

Estimation of Genetic Variability Parameters and Path Analysis for Seed Yield and Its Characters in Mungbean (*Vigna radiata* (L.) Wilczek)

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ABSTRACT

Thirty-four genotypes of mungbean were assessed during *kharif* 2022 using a Randomized Block Design (RBD) with three replications to estimate the genetic variability parameters, characters association and path analysis for different characters. The results were revealed mean sum of squares due to genotypes showed significant differences for all the characters, suggested that the genotypes were genetically diverse. Thus, it indicates sufficient opportunity for selection for different characters in mungbean improvement. The phenotypic coefficient of variation (PCV) was slightly higher than the corresponding genotypic coefficient of variation (GCV) for all the characters

suggesting the presence of environmental influence to some extent in the expression of these characters. High heritability were observed for all the characters indicated the scope of their improvement through selection. High genetic advance as percentage of mean along with high heritability was found for plant height, number of branches, number of pods per plant, pod length, 1000 seed weight and seed yield. These characters are governed by additive gene effects and therefore, may be enhanced through direct selection. 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, pod length and number of seeds per pod. At phenotypic level, highest positive direct effect on seed yield was found for number of branches, pod length, plant height, number of pods per plant and 1000 seed weight. At genotypic level, highest direct positive effect on seed yield were observed for number of branches, pod length, plant height, days to maturity, number of pods per plant, number of seeds per pod and 1000 seed weight.

Keywords Correlation, Genetic advance, Heritability, Mungbean, Path analysis.

INTRODUCTION

Mungbean [*Vigna radiata* (L.) Wilczek] also known as green gram is an ancient pulse crop widely cultivated in India. It has the diploid chromosome number $2n = 2x = 22$ (Karpechenko 1925) and 579 Mb genome

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size. It is believed to originated from the subcontinent of India (De Candolle 1886). Mungbean is a short-day, self-pollinated, warm-season crop, mainly grown in arid and semi-arid regions of India. It needs 22 to 35 °C mean temperature during crop production. It is tolerant to moisture stress and heat stress (Kumar *et al.* 2024a). Mungbean is considered as an outstanding source of protein. The seeds of mungbean contains protein (24-28%), oil (1.0- 1.5%), ash (4.5–5.5%), fiber (3.5-4.5%) and carbohydrates (62–65%) on dry weight basis (Srivastava *et al.* 2024). During 2022-2023, the mungbean production in India was 3.37 million tonnes over an area of 5.5 million hectares with an average seed yield of 570 kg/ha. More than 80% of mungbean production comes from ten major states viz., Rajasthan, Maharashtra, Madhya Pradesh, Karnataka, Bihar, Andhra Pradesh, Odisha, Tamil Nadu, Gujarat and Telangana (Anonymous 2022-23). The success of selection depends upon the presence and extent of genetic variability for yield and yield related characters in the breeding material (Adevale *et al.* 2010). Selection of superior parents with stronger heritability and genetic advance for any quantitative trait is a necessary prerequisite for any yield improvement program. (Khan *et al.* 2005). The correlation coefficient provides information about inter association among yield and its related characters. The seed yield in mungbean like in other crops has a very complex existence because its expression depends upon several other plant characters which have a positive and negative correlation with yield and among themselves. The observed correlation among yield and its related characters is the net outcome of the direct and indirect effects of the component character through other yield features. The total correlation coefficient between yield and its related characters may sometimes be misleading, as it may be an over or under estimate of its association with other characters (Karim *et al.* 2014). In these cases, direct selection on the basis of correlated response may not be fruitful. For critical evaluation, the correlation coefficient need to be split into direct and indirect effects using path coefficient analysis since, many characters affect a given character. Thus, the correlation and path coefficients in combination can give a better insight into cause and effect relationship between different pairs of characters (Srivastava *et al.* 2024). Therefore, the current study was conducted

to assess the genetic variability, correlation and path analysis in relation to various desirable characters in an elite set of IVT genotypes of mungbean, which will aid in isolating promising lines for hybridization programs and exploring high yield potential and quality of mungbean.

MATERIALS AND METHODS

In the *kharif* season of 2022, thirty four mungbean genotypes were evaluated at the Research Farm of Agricultural Research Sub-Station, Nagaur (Rajasthan). The genotypes of mungbean were assessed using a Randomized Block Design with three replications. Each genotype was sown in a 4.0 × 2.40 m² plot with eight rows spaced 30 cm away from one another. Plants were spaced 10 cm apart from one another. A random selection of ten plants was made from each genotype and replication for recording observations on traits such as plant height (cm), number of branches, number of pods per plant, length of pod (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. To grow a healthy crop, all the recommended package of practices for mungbean was followed. The data were subjected to analysis of variance (Panse and Sukhatme 1985) to determine genotypic coefficients of variation and phenotypic coefficients of variation (Burton and Devane 1953), broad sense heritability (Hanson *et al.* 1956). The genotypic and phenotypic correlation coefficients were calculated as defined by Singh and Choudhary (1985) and as per formula given by Johnson *et al.* (1955). The direct and indirect effects were estimated through path coefficient analysis as advocated by Wright (1921) and expanded by Dewey and Lu (1959).

RESULTS AND DISCUSSION

Development of high yielding varieties of mungbean needs a deep knowledge of the existing genetic variation for seed yield and its component characters. The mean sum of squares due to genotypes showed significant differences for all the characters in current study, suggested that the genotypes were genetically

Table 1. Analysis of variance for different characters in mungbean.

Source of variation	df	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	2.04	1.66	15.65	0.08	10.15	0.09	0.13	0.88	9238.79
Genotypes	33	31.88**	54.98**	767.63**	6.23**	154.83**	2.55**	4.41**	107.81**	126716.47**
Error	66	1.29	1.94	11.30	0.03	10.94	0.04	0.22	0.49	4842.90

** significant at 1% level.

diverse (Table 1). Thus, it indicates sufficient opportunity for selection for different characters in mungbean improvement. The mean performance of different

genotypes for different characters are presented in Table 2 revealed that days to maturity ranged from 71.00 to 84.67 days with overall mean is 75.77 and,

Table 2. Mean values of different characters in mungbean genotypes.

Genotypes	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)
KM-22-90	45.67	79.67	96.33	6.40	40.60	7.20	10.90	36.08	590.28
KM-22-91	47.67	84.00	75.33	7.70	27.72	8.17	13.40	35.05	815.97
KM-22-92	37.67	75.33	44.33	3.63	38.67	7.23	11.77	42.19	552.09
KM-22-93	40.67	72.67	56.67	4.73	35.58	9.30	10.73	46.79	583.33
KM-22-94	46.67	80.33	71.33	4.40	41.60	7.52	10.62	39.99	565.97
KM-22-95	41.67	72.67	56.00	4.23	39.60	6.73	11.50	33.62	510.41
KM-22-96	37.67	73.67	72.00	6.50	42.46	6.50	11.79	31.93	850.69
KM-22-97	43.67	82.00	94.67	2.40	26.60	8.50	11.69	50.41	666.65
KM-22-98	48.67	84.67	96.67	4.33	30.64	6.77	12.03	33.31	503.46
KM-22-99	39.33	73.00	82.33	3.23	32.52	9.43	12.43	55.10	849.65
KM-22-100	39.33	71.00	89.33	3.40	25.64	8.27	10.87	40.62	811.80
KM-22-102	39.00	75.33	83.67	3.23	31.39	8.60	8.71	41.15	899.31
KM-22-103	42.00	73.67	89.67	3.37	23.53	8.30	10.93	36.42	744.79
KM-22-104	41.67	76.33	71.33	4.17	22.54	8.77	12.27	37.65	624.31
KM-22-105	39.67	71.33	72.67	5.50	29.53	7.27	11.97	31.52	944.44
KM-22-106	38.67	71.00	65.33	3.23	22.65	7.17	12.13	28.62	566.32
KM-22-107	41.67	77.00	49.33	3.97	43.62	8.43	11.67	32.54	788.19
KM-22-108	39.67	73.00	55.33	4.83	24.67	7.07	10.63	31.76	559.03
KM-22-109	45.67	79.67	74.67	2.53	31.67	8.47	9.53	30.29	437.50
KM-22-110	42.33	73.33	72.67	3.03	35.46	7.50	12.40	32.27	694.44
KM-22-111	42.67	73.00	92.33	2.23	38.62	7.40	12.00	30.75	500.00
KM-22-112	41.00	74.67	91.33	2.50	21.64	9.43	12.73	45.71	726.39
KM-22-113	42.33	73.00	86.33	3.83	31.45	8.20	12.13	35.89	518.40
KM-22-114	48.67	83.33	84.00	2.73	20.73	6.33	7.70	43.48	241.32
KM-22-115	38.67	75.67	80.33	3.33	38.69	8.40	10.83	39.28	821.18
KM-22-116	39.67	72.67	60.67	3.00	29.65	7.90	12.17	36.12	859.38
KM-22-118	45.00	82.33	106.00	4.20	27.67	8.57	12.20	36.90	305.55
KM-22-119	38.00	71.67	47.67	7.93	45.52	10.33	13.33	40.82	1227.09
KM-22-120	41.67	71.33	88.00	5.43	22.65	7.43	12.60	44.56	775.00
KM-22-121	45.33	73.67	68.33	2.13	26.67	8.67	12.10	36.79	293.74
KM-22-122	47.67	83.00	82.00	3.33	25.61	7.60	11.25	34.77	447.91
KM-22-123	41.67	71.67	81.33	3.40	22.67	8.90	10.89	36.75	639.94
KM-22-124	40.67	72.67	48.00	4.37	27.57	7.37	13.10	32.89	534.73
KM-22-125	44.67	78.00	79.00	4.57	30.64	8.13	12.47	36.96	506.95
Overall mean	42.26	75.77	75.44	4.05	31.07	8.00	11.57	37.62	645.77
Minimum	37.67	71.00	44.33	2.13	20.73	6.33	7.70	28.62	241.32
Maximum	48.67	84.67	106.00	7.93	45.52	10.33	13.40	55.10	1227.09

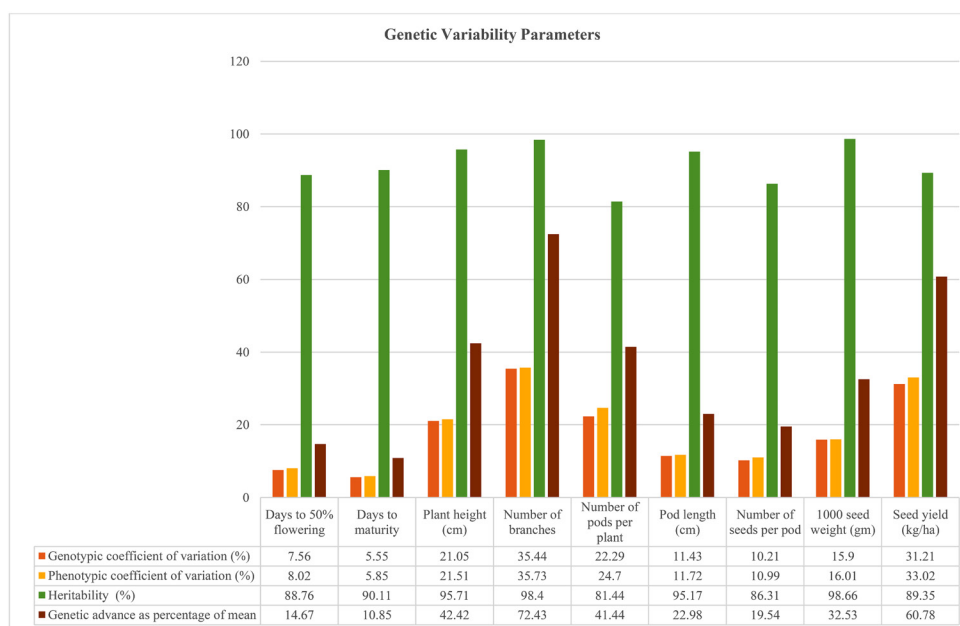


Fig. 1. Estimation of genetic variability parameters for different characters in mungbean.

KM-22-100 and KM-22-106 genotype showed early maturity. Plant height ranged from 44.33 to 106.00 cm. Number of pods per plant ranged from 20.73 to 45.52 with 31.07 overall mean. Number of branches, number of pods per plant, pod length and number of seeds per pod are considered as the most important yield component and are directly concerned with final yield in mungbean crop. These characters were showed a great variation in their mean values. Similar results were also observed by Singh *et al.* (2022).

In the current study, the estimation of genotypic coefficients of variation, phenotypic coefficients of variation, heritability and genetic advance as percentage of mean of different characters in mungbean genotypes are presented in Fig. 1. Figure showed that the phenotypic coefficient of variation (PCV) was slightly higher than the corresponding genotypic coefficient of variation (GCV) for all the characters suggesting the presence of environmental influence to some extent in the expression of these characters. These findings were also reported by Makeen *et al.* (2007). High PCV and GCV were observed for plant height, number of branches, number of pods per plant and seed yield. Similar results were also observed by Anand *et al.*

(2016), Desai *et al.* (2020), Kumar (2023), Prasanthi *et al.* (2024) and Kumar *et al.* (2024b). The estimation of heritability determines the heritable portion of this variation. Therefore, heritability estimates provide a clear idea of potential gains through selection. High heritability were observed for all the characters indicated the scope of their improvement through selection. Similar outcome was also observed by Bhutia *et al.* (2016), Shiv *et al.* (2017) and Singh *et al.* (2021). Maximum genetic advance as percentage of mean along with high heritability was observed for plant height, number of branches, number of pods per plant, pod length, 1000 seed weight and seed yield. These traits are governed by additive gene effects and therefore, may be improved through direct selection. Similar outcomes were observed by Tiwari *et al.* (2014), Choudhary *et al.* (2017) and Kumar *et al.* (2024b).

The correlation coefficient provides a measure of the relationship between characters and serves to assess the chance for mutual improvement of two characters by common selection. The estimates of genotypic and phenotypic correlation coefficients between different characters of mungbean genotypes

Table 3. Genotypic and phenotypic correlation coefficients between different 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	rg	1	0.841**	0.454**	-0.066	-0.217*	-0.230*	-0.196*	-0.102	-0.635**
	rp	1	0.762**	0.411**	-0.068	-0.185	-0.213*	-0.170	-0.097	-0.574**
Days to maturity	rg		1	0.401**	0.029	-0.056	-0.174	-0.238*	0.040	-0.433**
	rp		1	0.371**	0.025	-0.047	-0.173	-0.205*	0.042	-0.392**
Plant height (cm)	rg			1	-0.230*	-0.358**	0.006	-0.158	0.196*	-0.205*
	rp			1	-0.218*	-0.346**	-0.001	-0.143	0.185	-0.190
Number of branches	rg				1	0.364**	-0.025	0.357**	-0.123	0.465**
	rp				1	0.336**	-0.026	0.332**	-0.122	0.436**
Number of pods per plant	rg					1	0.003	0.089	-0.111	0.329**
	rp					1	-0.009	0.073	-0.097	0.254*
Pod length (cm)	rg						1	0.231*	0.485**	0.389**
	rp						1	0.213*	0.475**	0.376**
Number of seeds per pod	rg							1	-0.072	0.306**
	rp							1	-0.060	0.265**
1000 seed weight (gm)	rg								1	0.185
	rp								1	0.180

*, ** significant at 5% and 1% level, respectively.

are presented in Table 3. 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, pod length and number of seeds per pod. Days to 50% flowering was showed positive and significant correlation with days to maturity and plant height at genotypic and phenotypic levels. Number of branches was showed positive and significant correlation with number of pods per plant, number of seeds per pod and seed yield at genotypic and phenotypic levels. Number of pods per plant was showed positive and significant correlation with number of branches and seed yield at genotypic and phenotypic levels. Pod length was showed positive and significant correlation with number of seeds per pod, 1000 seed weight and seed yield at genotypic and phenotypic levels. Number of seeds per pod was showed positive and significant correlation with number of branches, pod length, 1000 seed yield and seed yield at genotypic and phenotypic levels. 1000 seed weight was showed positive and significant correlation with pod length at genotypic and phenotypic levels. Similar findings of positive and significant correlation had been reported by Hemavathy *et al.* (2015), Bhutia *et al.* (2016), Kate *et al.* (2017), Ahmad and Belwal (2020) and Salman *et al.* (2023).

The phenotypic and genotypic correlations were

further analyzed by path coefficient analysis, which includes dividing of the correlation coefficients into direct and indirect effects through pathways. Such analysis leads to identification of important component characters useful in indirect selection complex characters like seed yield. Since a character like seed yield is dependent on several mutually related component characters and change in any one of the components is likely to affect the whole network of cause and effect relationship. In the current study, path coefficient analysis was calculated at phenotypic level as well as genotypic level for all the characters. Path coefficient analysis was carried out by taking seed yield as dependent variable to partition the correlation coefficient into direct and indirect effect in order to determine the contribution of various characters towards the seed yield (Table 4). At phenotypic level, highest positive direct effect on seed yield was observed for number of branches, pod length, plant height, number of pods per plant and 1000 seed weight. These findings support the observations made by Raj *et al.* (2022). While highest direct negative effect was recorded for days to 50% flowering, days to maturity and number of seeds per pod. At genotypic level, highest direct positive effect on seed yield were observed for number of branches, pod length, plant height, days to maturity, number of pods per plant, number of seeds per pod and 1000 seed weight. While

Table 4. Direct (diagonal) and indirect (non-diagonal) effects of different 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	-0.75009	0.13021	0.09245	-0.02811	-0.01969	-0.05709	-0.00188	-0.00055	-0.635**
	P	-0.52486	-0.00583	0.0562	-0.02842	-0.01276	-0.05433	0.00039	-0.00393	-0.574**
Days to maturity	G	-0.63107	0.15477	0.08155	0.01247	-0.0051	-0.04324	-0.00229	0.00022	-0.433**
	P	-0.40005	-0.00764	0.05077	0.01071	-0.00322	-0.04427	0.00047	0.0017	-0.392**
Plant height (cm)	G	-0.34063	0.062	0.20357	-0.09848	-0.03245	0.00145	-0.00152	0.00105	-0.205*
	P	-0.21577	-0.00284	0.1367	-0.09166	-0.02382	-0.00028	0.00033	0.00753	-0.190
Number of branches	G	0.04923	0.00451	-0.0468	0.42837	0.033	-0.00632	0.00344	-0.00066	0.465**
	P	0.03552	-0.00019	-0.02983	0.41997	0.02314	-0.00662	-0.00076	-0.00498	0.436**
Number of pods per plant	G	0.16312	-0.00872	-0.07297	0.15614	0.09053	0.00079	0.00086	-0.00059	0.329**
	P	0.0972	0.00036	-0.04727	0.14105	0.06889	-0.00239	-0.00017	-0.00394	0.254*
Pod length (cm)	G	0.17218	-0.02691	0.00118	-0.01088	0.00029	0.24869	0.00223	0.0026	0.389**
	P	0.11162	0.00132	-0.00015	-0.01088	-0.00065	0.25545	-0.00049	0.01935	0.376**
Number of seeds per pod	G	0.14689	-0.03682	-0.03217	0.15312	0.00806	0.05753	0.00962	-0.00039	0.306**
	P	0.08908	0.00156	-0.01954	0.13947	0.00503	0.05447	-0.00229	-0.00245	0.265**
1000 seed weight (g)	G	0.0765	0.00623	0.03992	-0.05252	-0.01004	0.12051	-0.00069	0.00537	0.185
	P	0.05066	-0.00032	0.02527	-0.0514	-0.00666	0.12135	0.00014	0.04073	0.180

Residual effect at genotypic levels and phenotypic levels are 0.30293 and 0.41859, respectively.

Bold values indicate direct effect.

highest direct negative effect was recorded for days to 50% flowering. The residual effects were low at genotypic level as compared to phenotypic level. Same findings were observed by Mohammed *et al.* (2020) and Mahla *et al.* (2022).

CONCLUSION

In previous discussion it can be concluded that the high magnitude of the phenotypic variances than genotypic variances showing the pronounced effects of environment. Higher heritability coupled with high genetic advance as percentage of mean showed additive effects and more gain of selection in next generations. Improvement in seed yield of mungbean could be brought through selection of component characters directly concerned with final yield such as number of branches, number of pods per plant, pod length and number of seeds per pod.

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