



Genetic Variability, Character Association and Path Analysis for Various Characters in Mungbean [*Vigna radiata* (L.) Wilczek]

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Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

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ABSTRACT

In order to estimate the genetic variability parameters, characters association and path analysis for the various traits, thirty-five genotypes of mungbean were evaluated during *Kharif* season 2023 at the Research Farm of Agricultural Research Sub-Station, Nagaur (Rajasthan) using a randomized block design (RBD) with three replications. Based on the results, there were significant differences in the mean sum of square resulting from genotypes for each trait studied, indicating that the genotypes were genetically distinct. The PCV values was higher than GCV values for all the characters which reflect the impact of environment on the expression of traits. The estimates of GCV and PCV were higher for number of branches, number of pods per plant and seed yield. Highest heritability estimates were recorded for all the traits. High genetic advance as a percentage of mean along with high heritability was observed for plant height, number of branches, number of pods per plant, 1000 seed weight and seed yield. The correlation of seed yield was positive and significant at phenotypic and genotypic level with characters *viz.*, number of branches, number of pods per plant and number of seeds per pod. Path analysis revealed that at phenotypic level, highest positive direct effect on seed yield was observed for number of pods per plant followed by days to 50% flowering, number of seeds per pod, pod length and number of branches. At genotypic level, highest direct positive effect on seed yield were observed for number of pods per plant followed by days to 50% flowering, number of seeds per pod and plant height.

Keywords: Correlation; genetic advance; heritability; mungbean and path analysis.

1. INTRODUCTION

Mungbean [*Vigna radiata* (L.) Wilczek] is an important annual pulse crop. It has chromosome number $2n = 2x = 22$, which is diploid [1]. Its genomic size is 579 Mb. It is also known as moong, green gram, green soy, green bean, mash bean and golden gram [2]. It is believed to originated from the subcontinent of India [3]. Mungbean cultivation can enhance the chemical, biological and physical qualities of soil by biologically fixing atmospheric nitrogen [4]. In terms of area and production, Rajasthan leads among the states with 46% and 45% respectively. Madhya Pradesh follows with 9% and 14%, Maharashtra with 9% and 8%, Karnataka with 9% and 6%, Odisha with 5% and 4%, Bihar with 4% and 5%, Tamil Nadu with 4% and 3%, Gujarat with 3% and 4%, Andhra Pradesh with 3% for both and Telangana with 2% for both. Mungbean cultivation covers 5.50 million hectares, yielding an average of 3.17 million tonnes and 570 kg/ha of productivity [5]. Genetic variability within the various characters that contribute to yield is a crucial criterion for improving yield; yet, in highly self-pollinated crops such as mungbean, natural variation is restricted, meaning that selection opportunities are limited. The presence and degree of genetic diversity for yield and traits that contribute to yield in the breeding material determines the effectiveness of selection [6]. Selection of superior parents with higher heritability and genetic advance for any quantitative trait is a

necessary precondition for any yield improvement program [7]. An effective method for describing the strength and degree of relationship between important plant traits is correlation coefficient analysis. It also offers fundamental selection criteria and provide to directional model based on yield and its components in the field experiments. Yet the information it supplies about the nature of association is often incomplete. Path coefficient analysis is a powerful statistical method specifically made to measure how various components interact and influence seed yield both directly and indirectly. With this method, yield attributing characters may be ranked and particular traits that result in a particular connection can be headed [8]. An understanding of the contribution of various character to seed yield is provided by correlation and path studies [9]. Therefore, the objective of the present research is to assess the genetic variability, heritability, genetic advance, correlation and path analysis with respect to different desirable characters in the elite set of AVT genotypes of mungbean. This will be helpful in the identification of promising lines for the hybridization program and enable the investigation of mungbean quality and high yield potential.

2. MATERIALS AND METHODS

Thirty-five genotypes of mungbean were assessed during the *Kharif* season of 2023, the

genotypes of mungbean were assessed using a randomized block design (RBD) with three replications at the Research Farm of Agricultural Research Sub-Station, Nagaur (Rajasthan). At the experimental site, the ground water had a salinity with a PH 7.8, an electrical conductivity of 5.7 ds m^{-1} and a total dissolved solids (TDS) of 4500 mg/l . It contained 0.55% organic carbon. Each genotype was sown in a $4.0 \times 1.80 \text{ m}^2$ plot with six rows that were 30 cm apart from one another. Plants were kept 10 cm apart from one another. Ten plants were chosen at random from each genotype and replication to recorded observations at various stages of crop growth on characteristics such as plant height (cm), number of branches, number of pods per plant, pod length (cm), number of seeds per pod and seed yield (kg/ha). However, observations on days to 50% flowering, days to maturity and 1000 seed weight (g) were recorded on a plot-by-plot basis. All the recommended package of practices for mungbean was followed to raise a healthy crop. To find the genotypic and phenotypic coefficients of variation [10] and broad sense heritability [11], the data were put *via* analysis of variance [12]. The estimation of the genotypic and phenotypic correlation coefficients followed the methodology of Singh and Choudhary [13] and the formula provided by Johnson et al. [14]. Path coefficient analysis was used to assess the direct and indirect impacts of various characters on yield and its analysis suggested by Wright [15] and Dewey and Lu [16] further explanation.

3. RESULTS AND DISCUSSION

3.1 Genetic Variability Parameters

For each trait under investigation, the mean sum of squares due to genotypes revealed significant differences, indicating that the genotypes were genetically distinct (Table 1). This shows that there is enough scope in the current gene pool to choose promising lines for seed yield and its contributing characters. It suggests that there is a lot of scope for development in mungbean by selecting for various characters. The genetic variability parameters such as genotypic coefficient of variation, phenotypic coefficient of variation, heritability and genetic advance as percentage of mean for the traits are presented in Table 2. The PCV values was higher than GCV values for all the traits which reflect the impact of environment on the expression of traits. These outcomes concur with the research conducted by Siddique et al. [17] and Makeen et al. [18]. The estimates of GCV and PCV were

higher for number of branches, number of pods per plant and seed yield; moderate for pod length and 1000 seed weight; lowest for days to 50% flowering and days to maturity. Plant height was showed moderate GCV and highest PCV. Number of seeds per pod was showed low GCV and moderate PCV. Similar findings have been made by Hemavathy et al. [19] found maximum PCV and GCV values for seed yield and number of pods per plant. Anand et al. [20] reported high GCV and PCV values for number of pods per plant, seed yield per plant and a low genotypic co-efficient of variation for days to 50 per cent flowering and days to maturity. Desai et al. [21] in mungbean and reported high PCV and GCV values for seed yield per plant and number of pods per plant. Highest heritability estimates were recorded for all the traits. Singh et al. [22] reported high broad sense heritability for the all characters. The highest genetic advance as percentage of mean was observed for plant height, number of branches, number of pods per plant, 1000 seed weight and seed yield. The characters such as days to 50% flowering, days to maturity, pod length and number of seeds per pod were showed moderate genetic advance as percentage of mean. In the current study, high genetic advance as a percentage of mean along with high heritability was observed for plant height, number of branches, number of pods per plant, 1000 seed weight and seed yield. The combination of high heritability and genetic advance suggested that selection for these traits could be effective. Nand and Anuradha [23] reported high heritability coupled with high genetic advance over mean for number of pods per plant, number of seeds per pod and seed yield per plant.

3.2 Correlation Coefficient Analysis

For the majority of the traits, the genotypic correlation coefficients were generally higher than the corresponding phenotypic correlation coefficients (Table 3). This suggests that genetic variance predominates in the expression of traits and that the environment has a masking effect on the overall expression of traits. At the phenotypic and genotypic levels, the number of branches, number of pods per plant and seeds per pod exhibited a positive and statistically significant association with seed yield. Days to 50% flowering was exhibited positive and significant association with days to maturity and plant height at genotypic and phenotypic levels. Number of branches was exhibited positive and significant association with number of pods per

Table 1. Analysis of variance for various morphological characters in mungbean

Source of variation	d.f	Mean Sum of Squares								
		Days to 50% flowering	Days to maturity	Plant height (cm)	Number of branches	Number of pods per plant	Pod length (cm)	Number of seeds per pod	1000 seed weight (g)	Seed yield (kg/ha)
Replications	2	2.60	1.41	1.76	0.01	0.62	0.05	0.15	2.99	77.53
Genotypes	34	30.72**	51.08**	670.28**	4.30**	150.47**	2.47**	4.12**	105.66**	107039.74**
Error	68	1.46	2.64	17.99	0.07	3.95	0.23	0.48	4.81	1058.57

**Significant at $P = 0.01$

Table 2. Estimation of genetic variability parameters for various morphological characters in mungbean

Characters	Range	Mean	Genotypic coefficient of variation (%)	Phenotypic coefficient of variation (%)	Heritability (%)	Genetic advance as percentage of mean
Days to 50% flowering	37.00-48.00	41.60	7.51	8.05	86.96	14.42
Days to maturity	71.33-85.00	76.18	5.28	5.69	85.93	10.07
Plant height (cm)	44.67-95.36	74.53	19.79	20.59	92.36	39.17
Number of branches	2.13-6.60	3.96	29.97	30.74	95.04	60.19
Number of pods per plant	20.06-44.85	30.36	23.02	23.93	92.50	45.60
Pod length (cm)	6.34-10.33	7.99	10.81	12.40	76.01	19.42
Number of seeds per pod	7.70-13.40	11.53	9.55	11.30	71.39	16.62
1000 seed weight (gm)	28.62-55.10	37.52	15.45	16.52	87.47	29.77
Seed yield (kg/ha)	250.03-850.00	522.63	35.96	36.50	97.09	73.00

Table 3. Genotypic and phenotypic correlation coefficients between various morphological characters in mungbean

Characters		Days to 50% flowering	Days to maturity	Plant height (cm)	Number of branches	Number of pods per plant	Pod length (cm)	Number of seeds per pod	1000 seed weight (g)	Seed yield (kg/ha)
Days to 50% flowering	r _g	1	0.845**	0.434**	0.026	0.100	0.102	0.015	-0.099	0.171
	r _p	1	0.724**	0.397**	0.020	0.093	0.064	0.060	-0.080	0.158
Days to maturity	r _g		1	0.376**	0.007	0.168	0.079	-0.049	0.046	0.106
	r _p		1	0.321**	0.008	0.141	0.076	-0.071	0.016	0.094
Plant height (cm)	r _g			1	0.108	0.134	0.328**	0.092	0.244*	0.153
	r _p			1	0.132	0.195*	0.338**	0.183	0.291**	0.185
Number of branches	r _g				1	0.311**	-0.084	0.280**	0.109	0.298**
	r _p				1	0.326**	0.002	0.289**	0.141	0.314**
Number of pods per plant	r _g					1	0.090	0.142	0.228*	0.889**
	r _p					1	0.136	0.214*	0.279**	0.886**
Pod length (cm)	r _g						1	0.208*	0.720**	0.079
	r _p						1	0.254**	0.668**	0.115
Number of seeds per pod	r _g							1	0.254**	0.305**
	r _p							1	0.308**	0.318**
1000 seed weight (gm)	r _g								1	0.136
	r _p								1	0.170

*Significant at $P = 0.05$ and **Significant at $P = 0.01$

Table 4. Direct (diagonal) and indirect (non-diagonal) effects of various morphological characters on seed yield in mungbean at genotypic (G) and phenotypic (P) levels

Characters		Days to 50% flowering	Days to maturity	Plant height (cm)	Number of branches	Number of pods per plant	Pod length (cm)	Number of seeds per pod	1000 seed weight (g)	Correlation with seed yield (kg/ha)
Days to 50% flowering	G	0.3578	-0.2866	0.0045	-0.0010	0.0906	-0.0022	0.0028	0.0049	0.171
	P	0.1497	-0.0933	-0.0045	0.0001	0.0827	0.0037	0.0084	0.0115	0.158
Days to maturity	G	0.3022	-0.3393	0.0039	-0.0003	0.1528	-0.0017	-0.0089	-0.0023	0.106
	P	0.1084	-0.1288	-0.0036	0.0001	0.1257	0.0044	-0.0099	-0.0023	0.094
Plant height (cm)	G	0.1553	-0.1274	0.0104	-0.0043	0.1218	-0.0070	0.0166	-0.0120	0.153
	P	0.0595	-0.0413	-0.0113	0.0002	0.1747	0.0198	0.0257	-0.0418	0.185
Number of branches	G	0.0093	-0.0024	0.0011	-0.0400	0.2825	0.0018	0.0506	-0.0054	0.298**
	P	0.0031	-0.0010	-0.0015	0.0014	0.2913	0.0001	0.0405	-0.0203	0.314**
Number of pods per plant	G	0.0356	-0.0570	0.0014	-0.0124	0.9091	-0.0019	0.0257	-0.0112	0.889**
	P	0.0139	-0.0181	-0.0022	0.0005	0.8939	0.0079	0.0299	-0.0401	0.886**
Pod length (cm)	G	0.0367	-0.0267	0.0034	0.0034	0.0818	-0.0215	0.0376	-0.0354	0.079
	P	0.0096	-0.0098	-0.0038	0.0001	0.1212	0.0585	0.0356	-0.0962	0.115
Number of seeds per pod	G	0.0055	0.0168	0.0010	-0.0112	0.1295	-0.0045	0.1806	-0.0125	0.305**
	P	0.0090	0.0091	-0.0021	0.0004	0.1909	0.0149	0.1400	-0.0443	0.318**
1000 seed weight (gm)	G	-0.0353	-0.0157	0.0025	-0.0044	0.2073	-0.0154	0.0458	-0.0492	0.136
	P	-0.0120	-0.0021	-0.0033	0.0002	0.2490	0.0391	0.0431	-0.1439	0.170

Residual effect at genotypic levels and phenotypic levels are 0.13018 and 0.17176, respectively

plant, number of seeds per pod and seed yield at genotypic and phenotypic levels. Number of pods per plant was exhibited positive and significant association with number of branches, 1000 seed weight and seed yield at genotypic and phenotypic levels. Pod length was displayed positive and significant association with plant height, number of seeds per pod and 1000 seed weight at genotypic and phenotypic levels. Number of seeds per pod was displayed positive and significant association with number of branches, pod length, 1000 seed yield and seed yield at genotypic and phenotypic levels. 1000 seed weight was displayed positive and significant association with plant height, number of pods per plant, pod length and number of seeds per pod at genotypic and phenotypic levels. Similar findings of positive and significant correlation had been reported by Narasimhulu et al. [24], Bhutia et al. [25], Ramakrishnan et al. [26], Sandhiya and Shanmugavel [27] and Varma et al. [28].

3.3 Path Coefficient Analysis

Path coefficient analysis was performed for each morphological trait at both the genotypic and phenotypic levels. Using seed yield as the dependent variable, path coefficient analysis was used to split the correlation coefficient into direct and indirect effects, thereby identifying the relative contributions of different characters to the seed yield. At the phenotypic level, the number of pods per plant, days to 50% flowering, number of seeds per pod, pod length and number of branches showed the strongest positive direct effects on seed yield (Table 4). These findings support the observations made by Ahmad and Belwal [29] and Raj et al. [30]. While highest direct negative effect was recorded for 1000 seed weight, days to maturity and plant height. At genotypic level, highest direct positive effect on seed yield were observed for number of pods per plant followed by days to 50% flowering, number of seeds per pod and plant height. While highest direct negative effect was recorded for days to maturity, 1000 seed weight, number of branches and pod length. The residual effects were low at genotypic level as compared to phenotypic level. Same results were reported by Eswaran and Senthilkumar [31], Mohammed et al. [32] and Mahla et al. [33].

4. CONCLUSION

Considering an aforementioned result, it is clear that direct selection based on number of

branches, number of pods per plant and number of seeds per pod can help in the improvement of seed yield in mungbean.

DISCLAIMER (ARTIFICIAL INTELLIGENCE)

Author(s) hereby declare that NO generative AI technologies such as Large Language Models (Chat GPT, COPILOT, etc.) and text-to-image generators have been used during writing or editing of manuscripts.

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COMPETING INTERESTS

Authors have declared that no competing interests exist.

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