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RESEARCH PAPER

Genetic variability and correlation studies on seed yield and yield components in advanced breeding lines of mungbean [*Vigna radiata* (L.) Wilczek.]

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Abstract: The present investigation was undertaken to evaluate eighteen diverse mungbean [*Vigna radiata* (L.) Wilkeezek] advanced breeding lines developed at AICRP on MULLaRP for the estimation of genetic variability, heritability and genetic advance, correlation coefficient for eleven quantitative traits and their association level with seed yield. The genotypes differed significantly for all characters under study. High genotypic and phenotypic coefficient of variation was observed for seed yield, number of pods per plant, branches per plant and clusters per plant. Association analysis indicated that, number of branches per plant, number of clusters per plant, number of pods per plant and chlorophyll content had positive correlation with seed yield. Maximum direct effect on seed yield was observed through number of branches per plant, the number of clusters per plant and dry matter. From the present findings it could be suggested that on the basis of genetic parameter correlation and path analysis, number of branches per plant, number of clusters per plant and number of pods per plant should be given topmost priority while formulating a selection strategy for improvement in seed yield of mungbean.

Key words: Correlation, Genetic Variability, Heritability, Mungbean, Path analysis, Selection

Introduction

Mungbean (*Vigna radiata* L.) holds significant importance as a pulse crop in India and is believed to have originated in this country. It is a short-duration legume crop primarily cultivated as a fallow crop in rotation with rice. This rotation is preferred due to its ability to enhance soil nitrogen content. India stands as the leading producer, contributing to over 70 per cent of the world's mungbean production.

Mungbean, a key player in India's *kharif* and summer pulses, boasts a protein content of approximately 25 per cent. It serves as an exceptional and cost-effective source of high-quality, easily digestible protein, surpassing meat, fish and eggs. Beyond its role in providing dietary proteins and income for resource-limited farmers, food legumes like mungbean play a vital role in sustainable crop production. Mungbean becomes an integral part of cropping systems for maintaining soil health by fixing atmospheric nitrogen, accessing water and nutrients from deeper soil layers and enriching the soil through the addition of organic matter *via* leaf litter.

Seed yield in mungbean, much like in other crops, is a multifaceted trait influenced by various contributing factors. Understanding the genetic variability among these factors is a crucial aspect of crop improvement. Correlation coefficient analysis serves as a robust technique for assessing the degree and extent of relationships between key plant characteristics. It offers essential criteria for selection and guides the development of a model centered on yield and its components in field experiments. In contrast, path coefficient analysis is a highly effective statistical method tailored to quantify the interrelationships among different components and their direct and indirect impacts on seed yield. This technique allows for the ranking of yield contributing characteristics and identification of specific traits responsible for observed correlations (Rao *et al.,* 2006). It's important to note that earlier studies on correlation and path analysis in mungbean, have resulted in consistent results, varying with the materials and environmental conditions used (Yaqoob *et al.,* 1997).

Correlation and path studies provide valuable insights into the contributions of different traits to seed yield, as emphasized by Vandana and Dubey in 1993. Therefore, the present study was initiated to evaluate genetic variability, heritability, genetic advance, as well as correlation and path analysis regarding various desirable traits in 18 different genotypes of mungbean. This research aims to identify promising lines for hybridization programs and uncover the high yield potential and quality of mungbean.

Material and methods

The experimental materials comprised of 18 mungbean genotypes. The experiment was laid out in a randomized complete block design (RCBD) with two replications in experimental fields Main Agricultural Research Station, University of Agricultural Sciences, Dharwad during *summer* 2022-23. Spacing between rows and plant to plant was kept 30 cm and 10 cm respectively. All the recommended cultural practices were followed up to harvest. At maturity data were recorded for plant height, days to 50% flowering, days to maturity, number of branches per plant, number of clusters per plant, number of pods per plant, number of pods per plant, pod length number of seeds per pod, 100 seed weight, single plant yield and seed yield per plot on five randomly selected plants from four middle rows of each genotype Standard statistical

Table 1. Analysis of variance for yield and its components in mungbean genotypes

Source of Variation	D. f	Days to50 per cent flowering	Days to maturity	Plant height	No. of branches per plant	No. of clusters per plant	No.of pods per plant	Pod length	No. of seeds /pod	Seed yield perplant	100 seeds weight	Seed yield per plot
Replication	1	1.36	16	0.007	3.87	0.126	0.78	0.346	0.034	0.080	1.071	96
Genotype	17	4.60**	15.58**	18.478*	0.295*	2.22**	107.60**	0.808**	0.941**	3.106**	0.447**	120334*
Error	17	0.41	4.41	7.48	0.175	0.92	1.83	0.00014	1.18	0.035	0.065	104

procedure was used for the analysis of variance, genotypic and phenotypic coefficients of variation (Burton, 1952) and heritability (Hanson *et al.* 1956). The genotypic and phenotypic correlation coefficients were computed using genotypic and phenotypic variances and covariances. The path co-efficient analysis was done according to the method by Dewey and Lu (1959).

Results and discussion

In the present study the analysis of variance revealed highly significant differences for all eleven characters among the genotypes, indicating existence of sufficient variation in the material studied. (Table 1)

The magnitude of phenotypic co-efficient of variation was higher than genotypic coefficient of variation for all the traits under study (Table 3) These results are accordance with the findings of Siddique *et al.,* (2006) and Makeen *et al.,* (2007). Traits like number of branches (34.65%, 23.60%), clusters per plant (23.64%, 32.60%), number of pods per plant (25.24%, 32.06 %), seed yield per plant (22.86%, 30.54 %) and yield per plot (31.43%, 29.36%) reported high PCV and GCV suggesting substantial amount of genetic variability. Pod length recorded moderate PCV and high GCV. A moderate estimate of PCV was exhibited by plant height and 100 seed weight. A moderate estimate of GCV was exhibited by number of seeds per plant and 100 seed weight. Similar findings have been made by Desai *et al.* (2020) in mungbean and reported high PCV and GCV values for seed yield per plant, number of pods per plant and number of clusters per plant. Hemavathy *et al.* (2015) reported high PCV and GCV values for seed yield, number of pods per plant and clusters per plant. Anand *et al.* (2016) 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 (Table 2).

Branches per plant (90.81 per cent, 64.81 per cent), number of clusters per plant (92.30 per cent, 44.96 per cent), number of pods per plant (95.88 per cent, 49.85 per cent), pod length (91.67 per cent, 20.47 per cent), seed yield per plant(90.21 per cent, 42.48 per cent) and seed yield per plot (88.50 per cent, 50.05 per cent) recorded high estimates heritability coupled with high genetic advance over mean. Singh *et al.*(2021) reported high broad sense heritability for the all characters and moderate heritability for days to maturity. Nand and Anuradha (2013) 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. Varma *et al.* (2018) reported high heritability and genetic advance for plant height, pods per plant, days to 50 per cent flowering and maturity indicating an additive gene effect. The combination of high heritability and genetic advance suggested that selection for these traits could be effective.

Correlation studies indicated that, seed yield per plant was significantly positively associated with number of branches per plant (0.628) , number of clusters per plant (0.695), number of pods per plant (0.962), chlorophyll content (0.628) and significant negative correlation with days to maturity (-0.485). These results are in confirmation with Raje and Rao (2000) for branches per plant, clusters per plant, pods per plant, pods per cluster and seeds per pod. Sandhiya and Shanmugavel (2018) reported that seed yield per plant had a positive significant correlation with the traits of number of pods per plant, number of clusters per plant. Thus, these traits should be given due importance, while formulating the selection procedure for improving the seed yield (Table 3).

The correlation values decide only the nature and degree of association existing between pairs of characters. A character like seed yield is dependent in several mutually associated

Table 2. Estimation of genetic variability parameters for seed yield and its components in green gram

Characters	Mean	Range		Coefficient of variation		Heritability (h^2)(%)	GA	GAM
		Min.	Max.	PCV (%)	GCV (%)			
Days to50 per cent flowering	44.84	42.25	47.75	3.11	2.62	71.18	2.07	4.56
Days to maturity	70.97	69.25	77.75	3.76	3.46	84.81	4.73	6.56
Plant height (cm)	29.78	23.92	34.83	10.07	9.63	91.34	5.61	18.95
No. of branches	2.94	2.17	4.28	34.65	33.02	90.81	2.41	64.81
No. of clusters	5.26	3.83	6.59	23.64	22.71	92.30	2.25	44.96
No. of pods	18.46	13.03	29.37	25.24	24.71	95.88	9.47	49.85
Pod length (cm)	8.13	7.01	9.34	10.84	10.38	91.67	1.59	20.47
No. of seeds/ pod	9.63	8.7	10.88	8.31	7.78	87.68	1.44	15.01
100 seed weight (gm)	4.52	3.76	5.96	12.69	10.53	70.65	0.85	18.74
Seed yield / plant (gm)	5.61	3.09	8.73	22.86	21.71	90.21	2.29	42.48
Seed yield /plot (kg/ha)	514.85	174.2	803.75	27.46	25.83	88.50	275.32	50.05

Table 3. Estimates of phenotypic correlation coefficients in mungbean

Characters	DFF	DM	PH	NB	NC	NP	PL	NS/P	TW	Chl.	DRM	SY/PNT
DFF	1.000											
DM	0.655*	1.000										
PH	0.400	0.205	1.000									
NB	0.046	-0.167	0.032	1.000								
NC	0.132	-0.049	0.115	0.578*	1.000							
NP	-0.442	-0.315	-0.093	0.566*	0.564*	1.000						
PL	-0.187	0.036	0.014	0.247	0.481*	0.672**	1.000					
NS/P	-0.165	-0.165	-0.353	0.266	0.436	0.478*	0.389	1.000				
TW	-0.297	0.051	-0.344	-0.199	-0.028	-0.178	0.057	0.031	1.000			
Chl.	0.003	-0.127	-0.085	0.606**	0.686**	0.728**	0.534*	0.468*	-0.372	1.000		
DRM	0.349	0.136	0.694**	0.209	0.052	-0.080	-0.101	-0.200	-0.370	0.010	1.000	
SY/PNT	-0.186	-0.485*	-0.4009	0.628**	0.695**	0.962**	0.411	0.518*	0.606	0.628**	-0.050	1.000

Table 4. Direct and Indirect effects for seed yield and its component characters at phenotypic path level

Characters	DFF	DM	PH	NB	NC	NP	PL	SP	TW	Chl.	DRM	r
DFF	-0.5449	-0.0256	-0.0561	0.0282	0.0663	0.2588	-0.0316	-0.0313	0.003	0.0004	0.1459	-0.186
DM	-0.4881	-0.0391	-0.0288	-0.1016	-0.0245	0.1841	0.0061	-0.0314	-0.0005	-0.0176	0.0566	-0.485*
PH	-0.2981	-0.0080	-0.4433	0.0196	0.0577	0.0546	0.0023	-0.0671	0.0035	-0.0118	0.2897	-0.4009
NB	-0.0345	0.0065	-0.0045	0.6094	0.2912	-0.3311	0.0418	0.0506	0.0020	0.0844	-0.0875	0.628**
NC	-0.0981	0.0019	-0.0161	0.3526	0.5032	-0.3298	0.0814	0.0830	0.0003	0.0954	0.0216	0.695**
NP	0.3293	0.0123	0.0131	0.3448	0.2836	0.1054	0.1137	0.0910	0.0018	0.1015	-0.4336	0.9628**
PL	0.1394	-0.0014	-0.0019	0.1505	0.2423	-0.3935	0.1691	0.0739	-0.0006	0.0745	-0.0421	0.411
NS/P	0.1227	0.0065	0.0495	0.1621	0.2198	-0.2800	0.0657	0.1901	-0.0003	0.0651	-0.0835	0.518*
TW	0.2209	-0.0020	0.0483	-0.1208	-0.0144	0.1040	0.0095	0.0060	-0.2098	-0.0518	-0.1545	0.6062
Chl.	-0.0023	0.0050	0.0119	0.3692	0.3447	-0.4265	0.0904	0.0889	0.0037	0.1392	0.0042	0.628**
DRM	-0.2602	-0.0053	-0.0973	-0.1276	0.0260	0.0471	-0.0170	-0.0380	0.0037	0.0014	0.4177	-0.05

Residual effect: 0.103

DM: Days to Maturity, DFF: Days to 50% flowering, NB: No. of Branches per plant, NC: Number of clusters per plant ,PH: Plant height, NP: No. of Pods, NS/P: No. of Seeds /Pod, PL: Pod length(cm), Y/PNT : Yield per plant, TW: 100 Seed weight, Y/PLT: Yield per plot

r – Correlation coefficient of seed yield per plant

component characters and change in any one of the components is likely to affect the whole network of cause and effect of relationship. This in turn might affect the true association of component characters, both in magnitude and direction and tend to vitiate association of yield and yield components. Hence it is necessary to partition the phenotypic correlation of component characters into direct and indirect effects (Biradar *et al.,* 2007).

The phenotypic path coefficient analysis showed that several factors had a high positive direct impact on seed yield per plant. These factors include the number of branches per plant (0.6094), the number of clusters per plant (0.5032) and dry matter (0.4177). Conversely, there was a high negative direct effect on seed yield from factors such as the number of days to 50 per cent flowering (-0.5449) and plant height (-0.4433). Similar results for positive direct effects were observed for number of branches, the number of clusters per plant, the number of pods per plant, pod length and the number of seeds per pod (Ahmad and Belwal, 2019), for days to maturity and plant height (Verma *et al.,* 2018), for days to fifty per cent flowering (Raj *et al.,* 2022), for days to maturity, plant height, chlorophyll content and 100 seed weight Mahla *et al.* (2022). Therefore, these characteristics should be prioritized when selecting mungbean genotypes to enhance productivity (Table 4).

Conclusion

The high estimates of phenotypic and genotypic coefficient of variation (>20%) were found for number of branches, clusters per plant, number of pods per plant, seed yield per plant and yield per plot. High heritability coupled with high genetic advance in per cent of mean was recorded for as branches per plant, number of clusters per plant, number of pods per plant, pod length, seed yield per plant and seed yield per plot. Number of clusters per plant, branches per plant, seeds per pod and pods per plant showed positive and significant correlations and considerable direct positive effects on seed yield. It is concluded that these characters are the most important contributing factors to seed yield and should be used as selection criteria for yield improvement in mungbean. Therefore, selection for seed yield of mungbean, especially among these accessions should be made through the selection for large plants with high number of clusters per plant, branches per plant, pods per plant and seeds per pod.

References

Ahmad S and Belwal V, 2019, Morphological characterization and evaluation of mungbean (*Vigna radiata* (L.) Wilczek) germplasm for various yield attributing traits. *International Journal of Current Microbiology and Applied Sciences*, 9(1): 2319-7706.

Anand G, Anandhi K and Paulpandi V K, 2016, Genetic variability, correlation and path analysis for yield and yield components in F_6 families of green gram [*Vigna radiata* (L.) Wilczek] under rainfed condition. *Electronic Journal of Plant Breeding*, 7(2): 434-437.

Biradar K, Salimath S P M and Ravikumar R L, 2007, Genetic studies in greengram and association analysis. *Karnataka Journal of Agricultural Sciences*, 20: 843-844.

Burton G W and De Vane E M, 1953, Estimating heritability in tall fescue (*Festuca arundinaceae*) from replicated clonal material. *Journal of Agronomy*, 51: 515-518.

Desai V K, Parmar L D, Chaudhary A R and Chaudhary N B, 2020, Genetic variability, correlation, path coefficient and stability analysis for yield and its attributing traits in summer greengram [*Vigna radiata* (L.) Wilczek] accessions. *International Journal of Current Microbiology and Applied Sciences*, 9(6): 2942-2955.

Dewey D R and Lu K, 1959, A correlation and path coefficient analysis of components of crested wheatgrass seed production. *Agronomy Journal*, 51(9): 515-518.

Garg G K, Verma P K, Kesh H and Kumar A, 2017, Genetic variability, character association and genetic divergence for seed quality traits in mungbean [*Vigna radiata* (L.) Wilczek]. *Indian Journal of Agricultural Research*, 51(6): 521-528.

Garg G K, Verma P K, Kesh H and Kumar A, 2017, Genetic variability, character association and genetic divergence for seed quality traits in mungbean [*Vigna radiata* (L.) Wilczek]. *Indian Journal of Agricultural Research*, 51(6): 521-528.

Hanson G H, Robinson H F and Comstock R E, 1956, Biometrical studies of yield in segregating populations of Koren Lependeza. *Journal of Agronomy*, 48(1): 267-282.

Hemavathy A T, Shunmugavalli N and Anand G, 2015, Genetic variability, correlation and path co-efficient studies on yield and its components in mungbean [*Vigna radiata* (L) Wilczek], *Legume Research*, 38(4): 442-446.

Mahla P, Ram M, Dalip, Nehra A and Chawla R, 2022, Study of genetic association and path coefficient in green gram [*Vigna radiata* (L.) wilczek] genotypes. *Biological Forum- An International Journal*,14(2): 766-770.

Makeen K, Garard A, Arif J and Archana K S, 2007, Genetic variability and correlation studies on yield and its components in mungbean (*Vigna radiata* (L). Wilckez). *Journal of Agronomy* 6: 216-218.

Nand M J and Anuradha C , 2013, Genetic variability, correlation and path coefficient analysis for yield and yield components in mungbean (*Vigna radiata* L. Wilczek). *The Journal of Research ANGRAU*, 41:31-39.

Raj K, Varghese S, Jayaswal D, Jayaswall K, Yadav K, Mishra G, Vyas R P, Singh H C, Prakash H G, Singh A N and Kumar S, 2022, Agro-morphological and genetic variability analysis in oat germplasms with special emphasis on food and feed. *Plos one*, 18(2): 0280450.

Raje R S and Rao S K, 2000, Association analysis for yield and its components in mungbean (*Vigna radiata* L. Wilczek). *Legume Research-An International Journal*, *23*(1): 42-48.

Rao C M, Rao Y K and Mohan R, 2006, Genetic variability and path analysis. *Legume Research-An International Journal*, 29(3): 216-218.

Sandhiya V and Shanmugavel S, 2018, Genetic variability and correlation studies in green gram [*Vigna radiata* (L.) Wilczek]. *Electronic Journal of Plant Breeding*, 9(3): 1094-1099.

Siddique M, Faisal M, Anwar M and Shahid I A, 2006, Genetic divergence, association and performance evaluation of different genotypes of mungbean (*Vigna radiata*). *International Journal of Agriulture and Biology*, 6: 793-795.

Singh S P, Chauhan M P, Nath S, Singh V K, Tiwari A, Singh P, Dwivedi D K and Rai V R, 2021, Estimation of genetic variability, heritability and genetic advance in mungbean [*Vigna radiata* (L.) Wilczek] in summer season under late sown condition. *The Pharma Innovation Journal*, 10(6): 1241-1243.

Vandana S K and Dubey D K, 1993, Path analysis in faba bean, *FABIS* Newsletter, 32, 23-23.

Yaqoob M, Malik A J, Malik B A, Khan H U and Nawab K, 1997, Path coefficient analysis in some mungbean (*Vigna radiata* L.). Mutants under rainfed conditions. *Sarhad Journal of Agriculture*, 13(2): 129-133.