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Study of genetic variability and association on yield and yield components in Mungbean (*Vignaradiata* L.)

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Abstract
Thirty five genotypes of Mungbean were evaluated in RBD for estimation of genetic variability, heritability, genetic advance, correlation coefficient for yield and its component traits. The estimates of heritability in broad sense were found higher in seeds per pod, Seed yield per plot and branches per plant. The genotypes showed wide and highly significant variation for all the traits. The estimates of GCV and PCV for pods per plant, number of cluster per plant, plant height and seed yield per plot showed very little differences indicating the greater role of genetic factors in the expression of these traits and ample scope for improvement. High heritability along with high genetic advance as percent of mean was observed for seed yield per plot, days to maturity, plant stand and plant height preponderance of additive gene action. The characters, Seed yield per plant showed highly significant and positive correlation with cluster per plant and plant height.

Keywords: Genetic variability, heritability, correlation, yield component

Introduction

Pulses in India have long been considered as only source of poor man's protein. Mungbean (*Vigna radiate* L.) is one of the most widely adapted; drought-tolerant, versatile, green manuring and nutritious legumes. It is a self-pollinating, short duration legume crop that belongs to family Taxaceae with 2n=22 number of chromosomes. It harvested in two months after sowing, which makes an ideal fit for fallow crop in wheat and rice production system. It can improve the soil fertility by fixing atmospheric nitrogen through their root nodules (Malik, 1994) [16]. India ranks first in the world in terms of pulse production. The production of Mungbean in India is 2.41 million tons in the year 2018-19 as by Directorate of Economics and Statistics, among the various grains it is well suited to a large number of cropping systems and constitutes an important source of protein in cereal based predominantly vegetarian diets. Mungbean is largely cultivated for their protein content (22 to 24%), rich in amino acid which predominantly deficit in cereal besides the protein is easily digested without flatulence (Baskaran *et al*., 2009) [2]. For yield improvement, it is essential to have knowledge on variability of different characters. The lack of genetic variability for high yield potential is the major constraint to achieve a major breakthrough in mungbean production. The grain yield was hampered due to various biotic and abiotic stresses. Investigation and better understanding of the variability existing in a population constitute base for an efficient and effective breeding work (Bello *et al*., 2012) [3]. Genetic parameters such as genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) are useful in detecting the amount of variability present in germplasm. Burton (1952) [23] suggested that the GCV along with heritability estimate could provide better picture of the advance to be expected by phenotypic selection. Heritability estimates along with genetic advance are normally more helpful in predicting the gain under selection than heritability estimates alone (Johnson *et al.* 1955) [12]. The statistics which measure the degree and direction of association between two or more variables is known as correlation. Yield is one such complex character that results due to the actions and interactions of various component characters (Grafius, 1960) [8]. Studies on correlation between different yield components are prerequisite for improvement of yield. The present study is focused on to assess the genetic variability present in the population by using coefficient of variation and study the heritability of the character and the correlation among yield and component traits.

Material and method

The experiment under present investigation was conducted in a well prepared field during *Kharif* 2017 at agriculture farm, department of crop sciences, faculty of agriculture, Nana Ji Deshmukh new agriculture campus, Mahatma Gandhi Chitrakoot Gramodaya Vishwavidyalaya, Chitrakoot, Satna. The place of experiment in Chitrakoot is situated at $25^0$10' North latitude and $80^0$85' East longitude. The altitude is about 200 meter above mean sea level. Thirty six Mungbean genotypes were raised in randomized block design with three replications. Each genotype was grown in 3 meter long row with 45cm apart. Recommended agronomic practices and plant protection measures were adopted to raise a good crop. Five competitive plants from each plot were randomly selected for recording of observations for ten characters namely plant stand, days to 50% flowering, branches per plant, cluster per plant, pods per plant, seeds per pod, plant height, days to maturity, hundred Seed weight and seed yield per plot. Average of the data from the sampled plants of each plot in respect of different characters was used for various statistical analyses.

Result and discussion

The analysis of variance

The analysis of variance for all the characters under study was presented in Table 1. These were showed that there is a highly significant difference for all characters among thirty five germplasm. Current study indicating wide genetic variation for all the characters associated with the Mungbean genotypes.

Table 1: Analysis of variance for yield and yield attributes

Source of variation	DF	Mean sum of square									
		PS	DF	BP	CPP	PP	SP	PH	DM	SW	SYP
Replication	2	3.7	0.41	1.03	0.52	2.31	0.29	12.36	24.87	0.51	588.67
Treatments	34	178.7 **	38.4 **	7.2 **	1.7 **	160.5 *	5.9 **	171.8 **	194.4 **	1.3 **	12878.2 **
Error	68	38.92	5.36	0.69	0.35	71.47	0.25	40.38	27.01	0.18	1198.08

*and ** indicating significant difference at $p<0.01$ and $p<0.001$ respectively, ANOVA: Analysis of variance DF: Degree of freedom, PS: plant stand, DF: Days to 50% flowering, BP: Branches per plant, CPP: Cluster per plant, PP: Pods per plant, SP: Seeds per pod, PH: Plant height, DM: Days to maturity, SW: 100 Seed weight, SYP: Seed yield per plot

Genetic variability studies

The extent of variability as measured by GCV and PCV provides information regarding the relative amount of variation in different characters. Differences between phenotypic coefficient of variation and genotypic coefficient of variation were narrow for all the characters under investigation, suggesting that these traits studied have low environmental influence. The magnitude of Phenotypic Coefficient of Variation (PCV) and Genotypic Coefficient of Variation (GCV) was observed highest in case of branches per plant Followed by seeds per pod and thousand grain Weight (g) (Table 2) indicated that there is greater diversity for these traits in mung bean. Hence direct selection for these traits would be effective for the improvement of this crop; similar findings were reported by Rahim *et al*. (2010) [21], Srivastava and Singh (2012) [30] reported high GCV, heritability and genetic advance for seed yield per plant, number of pods per plant and thousand grain weight. Whereas plant height, days to fifty percent flowering and percentage of plant stand had minimal magnitude, genotypic and phenotypic coefficient of variation. Suggesting the little role of environment in the expression of these characters. The results are in accordance with that of Srivastava and Singh (2012) [30] reported high GCV, heritability and genetic advance for seed yield per plant, no. of pods per plant and thousand grain weight. High genetic advance percent of mean were observed for seed yield per plot (g), followed by days to maturity, percentage of plant stand and thousand grain weight (g). Similar findings of high genetic advance were reported by Tushar Kumar Asari (2019) [33] for High GCV and PCV observed for primary branches per plant, pods per plant, seed yield per plant Rahim *et al.* (2010) [21] Srivastava and Singh (2012) [30], Suresh *et al.* (2013) [32] and Kumar *et al.* (2013) [12] reported high GCV, heritability and genetic advance for seed yield per plant, number of pods per plant and thousand grain weight. High heritability along with high genetic advance as percent of mean was observed for primary branches per plant, seed per pods and seed yield indicating the preponderance of additive gene action and hence simple selection would be more effective for improvement of these characters (table 3). Similar results were reported by Shiv *et al*. (2017) [28], Ramakrishna *et al*. (2018) [5], Jagdhane *et al*. (2017) [11] for primary branches per plant and pods per plant, Sana *et al*. (2017) [27] and Katiyar *et al*. (2015a) [13] for pods per plant and seed yield per plant. Vikas *et al*. (1998) [4] for plant height, cluster per plant, days to 50% flowering, pods per plant and biological yield Rahim *et al*. (2010)) [21].

Table 2: Estimation of GCV, PCV and other genetic parameters for different characters

Character	Mean	Range	CV%	GCV	PCV	h^2	GA	GA% of mean
PS	88.45	52.3- 97.67	7.05	7.72	10.46	54.49	10.38	11.74
DF	38.52	32.7-54.67	6.01	8.61	10.5	67.25	5.6	14.55
BP	6.08	3.2 -9.67	13.67	24.15	27.75	75.73	2.63	43.29
CPP	4.43	2.8- 5.87	13.39	15.37	20.38	56.84	1.06	23.87
PP	38.1	22.7- 50.80	22.16	14.28	26.36	29.34	6.08	15.93
SP	6.97	4.3- 9.20	7.23	19.69	20.98	88.13	2.65	38.08
PH	87.81	52.6- 96.33	7.24	7.54	10.45	52.03	9.84	11.2
DM	66.59	49- 83.33	7.81	11.22	13.66	67.37	12.63	18.97
SW	3.79	2.2-5.10	11.15	16.12	19.6	67.67	1.04	27.32
SYP	475.82	307.9-571.63	7.27	13.11	15	76.47	112.4	23.62

CV%: percentage of coefficient of variation, GCV: Genotypic coefficient of variation, PCV: Phenotypic coefficient of variation, h^2: Heritability, GA: Genetic advance and GA % of mean: Genetic Advance percent of mean

Correlation coefficient analysis

Correlation studies among the ten characters indicated different degree of association between characters at genotypic and phenotypic levels. Both positive and negative correlation was found between different pairs of characters. The correlation coefficient at phenotypic level was in general higher than their genotypic correlations ones in magnitude for all the characters indicating the existence of strong inherent associations between various traits (Table 3). This is in agreement with the earlier reports of Rahim *et al*. (2010) [21] and Sakthivel G. *et al*. (2019) [26].

The genotypic and phenotypic correlation among yield and yield contributing traits revealed that cluster per plant and plant height was positively correlated with the seed yield per plot while days to 50% flowering followed by days to maturity showed negatively correlated. Seed per pod showed significant and positive correlation with cluster per plant. And days to 50% flowering was positively correlated with days to maturity at both genotypic and phenotypic level. Plant height expressed significant negative correlation with number of branches per plant. Similar findings were reported by C.K. Divya Ramakrishnan *et al*. (2018) [5], whereas significant positively correlated with percentage of plant stand and cluster per plant at phenotypic level.

The seed yield per plot showed highly significant and negative correlation with days to 50% flowering followed by days to maturity, whereas seed yield per plot showed significant and negative correlation with days to maturity followed by days to 50% flowering while plant height exhibited positive correlation at phenotypic level. Similar the findings were reported by Patil and Deshmukh (1988) [19], Singh *et al*. (1988) [29] Satyan *et al*. Pundir *et al*. (1992) [31] Sharma and Gupta (1994) [26], Kumar *et al*. (1995) [15], Henry and Mathur (2007) [9], Rahim *et al*. (2010) [21] Srivastava and Singh (2012) [30], Kumar *et al*. (2013) [14] and Suresh *et al*. (2013) [32]. Rama Krishnan *et al*. (2018) [5] for clusters per plant, pods per plant and seeds per pod. Tushar Kumar *et al*. (2019) [33] for Days to 50% flowering and days to maturity.

Table 3: Estimates of Phenotypic Correlations

Character	PS	DF	BP	CPP	PP	SP	PH	DM	SW	SYP
PS	1	-0.07	0.268**	0.298**	0.014	0.189	0.923**	-0.176	0.229*	0.074
DF		1	0.183	-0.265**	-0.237*	-0.189	-0.156	0.218*	0.087	-0.296**
BP			1	0.03	-0.035	-0.111	-0.258**	0.102	-0.125	0.064
CPP				1	-0.12	0.288**	0.337**	-0.123	-0.104	0.143
PP					1	0.117	-0.011	0.083	-0.049	0.067
SP						1	0.213*	-0.145	0.113	0.03
PH							1	-0.245*	0.225*	0.145
DM								1	-0.091	-0.357**
SW									1	0.005
SYP										1

*and ** significant difference at $p<0.05$ and $p<0.01$ respectively

Efficiency of selection in any breeding programme mainly depends upon the knowledge of association of characters. Although correlation coefficient indicates the nature of association among the traits. Thus identification of important components and information about their association with yield among each other are very useful for developing effective breeding strategy for evolving high yielding varieties. The correlation coefficient is measure of degree of symmetrical association between two variables or character, which helps us in understanding the nature and magnitude of association between yield and its component traits.

Table 4: Mean Performance of Mungbean genotypes

S. No.	Genotypes	PS	DF	BP	CPP	PP	SP	PH	DM	SW	SYP
1	NMK15-08	94	37.33	6.13	4.93	40.93	8.27	94.27	64	3.4	564.86
2	VGG16-055	86	32.67	5.87	4.2	50	9.2	86.07	63.33	3.37	478.24
3	MDGGV-18	92.33	37.33	4.47	3.73	43.73	6.13	92.6	67.67	3.3	488.98
4	BM4(Ch)	94.67	37	6	5.13	46.93	7.2	89.47	49	2.77	517.11
5	AKM12-28	91	38.67	4.33	4.8	41.07	7.27	91	66.67	3.47	484.32
6	RMG1097	91	38.33	8.73	4.67	38.4	7.27	91.07	68.33	3.47	522.38
7	PusaM1772	89	38.33	5.3	5.4	50.8	8.27	89.07	72.33	3.5	404.35
8	PKV AKM4(Ch)	92.33	39.67	4.67	4.4	46.27	8.73	87.07	68	5.1	465.84
9	PM 14-3	88	39.33	4.47	2.8	43.2	6.33	88.2	70.67	4.33	324.1
10	SKNM 1502	91.67	38.33	4.33	4.8	44.4	4.53	87.2	71	3.8	476.78
11	SML1808	97.67	32.67	4.8	4.13	42.27	7.73	93.53	73.33	4.27	538.94
12	IGKM2016-1	81	39.67	5.27	3	43.6	6.8	81.07	69.67	4.83	417.02
13	MH 1323	87.33	35	3.2	4.47	40.67	8.37	87.53	66.33	3.4	480
14	LGG 607	89	54.67	7.4	3.4	26.27	5.07	79.8	83.33	3.43	316.61
15	AKM 8802(Ch)	91.33	39.67	8.33	4.5	32.53	4.73	91.33	76	4.43	509.11
16	SKNM1504	92.67	38.67	5.4	5.13	28.93	7.33	92.67	68.33	4.23	307.97
17	PM14-11	85.67	38	5.33	4.47	38.27	7.4	85.67	75.33	3.73	488.5
18	ML 2479	92.67	40.33	4.17	4.67	34.4	7.03	93.13	64.67	3.47	486.34
19	AKM 12-24	81.67	40	4.37	3.2	23.33	4.27	81.67	64.33	4.73	549.17
20	NDMK16-324	85.67	39.67	5.63	5.07	25.87	7.33	85.67	67.33	2.77	465.94
21	JAUM 0936	96.33	38.67	7.67	4.27	38.93	6.73	96.33	71.33	4.27	531.8
22	SVM- 6133	94.67	39.33	6.9	5.73	35.73	8.53	94.67	72.33	3.5	401.81
23	VGG 16-036	90.67	34.33	5.97	4.6	36.4	4.73	91.2	59.67	3.07	464.69

24	IPM 512 -1	80.67	40	7.1	4.27	33.6	6.87	80.4	49.67	3.63	523.54
25	TMB 126	96	40.67	6.1	3.13	44.8	5.8	95.73	58	4.47	462.58
26	KM 2355	89.67	39	5.13	5.2	43.33	6.8	90	71.33	3.7	495.17
27	COGG 13-39	89.67	41.67	8	4.33	34.93	8.73	90.13	57	4.37	531.03
28	IPM 410-9	84.67	39.67	8.53	5.87	37.33	7.8	85.2	69	4.73	517.82
29	RMB 12-07	92	40	7.27	4.67	22.77	8.8	92.47	56	4.3	448.75
30	MGG-387	85.67	35.67	8.2	4.47	39.73	5.2	86.07	67.33	2.97	571.63
31	OBGG 58	83.33	34.33	6.13	5.33	36.93	6.4	84.13	54.33	4.27	531.89
32	NVL 855	83	38	5.6	4.07	43.33	8.53	83.4	76.33	3.47	534.38
33	Pusa M1771	88.67	36.33	5.47	4.13	24.8	8.67	89.2	60	4.27	472.37
34	BM 2012-9	52.33	39.33	9.67	3.2	40.67	5.33	52.6	81.33	2.2	405.41
35	OBGG-56	93.67	36	6.93	4.73	40.13	5.67	93.67	57.33	3.77	474.26
Mean		88.45	38.52	6.08	4.43	38.15	6.97	87.81	66.59	3.79	475.82
C.V.(%)		7.05	6.01	13.67	13.39	22.16	7.23	7.24	7.81	11.15	7.27
S.E.±m		3.6	1.34	0.48	0.34	4.88	0.29	3.67	3	0.24	19.98
C.D. 5%		10.16	3.77	1.35	0.97	13.77	0.82	10.35	8.47	0.69	56.4
Range Lowest		52.33	32.67	3.2	2.8	22.77	4.27	52.6	49	2.2	307.97
Range Highest		97.67	54.67	9.67	5.87	50.8	9.2	96.33	83.33	5.1	571.63

The mean performance for all the characters presented in table 4.The maximum and minimum values for different characters were underlined. Among the 38 genotypes BM2012-9 had the minimum plant stand percent 52.33% and SML-1808 had the maximum 97.67% plant stand percent. SML-1808 is the short duration line having 32.67 days to 50% flowering and LGG-607 had long duration 54.67 days. Number of primary branches was found minimum in MH 13233.20 and maximum 9.67 in BM2012-9. Genotypes PM 14-3 had the minimum 2.80 and IPM 410-9 had the maximum number of cluster per plant. RMB 12- had the minimum 22.27 and Pusa M1772 had maximum 50.80 number of pod per plant. AKM 12-24showed lowest 4.27number of seeds per pod VGG16-055 had highest 9.20 number of seeds per pod. BM2012-9 showed the highest values 62.60 for plant height and the smallest seed size 2.20g for 100 seed weight. JAUM 0936 had highest 96.33for plant height and boldest seed size5.10 was found in PKV AKM4 (Ch.) (5.10 g) Days to maturity ranged from BM 4(Ch.) 49.00 days to 83.33 days in LGG 607. Largest571.63 g amount of variability was found for seed yield per plot in MGG-387 and minimum 307.97g in SKNM 1504 for seed yield per plot. Similar results also reported by V. Sandhiya *et al*. (2018) [34]

Conclusion

All the characters recorded high heritability indicating the high influence of genetic components. Traits seed per pod, branches per plant, and seed yield per plant were governed by additive gene action as they possessed high heritability along with high genetic advance. Cluster per plant and plant height were significant and positively correlated with seed yield per plant. Hence, these traits should be given consideration while selecting for increasing yield.

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