RESEARCH ARTICLE

STUDIES ON GENETIC VARIABILITY PARAMETERS IN MUNGBEAN (*VIGNARADIATA* L.)

S. Mounika*, J.V. Ramana[1], D. Ratna Babu[1] and Lal Ahamed M.[1]

Department of Molecular Biology and Biotechnology, APGC, Lam, Guntur, Andhra Pradesh
[1] Department of Genetics and Plant Breeding, Agricultural College, Bapatla, Andhra Pradesh
Email: monikayadavs1996@gmail.com

Received-03.06.2021, Revised-19.06.2021, Accepted-29.06.2021

Abstract: Mungbean is a very important pulse crop and development of new varieties with desirable traits forms an important breeding objective. Evaluation of germplasm for yield and yield contributing traits is crucial to know the variability and their exploitation in the breeding programmes. In the present study, 48 genotypes were evaluated for different yield and yield characters. Analysis of variance for all the traits was significant revealing availability of sufficient variability for these traits in the studied material. The genotypic coefficients of variation for all the characters studied were lesser than the phenotypic coefficients of variation indicating the presence of interaction between genotypes with environment. Wide genetic variability was observed for the characters *viz*., pod length, seeds/pod, where as it was narrow for the characters *viz.*, days to 50% flowering, plant height, clusters/plant, branches/plant, pods/plant, days to maturity and yield/plant. High heritability with high genetic advance as per cent of mean was recorded for plant height, clusters/plant, branches/plant, seeds/pods, pods/plant and yield/plant indicating the preponderance of additive gene action in the inheritance of these traits and offers the scope for further improvement through simple selection procedures. High heritability coupled with low genetic advance as per cent of mean was observed for days to maturity indicating the role of non-additive gene action in the inheritance of this trait and the non-additive component may be exploited through heterosis breeding. The traits, plant height, clusters/plant, branches /plant, pods/plant, seeds/pod andyield /plant indicated the preponderance of additive gene action in their expression and can be exploited using direct simple selection.

Keywords: Genetic advance, Heritability, Mung bean, Variability

INTRODUCTION

Mung bean is an important pulse crop of India after chickpea and pigeon pea. Similar to other leguminous crops, mung beanalso enriches soil nitrogen content. It is a self-pollinating diploid grain legume crop (2n=2x=22) widely cultivated because of its adaptation to low water requirement, low soil fertility and short growth duration. It is a preferred legume in crop rotation. It is a rich source of proteins, vitamins, and minerals along with the properties like easy digestibility and low proportions of flatulence factors.

India is the primary producer and contributes to about 75% of the world production of mung bean*i.e*., 14% of total pulse cultivated area and 7% of total production. The cultivated area in India under mung bean is 4.24 million ha and with a productionand productivity of 2.02 million tonnes and 477 kg/ha, respectively (Indiastat, 2017-18).

Exploitation of germplasm in the breeding programmes forms an important objective and is carried outwidely to select the suitable genotypes for the immediate use in the breeding programmes. The germplasm is also studied to know the variability parameters as the success of the programme depends on the available variability for yield and yield components. Yield is a polygenic trait and the successful improvement in yield is highly dependent on the yield components. Hence, studying the nature and magnitude of variability present in the material is very crucial (Kale *et al.*, 2007). A wide variability in the material will give better chances of desired genotype selection. Along with variability, knowledge on other genetic variability parameters like heritability and genetic advance will predict the transmission of character to the progeny and helps in choosing a suitable breeding strategy to achieve the desired objective. There are reports that variability and heritability will give better idea of expected genetic advance during selection. Keeping this in view,in the present study, forty-eight genotypes collected from different parts of the country were studied to know the extent variability present in these genotypes.

MATERIALS AND METHODS

The present investigation was carried out during *rabi*, 2019-2020 at Regional Agricultural Research Station, Lam, Guntur with 48 genotypes of mung bean collected from different parts of the country in a randomized block design with three replications. The spacing adopted for sowing was 30 cm row to row and 10 cm plant to plant. Recommended package of practices and need based plant protection measureswere followed to raise the good crop. The data were recorded on ten randomly selected plants of each replication for nine quantitative characters i.e., days to 50% flowering, plant height, no. of branches/plant, no. of clusters/plant, no. of pods/plant, pod length, no. of seeds/pod, and seed yield/plant. The data on days to 50% flowering and days to maturity were recorded on plot basis. The

---

*Corresponding Author

data was subjected to statistical analysis to estimate the analysis of variance, genotypic and phenotypic coefficients of variation (Burton and Dewane,1953), heritability in broad sense and genetic advance (Johnson *et al.*, 1955).

RESULTS AND DISCUSSION

The analysis of variance revealed significant differences among the genotypes for all the characters indicating the presence of significant genetic variability in the genotypes studied (Table 1).Similar results of significant values for ANOVA was reported by Hemavathy*et al.* (2015), Dhoot *et al.* (2017), Sheena *et al.* (2021) andSanthiPriyaand RatnaBabu(2021)in mung bean. The estimated values of mean, range, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability ($h^2_{(b)}$) and genetic advance as per cent of mean (GAM) are presented in Table 2.

Days to 50% flowering

The mean value noted for the trait, days to 50% flowering, in the germplasm was 34.25 days with the range from 29.66 (LGG-603) to 38.66 days (MH-318). The estimates of PCV and GCV were low (7.8 and 5.2) and there was less difference between phenotypic and genotypic variance indicating low environmental influence. Sheena *et al.* (2021) also reported similar trend in their study.Moderate heritability in broad sense (45%) with low genetic advance as per cent of mean (7.3) was observed for this trait indicating the role of non-additive gene action in the inheritance of this trait and can be exploited by heterosis breeding. Nand and Anuradha (2013) reported high heritability and moderate genetic advance for this trait..

Plant height

The range of variation for this character varied from13.6 cm (MH-318) to 68.38cm (LGG-604) with a mean of 39.85cm. The estimates of PCV and GCV were high (40.7 and 37.7) indicating high variability for this trait in the evaluated germplasm lines which can be exploited for generating varied genotypes for different climatic conditions. High heritability (87%) along with high genetic advance (72.08) was observed for plant height indicating the role of additive gene action in the expression and desired results may be obtained by simple selection. Rahim *et al.* (2010), Reddy *et al.* (2011), Sao *et al.* (2014) and Kaur *et al.* (2017) also reported additive gene action for this trait.

Number of clusters/plant

The trait, number of clusters/ plant, recorded mean values of 4.3 and the range was 2.1 (PusaRatna) to 10.6 (LGG-595). The estimates of PCV and GCV were moderate (45.8 and 42.0) indicating existence of medium variability for this parameter in the studied material. High heritability (84%) and high genetic advance (79.4) were observed for number of clusters/plant indicating the predominant role of additive gene action and desired results may be obtained by simple selection. Azam*et al.* (2018) reported additive gene action and high heritability for this trait in their study.

Number of branches /plant

The mean no. of branches per plant in the studied material was 3.78 while the range observed was 1.4 (IPM 288) to 7.9 (Pusa Vishal). The estimates of PCV and GCV were low (48.6 to 49.9) and there was less difference between phenotypic and genotypic variances indicating less environmental influence on the expression and the presence of less variability among the genotypes for this trait. High heritability (93%) and high genetic advance as per cent of mean (93.2) were observed for branches/plant indicating the preponderance of additive gene action in the inheritance of branches per plant and offers the scope for improvement through simple selection procedures. Rao *et al*. (2006) andSheena *et al.* (2021) also reported additive gene action and high heritability for this trait in greengram while Geeta Chaudhary *et al*. (2012) in chick pea.

Pod length

The range for pod length was 4.90 (LGG-644) to 8.92 cm (WGG-42) with a mean value of 6.31 cm. The estimates of PCV and GCV were moderate (18.3 to 11.7) and difference between the phenotypic and genotypic variance was medium indicating the role of environmental influence on the expression of the trait. Medium heritability (40) with medium genetic advance (15.38) was observed for pod length indicating the role of non-additive gene action in the expression of this trait.Similar results were reported by Reddy *et al*. (2011) in mung bean.

Number of seeds/pod

The mean value noted for seeds per pod was 9.23 ranging from 6.4 (MH 96-1) to 12.8 (LGG-603). The estimates of PCV and GCV were moderate (19.7 to 15.2) indicating moderate variability in the studied material for this trait. High heritability (59%) with high genetic advance (24.3) was observed for no. of seeds/pod indicating the operation of additive gene action in the inheritance of this trait that could be targeted by phenotypic selection and further genetic improvement through simple selection method. Similar results were also reported by Singh *et al.* (2009) and Reddy *et al*. (2011).

Number of pods/plant

The trait, pods per plant, showed a mean value of 12.6 and the range was 5.7 (MH-318) to 24 (LGG-625). The estimates of PCV and GCV were high (32.6 to 30.0) and the values of phenotypic and genotypic variance was closer to each other indicating less environmental influence. These results are in accordance with the earlier reports of Sheena *et al.* (2021)in mung bean.High heritability (84%) with high genetic advance as percent of mean (57.03) was observed for pods/plant indicating the role of additive gene action and desired result may be obtained by simple selection method. Rahim *et al.*

(2010), Reddy *et al.* (2011), Godakh*et al.* (2013), Kaur *et al.* (2017) and Sheena *et al.* (2021) also reported additive gene action in the expression of this trait.

Days to maturity

The mean value noted for days to maturity was 67.9 days while the range observed was 58 days in MGG-385 to 80 days in LGG-644 and LGG -407. The estimates of PCV and GCV were low (7.5 to 5.9) and the less difference between phenotypic and genotypic variances indicated low environmental influence on the expression of this trait. Sheena *et al*. (2021) also recorded similar results in their study for this trait.High heritability (62) with low genetic advance as per cent of mean (9.7) was observed indicating the operation of additive and non-additive gene actions in the expression of this trait. Similar results were also reported by Rao *et al*. (2006) and Sheena *et al.* (2021).

Yield/plant

The range of values for yield per plant in the studied germplasm was 2.33g (MH-318) to 9.30g (LGG-595) with a mean value of 5.04g. The estimates of PCV and GCV were low (40.6 to 37.3) and there was less difference between phenotypic and genotypic variances indicating medium environment influence on the expression of this trait. Singh*et al*. (2009) also noted the similar PCV and GCV values for this trait. High heritability (84%) with high genetic advance as per cent of mean (70.6) was observed indicating the role of additive gene action and desired result may be obtained by following simple selection procedures. Reddy *et al*. (2011), Kaur *et al.* (2017) and Sheena *et al*. (2021) also reported additive gene action in the expression of this trait in their studies.

High heritability in conjunction with high genetic advance as per cent of mean were recorded for the traits, plant height, clusters/plant, branches/plant, pods/plant, seeds/pod andyield /plant indicating the preponderance of additive gene action in the inheritance of these traits and offers the scope for further improvement through breeding procedures with simple selection.

Table 1. Analysis of variance of components in greengram (*Vignaradiata* L.)

Source	d.f.	Days to 50% flowering	Plant height (cm)	Clusters/ plant	Branches/ plant	Pod length	Seeds/pod	Pods/plant	Days to maturity	Yield/ plant (gm)
		Mean squares								
Replications	2	7.153	87.52	0.012	0.012	1.55	0.92	0.28	18.74	1.19
Treatments	47	13.69***	710.64***	10.73***	9.68***	2.43***	7.32***	46.1***	59.43***	11.32***
Error	94	3.91	31.84	0.637	0.23	0.79	1.34	2.58	10.04	0.66

*** = Significance at 5% level

Table 2. Mean, genetic variability, heritability (broad sense) and genetic advance as per cent of mean for yield and yield components in greengram (*Vignaradiata*L.)

S. No.	Character	Mean	Range		Coefficient of variation		Heritability (%)	Genetic advance as per cent of mean
			Minimum	Maximum	GCV (%)	PCV (%)	(broad sense)	
1	Plant height (cm)	39.85	13.60	68.38	37.70	40.30	87	72.08
2	Days to 50% flowering	34.20	29.60	38.66	5.27	7.81	45	7.31
3	Number of Clusters/plant	4.36	2.12	10.60	42.00	45.80	84	79.44
4	Number of Branches/plant	3.78	1.40	7.90	46.90	48.60	93	93.24
5	Pod length (cm)	6.31	4.90	8.92	11.70	18.30	40	15.38
6	Number of Seeds/pod	9.23	6.40	12.80	15.20	19.70	59	24.33
7	Number of Pods/plant	12.60	5.79	24.00	30.00	32.60	84	57.03
8	Days to maturity	67.90	59.00	80.00	5.97	7.58	62	9.70
9	Yield /plant	5.04	2.33	9.300	37.30	40.60	84	70.62

PCV = Phenotypic coefficient of variation GCV = Genotypic coefficient of variation

ACKNOWLEDGEMENTS

The First author is thankful to the Acharya NG Ranga Agricultural University for providing the financial help in the form of stipend during M.Sc. (Ag.) programme.

REFERENCES

Burton, G.W. and Dewane, E.H. (1953). Estimating heritability in tall Fasciae (*Fescuta arundinacea* L.) from replicated clonal material. *Agronomy Journal*.45: 478-481.

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.

Chaudhary, Geeta, Dahiya, B.S., Singh, Dhirendra, Kumar, Jitendra, Singh, Gyanendra, Tomar, Rahul and Dahiya, Arti (2012). Genetic variability in different environment in chickpea (*Cicer arietinum* L.).*Journal of Plant Development Sciences*.4 (2): 299-303.

Godakh, 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). *Bioinfolet*.10(2A): 441- 447.

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.

Indiastat (2017-18). Ministry of Agriculture, government of India. 2017-18. *http://www.indiastat.com*

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

Kale, U.R., Kalpande, S., Annapurve, S.N. and Gite, V.K. (2007). Yield components analysis in American cotton (*Gossypiumhirsutum* L.). *Madras Agricultural Journal*. 94 (7-12): 156-161.

Kaur, S., Bains, T.S. and Singh, P. (2017). Creating variability through interspecific hybridization and its utilization for genetic improvement in mungbean [*Vigna radiata* (L.) Wilczek]. *Journal of Applied and Natural Science*. 9 (2): 1101-1106.

Makeen, K., Abrahim, G., Jan, A. 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.

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

Rahim, M.A., Mia, A.A., Mahmud, F., Zeba, N. and Afrin, K.S. (2010). Genetic variability, character association and genetic divergence in mung bean (*Vignaradiata* (L.) Wilczek). *Pakistan Orthodontic Journal.* 3(1):1-6.

Rao, M., Rao, K.Y. and Reddy, M. (2006). Genetic variability and path analysis in mung bean. *Legume Research.* 29(3): 216-218.

Reddy, D.K.R., Venkateswarlu, O., Obaiah, M.C. and Jyothi, G.L.S. (2011). Studies on genetic variability, character association and path coefficient analysis in green gram (*Vigna radiata* (L.) Wilczek). *Legume Research*. 34(3): 202-206.

SanthiPriya, Ch. and RatnaBabu, D. (2021). Genetic parameters of variation and character association for seed yield and its attributes in mungbean (*Vigna radiata* L. Wilczek). *Legume Research.* Doi: 10.18805/LR-4498.

Sao, M.S., Nair, S.K., Sao, Fakeer Chand, Yadav, Sanjay Kumar and Paikara, Sourabh (2014). Genetic variability, correlation and pathcoefficient analysis of some yield components of mungbean (*Vigna radiata* L.).*Journal of Plant Development Sciences*. 6 (3): 461-464.

Sheena Sabatina, A., Lal Ahamed, M., Ramana, J.V. and Harisatyanarayana, N. (2021). Genetic variability studies in mungbean (*Vignaradiata* L.). *The Pharma Innovation Journal*. 10(6): 906-909.

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