Correlation and Path Analysis Studies of Pod Yield and its Component Traits in Mungbean [*Vigna radiata* (L.) Wilczek] Genotypes

Anita[1], S.R. Kumhar[1], Anil Kumar[1], Suchitra[1], Anil Kulheri[1], Pooja Kanwar Shekhawat[1], Giradhari Lal Yadav[1]

10.18805/LR-4906

ABSTRACT

Background: Mungbean is an important pulse crop grown in India. The mungbean is an excellent source of protein (27%) and its essential amino acid comparable with that of soybean and kidney bean. Estimates of correlation coefficient are useful in identifying the component traits which can be used for yield improvement of mungbean. Path coefficient analysis provides a thorough understanding of contribution of various characters by partitioning the correlation coefficient into components of direct and indirect effects. This study aimed to quantify the relationship and contributions of various traits to seed yield.

Methods: The present investigation was undertaken to assess the correlation and path analysis on yield and its components in 38 genotypes of mungbean. The genotypes were raised in randomized block design with three replications during *Kharif* 2019 at Agricultural Research Station Farm, Agriculture University, Jodhpur, Rajasthan.

Result: The experimental results showed that positive correlation and positive direct effect on seed yield were observed for plant height, number of pods per plant, number of seeds per pod and 100 seed weight. Therefore these traits can be used for mungbean improvement program as well as developing high yielding varieties of mungbean.

Key words: Correlation, Mungbean, Path coefficient, Seed yield.

INTRODUCTION

Pulses compliment the daily human diet of Indians along with cereals. They are rich source of proteins with satisfactory proportion of carbohydrates. Among pulses, mungbean [*Vigna radiata* (L.) Wilczek] also known as green gram is an ancient pulse crop widely cultivated in India. It is a diploid species with chromosome number 2n=2x=22 belongs to the family Leguminosae (Fabaceae), sub-family Papilionaceae and botanically recognized as *Vigna radiata* (L.) Wilczek and it is essentially a self-pollinated crop. Mungbean is native of South Asia (India). *Vigna radiata* var. sublobata is the probable progenitor of mungbean. High protein, easy digestibility and low flatulence production made the crop more acceptable by the people world over. Because of short duration, wide adaptation, low water requirement and photo insensitiveness, it can be grown in various crop rotation practices. It is primarily grown in India, Pakistan, Bangladesh, Sri Lanka, Nepal and other Southeast Asian countries (Singh *et al.*, 2015).

Mungbean is short day, warm season crop mainly grown in arid and semi-arid regions. It is a drought resistant crop with ability to grow under harsh climate and medium to low rainfall conditions and requires fewer quantities of inputs to grow well and mature. It grows on a variety of soils including black, red lateritic, gravelly and sandy soils with well drained fertile sandy loam soil of pH between 6.2 to 7.2 is the best for mungbean cultivation. Water logged and saline soils are not suitable for mungbean cultivation (Sharma, 2016). Estimates of genetic parameters provide an indication of the relative importance of the various types of gene effects affecting the total variation of a plant character. Therefore, the present study was conducted to assess genetic variability, heritability and genetic advance in mungbean genotype during *kharif* season under rainfed in Rajasthan. So that promising genotypes could be identified for breeding programme to develop high yielding varieties of mungbean.

Studies of correlation allow breeders to understand the strength of the relationship between different characters as well as the direction of changes expected during selection. Correlation and path analysis will determine the magnitude of association between yield and its components and also bring out relative importance of their direct and indirect effects, thus providing an obvious understanding of their association with seed yield. Path analysis is standardized partial regression coefficient which splits the correlation

[1]Department of Genetics and Plant Breeding, College of Agriculture, Agriculture University, Jodhpur-342 304, Rajasthan, India.

Corresponding Author: Anita, Department of Genetics and Plant Breeding, College of Agriculture, Agriculture University, Jodhpur-342 304, Rajasthan, India. Email: akhedar1993@gmail.com

How to cite this article: Anita, Kumhar, S.R., Kumar, A., Suchitra, Kulheri, A., Shekhawat, P.K. and Yadav, G.L. (2025). Correlation and Path Analysis Studies of Pod Yield and its Component Traits in Mungbean [*Vigna radiata* (L.) Wilczek] Genotypes. Legume Research. 48(1): 26-31. doi: 10.18805/LR-4906.

Submitted: 04-03-2022 **Accepted:** 02-11-2022 **Online:** 12-11-2022

coefficient into the measure of direct and indirect effect and measure the direct and indirect contribution of each independent variable on the depend variable (Wright, 1921).

Materials and Methods

The investigation was conducted during *Kharif*, 2019 under rainfed conditions at experimental field of Agricultural Research Station, Agriculture University, Mandor, Jodhpur, Rajasthan. The material comprised of 38 genotypes/varieties of mungbean which were sown by adopting randomized block design (RBD) with three replications is presented in Table 1. Each genotype was sown in 4 m length of five rows with the spacing of 30 cm between rows and 10 cm from plant to plant. The recommended agronomic practices were followed to raise a good crop. Observations were recorded on days to 50% flowering, days to maturity, plant height (cm), number of pods per plant, pod length (cm), number of branches per plant, number of seeds per pod, 100 seed weight (g), seed yield per plant (g), harvest index (%) and protein content (%). The estimates of correlation and path coefficient analysis were calculated by using data.

Table 1: List of mungbean genotypes used in the present study.

Name of genotypes	Source
IPM 02-3M 02-	IIPR, Kanpur, U.P.
IPM 604-1	IIPR, Kanpur,U.P.
Virat	IIPR, Kanpur, U.P.
Shikha	IIPR, Kanpur, U.P.
SKNM 1514	SDAU, S. K. Nagar, Gujarat
SKNM 1516	SDAU, S.K. Nagar, Gujarat
GM 4	SDAU, S.K. Nagar, Gujarat
GM 6	SDAU, S.K. Nagar, Gujarat
ML 818	PAU, Ludhiana, Punjab
ML 2483	PAU, Ludhiana, Punjab
SML 1901	PAU, Ludhiana, Punjab
SML 668	PAU, Ludhiana, Punjab
MH 2-15	Hisar, Haryana
MH 421	Hisar, Haryana
MH 1344	CCS HAU, Hisar, Haryana
SVM 6262	SVHS, Hisar, Haryana
VGG17-002	NPRC, Vamban, T.N.
VGG 17-009	NPRC, Vamban, T.N.
VGG 16-055	NPRC, Vamban, T.N.
Pusa M 1871	IARI, New Delhi
Pusa M 1872	IARI, New Delhi
OBGG 101	OUAT, Bhubaneswar, Odisha
OBGG 102	OUAT, Bhubaneswar, Odisha
IGKM 05-6-27	IGKVV, Raipur, Chhattisgarh
IGKM 06-18-3	IGKVV, Raipur, Chhattisgarh
PM 1511	GBPUAT, Pantnagar, Uttarakhand
PM 1522	GBPUAT, Pantnagar, Uttarakhand
CO-6	Coimbatore, T.N.
COGG-912	Coimbatore,T.N.
GAM 5	Anand, Gujarat
LGG 630	ARS, Lam, A.P.
DGGV- 59	ARS, Dharwad, Karnataka
MGG 399	ARS, Madhira, Telangana
TRCM 171-B-B-12-6	Agartala,Tripura, Bangladesh
OUM 11-5	Berhampur, Odisha
JLM 707-5	MPKV, Jalgaon, M.H.
AKM- 1604	PDKV, Akola, M.H.
SKAU-M-365	Srinagar, J and K

Results and Discussion

Analysis of variance revealed highly significant difference among for all eleven characters Table 2. The phenotypic and genotypic correlations between seed yield and its contributing traits for 38 genotypes/varieties were estimated and are presented in Table 3. In general, for most of the characters under study, the genotypic correlation coefficients were higher in magnitude than phenotypic correlation coefficients. High genotypic correlations as compared to their phenotypic counterparts indicated strong inherent association between the characters studied and its expression is lessened due to influence of environment. Among the eleven characters studied under this experiment, only five traits *viz.,* plant height, number of pods per plant, number of branches per plant, number of seeds per pod and 100 seed weight exhibited significant positive association at both genotypic and phenotypic levels with seed yield per plant. The correlations of seed yield per plant (g) was positive and significant at both level with characters *viz.*, plant height, number of pods per plant and number of branches per plant (Patel *et al*., 2014; Kapadia *et al*., 2015; Muthuswamy *et al.,* 2019 and Ahmad and Belwal, 2020), number of seeds per pods (Singh *et al*., 2009; Pulagmpalli and Lavanya, 2017; Kumar *et al*., 2018; Muthuswamy *et al.,* 2019), 100 seed weight (Raturi *et al.,* 2015; Kumar *et al*., 2018 and Ahmad and Belwal, 2020). The correlations of seed yield per plant (g) with days to 50% flowering and pod length were highly positive and significant at genotypic level.

The seed yield per plant was dependent character and output of direct and indirect effects of independent characters (variables) like days to 50% flowering, days to

Table 2: Analysis of variance (ANOVA) for seed yield and other traits in 38 mungbean genotypes/varieties.

Characters	Replications	Genotypes	Error
Degree of freedom	2	37	74
Days to 50% flowering	0.08	41.10**	1.23
Days to maturity	1.32	24.30**	2.19
Plant height (cm)	1.34	278.49**	1.37
No. of pods per plant	0.57	46.79**	0.81
Pod length (cm)	0.30	0.90**	0.37
No. of branches per plant	0.01	0.35**	0.01
Number of seeds per pod	0.27	1.97**	0.48
100 seed weight (g)	0.09	1.15**	0.02
Seed yield per plant (g)	0.33	8.48**	0.64
Harvest index (%)	1.72	132.74**	5.61
Protein content (%)	1.38	6.55**	1.62

** = Significant at 1%, * = Significant at 5%.

Table 3: Phenotypic and genotypic correlation coefficient between different characters in mungbean.

Characters	Level	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of pods per plant	Pod length (cm)	Number of branches per plant	Number of seeds per pod	100 seed weight (g)	Harvest index (%)	Protein content (%)	Seed yield per plant (g)
Days to 50% flowering	G	1.000	0.6130**	0.5073**	0.5355**	-0.0121	0.3633**	0.2048*	-0.1798	-0.2916**	-0.0685	0.2103*
	P	1.000	0.5358**	0.4885**	0.4925**	0.0181	0.3389 **	0.1457	-0.1634	-0.2624 **	-0.0397	0.1831
Days to maturity	G		1.000	0.3971**	0.3019**	-0.4688**	0.2374*	0.0111	0.0126	-0.3312**	-0.2316*	0.1299
	P		1.000	0.3522**	0.2684**	-0.2557**	0.1933 *	0.0060	0.0179	-0.2692 **	-0.2138 *	0.0294
Plant height (cm)	G			1.000	0.4016**	-0.1874*	0.2153*	0.0796	-0.1106	-0.1971*	-0.1954*	0.3024**
	P			1.000	0.3893**	-0.0810	0.1964 *	0.0674	-0.1103	-0.1889 *	-0.1337	0.2667**
No. of pods per plant	G				1.000	-0.1065	0.6340**	0.1739	-0.0885	0.0265	-0.0289	0.6162**
	P				1.000	-0.0356	0.5835 **	0.1575	-0.0770	0.0205	-0.0426	0.5517**
Pod length (cm)	G					1.000	0.1052	0.3463**	0.3415**	0.0126	-0.0031	0.2467**
	P					1.000	0.0636	0.3669 **	0.2282 *	-0.0245	0.0400	0.1481
No. of branches per plant	G						1.000	0.0606	0.1738	-0.0580	-0.0640	0.4129**
	P						1.000	0.0559	0.1540	-0.0635	-0.0663	0.3511**
Number of seeds per pod	G							1.000	0.1364	0.0229	-0.2666**	0.5892**
	P							1.000	0.0581	-0.0053	-0.1704	0.4013**
100 seed weight (g)	G								1.000	-0.0338	-0.1107	0.3362**
	P								1.000	-0.0382	-0.0759	0.2879**
Harvest index (%)	G									1.000	-0.1532	-0.0205
	P									1.000	-0.1114	-0.0199
Protein content (%)	G										1.000	-0.2763**
	P										1.000	-0.1593
Seed yield per plant (g)	G											1.000
	P											1.000

** = Significant at 1%., * = Significant at 5%.

Table 4: Path coefficient analysis showing direct (bold) and indirect effects of different characters on seed yield per plant.

Characters	Level	Days to 50% Flowering	Days to maturity	Plant height (cm)	No. of pods per plant	Pod length (cm)	Number of branches per plant	Number of seeds per pod	100 seed weight (g)	Harvest index (%)	Protein content (%)	Correlation with seed yield per Plant
Days to 50%Flowering	G	-0.4150	-0.2544	-0.2106	-0.2222	0.0050	-0.1508	-0.0850	0.0746	0.1210	0.0284	0.2103*
	P	-0.0647	-0.0347	-0.0316	-0.0319	-0.0012	-0.0219	-0.0094	0.0106	0.0170	0.0026	0.1831
Days to maturity	G	0.0903	0.1474	0.0585	0.0445	-0.0691	0.0350	0.0016	0.0019	-0.0488	-0.0341	0.1299
	P	-0.1027	-0.1916	-0.0675	-0.0514	0.0490	-0.0370	-0.0012	-0.0034	0.0516	0.0410	0.0294
Plant height (cm)	G	0.0811	0.0635	0.1599	0.0642	-0.0300	0.0344	0.0127	-0.0177	-0.0315	-0.0312	0.3024**
	P	0.0654	0.0471	0.1338	0.0521	-0.0108	0.0263	0.0090	-0.0148	-0.0253	-0.0179	0.2667**
No. of pods per plant	G	0.4027	0.2270	0.3020	0.7520	-0.0801	0.4768	0.1308	-0.0665	0.0200	-0.0218	0.6162**
	P	0.2814	0.1534	0.2225	0.5714	-0.0203	0.3334	0.0900	-0.0440	0.0117	-0.0243	0.5517**
Pod length (cm)	G	-0.0026	-0.1021	-0.0408	-0.0232	0.2178	0.0229	0.0754	0.0744	0.0027	-0.0007	0.2467**
	P	-0.0009	0.0124	0.0039	0.0017	-0.0486	-0.0031	-0.0178	-0.0111	0.0012	-0.0019	0.1481
Number of branches per plant	G	-0.0291	-0.0190	-0.0172	-0.0507	-0.0084	-0.0800	-0.0048	-0.0139	0.0046	0.0051	0.4129**
	P	-0.0083	-0.0047	-0.0048	-0.0142	-0.0015	-0.0244	-0.0014	-0.0038	0.0015	0.0016	0.3511**
Number of seeds per pod	G	0.0826	0.0045	0.0321	0.0701	0.1397	0.0244	0.4033	0.0550	0.0092	-0.1075	0.5892**
	P	0.0432	0.0018	0.0200	0.0467	0.1089	0.0166	0.2968	0.0172	-0.0016	-0.0506	0.4013**
100 seed weight(g)	G	-0.0383	0.0027	-0.0236	-0.0188	0.0727	0.0370	0.0291	0.2130	-0.0072	-0.0236	0.3362**
	P	-0.0535	0.0058	-0.0361	-0.0252	0.0747	0.0504	0.0190	0.3273	-0.0125	-0.0248	0.2879**
Harvest index(%)	G	0.0312	0.0354	0.0211	-0.0028	-0.0013	0.0062	-0.0024	0.0036	-0.1070	0.0164	-0.0205
	P	0.0194	0.0199	0.0140	-0.0015	0.0018	0.0047	0.0004	0.0028	-0.0739	0.0082	-0.0199
Protein content (%)	G	0.0074	0.0249	0.0210	0.0031	0.0003	0.0069	0.0286	0.0119	0.0165	-0.1074	-0.2763**
	P	0.0037	0.0199	0.0125	0.0040	-0.0037	0.0062	0.0159	0.0071	0.0104	-0.0931	-0.1593

Note: Residual effect: Phenotypic = 0.31841 and Genotypic = 0.68614.

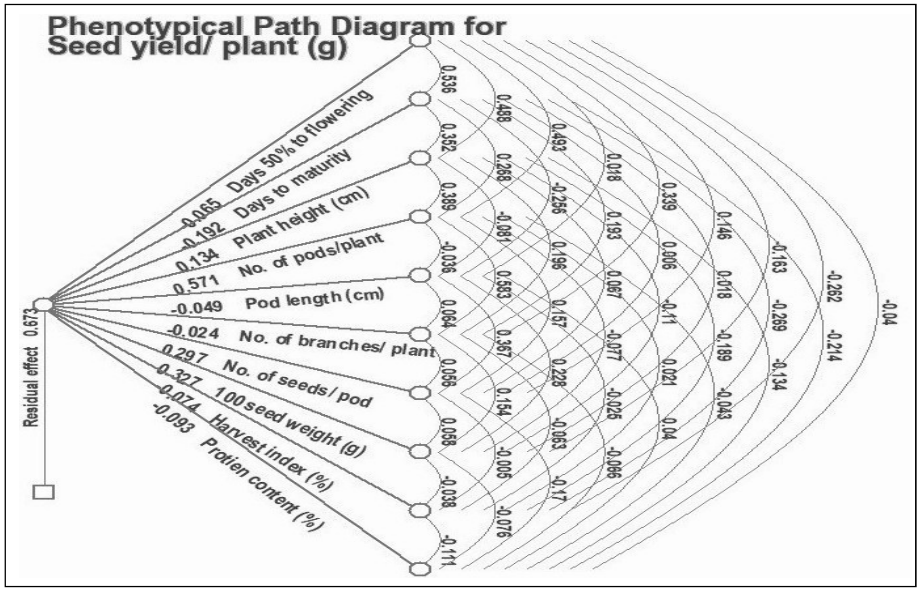


Fig 1: Path diagram for seed yield per plant in mungbean.

maturity, plant height (cm), number of pods per plant, pod length (cm), number of branches per plant, number of seeds per pod, 100 seed weight (g), harvest index (%) and protein content (%). The direct and indirect contribution of each character towards seed yield per plant is presented in Table 4, Fig 1. Results of path coefficient analysis of different characters contributing towards seed yield per plant showed that number of pods per plant (0.7520) had highest positive direct effect on seed yield per plant followed by number of seeds per pod (0.4033), pod length (0.2178), 100 seed weight (0.2130), plant height (0.1599) and days to maturity (0.1474) at genotypic level. These finding were supported the observations made earlier by (Rao *et al*., 2006; Ahmad and Belwal, 2020). Whereas, days to 50% flowering (-0.4150) had the highest negative direct effect on seed yield per plant followed by protein content (Kumar, 2011), harvest index (Gadakh *et al*., 2013) and number of branches per plant (Aqsa *et al.,* 2010; Muthuswamy *et al.,* 2019) at genotypic level.

At phenotypic level, highest direct positive effect on seed yield per plant was observed for number of pods per plant had the highest positive direct effect on seed yield per plant followed by 100 seed weight, number of seeds per pod, plant height. Direct negative effect on seed yield per plant was also observed for days to maturity had the highest negative direct effect on seed yield per plant followed by protein content, harvest index, days to 50% flowering, pod length and number of branches per plant.

Conclusion

Correlation relieved that seed yield per plant was positive significant correlation with plant height, number of pods per plant, number of branches per plant per plant, number of seeds per pod and 100 seed weight at both levels. The traits days to 50% flowering and pod length showed positive significant correlation with seed yield per plant at genotypic level only. Protein content exhibited negative significant correlation with seed yield per plant at genotypic level only. The selection for plant height, number of pods per plant, number of branches per plant per plant, number of seeds per pod and 100 seed weight may bring simultaneous improvement in seed yield. Path coefficient analysis revealed that the highest positive direct effect on seed yield exerted by number of pods per plant, followed by number of seeds per pod, 100 seed weight and plant height, therefore may be used for further improving yield attributes breeding programme of mungbean.

Acknowledgement

The authors are thankful to the Sitaram Kumhar, Sesame Breeder, Agricultural Research Station (Agriculture University, Jodhpur) and Department of Genetics and Plant Breeding, Agriculture University, Mandore, Jodhpur for providing the valuable genotypes to carry out this study.

Conflict of interest

The authors declare that there is no conflict of interest regarding the publication of this article. No funding or sponsorship influenced the design of the study, data collection, analysis, decision to publish or preparation of the manuscript.

References

Ahmad,S. and Belwal,V. (2020). Study of correlation and path analysis for yield and yield attributing traits in mungbean [*Vigna radiata* (L.) Wilczek]. International Journal of Chemical Studies. 8(1): 2140-2143.

Aqsa, T., Muhammad, S. and Irum, A. (2010). Genetic variability, trait association and path analysis of yield and yield components in mungbean. Journal of Botany. 42(6): 3915-3924.

Gadakh, S.S., Dethe, A.M. and Kathale, M.N. (2013). Genetic variability, correlations and path analysis studies on yield and its components in mungbean [*Vigna radiata* (L.) Wilczek]. Bioinfo'let. 10(2a): 441-447.

Kapadia, V.N, Raiyani, A.M. and Parmar, M.B. (2015). Genetic studies of variability correlation and path coefficient analysis for mungbean [*Vigna radiata* (L.) Wilczek] yield and its yield component. Trends in Biosciences. 8(5): 1270-1273.

Kumar, A., Sharma, N.K., Kumar, R., Sanadya, S.K. and Sahoo, S. (2018). Correlation and path analysis for seed yield and components traits in mungbean under arid environment. International Journal of Chemical Studies. 6(4): 1679-1681.

Kumar, S. (2011). Genetic analysis for yield its components and protein content in some genotypes of mungbean [*Vigna radiata* (L.) Wilzeck]. M.Sc. thesis, Indira Gandhi Krishi Vishwavidyalaya, Raipur. 100 pp.

Muthuswamy, A., Jamunarani, M. and Ramakrishnan, P. (2019). Genetic variability, character association and path analysis studies in mungbean [*Vigna radiata* (L.) Wilczek]. International Journal of Current Microbiology and Applied Sciences. 8(4): 1136-1146.

Patel, S.R., Patel, K.K. and Parmar, H.K., (2014). Genetic variability, correlation and path analysis for seed yield and its components in greengram [*Vigna radiata* (L.) Wilczek]. The Bioscan. 9(4): 1847-1852.

Pulagampalli, R. and Lavanya, G.R. (2017). Variability, heritability, genetic advance and correlation coefficients for yield component characters and seed yield in green gram [*Vigna radiata* (L.) Wilczek]. Journal of Pharmacognosy and Phytochemistry. 6(4): 1202-1205.

Raturi, A., Singh, S.K., Sharma, V. and Pathak, R. (2015). Genetic variability, heritability, genetic advance and path analysis in mungbean [*Vigna radiata* (L.) Wilczek]. Legume Research. 38(2): 157-163. doi: 10.5958/0976-0571.2015.00024.7.

Rao, C.M., Rao, Y.K. and Reddy, M. (2006). Genetic variability and path analysis in mungbean [*Vigna radiata* (L.) Wilczek]. Legume Research. 29(3): 216-218.

Singh, S.K., Singh I.P., Singh B.B and Singh O. (2009). Correlation and path coefficient studied and its components in mungbean [*Vigna radiata* (L.) Wilczek]. Legume Research. 32(3): 180-185.

Sharma, N.K. (2016). Mungbean Production Strategy. Swami Keshwanand Rajasthan Agricultural University, Bikaner. DOR/SKRAU/NFSM Publication-2: 19 p.

Singh, C., Singh, P. and Singh, R. (2015). Modern Techniques of Raising Field Crops. Oxford and IBH Publishing Co. Pvt. Ltd., New Delhi: 386 p.

Wright, S. (1921). Correlation and causation. Journal of Agricultural Research. 20: 257-87.