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Analysis of Genetic Parameters for Yield, Quality and Related Traits in Mungbean [*Vigna radiata* (L.) Wilczek] Genotypes

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ABSTRACT

Background: The present investigation was effectuated to study mungbean germplasms with an objective to estimate the genetic variability parameterssuch as coefficient of variation, heritability andgenetic advance for yield and its contributing traits.

Method: The experimental material comprises of forty mungbean genotypes evaluated during *Kharif*-2017. An experimental study was conducted with emphasis on the selection of superior along with highly variable genotypes thatwere analyzed in Randomized Block Design (RBD) with three replications.

Result: The results of the analysis of variance (ANOVA) revealed thatthe genotypic variations were significant for all of the traits and magnitude of variation was found high for clusters per plant followed by harvest index and seed yield per plant. High heritability coupled with high genetic advance was recorded for clusters per plant (96.00%, 65.48%), seed yield per plant (96.00%, 45.78%), pods per plant (93.00%, 44.81%), harvest index (86.00%, 44.42%). Thus, the present findings could be beneficial to develop superior genotypes through selection in mungbean breeding program.

Key words: Variability, Heritability, Mungbean, Selection.

INTRODUCTION

Mungbean [*Vigna radiata* (L.) Wilczek] (2n=2x=22) also known as greengram/green bean/mash bean or golden gram belongs to the family *Leguminaceae* and is an excellent source of easily digestible proteins with low flatulence which complements the staple diet in Asia. Its seeds are utilized in making dal, curries, soup, sweets and snacks *etc*. The sprouted seeds contain a goodamount of vitamins such as Thiamine, Niacin and Ascorbic acid (Dahiya *et al.* 2015). Thus, mungbean sprouts are increasingly becoming popular in certain vegetarian diets. The grains contain approximately 25-28% protein, 1.0-1.5% oil, 3.5-4.5% fibre, 4.5-5.5% ash content and 62-65% carbohydrates on dry weight basis. Greengram also contains vitamin A, vitamin C, iron, calcium, magnesium, phosphorus, potassium, zinc and foliate. Unlike other pulses, it doesn't produce flatulent effects in the stomach (Dahiya *et al.* 2015). Therefore, it is fed to babies and to the elders as a convalescents. Greengram is a widely cultivated crop throughout South Asia including India, Pakistan, Bangladesh, Sri Lanka, Thailand, Cambodia, Vietnam, Indonesia, Malaysia and South China. In India, it is the third most important pulse crop after chickpea and pigeonpea. It is grown mainly as a *Kharif* crop. However, it can be cultivated in the *Rabi* season as well in the eastern and southern parts of the country. It is suited for crop rotation, intercropping and mixed cropping systems owing to its short duration.

In any crop improvement program,the study of the amount of variability present in crop species is a pre-requisite, as it provides the basis for effective selection of desirable genotypes towards crop improvement. A clear understanding of variability in various quantitative characters existing in the breeding material helps plant breeders for selecting superior genotypes based on different genetic parameters such as genotypic variation, heritability, genetic gain, *etc*. to understand the nature and magnitude of variation for the available plant characters (Burton and Devane, 1953). Hence, it is necessary to estimate the relative amount of genetic and non-genetic variability exhibited by the traits under the study. The average yield of mungbean is very low in India and year-to-year variation in yield is remarkably high. Therefore, there is an urgent need to design a breeding program that can enhance productivity and stabilize the yield. It has also been well established that the greater the genetic variability in the population

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greater will be the chance of obtaining desirable gene contribution. Previous studies have been in consonance with the present study with respect to greengram (Kushwaha *et al.* 2013, Degefa *et al.* 2014, Jebaraj *et al.* 2015, Baisakh *et al.* 2016 and Kumar *et al.* 2020) and other related pulses (Punia *et al.* 2014 in urdbean, Sahoo *et al.* 2019) in mothbean. Asthe population in the country is rapidly increasing, therefore, there is an urgent need to provide high yield varieties to meet this increasing demand. Therefore,the present study has been undertaken to study genetic variability for different quantitative characters in greengram germplasms.

MATERIALS AND METHODS

The research experiment was carried out during *Kharif* 2017 comprising of 40 greengram genotypes at the Experimental Farm, Sam Higginbottom University of Agriculture, Technology and Sciences, Allahabad, Uttar Pradesh India (Table 1). All the genotypes to be used for present study were procured from Department of Genetics and Plant Breeding, SHUATS, Allahabad. Recommended agronomic packages of practices were followed for obtaining a good crop. The technique of random sampling was adopted for recording the observations of various quantitative characters of greengram. Five plants of each treatment from each replication were selected at random while recording the data on various characters. Data of five plants were averaged replication wise and mean data was used for statistical analysis. Observations were recorded for thirteen characters *viz.*, days to 50% flowering (DF), days to maturity (DM), plant height (PH), number of primary branches per plant (PBP), number of clusters per plant (CPP), number of pods per plant (PPP), pod length (PL), seeds per pod (SPP), biological yield per plant (BYP), protein content (PC), seed index (SI), harvest index (HI) and seed yield per plant (SYP). Mean performance for genotypes to be used in present study has been reported earlier in International Conference (Kumar *et al.* 2020).

Macro Kjeldahl method

To estimate protein content, each grinded mungbean sample (1 g) was digested with concentrated sulphuric acid in the presence of cuproic sulphate and sodium sulphate and heated to release ammonia gas which is distilled into a boric acid solution. The total nitrogen persent in ammonia was estimated through titration with 0.1 M HCl until the purple-pink color was observed. The assumed nitrogen value was multiplied with a factor of 6.25 to get total protein in the sample (AOAC, 1975).

Analysis of variance

The analysis of variance (ANOVA) was worked out to test the differences among the genotypes by F-test. It was carried out according to the procedure of randomized block design for each character as per methodology advocated by Panse and Sukhatme (1985).

Genetic variability parameters

Following genetic variability parameters worked out-

Mean

Mean value of each character was worked out by dividing the totals by the corresponding number of observations.

Range

It was taken as the difference between the highest and lowest mean value for each character.

Components of variance

Two types of variance components (genetic and phenotypic variances) were calculated by the formula suggested by Burton and Devane (1953).

Coefficient of variations (CV)

It is the measure of variability evolved. The coefficient of variation is the ratio standard deviation of the variable traits to its mean and expressed in percentage which was suggested by Sivasubramanian and Madhavamenon (1973). As genotypic value is more important for crop improvement program so that CV could be divided into two part namely genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV).

Heritability

Heritability is the ratio of genotypic variance to the total variance that was calculated by the formula given by Lush (1949) and Burton and Devane (1953). Since in present study genetic variability analysed in different germplasm therefore, only broad sense heritability could be worked out.

Genetic advance

Improvement in the mean genotypic value (performance) of selected plants (progeny or lines) over the parental population (base population) is known as genetic advance which was calculated according to the formula suggested by Johanson *et al.* (1955).

RESULTS AND DISCUSSION

Analysis of Variance (ANOVA)

Genetic variability in any crop improvement program is the basic requirement for deciding the effectiveness of selection. Its existence is essential for resistance to biotic and abiotic factors as well as for wide adaptability. The assessment of genetic variability was the main objective of the present investigation. The analysis of variance presented in Table 2 indicated that the mean squares of genotypes was significantly different at 5% level of significance for days to flower initiation, days to 50% flowering (DF), days to maturity (DM), plant height (PH), number of primary branches per plant (BPP), number of clusters per plant (CPP), number of pods per plant (PPP), pod length (PL), seeds per pod (SPP), biological yield per plant (BYP), rotein Content (PC), seed Index (SI), harvest index (HI) and seed yield per plant (SYP).

Table 1: List of the genotypes used for present study.

S. no.	Name of genotypes
1	IPM 5-07
2	PUSA 1471
3	PUSA 1472
4	KM 2342
5	HUM 27
6	COGG 10-10
7	SGC 20
8	IGKM 05-26-3
9	RMG 1030
10	COGG 12-10
11	NVL 641
12	ML 2050
13	PM 9-11
14	IPM 9901-8
15	BM 2002-1
16	BM 2003-2
17	BPMR 145
18	ML 2333
19	BM 4
20	NDMK 13-1
21	KM-11-563
22	KM-11-575
23	KM-11-586
24	RMG-1040
25	ML-2024
26	BGS-9
27	BGS-11
28	MSJ-118
29	RMG-1083
30	PUSA-871
31	RMG-1039
32	RMG-268
33	RMG-1093
34	SML-668
35	JLM-1751
36	JLM-1752
37	JLM-1754
38	JLM-1757
39	JLM-1758
40	SAMARAT ©

The results indicated a wide range of variability among the genotypes. Similar results were recorded by Byregowda *et al.* (1997), Das and Chakraborty (1998), Kapoor *et al.* (2005), Eswari and Rao (2006), Hanif *et al.*(2006), Wani *et al.* (2009), Khan *et al.*(2008), Kamleshwar *et al.*(2013), Kushwaha *et al.* (2013), Degefa *et al.* (2014), Jebaraj *et al.* (2015), Baisakh *et al.* (2016) and Kumar *et al.* (2020) in greengram.

Genetic variability parameters

One of the important considerations in any crop improvement programme is the detailed study of genetic variability. Variability is measured by estimation of the mean genotypic and phenotypic coefficient of variation, heritability, genetic advance and genetic advance as percentage mean. Environment plays an important role in the expression of phenotype and genotype,a fact which is inferred from phenotypic observation. Hence, variability can be observed through biometric parameters like the genotypic coefficient of variation, heritability and genetic advance. This would help a breeder in evolving selection programs for genetic improvement of the crop plant.The estimates of variance, coefficient of variation, heritability and genetic advance for all the thirteen characters studied have been presented in Table 3.

Phenotypic and genotypic coefficient of variation

In the present investigation, it is depicted from Table 3 that in general, estimates of the phenotypic coefficient of variation were found higher than their corresponding genotypic coefficient of variation, indicating the little influence of environment on the expression of these characters. However, good correspondence was observed between genotypic coefficient of variation and phenotypic coefficient in all characters.

A wide range of phenotypic coefficient of variation (PCV) observed for all the traits ranged from 33.15 (number of clusters per plant) to 3.41 (days to maturity). A higher magnitude of PCV was recorded for number of clusters per plant (33.15), harvest index (24.80), the number of pods per plant (23.37), seed yield per plant (23.15), seed index (21.25) and the number of branches per plant (20.64). A moderate value of PCV was observed for the number of seed plants (17.51), plant height (15.83), biological yield per plant (14.00),and pod length (12.65). Whereas daysto 50% flowering (4.85), protein content (4.62) and days to

Table 2: Analysis of variance for thirteen characters of mungbean genotypes under present study.

Source of variation	Degree of freedom	Mean square												
		DF	DM	PH	BPP	CPP	PPP	PL	SPP	BYP	SYP	SI	HI	PC
Replication	3	0.77	0.46	6.24	0.03	0.06	0.06	0.06	0.18	0.54	0.03	0.07	12.53	0.22
Genotype	39	12.40**	16.74**	208.48**	2.29**	19.66**	49.86**	3.12**	11.89**	16.79**	5.60**	1.92**	248.75**	3.01**
Error	117	1.23	0.51	4.31	0.07	0.21	0.91	0.07	0.20	0.90	0.06	0.05	9.01	0.37

** Significant at 5% level.

Table 3: Estimates of genetic variability parameters for thirteen traits of mungbean genotypes.

Characters	Mean	PV	GV	PCV (%)	GCV (%)	Heritability (%)	GA	GA (as % of Mean)
DF (Nos)	41.39	4.02	2.79	4.85	4.04	69.00	2.87	6.92
DM (Nos)	62.54	4.57	4.06	3.42	3.22	89.00	3.91	6.26
PH (cm)	47.00	55.35	51.04	15.83	15.20	92.00	14.13	30.07
BPP (nos)	3.84	0.63	0.56	20.64	19.41	88.00	1.44	37.60
CPP (nos)	6.79	5.07	4.86	33.15	32.46	96.00	4.45	65.48
PPP (nos)	15.52	13.14	12.24	23.37	22.55	93.00	6.95	44.81
PL (cm)	7.23	0.84	0.76	12.65	12.07	91.00	1.72	23.73
SPP (nos)	10.09	3.12	2.92	17.51	16.93	93.00	3.40	33.73
BYP (g)	15.77	4.87	3.97	14.00	12.64	81.00	3.71	23.50
SYP (g)	5.19	1.44	1.38	23.15	22.68	96.00	2.38	45.78
SI (g)	3.38	0.52	0.47	21.25	20.22	90.00	1.34	39.61
HI (%)	33.48	68.94	59.94	24.80	23.13	87.00	14.87	44.42
PC (%)	21.97	1.03	0.66	4.62	3.70	64.00	1.34	6.09

Note: Units for mean, GV, PV and GA are similar as unit of concerned trait.

maturity (3.41) depicted the least phenotypic coefficient of variation. Loganathan *et al.* (2001) recorded high Phenotypic Coefficient of Variation for number of clusters per plant and seed yield per plant and Kumar *et al.* (2010) also reported moderate PCV for number of seeds per plant, followed by seed yield per plant, number of pods and number of branches per plant.

Genotypic coefficient of variation (GCV) ranged from 32.46 (number of clusters per plant) to 3.22 (days to maturity). A higher magnitude of PCV was recorded for number of clusters per plant (32.46), harvest index (23.13), seed yield per plant (22.68), number of pods per plant (22.55) and seed index (20.22). A moderate value of GCV was observed for the number of branches per plant (19.41),the number of seed plant (16.93), plant height (15.20), biological yield (12.64) and pod length (12.07). Whereas, days to50% flowering (4.04), protein content per plant (3.70) and days to maturity (3.22) depicted the least phenotypic coefficient of variation. Sirohi *et al.* (2006) observed significant variability for GCV for clusters per plant, productive branches per plant, productive pods per plant, biological yield and seed yield. Kumar *et al.* (2010) also reported moderate GCV for number of seeds per plant, followed by seed yield per plant, number of pods and number of branches per plant. Das *et al.* (1998) reported that plant height, branches per plant, pods per plant, pod length and yield per plant had a high genotypic coefficient of variation suggesting the possibility of improvement of greengram by selective breeding.On an average, the higher magnitude of GCV and PCV were recorded for pods per plant, branches per plant, clusters per plant and seed yield suggesting sufficient variability and thus, scope for genetic improvement through selection for these traits.Similar finding was also reported by Neelavati and Govindarasu (2010). The magnitudinal differences were medium to low in GCV and PCV for cluster per plant, harvest index, seed yield per plant and the number of pods per plant suggesting the little role of environment in the expression of these characters. These findings are in agreement with the finding of Das *et al.* (1998).The studies on GCV and PCV indicated that the presence of a high amount of variation and the role of the environment on the expression of these traits. The magnitude of PCV was higher than GCV for all the characters which may be due to a higher degree of interaction of genotypes with the environment. The differences between PCV and GCV were less to moderate for most of the characters indicating a lesser contribution of environment towards an expression of these characters.

Heritability

Heritability is a measure of the extent of phenotypic variation caused by the action of genes. For making effective improvement in the character for which selection is practiced, heritability has been adopted by a large number of workers as a reliable indicator.In the present investigation heritability and genetic advance have been worked out for all the thirteen quantitative characters and are presented in Table 3.

In a broad sense, high estimates of heritability were recorded for all the characters under study, which ranged from 63.00% (protein content) to 96.00 % (seed yield per plant). High heritability was observed for maximum traits *viz*., number of clusters per plant (96.00%), number of pods per plant (93.00%), number of seeds per plant (93.00%), plant height (92.00%), pod length (91.00%), seed index (90.00%), days to maturity (89.00%), number of branches per plant (88.00%), harvest index (87.00%), biological yield (81.00%) whereas remaining traits reported moderate to low heritability.High heritability was recorded for the plant height, seed yield per plant, seed index, pods per plant and days to 50%flowering indicating that these traits are likely to be controlled by an additive genetic component. Das *et al.* (1998) and Loganathan *et al.* (2001) also reported high heritability for plant height, number of seeds per pod, number of pods per plant and harvest index.

Genetic advance as percent of mean

The estimate of genetic advance as a percent of mean reported from 6.08 % (protein content) to 65.48 % (number of clusters per plant). High amount of Genetic Advance as 5% of mean was reported for number of clusters per plant (64.48%),seed yield per plant (45.78%), number of pods per plant (44.81%), harvest index (44.42%), seed index (39.61%) whereas moderate for number of branches per plant (37.60%),number of seeds per plant (33.73%), plant height (30.07%), pod length (23.73%), biological yield per plant (23.50%) and low for days to 50% flowering (6.92%),days to maturity (6.26%) and protein content (6.09%). Wani *et al.* (2007) reported high heritability coupled with high genetic advance for the number of pod per plant, plant height and harvest index suggested the additive genetic control in the inheritance of these characters.High heritability with high genetic advance was recorded for plant height, branches per plant, biological yield per plant and seed yield, suggesting that mostly these traits were under the control of additive gene action and selection will be more useful for yield improvement. Similar results were observed by Jebaraj*et al.* (2015), Baisakh *et al.* (2016) and Kumar *et al.* (2020) for plant height, branches per plant and seed yield in mungbean. Moderate heritability with high genetic advance was found for harvest index, indicating the lesser influence of environment with additive gene action, hence, amenable for selection. High heritability with moderate genetic advance was observed for pods per plant, pod length and seeds per pod, indicating that these traits were less influenced by the environment but governed by both additive and non-additive gene action. Hence,the simple selection method is suggested for the improvement of these traits in the later generations.

CONCLUSION

The analysis of variance revealed the occurrence of genetic variability among genotypes. In general,the phenotypic coefficient of variation was greater than the genotypic coefficient of variation for all the agro-morphometric traits. High magnitude of GCV and PCV were recorded for clusters per plant, harvest index, seed yield per plant and pods per plant. High heritability coupled with high genetic advance as percent of mean was observed for clusters per plant and seed yield per plant, hence these parameters could be used for selection. Plant height, branches per plant, biological yield, harvest index and seed yield were important traits and should be prioritized while deciding the criteria for selection, which would be useful in yield improvement. It was concluded that in the case of biological yield and seed yield apart from thehigh genotypic coefficient of variation,the estimates of heritability with genetic advance were high,and hence direct mass selection may be rewarded for these two traits.

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Authors' contribution

Conceptualization of research; designing of the experiments; execution of field experiments and data collection; analysis of data and interpretation; preparation of the manuscript.

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