RESEARCH ARTICLE Legume Research- An International Journal, Volume 47 Issue 11: 1851-1857 (November 2024)

Genetic Variability and Correlation Studies for Yield and Yield Attributing Traits in Mungbean [*Vigna radiata* (L.) Wilczek]

Labhya Rani Gogoi[1], Partha Pratim Behera[1], Nayanmoni Borah[1], Ramendra Nath Sarma[1] 10.18805/LR-5241

ABSTRACT

Background: Mungbean is one important short duration pulse mostly grown in South and Southeast Asia. The level of variability available in the germplasm influences how well a breeding programme would be productive. Understanding the nature and extent of genetic diversity in breeding material is greatly helped by estimates of genetic variability parameters and character associations. The current study aimed to study genetic variability and character associations in mungbean for yield and its attributes, pre-requisite for formulating an effective breeding programme.

Methods: The present experiments were carried out with 107 mungbean genotypes collected from NBPGR (New Delhi) and AAU-Zonal Research Station, Shillongani. The genotypes were evaluated in randomized complete block design over two replications for yield and yield attributing traits at the experimental farm Assam Agricultural University, Jorhat during 2020-2021.

Result: The traits like yield per plant, number of branches per plant, clusters per plant, pods per plant, plant height, 100 seeds weight and peduncle length exhibited a high to medium magnitude of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV). Additionally, these traits showed high heritability and high genetic advance. The correlation studies revealed significant positive relationships between yield and all the assessed traits, with the exception of shelling percentage. The results of the path analysis indicated that a few traits, such as the number of pods per plant and the weight of 100 seeds, had a significant positive impact on seed yield. This suggests that when selecting for seed yield in mungbean, it would be advantageous to take into account these traits.

Key words: Correlations, Genotypic coefficient of variation, Heritability, Mungbean, Path coefficient, Phenotypic coefficient of variation, Variability.

INTRODUCTION

Mungbean [*Vigna radiata* (L.) Wilczek], also known as green gram or moong, is a legume crop that is widely grown in many parts of the world, particularly in South and Southeast Asia (Pratap *et al*., 2020). Mungbean belongs to the *Fabeaceae* family in the genus *Vigna* and is a self pollinating diploid grain legume, 2n = 22 (Karpechenko, 1925). It is often preferred to other pulse crop because of its better digestibility and lower content of raffinose, stachyose and verbacose leading to less flatulence problem (Poehlman, 1991). It is a short duration crop and can be grown across seasons in varying cropping systems and crop rotations (Malik, 1994). It can be grown successfully in extreme environments (*e.g*., high temperatures, low rain fall and poor soils) with few economic inputs (Das *et al*., 2014). After chickpea and pigeon pea in terms of production and area, mungbean is the third most significant pulse crop in India. India is a major producer of mungbean and at the same time India identified as the largest consumer of mungbean in the world (Sneha *et al*., 2020). In India, the total area covered under mungbean is 4.607 million (m) ha with a production of 2.448 m tons and a productivity of 513 kg/ha in the country during 2017-18 to 2021-2022 (Directorate of Pulses Development, 2022). Currently, the realized average productivity of mungbean is well below the economic level (Rahmianna *et al*., 2021).

[1]Department of Plant Breeding and Genetics, Assam Agricultural University, Jorhat-785 013, Assam, India.

Corresponding Author: Labhya Rani Gogoi, Department of Plant Breeding and Genetics, Assam Agricultural University, Jorhat-785 013, Assam, India. Email: labhrj@gmail.com

How to cite this article: Gogoi, L.R., Behera, P.P., Borah, N. and Sarma, R.N. (2024). Genetic Variability and Correlation Studies for Yield and Yield Attributing Traits in Mungbean [*Vigna radiata* (L.) Wilczek]. Legume Research. 47(11): 1851-1857. doi: 10.18805/LR-5241.

Submitted: 01-09-2023 **Accepted:** 22-02-2024 **Online:** 04-04-2024

High yield is the basic objective of all crop breeding programmes. In any program aimed at genetic improvement of yield, existence of variability is the basic requirement (Azam *et al*., 2018). The available genetic variability for the traits of interest, especially yield and its attributes are to be exploited by mungbean breeders in order to broaden and strengthen genetic potential. Yield is a complex character and depends upon the action and interaction of a number of factors. The relative contributions of these different characters to seed yield can be estimated by correlation analysis. However, correlation studies do not provide an exact picture of the relative importance of direct and indirect influence of each of them. The path coefficient analysis further allows the partitioning of correlation coefficients of yield-related characters into their direct and indirect effects.

Keeping all these points in view, the present study was planned to assess the genetic diversity, parameters of variability and associations among yield and yield attributing traits in mungbean order to identify the most promising traits of interest and genotypes to be considered in future mungbean crop improvement programmes.

MATERIALS AND METHODS

A total of 107 genotypes of mungbean were included in the study. The majority (103) were collected from NBPGR and rest 4 genotypes collected from AAU- Zonal Research Station, Shillongani. The investigation was carried out during *kharif* and summer seasons each of 2020 and 2021 at the Instructional-Cum-Research (ICR) Farm of Assam Agricultural University. The experiment was laid out in a randomized block design in each environments with two replications. Each genotype was grown in two rows of 3 meter length with row to row and plant to plant spacing of 30 cm and 10 cm, respectively. The observations on 13 characters were recorded on five randomly selected plants in each of the two replications were days to 50% flowering, peduncle length (cm), days to 50% maturity, number of branches (only pod bearing branches) per plant, flowering period (days), number of cluster, number of pod per plant, plant height (cm), pod length (cm), seeds per pod, 100 seeds weight, shelling percentage and yield per plant.

All phenotypic data recorded in four environment were subjected to combined analysis of variance (ANOVA). The genetic parameters *viz*., phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV), heritability in the broad sense and genetic advance as per the standard procedure described by Singh and Chaudhary (1985) using the pooled data. The pooled data were also used for correlation and path coefficient analysis following Singh and Chaudhary (1985) and Dewey and Lu (1959), respectively. These analyses were done in R platform in R version 3.6.3 (R core Team, 2021) using the R package 'variability' (Popat *et al*., 2020).

RESULTS AND DISCUSSION

The combined analysis of variance for the 107 genotypes across four environments indicated significant genotypic differences for yield and yield-attributing traits (Table 1), indicating that genotypes were genetically diverse. The environment component also showed substantial variation for all the traits under study. Thus, the substantial genotypic differences for all traits warrant further investigation.

Analysis of variability parameters

In general, the magnitude of PCV was found to be higher than the corresponding GCV for all the traits, but the differences are quite small (Table 2). This reflected their high heritability values and indicated the less influence of environment on the expression of these traits. Similar results were also obtained by Singh *et al.* (2009a) and Kumar *et al.* (2013). The magnitude of both GCV and PCV were

Table 1: Combined analysis of variance for yield and yield attributing traits in mungbean.

Sources of variation	df	Mean squares												
		dfl	lpl	nb	dpm	pht	nc	npp	nsp	swt	fpd	pl	sp	ypp
GEN	106	44.517**	18.017**	1.177**	77.028**	366.307**	17.255**	234.347**	3.737**	1.728**	27.814**	1.488**	88.198**	71.814**
ENV	3	5666.359**	214.525**	10.109**	3791.104**	2340.230**	264.875**	3708.924**	125.701**	3.067**	1758.252**	52.307**	3605.718**	914.623**
GEN × ENV	318	9.619**	9.976**	0.701**	19.037**	60.345**	5.666**	65.089**	1.998**	0.249**	5.293**	0.527**	44.472**	21.025**
REP/ENV	4	50.116**	0.063	0.192	31.808	2.514	0.921	10.638**	6.979**	0.748**	2.805**	0.429**	35.869**	21.010**
Error	424	0.965	0.966	0.157	0.954	1.882	0.4	2.469	0.86	0.028	0.589	0.118	2.114	1.766
CV (%)		2.168	7.885	26.915	1.570	3.010	8.297	5.511	8.546	4.617	3.712	4.731	2.071	11.686

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

(df= Degree of freedom, dfl= Days to 50% flowering, dpm= Days to 50% pod maturity, fpd= Flowering period, lpl= Peduncle length, nb= No. of branches per plant, nc= No. of clusters per plant, npp= No. of pods per plant, nsp= No. of seeds per pod, pht= Plant height, pl= Pod length, sp= Shelling percentage, swt= 100 seeds weight, ypp= Yield per plant).

high for yield per plant and number of branches per plant. This indicated the presence of wide variation for these two traits allowing further improvement by simple selection of the individual traits. The moderate GCV and PCV for clusters per plant, number of pods per plant, plant height, 100 seeds weight and peduncle length suggested the presence of considerable variation for above said characters to allow selection for individual traits. High estimate of GCV for seed yield per plant was observed by Patel (2000); Longnathan *et al.* (2001); Samad and Lavanya (2005); Makeen *et al.* (2007); Jyothsna *et al.* (2013) and Hemavathy *et al.* (2015) and for branches per pant was observed by Narasimhulu*et al.* (2013); Patel *et al.* (2014) and Singh *et al.* (2014). But shelling percentage, days to 50% pod maturity, days to 50% flowering, number of seeds per pod, pod length and flowering period estimated to have low GCV and PCV which indicated the narrow range of variability thereby restricting for further improvement of these characters through simple selection. Similar finding had been earlier reported by Mehandi *et al.* (2013) and Patel *et al.* (2014).

The magnitude of broad-sense heritability was observed to be high for all the thirteen characters indicating least environmental effects on their expression. The highest heritability value was recorded for plant height, followed by number of pods per plant and days to 50% pod maturity. Patel (2000), Reddy *et al.* (2003) and Makeen *et al.* (2007); Payasi (2015) and Hemavathy *et al.* (2015) also reported high heritability for the traits studied in this experiment. According to Johnson *et al.* (1955) the heritability values together with genetic advance would be more useful for correlating selection criteria than heritability alone. High heritability coupled with high GA, were evident for the number of branches per plant, yield per plant, pods per plant, clusters per plant and plant height. This indicated the predominance of additive gene action, implying the potential efficacy of simple selection for trait improvement. These results were agreed upon by Shiv *et al.* (2017); Ramakrishan *et al.* (2018); Jagdhane *et al.* (2017) for primary branches per plant and pods per plant, Sana *et al.* (2017) and Katiyar *et al.* (2015) for pods per plant and seed yield per plant. High heritability and moderate genetic advance were seen for flowering period, pod length, days to 50% flowering and days to 50% pod maturity indicating these characters can also be improved by phenotypic selection.

Correlations and path coefficient analysis

Correlation analysis revealed that the association between yield and yield contributing traits was found positive and significant at both genotypic and phenotypic level for all the traits except shelling percentage (Table 3). It suggested that direct selection for these component traits could enhance yield. As a result, greater attention should be placed on these components during selection for higher yield. Similar results for yield per plant were reported by Makeen *et al.* (2007) with clusters per plant, pods per plant and seeds per pod (genotypic correlation only); Parihar *et al.* (2018) with days to maturity, seeds per pod and test weight.

Among the other traits, the correlation was positive between days to 50% flowering with days to 50% pod maturity, flowering period, number of branches, number of cluster, number of pods per plant, number of seeds per pod and plant height at both the genotypic and phenotypic level. The results confirmed the earlier findings of Srivastava and Singh (2012) and Patel *et al.* (2014) for 50% flowering with primary branches per plant, clusters per plant and pods per plant;Titumeer *et al.* (2014) for 50% flowering with primary branches per plant, pods per plant and seed yield per plant; and Khanpara *et al.* (2012) for 50% flowering with days to maturity, pods per plant and seed yield per plant. The results were also in agreement with Kritika (2017), Dhoot *et al.* (2017) for 50% flowering with days to maturity and Rohman *et al.* (2003); Kritika (2017); Dhoot *et al.* (2017) for 50% flowering with plant height. Days to 50% pod maturity showed a highly significant and positive correlation with flowering period, number of branches, number of clusters, number of pods per plant, number of seeds per pod and plant height at both the genotypic and phenotypic levels. Anita *et al.* (2022),

Table 2: Variability parameters of yield and yield attributing traits in mungbean using pooled data.

Traits	Range	GCV	PCV	h^2_{bs}	GAM
Days to 50% flowering	39.816-53.729	5.117	5.295	93.380	10.185
Peduncle length	8.078-15.743	11.680	12.385	88.940	22.692
No. of branches per plant	0.641-2.645	24.299	27.746	76.700	43.838
Days to 50% pod maturity	53.089-74.943	4.947	5.033	96.640	10.018
Plant height	35.167-67.556	14.807	14.886	98.940	30.341
No. of clusters per plant	4.816-11.554	19.016	19.526	94.840	38.149
No. of pods per plant	17.880-41.664	18.853	19.112	97.300	38.310
No. of seeds per pod	8.925-12.395	5.486	7.018	61.110	8.834
100 seeds weight	1.954-5.010	12.672	12.890	96.630	25.661
Flowering period	15.554-28.096	8.906	9.131	95.140	17.896
Pod length	6.194-8.684	5.751	6.117	88.400	11.140
Shelling percentage	60.889-79.076	4.680	4.777	96.010	9.447
Yield per plant	5.866-19.199	26.004	26.683	94.970	52.203

Parihar *et al.* (2018) and Dhoot *et al.* (2017) observed positive correlations between days to maturity and plant height, number of pods per plant and number of branches, as well as between days to maturity and plant height by Dhoot *et al.* (2017). At both the genotypic and phenotypic levels, there was a positive correlation between the flowering period and the number of branches, clusters per plant, pods per plant and plant height. The peduncle length exhibited a positive correlation with the number of branches, the number of clusters, pods per plant, seeds per pod and the plant height at both genotypic and phenotypic levels. Almost all traits, including flowering period, peduncle length, number of clusters, pods per plant, seeds per pod and plant height showed a highly significant and positive correlation with the number of branches. Similar results were reported by Patel *et al.* (2014) and Titumeer *et al.* (2014). However, correlation of number of branches with the shelling percentage was negative. The correlation of number of cluster per plant was highly significant and positive with number of pod per plant, number of seed per pod, plant height and pod length at both the level. These results were in agreement with the findings of Hemavathy *et al.* (2015), Anand *et al.* (2016) and Parihar *et al.* (2018). Number of pods per plant correlated positively with seeds per pod, plant height and pod length. Pod length correlated positively with plant height at both levels. Positive associations existed between number of seeds per pod, pod length and plant height. These results are agreement with Biradar *et al.* (2007); Titumeer *et al.* (2014) and Makeen *et al.* (2007) for pod length with seed per pod and Alom *et al*; (2014), Khajudpar and Tantasawat (2011); Singh *et al.* (2014) for pod length with seed per pod and 100 seeds weight. Since, the correlation was quite complex among the yield attributing traits, it emphasized the importance of path analysis.

Path coefficient analysis based on genotypic correlation is presented in Table 4. The path coefficient analysis revealed that number of pods per plant had the highest positive direct effect on yield per plant (0.771), followed by 100 seeds weight (0.522) and seeds per pod (0.240); indicating their effect for positive correlation with the yield. Most of the traits showed positive direct effect and negative direct- as well as negative indirect-effects were negligible. The indirect effect of number of clusters, number of branches and plant height were positive and high via number of pods per plant. Similarly, days to 50% maturity, peduncle length and number of seed per pod recorded moderate positive indirect effect via number of pods per plant. This might be the reason for positive correlations of yield with all these traits. These positive direct effects of different traits in mungbean were supported by previous studies of Khajudpar and Tantasawat, (2011); Srivastava and Singh (2012) for pods per plant, seeds per pod, 100 seeds weight, Ambachew *et al.* (2015) for 100 seeds weight and pods per plant and Singh *et al.* (2009a) for plant height. The results showed that the characters

Table 3: Genotypic (above diagonal) and phenotypic (below diagonal) correlations among yield and yield attributing traits in mungbean.

Traits	dfl	dpm	fpd	lpl	nb	nc	npp	nsp	pht	pl	sp	swt	ypp
dfl	1	0.879**	0.321**	-0.039	0.280**	0.255**	0.215*	0.261 **	0.422**	-0.149	-0.001	-0.125	0.164*
dpm	0.860**	1	0.533**	-0.062	0.297**	0.327**	0.302**	0.218 *	0.570**	-0.034	0.038	0.054	0.310**
fpd	0.300**	0.514**	1	-0.029	0.201*	0.225*	0.207*	0.104	0.461**	0.005	0.009	0.093	0.223*
lpl	-0.044	-0.062	-0.022	1	0.386**	0.301**	0.321**	0.368 **	0.239*	0.112	-0.116	-0.022	0.290**
nb	0.252**	0.262**	0.154*	0.294**	1	0.751**	0.654**	0.412 **	0.393**	0.114	-0.233*	0.071	0.614**
nc	0.246**	0.310**	0.209**	0.274**	0.645**	1	0.963**	0.350 **	0.493**	0.166**	-0.135	0.071	0.830**
npp	0.205**	0.290**	0.195**	0.298**	0.568**	0.946**	1	0.310 **	0.502**	0.181**	-0.13	0.073	0.849**
nsp	0.198**	0.168*	0.058	0.271**	0.277**	0.276**	0.248**	1	0.139	00.310**	-0.101	-0.127	0.385**
pht	0.412**	0.558**	0.446**	0.220**	0.344**	0.482**	0.497**	0.109	1	0.222*	0.053	0.327**	0.575**
pl	-0.13	-0.027	0.005	0.102	0.081	0.159*	0.174*	0.259**	0.213**	1	-0.034	0.572**	0.473**
sp	0.003	0.041	0.008	-0.11	-0.208**	-0.132	-0.126	-0.087	0.053	-0.031	1	0.127	-0.028
swt	-0.116	0.0512	0.093	-0.013	0.047	0.06	0.068	-0.088	0.317**	0.535**	0.119	1	0.533**
ypp	0.154*	0.293**	0.204**	0.272**	0.519**	0.802**	0.835**	0.398**	0.559**	0.451**	-0.033	0.528**	1

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

(df= Degree of freedom, dfl= Days to 50% flowering, dpm= Days to 50% pod maturity, fpd= Flowering period, lpl= Peduncle length, nb= No. of branches per plant, nc= No. of clusters per plant, npp= No. of pods per plant, nsp= No. of seeds per pod, pht= Plant height, pl= Pod length, sp= Shelling percentage, swt= 100 seeds weight, ypp= Yield per plant).

Table 4: Path coefficients at genotypic level showing direct (diagonal) and indirect effects of different yield attributing traits in mungbean.

Traits	dfl	dpm	fpd	lpl	nb	nc	npp	nsp	pht	pl	sp	swt	Correlation with yield
dfl	-0.004	0.001	-0.004	0.001	0.004	-0.008	0.165	0.062	0.005	0.005	0.001	-0.065	0.164*
dpm	-0.003	0.001	-0.006	0.002	0.005	-0.010	0.233	0.052	0.007	0.001	0.001	0.028	0.310**
fpd	-0.001	0.001	-0.011	0.001	0.003	-0.007	0.160	0.025	0.005	0.000	0.000	0.049	0.223*
lpl	0.001	0.001	0.000	-0.028	0.006	-0.009	0.247	0.088	0.003	-0.004	-0.003	-0.011	0.290**
nb	-0.001	0.001	-0.002	-0.011	0.015	-0.023	0.504	0.099	0.005	-0.004	-0.006	0.037	0.614**
nc	-0.001	0.001	-0.003	-0.008	0.012	-0.030	0.743	0.084	0.006	-0.006	-0.003	0.037	0.830**
npp	-0.001	0.001	-0.002	-0.009	0.010	-0.029	0.771	0.074	0.006	-0.006	-0.003	0.038	0.849**
nsp	-0.001	0.001	-0.001	-0.010	0.006	-0.011	0.239	0.240	0.002	-0.011	-0.003	-0.066	0.385**
pht	-0.001	0.001	-0.005	-0.007	0.006	-0.015	0.387	0.033	0.012	-0.008	0.001	0.171	0.575**
pl	0.001	-0.001	-0.001	-0.003	0.002	-0.005	0.140	0.074	0.003	-0.035	-0.001	0.299	0.473**
sp	0.000	0.000	-0.001	0.003	-0.004	0.004	-0.100	-0.024	0.001	0.001	0.025	0.066	-0.028
swt	0.001	0.001	-0.001	0.001	0.001	-0.002	0.056	-0.030	0.004	-0.020	0.003	0.522	0.533**

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

Residual effect: 0.012.

(df= Degree of freedom, dfl= Days to 50% flowering, dpm= Days to 50% pod maturity, fpd= Flowering period, lpl= Peduncle length, nb= No. of branches per plant, nc= No. of clusters per plant, npp= No. of pods per plant, nsp= No. of seeds per pod, pht= Plant height, pl= Pod length, sp= Shelling percentage, swt= 100 seeds weight, ypp= Yield per plant).

which were most important for correlation studies also proved important by path analysis. Thus, it can be suggested that correlation and path analysis study should be consider together for rapid gain for final improvement in seed yield.

In this study, the lower value of the residual effect (0.012) showed that the observed component traits could explain all of the variation in yield per plant. It revealed that the variables studied in the present investigation explained 99% of the variability in the yield and other attributes besides the traits have been studied to contribute to seed yield per plant (Srivastava and Singh, 2012).

SUMMARY AND CONCLUSION

The genotypes used in the present study showed the existence of substantial variation for all the traits under study. Considering the variability estimates, correlations and the path analysis, the traits namely yield per plant, number of clusters per plant, number on branches per plant, number of pods per plant, plant height and 100 seeds weight, these traits should be given due consideration in selection process of mungbean breeding. As a result, selecting plants with more pods, larger seeds, more clusters, more branches and higher heights will enhance the yield per plant in mungbean.

ACKNOWLEDGEMENT

The authors are grateful to National Bureau of Plant genetic Resources, New Delhi and AAU-Zonal Research Station, Shillongani for providing the genotypes as a part of Ph.D research of the first author.

Ethics and conflict of interest

No ethical issues are involved. Authors declare that there is no conflict of interest.

REFERENCES

Alom, K.M., Rashid, M.H. and Biswas, M. (2014). Genetic variability, correlation and path analysis in mungbean (*Vigna radiata* L.). Journal of Environmental Sciences and Natural Resources. 7: 131-138.

Ambachew, D., Mekbib, F., Asfaw, A., Beebe, E.S. and Blair, W.M. (2015). Trait associations in common bean genotypes grown under drought stress and field infestation by BSM bean fly. The Crop Journal. 3: 305-316.

Anand, G., Anandhi, K. and Paulpandi, V.K. (2016). Genetic variability, correlation and path analysis for yield and yield components in F6 families of Greengram [*Vigna radiata* (L.) Wilczek] under rainfed condition. Electronic Journal of Plant Breeding. 7(2): 434-437.

Anita, K.S.R., Kumar, A., Suchitra, Kulheri, A., Shekhawat, P.K. and Yadav, G.L. (2022). Correlation and path analysis studies of pod yield and its component traits in mungbean [*Vigna radiata* (L.) Wilczek] genotypes. Legume Research-An International Journal. 1: 6. doi: 10.18805/LR-4906.

Azam, M., Hossain, M., Alam, M., Rahman, K., Hossain, M. (2018). Genetic variability, heritability and correlation path analysis in mungbean [*Vigna radiata* (L.) wilczek]. Bangladesh Journal of Agricultural Research. 43(3): 407-416.

Biradar, K.S., Salimath, P.M. and Ravikumar, R.L. (2007). Genetic studies in greengram and association analysis. Karnataka Journal of Agricultural. 20(4): 843-844.

Das, S., Das, S.S., Ghosh, P. (2014). A comparative analysis of genetic diversity across certain mung bean and urd bean cultivars of West Bengal, using ISSR markers. Asian Journal of Plant Science and Research. 4: 56-61.

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

Dhoot, R., Modha, K.G., Kumar, D. and Dhoot, M. (2017). Correlations and Path Analysis Studies on Yield and its Components in Mungbean [*Vigna radiata* (L.) Wilczek]. International Journal of Current Microbiology and Applied Sciences. 6(5): 370-378.

Directorate of Pulses Development, (2022). Annual Report 2021-22. Retrieved from https://dpd.gov.in/Annual Report (2021-22).pdf.

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. doi: 10.5958/0976-0571.2015.00050.8.

Jagdhane, N.M., Suresh, B.G., Ram, B.J. and Yadav, P. (2017). Genetic variability and character association for seed yield in mungbean [*Vigna radiata* (L.) Wilczek]. Journal of Pharmacognosy and Phytochemistry. 6(4): 1388-1390.

Johnson, H.W., Robinson, H.F. and Comstock, R.E. (1955). Estimates of genetic and environmental variability in soybeans. Journal of Agronomy. 47(7): 314-318.

Jyothsna, N.M. 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(3): 31-39.

Karpechenko, G.D. (1925). On the chromosomes of Phaseolinae. Bulletin Applied Botany Genetics Plant Breeding. 14: 143-148.

Katiyar, M., Kumar, S. and Kumar, N. (2015). Path analysis, association and variation of grain yield attributes in mung bean [*Vigna radiata* (L.) Wilczek]. International Journal of Advanced Research. 3(6): 2410-2413.

Khajudpar, P. and Tantasawat, P. (2011). Relationships and variability of agronomic and physiological characters in mungbean. African Journal of Biotechnology. 10(49): 9992-10000.

Khanpara, M.D., Vachhani, J.H., Jivani, L.L., Jethava, A.S. and Vaghasia, P.M. (2012). Correlation and path coefficient analysis in green gram [*Vigna radiate* (L.) Wilczek]. Asian Journal of Biological Sciences. 7(1): 34-38.

Kritika, R.Y. (2017). Correlation and path coefficients analysis for seed yield and micronutrients in mungbean [*Vigna radiata* (L.) Wilczek]. Indian Journal of Pure and Applied Biosciences. 5(1): 908-917.

Kumar, P., Pal, M., Joshi, R. and Sairam, R.K. (2013). Yield growth and physiological response of mungbean (*Vigna radiata* L.) genotypes to waterlogging at vegetative stage. Physiology and Molecular Biology of Plants. 19(2): 209-220.

Loganathan, P., Saravanan, K. and Ganesan, J. (2001). Genetic variability in greengram. Research on Crops. 2: 396-397.

Makeen, K., Garard, A., Arif, J. and Singh, A.K. (2007). Genetic variability and correlations studies on yield and its components in mungbean [*Vigna radiata* (L.) Wilczek]. Journal of Agronomy. 6(1): 216-218.

Malik, B.A. (1994). Grain Legume. In: Crop Production, [(eds) Bashir, E. and Bantel, R.] (Islamabad: National Book Foundation). 277-328.

Mehandi, S., Singh, C.M. and Kushwaha, V.K. (2013). Estimates of genetic variability and heritability for yield and yield component traits in mung bean [*Vigna radiata* (L.) Wilczek]. The Bioscan. 8(4): 1481-1484.

Narasimhulu, R., Naidu, N. V., ShanthiPriya, M., Rajarajeswari, V. and Reddy, K.H.P. (2013). Genetic variability and association studies for yield attributes in mungbean [*Vigna radiata* (L.) Wilczek]. Indian Journal of Plant Sciences. 2(3): 82-86.

Parihar, R., Agrawal, A.P., Sharma, D.J. and Minz, M.G. (2018). Character association and path analysis studies on seed yield and its yield attributing traits in mungbean [*Vigna radiata* (L.) Wilczek]. Journal of Pharmacognosy and Phytochemistry. 7(1): 2148-2150.

Patel, C.R. (2000). Variability, correlation, path coefficient and genetic divergence in green gram. Thesis Abstracts. 26: 241-242.

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

Payasi, D.K. (2015). Genetic variability analysis for seed yield and its components in mungbean [*Vigna radiata* (L.) Wilczek]. International Journal of Plant Breeding and Genetics. 9: 177-188.

Poehlman, J.M. (1991). The mung bean Oxford and IBH Publishing Co. Pvt. Ltd., New Delhi, India.

Popat, R., Patel, R. and Parmar, D. (2020). Variability: Genetic Variability Analysis for Plant Breeding Research. Package Version 0.1.0.

Pratap, A., Douglas, C., Prajapati, U., Kumari, G., War, A.R., Tomar, R. and Dubey, S. (2020). Breeding progress and future challenges: Biotic stresses. The Mungbean Genome. pp 55-80.

R Core Team, (2021). R: A language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, Austria. URL: https://www.R-project.org/.

Rahmianna, A.A., Basuki, T., Kote, M., Seran, Y.L. and Rachaputi, R.C. (2021). Increasing productivity of mungbean [*Vigna radiata* (L.) Wilczek] under subsistence farming in Eastern Indonesia. In IOP Conference Series: Earth and Environmental Science. 911(1): 012029. doi: 10.1088/1755-1315/911/1/012029.

Ramakrishnan, C.K.D., Savithramma, D.L. and Vijayabharathi, A. (2018). Studies on genetic variability, correlation and path analysis for yield and yield related traits in greengram [*Vigna radiata* (L.) Wilczek]. International Journal of Current Microbiology and Applied Sciences. 7(3): 2753-2761.

Reddy, V.L.N., Reddisekhar, M., Reddy, K.R. and Reddy, K.H. (2003). Genetic variability for yield and its components in mungbean, [*Vigna radiata* (L.) Wilczek]. Legume Research. 26(4): 300-302.

Rohman, M., Iqbal Hussain, A.S.M., Arifin, S.M., Akhter, Z. and Hasanuzzaman, M. (2003). Genetic variability, correlation and path analysis in mung bean [*Vigna radiate* (L.) Wilczek]. Asian Journal of Plant Sciences. 2: 1209-1211.

Samad, S.S. and Lavanya, G.R. (2005). Variability studies for yield parameters in mungbean [*Vigna radiata* (L.) Wilczek]. Journal of Maharashtra Agricultural Universities. 30(2): 168-170.

Sana, A.Y., Pithia, M.S., Raval, L.J. and Vora, Z.N. (2017). Genetic variability, heritability and genetic advance for seed yield and its components in F2 generations of mung bean [*Vigna radiata* (L.) Wilczek]. Indian Journal of Pure and Applied Biosciences. 5(2): 532-535.

Shiv, A., Ramtekey, V., Vadodariya, G.D., Modha, K.G. and Patel, R.K. (2017). Genetic variability, heritability and genetic advance in F3 progenies of mung bean [*Vigna radiata* (L.) Wilczek]. International Journal of Current Microbiology and Applied Sciences. 6(12): 3086-3094.

Singh, A., Singh, S.K., Sirohi, A. and Yadav, R. (2009a). Genetic variability and correlation studies in green gram [*Vigna radiata* (L.) Wilczek]. Progressive Agriculture. 9(1): 59-62.

Singh, C.M., Mishra, S.B. and Pandey, A. (2014). Pattern of agro-morphological trait relationship and genetic divergence in greengram [*Vigna radiata* (L.) Wilczek]. Electronic Journal of Plant Breeding. 5(1): 97-106.

Singh, R.K. and Chaudhary, B.D. (1985). Biometrical Methods in Quantitative Genetic Analysis. Kalyani Publishers, New Delhi, Ludhiana, India. pp 39-78.

Sneha, M., Saravanan, S., Premkumari, S. M. and Pillai, M.A. (2020). An appraisal of genetic divergence in some indigenous collections of mungbean [*Vigna radiata* (L.) Wileczek]. Electronic Journal of Plant Breeding. 11(2): 620-625.

Srivastava, R.L. and Singh, G. (2012). Genetic variability, correlation and path analysis in mungbean [*Vigna radiata* (L.) Wilczek]. Indian Journal of Life Sciences. 2(1): 61-65.

Titumeer, S.M., Rahim, M.A. and Zeba, N. (2014). Genetic variability, character association and genetic divergence in mungbean [*Vigna radiata* (L.) Wilczek]. Agronomski Glasnik. 6: 305-325.