LR-4463
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RESEARCH ARTICLE Legume Research- An International Journal, Volume Issue : ()

Genetic Relationship and Assessment of Variability of Mungbean [*Vigna radiata* (L.) Wilzek] Genotypes Based on Morphological Traits

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10.18805/LR-4463

ABSTRACT

Background: The present investigation was undertaken to examine the genetic variability and relationship between traits among the 73 germplasm lines of mungbean collection of diverse nature. Genetic variability and association studies play an important role in developing a new genotype. The mungbean productivity remains low in India because of low genetic base for yield improvement, absence of variability for yield traits, poor ideotype of mungbean plant, inadequate management of the crop, weed infestation and susceptibility to biotic and abiotic stresses. Genetic variability is most important factor of success of any crop improvement programme.
Methods: An experiment was conducted in a completely randomized block design with two replication at Regional Agricultural Research Station, Sagar, Madhya Pradesh in high productive black cotton soils during *kharif* 2016 on 73 mungbean genotypes.
Result: The study revealed that the mean sums of squares due to genotype were highly significant for all the morphological traits. High estimates of heritability and genetic advance were recorded for clusters per plant, no. of branches per plant, days to maturity, seed yield, days to 50% flowering; plant height and no. of pods per plant indicating the role of additive gene effects with low environmental influence for the determination of these traits and simple phenotypic selection may be effective. The results also indicated improvement through direct selection for these traits can increase directly the grain yield in mungbean. Genotype Pusa Baisakhi, HUM-16, IPM-02-03, IPM-02-19, PM-5, AKM-9904, COGG-912 and RMG-991 were found good donors for these traits in recombinant breeding programme for yield enhancement in mungbean.

Key words: Association, Correlation, Diversity, Genetic variability, Genotype.

INTRODUCTION

Mungbean is a nutritious, short duration important pulse crop grown in India. It is a very ancient crop cultivated in China over more than 2000 years. Mungbean is also grown in many countries like Thailand, Philippines, Vietnam, Indonesia, Malaysia, South China and Korea. In India, mungbean is cultivated in 47.57 lakh hectare area with 23.48 lakh tonne production. But the productivity in India is 494kg per hectare (Source: DES, Ministry of Agriand FW, DAC and FW, Govt. of India 2018-19) which is very low when compared with other pulses. To increase productivity and production of this crop, development of new high yielding genotypes is a prime goal of mungbean breeding. It is a good source of digestive protein (28%) and easy to cook than other pulses. Mungbean is a rich sources of Iron (5.9-7.6) mg/100g (Dahiya *et al,.* 2015). It also contains 132 mg calcium and 367 mg phosphorus per 100g of seed. Therefore, mungbean is suitable for alleviating malnutrition in India. Mungbean is a short duration crop and it is highly suitable for multi cropping system. If we included in our cropping pattern, we can grow 3 to 4 crops in a year. Mungbean is also suitable for rice-wheat cropping system at Indo-Gangatic plain of India (Brar *et al*., 2004). It will be increase fertility level of soil, production and economic returns of farmers. Every year India imports around 1.5 lakh tonne mungbean and in curssizable depletion of foreign exchange reserves. It has a tap root system with nodule formation which has ability to survive in moisture stress conditions with fixation of atmospheric nitrogen in the soil. When rotated with wheat crop improved the nutritional value of wheat grain (Ilyas *et. al.* 2018). The mungbean productivity remains low in India because of its low genetic base for improvement of high yielding genotypes, absence of variability, poor ideotype of mungbean plant, poor management of crop, weed infestation and susceptibility to biotic and abiotic stresses (Souframanian and Gopal krishnan 2004). Genetic variability is most important factor of success of any crop improvement programme. The study of genetic variability present in different characters and their nature of heritability are the pre-requisites for an efficient crop improvement programme. Therefore the present study

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How to cite this article: Kumar, V. (2021). Genetic Relationship and Assessment of Variability of Mungbean [*Vigna radiata* (L.) Wilzek] Genotypes Based on Morphological Traits. Legume Research. DOI: 10.18805/LR-4463.

Submitted: 20-07-2020 **Accepted:** 15-12-2020 **Online:** 12-03-2021

was attempted to assess the genetic variability, heritability, genetic advance, GCV, PCV and correlation in morphological characters in73 mungbean genotypes.

MATERIALS AND METHODS

An experiment was conducted in a completely randomized block design with two replications at Regional Agricultural Research Station, Sagar, Madhya Pradesh in black cotton soils during *kharif* 2016. Each plot comprised 2 rows of 3 meter length with 30 cm distance between rows and 10 cm between plants. The all good agronomic practices for crop management are applied. Seventy-three Mungbean germplasm were used in the experiment obtained from Indian Agricultural Research Institute, New Delhi included released varieties advance lines, indigenous and exogenous lines. These lines are developed at different part of India for the cultivation (Table 1).

The data on nine morphological characters *viz.*, days to 50% flowering, days to maturity, plant height (cm), No. of branches/plant, No. of pods/plant, clusters/plant, pods/clusters, seeds/pods and seed yield/plot were recorded.

Analysis of variance and correlation coefficients for the observations were calculated by web agri state package 2.0 online data analysis software developed by ICAR- Central Coastal Agricultural Research Institute. The estimation PCV and GCV were calculated according to the formula given by Burton and De Vane (1953) and Singh and Choudhary (1985)-

$$\text{PCV}=\frac{\sqrt{\sigma_p^{\,2}}}{\overline{X}}\times 100 \quad \text{GCV}=\frac{\sqrt{\sigma_p^{\,2}}}{\overline{X}}\times 100$$

Where

$\sigma^2 g$ = genotypic variance, $\sigma^2 p$ =phenotypic variance,

$\overline{X}$ =General mean of character.

The genetic advance (GA) was estimated by following Robinson *et al.*

(1949) equation-GA= $K\sigma p h^2$

Where,

K = Constant, selection differential at 5% selection intensity *i.e.*, 2.06,

σp= Phenotypic standard deviation, h^2= Heritability in broad sense in fraction.

RESULTS AND DISCUSSION

Analysis of variance and genetic variability

The mean sum of squares for different morphological traits of mungbean genotypes is given in Table 2. All the traits under study showed considerable genetic variability. The analysis of variance of indicated that the mean sums of squares due to genotype were highly significant for all the morphological traits, suggesting presence of sufficient variation among genotypes for these characters.

An insight into the nature and magnitude of genetic variability present in the gene pool is of immense value for starting any systematic breeding programme because of considerable genetic variability in the base material ensures better chances of evolving desirable plant type. Patel *et al.,* (2012), Vir and Singh (2016) and Singh *et al.,* (2016) also revealed significant differences for all the traits studied.

The estimates of genetic variability *viz*, phenotypic coefficient of variation (PCV), genotypic coefficient variation (GCV), heritability, genetic advances are important in determining the method of selection to improve a particular plant population for a specific trait. The estimates in Table 3 indicated that high heritability is not necessary association with high genetic advance. It showed that the estimates phenotypic coefficient of variation (PCV) was higher than that genotypic coefficient variation (GCV) for all the morphological traits, indicating greater influence of environment on these traits as also reported earlier by Muthuswamy *et al*., (2019).

Table 1: List of Mungbean germplasm selected for experiment.

S. No.	Genotypes	S. No.	Genotypes
1.	PusaBaisakhi	38.	Ganga-8
2.	Pusa Vishal	39.	TM-96-2
3.	PusaRatna	40.	TM-96-25
4.	PS-16	41.	ML-512
5.	Pusa -105	42.	ML-818
6.	Pusa -0672	43.	ML-1299
7.	Pusa -0831	44.	ML-1451
8.	Pusa -0871	45.	ML-1464
9.	Pusa -1031	46.	ML-2037
10.	Pusa -1033	47.	AKM-9904
11.	Pusa -1333	48.	COGG-912
12.	Pusa -9072	49.	LGG-460
13.	Pusa -9531	50.	RMG-991
14.	MH-2-15	51.	RMG-1087
15.	MH-96-1	52.	EC-398885
16.	MH-318	53.	EC-398891
17.	MH-421	54.	EC-520024
18.	MH-521	55.	EC-520026
19.	MH-565	56.	EC-520029
20.	MH-805	57.	EC-520038
21.	HUM-1	58.	EC-520041
22.	HUM-2	59.	EC-550851
23.	HUM-6	60.	KM-11-10
24.	HUM-12	61.	SM-11-75
25.	HUM-16	62.	M-209
26.	IPM-02-03	63.	V-1138
27.	IPM-02-14	64.	V-3518
28.	IPM-02-15	65.	V-6173
29.	IPM-02-17	66.	Bhutan LM-1
30.	IPM-02-19	67.	Bhutan LM-2
31.	IPM-288	68.	Bhutan LM-95
32.	IPM-205-4	69.	China Mung
33.	IPM-205-7	70.	Parkesh Nepal
34.	IPM-406-1	71.	PLM-167
35.	IPM-409-4	72.	PLM-271
36.	PM-5	73.	BMGP-1
37.	PDM-139	-	-

High PCV with High GCV estimates were observed for clusters per plant, no. of branches per plant, days to maturity which are akin to the results of Azam *et al*., (2018) for pods per plant, plant height and 100 seed weight and Asari *et al*., (2019) observed for primary branches per plant, pods per plant, seed yield per plant and clusters per plant. Moderate PCV and GCV were found for days to 50% flowering, seed yield per plot, plant height and no. of pods per plant. Similar results were also reported by Singh *et al*., (2015) for no. of seed per pods and plant height, while Raturi *et al*., (2015) for seed yield, plant height and no of pods per plant. The lowest PCV and GCV estimates have been recorded for pods per cluster and such lowest estimates have been indicated by Alemu *et al*., (2014) for days to flowering and seeds per plant. Heritability and genetic advance serve as predictive function of genotypic performance in a succeeding generation but eventually guide the breeder in effective selection. High value of heritability coupled with high genetic advance as percentage of mean observed for clusters per plant, no. of branches per plant, days to maturity, seed yield, days to 50% flowering, plant height and no. of pods per plant. This clearly brought out the role of additive gene effects with low environmental influence in the inheritance of these traits suggesting phenotypic selection may be effective for improving these traits. These findings are in agreement with Malli *et al*., (2018) for the traits like biological yield per plant, branches per plant, no of pods per plant.

High heritability coupled with low genetic advance estimates for pods per clusters observed in the present study explains preponderance of the non additive gene action. The high heritability observed may due to be the favorable influence of environment. The presence of non additive gene action can be exploited better through recombination breeding. These findings are also in agreement with Roy chowdhury *et al*., (2012) for the trait plant height and Suresh *et al*., (2010) for days to maturity. Low heritability coupled with low genetic advance recorded for seeds per pods suggested that the trait is highly affected by environment and phenotypic selection would be ineffective. Similar estimates also reported by Mehandi *et al*., (2013) for the trait pod length (cm).

Correlation and character association

Correlation is essential for making efficient selection strategies by the geneticists and breeders. Correlation coefficient estimates are extensively used to measure the degree and direction of associations between various attributes including grain yield, consequently correlation coefficient analysis was done to understand the relative importance of the component traits and start an effective selection or breeding programme. The results in Table 4 indicated that genotypic correlation coefficients were higher than the phenotypic correlation coefficients for most of the traits. At genotypic level, seed per pod (r=0.478), no. of branches per plant (r=0.396), plant height (r=0.387), no. of pods per plant (r=0.273) and clusters per plant (r=0.197) were significant and positively correlated with seed yield per plot. Similar results were observed by Tah (2008). Dhole and Reddy (2018) also reported positive correlation coefficients for clusters per plant, pods per cluster and seeds

Table 2: Analysis of variance for different morphological characters of mungbean germplasm.

Source of variation	Degree of freedom	Mean sum of squares								
		Seed Yield /plot (g)	Days to 50 % flowering	Days to maturity	Plant height (cm)	No. of br./plant	No. of Pods/ plant	Clusters/ plant	Pods/ cluster	Seeds/ pod
Replications	1	448.877	0	4.993	38.322	2.712	16.987	1.887	1.842	44.938
Genotypes	72	3093.493**	9.007**	3.198**	99.445**	0.442**	27.904**	2.163**	1.593**	4.399**
Error	72	5.154	0.708	0.743	0.524	0.027	0.144	0.033	0.05	0.252
Sem±		1.605	0.594	0.609	0.511	0.116	0.268	0.128	0.158	0.354
CD (P=0.05%)		4.525	1.677	1.718	1.442	0.328	0.744	0.361	0.444	1.001

**Highly significant at 1% and 5 % level of significance

Table 3: Estimates of parameters of genetic variability for 9 characters in 73 Mungbean germplasm.

Character	Mean	Range		PV	GV	PCV %	GCV %	Heritability%	Genetic Advance	GA %over mean
		Min.	Max.							
Seed Yield(g/plot)	98.64	26.50	195.50	49.98	49.46	19.17	19.07	99.0	14.41	39.07
Days to 50 % flowering	39.68	34.50	44.50	0.23	0.20	19.52	18.36	88.4	0.88	35.57
Day to maturity	70.39	68.50	74.50	1.09	1.06	22.81	22.46	97.0	2.09	45.58
Plant height (cm)	36.87	22.15	59.90	0.80	0.77	17.83	17.47	95.9	1.77	35.24
No. of branches/ Plant	2.48	1.55	4.30	14.02	13.88	28.41	28.26	99.0	7.63	57.93
No. of Pods/plant	13.17	3.50	27.50	2.32	2.07	14.57	13.76	89.2	2.80	26.77
Clusters/plant	4.59	2.55	8.10	1549.32	1544.16	39.90	39.83	99.7	80.81	81.92
Pods/ cluster	5.02	3.10	7.80	4.85	4.14	5.55	5.13	85.4	3.87	9.77
Seeds/pod	10.46	6.75	13.60	54.73	1.22	10.51	1.57	2.2	0.34	0.48

Table 4: Estimate of Genotypic (above diagonal) and Phenotypic (below diagonal) correlation coefficients for morphological traits in Mungbean germplasm.

Character	Seed Yield/plot (g)	Days to 50 % flowering	Days to maturity (cm)	Plant height	No. of br./plant	No. of Pods/ plant	Clusters/ plant	Pods/ cluster	Seeds/ pod
Seed Yield(Kg/ha)	**1**	-0.219*	0.106	0.387**	0.396**	0.273**	0.197*	0.084	0.478**
Days to 50 % flowering	-0.210*	**1**	0.510**	0.394**	0.928**	0.367**	0.326**	0.001	-0.235*
Day to maturity	0.015	0.082	**1**	0.646**	0.185*	0.452**	0.295**	0.140	0.110
Plant height (cm)	0.386*	0.361**	0.096	**1**	0.419**	0.530**	0.447**	0.159	0.285**
No. of branches/Plant	0.320**	0.990**	0.031	0.397**	**1**	0.622**	0.535**	0.468**	0.324**
No. of Pods/plant	0.273**	0.334**	0.066	0.527**	0.592**	**1**	0.547**	0.277**	0.181*
Clusters/plant	0.198*	0.289**	0.041	0.440**	0.490**	0.535**	**1**	0.138	0.258**
Pod/ cluster	0.087	0.000	0.020	0.164	0.417**	0.276**	0.140	**1**	0.237**
Seed/pod	0.458**	-0.209*	0.015	0.273**	0.299**	0.175	0.263**	0.232**	**1**

**Highly significant at 1% and 5 % level of significance.

per pod. This result indicates improvement through direct selection of these traits can result directly in enhanced grain yield in mungbean. Days to 50% flowering (r=-0.219) showed significant and negative genotypic correlation with seed yield. This result was also in agreement with the studies of Mahanta and Sao (2019). Days to 50% flowering showed significant and positive correlation with no. of branches per plant (r=0.928), days to maturity (r=0.510), plant height (r=0.394), no. of pods per plant (r=0.367) and clusters per plant (r=0.326) while negative and significant correlation with seeds per pod (r=-0.235). Similar result has also been revealed by Varma *et al*., (2018) for days to maturity, primary branches, plant height but was negatively correlated with 100 seed weight, yield per plant, pod length, seed per pod, pods/ plant and cluster/ plant. Plant height (r=0.646) was significantly associated with days to maturity along with no. of pods per plant (r=0.452), clusters per plant (r=0.259) and no. of branches per plant (r=0.185). These results were also in agreement with Lal and Singh (2014) for plant height. Plant height showed significant and high correlation coefficient with no. of pods per plant (r=0.530), clusters per plant (r=0.447), no. of branches per plant (r=0.419) and seeds per pod (r=0.285).No. of branches per plant showed significant high positive association with no. of pods per plant (r=0.622), clusters per plant (r=0.535), pods per plant (r=0.324). Similar result was also revealed by Varma *et al*., (2018) for primary branches per plant was positively correlated with pods per plant.

Clusters per plant (r=0.547) was significantly and positively correlated with no. of pods per plant along with the pods per cluster (r=0.277) and seeds per pod (r=0.181) and showed significant and positive correlation coefficient with seeds per pod (r=0.258) and also pods per cluster was positively and significantly associated with seeds per pod (r=0.237).

CONCLUSION

The result of this study revealed that the morphological traits like clusters per plant, no of branches per plant, days to maturity showed high GCV and PCV. The results of heritability exhibits that high estimates of heritability and genetic advance were recorded for clusters per plant. It means that mainly the heritability is due to additive gene effects with low environmental influence for the determination of these traits and phenotypic selection may be effective with simple plant selection. The correlation results indicated that genotypic correlation coefficients higher than the phenotypic correlation coefficients for most of the traits. Correlation is essential for making efficient selection strategies by the geneticists and breeders.

ACKNOWLEDGEMENT

The author is greatly thankful to the Dr H. K. Dikshit, Principal Investigator, Mungbean, IARI, New Delhi for providing genotypes for conducting this experiment. I wish to give special thanks to IIPR Kanpur and Jawaharlal Nehru KrishiVishwaVidyalaya for finance and other facilities.

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