters plant^{-1}	No. of pod plant^{-1}	Pod length (cm)	No. of seed pod^{-1}	100 seed weight (g)	Protein percentage	Seed yield Plant^{-1}
Primary branches	G	-0.337^{NS}	-0.361**	0.088^{NS}	0.060^{NS}	0.208^{NS}	-0.077^{NS}	-0.136^{NS}	0.188^{NS}	0.289**	-0.064^{NS}
	P	-0.123^{NS}	-0.174^{NS}	0.100^{NS}	-0.064^{NS}	0.003^{NS}	-0.013^{NS}	-0.071^{NS}	0.031^{NS}	0.159^{NS}	0.016^{NS}
Plant height (cm)	G		0.227^{NS}	0.459*	0.348^{NS}	0.254^{NS}	0.324^{NS}	0.243^{NS}	0.031^{NS}	0.083^{NS}	0.315^{NS}
	P		0.195^{NS}	0.331**	0.293**	0.201^{NS}	0.300**	0.219*	0.039^{NS}	0.079^{NS}	0.292**
Days to 50% flowering	G			0.347^{NS}	0.347^{NS}	0.254^{NS}	0.195^{NS}	0.190^{NS}	-0.044^{NS}	0.005^{NS}	0.227^{NS}
	P			0.272*	0.282*	0.235*	0.183^{NS}	0.163^{NS}	-0.052^{NS}	0.012^{NS}	0.195^{NS}
Days to maturity	G				0.285^{NS}	0.199^{NS}	0.282^{NS}	0.349^{NS}	-0.054^{NS}	0.525**	0.310^{NS}
	P				0.228*	0.192^{NS}	0.212^{NS}	0.301**	-0.065^{NS}	0.402**	0.239*
No. of clusters plant^{-1}	G					0.826**	0.683**	0.669**	0.523**	-0.123^{NS}	0.743**
	P					0.674**	0.637**	0.613**	0.485**	-0.109^{NS}	0.661**
No. of pod plant^{-1}	G						0.639**	0.748**	0.705**	0.189^{NS}	0.764**
	P						0.545**	0.651**	0.604**	0.141^{NS}	0.668**
Pod length (cm)	G							0.810**	0.497**	0.150^{NS}	0.670**
	P							0.778**	0.476**	0.130^{NS}	0.618**
No. of seed pod^{-1}	G								0.513**	0.241*	0.819**
	P								0.487**	0.230*	0.769**
100 seed weight (g)	G									0.180^{NS}	0.480*
	P									0.162^{NS}	0.466**
Protein percentage	G										0.158^{NS}
	P										0.159^{NS}

*, ** significant at (p=0.05) and (p=0.01) respectively

were reported by Nalajala et al. (2022), Vadivel et al. (2020), Sineka et al. (2021). High heritability (>60%) along with moderate (>10%≥20%) genetic advance as a percentage of the mean was exhibited by pod length and number of seeds pod^{-1}. Whereas, days to 50% flowering exhibited high heritability coupled with low genetic advance as percent mean.

3.3. *Correlation studies*

Association analysis reveals the strength of relationships among various yield components, to assist in the direct selection of correlated characters to improve desirable characteristics such as overall yield. The present study aimed to determine the genotypic and phenotypic correlations among all possible combinations of characters within 27 mung bean genotypes. Due to the potential masking effect of environmental factors on trait expression in phenotypic correlation coefficients, the genotypic correlation coefficients, which reflect inherent genetic relationships, are considered to provide more accurate estimations. Table 3 represents the estimated correlation coefficients between various pairs of characters examined in this study. The seed yield plant^{-1} had highly significant and positive correlation (>0.65**) with number of clusters plant^{-1}, number of pods plant^{-1}, pod length, number of seed pod^{-1} and 100 seed weight at both phenotypic and genotypic levels. This suggests that selection for these characters could potentially lead to enhanced yield. These observations are in accordance with Nalajala et al. (2022), Kumar et al. (2017), Dutta et al. (2016), Prasanna et al. (2013), Bisht et al. (2014) Tabasum et al. (2010) and Makeen et al. (2007). In the present finding, genotypic and phenotypic correlations align with each other, although the genotypic correlations exhibit greater magnitudes for all the characters examined. A plant breeder benefits from a positive correlation between desirable characters as it facilitates simultaneous improvement of these characteristics.

3.4. *Path analysis*

The knowledge of correlation alone is often misleading as the correlation observed may not be always accurate. The only things determined by the correlation values are the nature and degree of the relationship between character pairs, it does not reveal how much a change in one variable will affect a change in another, However, path coefficient analysis is useful as it breaks down the correlation coefficient into direct and indirect effects and favoring for the assessment of the relative importance of each character involved in the yield attributing characters. In the current study, Table 4 depicts a path analysis that shows the direct and indirect effects of the different characters. The highest direct positive impact on seed yield plant^{-1} was exhibited by number of pods plant^{-1} followed by number of seed pod^{-1}, plant height, days to maturity, number of primary branches and number of clusters plant^{-1} at genotypic and phenotypic level. While characters viz., days to 50% flowering, pod length, 100 seed weight and protein percentage, were indirectly influencing the seed yield plant^{-1} through other characters. Path analysis revealed that the number of pods plant^{-1} and the number of seeds pod^{-1} were the most influential factors contributing to yield improvement. Number of pods plant^{-1}, number of seed pod^{-1}, number of primary branches, number of clusters plant^{-1} and plant height had shown highest positive direct effect in case of Degefa et al. (2013), Karthik et al. (2022) in black gram; 100 seed weight and days to 50% flowering in the study of Ahmad et al. (2015), pod length and days to maturity. In the present investigation the residual effect was 0.18.

Table 4. Direct (diagonal) and indirect effects of yield component characters on seed yield plant^{-1} in mung bean at genotypes level

Variables	Plant height (cm)	Primary branches	Days to 50% flowering	Days to maturity	No. of clusters plant^{-1}	No. of pod plant^{-1}	Pod length (cm)	No. of seed pod^{-1}	100 seed weight (g)	Protein percent-age
Plant height (cm)	0.05368	-0.00712	-0.03595	0.02287	0.00783	0.19320	-0.01353	0.11487	-0.0066	-0.0033
Primary branches	-0.03540	0.13029	0.00668	0.00367	-0.00140	0.10394	0.00619	-0.08440	-0.0331	-0.0326
Days to 50% flowering	0.02922	-0.00763	-0.06604	0.01667	0.00794	0.17697	-0.00814	0.09297	0.00994	0.0018
Days to maturity	0.02963	0.00187	-0.02657	0.04144	0.00667	0.13486	-0.01319	0.17180	0.01217	-0.066
No. of clusters plant^{-1}	0.02056	0.00126	-0.02564	0.01351	0.02046	0.61636	-0.02842	0.31375	-0.1394	0.028
No. of pod Plant^{-1}	0.01567	0.00440	-0.01766	0.00845	0.01906	0.66170	-0.02810	0.36332	-0.1977	-0.021
Pod length (cm)	0.01815	-0.00162	-0.01343	0.01366	0.01453	0.46455	-0.04002	0.36983	-0.1298	-0.014
No. of seed pod^{-1}	0.01380	-0.00288	-0.01374	0.01593	0.01436	0.53804	-0.03313	0.44682	-0.1344	-0.025
100 seed weight (g)	0.00140	0.00397	0.00257	-0.00197	0.01116	0.51213	-0.02033	0.23511	-0.2555	-0.029
Protein percentage	0.00876	0.03760	-0.00009	0.02176	0.00288	0.09442	-0.01212	0.14981	-0.0318	-0.1132

Residual effect 0.18

4. CONCLUSION

The study revealed significant genetic variation across all traits. High heritability in plant height, number of clusters, pod length, seed number, 100-seed weight, and protein%. Traits like plant height, clusters, 100-seed weight, protein percentage, and seed yield showed high-heritability and genetic advance. Seed yield correlated with most traits except plant height, primary branches, flowering time, maturity, and protein percentage. Path-analysis identified pod number and seeds pod^{-1} as key yield determinants, supporting indirect selection for pod-length, 100-seed weight, flowering time, and protein percentage.

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