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Research Article

Genetic variability and correlation studies in greengram (*Vigna radiata* L. Wilczek)

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Abstract

The present experiment was carried out during Kharif2016 to assess the genetic variability and correlation among yield and yield attributing characters of mungbean. Thirty six mungbeangermplasm were investigated for this study for 10 quantitative characters *viz.,* days to 50% flowering, plant height (cm), number of primary branches per plant, number of clusters per plant, number of pods per cluster, number of pods per plant, pod length (cm), number of seeds per pod, 100 seed weight (g) and seed yield per plant (g). On the basis of genetic variability study all the characters exhibited high heritability coupled with high genetic advance, indicating the preponderance of additive gene action. Selection based on this trait will be fruitful. Phenotypic correlation is higher than the genotypic correlation for all the characters under study. From the correlation studies, seed yield per plant showed positive significant correlation with the traits *viz.,* number of pods per plant, number of clusters per plant and number of pods per cluster. Hence, simultaneous selection for the above traits would be more rewarding to bring improvement in mungbean.

Key words

Mungbean (*Vignaradiata*), Variability, Correlation, Heritability.

Introduction

Greengram commonly known as mungbean (*Vignaradiata (L.)*Wilczek) is an economically important pulse crop ranking after chickpea and pigeonpea. The area of mungbean under cultivation is 3.38 m ha in India with an annual production of 1.61 m tonnes and productivity of 474 kg/ha during 2013-14 (Anonymous, 2014). It is a short duration legume harvested intwo months after sowing, which makes an ideal fit for fallow crop in wheat and rice production system. It canimprove the soil fertility by fixing atmospheric nitrogen through their root nodules (Malik, 1994). Mungbean is largely cultivated for their protein content (22 to 24%), rich in amino acid which predominantly deficit in cereal besides theprotein is easily digested without flatulence(Baskaran*et al*., 2009).The lack of genetic variability for high yield potential is the major constraint to achieve a major breakthrough in mungbeanproduction (Ramanujam, 1978). And the yield is also reduced 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). Heritability and genetic advance are important selection parameters. Heritability estimates along with genetic advance are normally more helpful in predicting the gain under selection than heritability estimates alone (Johnson *etal.,*1955). 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). Studies on correlation between different yield components are prerequisite for improvement of yield. So the present study is focussed 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.

Materials and Methods

The present investigation was carried out at the Department of Plant Breeding and Genetics, Agricultural College and Research Institute, Killikulam, during Kharif 2016. Thirty six mungbeangermplasm were raised in randomized block design with two replications. The seeds were raised with a spacing of 30×10 cm. On the tenth day after sowing, the crop was thinned out, leaving one healthy seedling per hill. Recommended agronomic practices and need based plant protection measures were taken. Each line was sown in two rows of 1.5 m. The data was collected on ten yield and yield contributing characters *viz.,* days to 50% flowering, plant height(cm), number of primary branches per plant, number of clusters per plant, number of pods per cluster, number of pods per plant, pod length(cm), number of seeds

per pod, 100 seed weight(g) and seed yield per plant (g). Among different genotypes, five plants were randomly selected and tagged for taking observations and the mean value was calculated for analysis on two replications. The observations were taken based on the descriptors. The cultivation practices like irrigation, weeding, fertilization and pesticide application *etc*. were followed on proper times. The analysis of variance of RBD and their significance for all the characters were worked out as suggested by Panse and Sukhatme (1967). The various genetic parameters *viz.*, ECV, GCV, PCV, heritability and GAM were calculated by adopting the formulae given by Johnson *et al.*, (1955). Genotypic correlation co- efficient was calculated byusing the formulae given by Al-Jibouri et al., (1958).

Results and Discussion

The analysis of variance for all the characters under study was presented in Table 1. This were showed that there is a highly significant differences for all characters among 36 germplasm under study indicating presence of wide genetic variation for different characters among the genotypes of mungbean. The mean performance of all the characters is presented in Table 2. The maximum and minimum values for different characters were underlined. Among the 36 genotypes LM 405 is the short duration line having 28 days to 50% flowering and Erode local had long duration 53 days. AGG 10 092 had the minimum plant height of 34.4 cm and Annur 2 had the maximum plant height of 100.9 cm. AGG 11 007 had the minimum values for most of the characters like number of clusters per plant, number of pods per cluster, pod length and number of seeds per pod and their value were 3.3, 1.8, 5.35cm and 6.9, respectively.Further, PLS 302 (23.4), EC 396120 (5.4), COGG 973 (11) and CO 6 (14.6) exhibited superiority for number of clusters per plant, number of pods per cluster, pod length and number of seeds per pod respectively. Pusa Vishal (1) and CO GG 11 03 (6) exhibits the minimum and maximum number of primary branches per plants.CO GG 365 showed the minimum 100 seed weight of 2.34 and COGG 973 had the maximum of 7.82 grams. LM 13 is having the 1.07g and CO 6 having the maximum of 12.6 gram of single plant yield.

The magnitude of genetic variance for all the characters under study is depicted in Table 3. The phenotypic coefficient of variation for all the characters under study is higher than the genotypic coefficient of variation indicating the involvement of both genotype and environment for variation. Hence, the selection for such traits often misleading. Similar results also reported byTabasum*et al*., (2010) and Sheetal*et al*., (2014). High heritability coupled with higher genetic advance was recorded for all the ten characters which indicated that most likely the heritability is due to additive gene effects and selection may be effective for all the characters. The findings were in agreement with earlier findings of Kumar *et al*., (2013), Pinchhyo*et al*., (2016) and Patel *et al*., (2014)**.**

Correlation coefficient among seed yield and its contributing characters are presented in Table 4. Among the ten yield component traits, three traits *viz*., number of clusters per plant (0.456), number of pods per cluster (0.474) and number of pods per plant (0.597) had significant and positive correlation with grain yield. These results are in agreement with those of Sheetal*et al*. (2014) and Anand*et al*. (2016) for number of pods per cluster while Hemavathy*et al*. (2015) and Sultana (2015) quoted similar results, for number of cluster per plant, Din *et al*. (2015), Baisakh*et al*. (2016) and Dhoot*et al*. (2017) reported the same results for number of pods per plant having positive correlation with single plant yield. Days to 50% flowering (-0.093) and plant height (-0.054) had negative correlation with single plant yield. The result was in concordance with Tabasum*et al*.(2010) PariharRoshan*et al*.(2018) and Pinchhyo*et al*.(2016). The characters *viz.*, number of primary branches per plant (0.034) pod length (0.254), number of seeds per pod (0.240) and 100 seed weight (0.087) had positivecorrelation with yield.Similar results have already been published by Gul*et. al.*,(2008)and Punia*et al*.(2014).From the results of present investigation it is inferred that the magnitude of PCV is higher than the GCV for all the characters under studied. So the selection for such traits may sometimes mislead. High heritability coupled with high genetic advance was recorded for all the ten characters and hence, additive gene action plays an important role. From the correlation studies, number of clusters per plant, number of pods per cluster and number of pods per plant had positive significant correlation with single plant yield so, selection for these traits will indirectly increase the seed yield per plant.

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Table 1. Analysis of variance for 10 characters of mungbean genotypes

Source of variation	Days to 50% flowering	Plant height (cm)	Number of branches per plant	Number of capsules per plant	Number of pods per cluster	Number of pods per plant	Pod length (cm)	Number of seeds per pod	100 seed weight (gms)	Seed yield per plant
Replication	0.89	211.49	0.09	1.23	0.13	32.27	0.00	0.20	0.30	0.14
Genotype	72.50**	442.93**	2.15**	46.28**	1.23**	178.44**	1.63**	5.83**	2.39**	11.39**
Error	1.49	163.03	0.06	0.32	0.10	6.74	0.10	0.39	0.07	0.33

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Table 2. Mean performance of 36 genotypes for different characters of mungbean

Genotypes	Days to 50% flowering	Plant height (cm)	Branches per plant (nos)	Capsule per plant (nos)	Pods per cluster (nos)	Pods per plant (nos)	Pod length (cm)	Seeds per pod (nos)	100 seed weight (g)	Seed yield per plant
PLS 302	37.50	61.90	4.00	23.40	2.40	32.90	6.30	10.40	3.63	2.99
BINAMUNG	35.00	58.40	4.00	10.70	3.60	37.30	6.82	8.20	3.12	2.40
LM 154	33.50	64.60	3.00	13.40	3.80	10.60	6.23	8.90	3.56	2.52
PLM 501	47.00	85.20	2.70	8.00	3.60	27.10	7.03	10.40	3.35	2.70
EC 396120	35.50	54.10	2.60	5.40	5.40	24.10	7.27	11.50	3.67	11.60
LM 13	49.50	70.50	1.60	7.30	2.80	27.00	6.31	10.00	2.83	1.07
EC 396100	38.00	57.60	2.80	13.10	3.00	16.10	7.93	9.00	5.18	3.72
CO 4	40.50	60.10	2.50	11.30	3.50	25.70	7.08	11.80	2.83	2.23
COGG 973	32.00	69.20	4.60	4.30	2.70	11.90	11.00	10.40	7.82	2.63
ANNUR 2	29.50	100.90	5.00	20.40	2.40	33.30	7.02	10.00	3.16	1.38
FRM 1320	40.50	52.80	2.30	9.00	2.20	15.90	7.57	12.50	5.31	3.37
VARAGU NESI PASI	46.50	48.30	3.50	11.40	2.40	30.90	6.80	8.90	2.80	4.51
LM 104	28.00	58.90	3.30	12.50	3.50	33.10	6.41	10.40	4.16	2.97
LM 15	39.00	100.50	3.10	12.00	3.70	45.20	6.36	9.60	2.37	2.10
PANT M 103	33.50	52.40	4.30	18.10	3.00	28.10	5.77	7.30	3.22	2.67
CO GG 365	41.00	55.60	2.50	11.30	3.50	30.20	6.73	7.10	2.34	4.50
EC 396126	39.00	74.20	2.50	8.50	2.00	19.90	7.49	10.70	3.63	4.86
CO 6	36.00	74.30	2.90	11.00	3.60	32.70	7.55	14.50	3.78	12.60
CO GG 930	36.50	71.50	2.70	5.20	3.70	35.40	6.64	8.60	3.12	2.65
CO GG 11 03	35.50	43.30	6.00	8.90	3.20	23.80	7.37	9.40	3.82	6.50
CO 8	36.00	53.60	1.60	5.30	3.50	21.30	6.30	8.60	3.78	1.40
CO 7	36.00	67.70	2.10	5.30	5.20	20.70	6.91	9.90	4.57	4.66
IPM 99 125	36.00	76.00	3.00	6.30	4.50	26.00	6.51	10.00	6.15	6.04
IPM 205-7	28.00	67.20	3.50	7.30	3.10	16.70	7.52	11.30	3.76	3.65
PUSA VISHAL	29.50	63.80	1.00	4.90	3.30	44.10	7.00	11.60	3.61	5.79
MH 565	30.50	46.10	2.20	8.50	3.60	37.80	7.16	9.40	3.16	4.80
IPM 0214	34.50	73.30	3.00	5.20	3.40	15.60	6.21	9.50	4.81	4.65
PUSA RATNA	28.50	61.00	2.40	6.60	4.50	41.70	7.22	7.10	3.50	2.70
IPM 0219	32.50	38.90	3.00	3.90	3.50	18.70	7.22	10.60	4.59	4.18
FRM 1317	41.50	68.20	4.00	15.10	3.00	37.80	8.01	12.20	3.97	5.12
AGG 10 092	38.00	34.40	2.70	5.10	3.50	25.50	7.50	10.50	3.04	3.39
AGG 10 087	46.00	63.50	1.40	7.50	3.40	42.40	7.07	10.90	2.60	2.67
AGG 09 073	42.00	68.20	2.50	11.10	3.60	31.80	6.93	12.70	2.90	3.00
ERODE LOCAL	53.00	76.20	4.50	16.50	3.00	25.90	6.84	11.10	2.86	3.95
AGG 11 007	39.00	44.60	3.30	3.30	1.80	11.90	5.35	6.90	3.12	2.90
AGG 11 002	40.50	81.10	2.60	5.00	2.40	32.80	7.80	12.20	3.47	4.62

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Table 3. Estimation of genetic components for yield and its components in mungbean

Traits	GCV	PCV	Heritabilithy	GA	GA%	CV%
DFF	22.67	22.91	97.97	73.91	197.83	3.26
PH	29.78	35.87	68.91	372.25	583.14	20.00
NPB	48.22	48.87	97.37	2.18	72.31	7.92
NCPP	71.47	71.72	99.30	47.51	499.92	5.98
NPPC	32.79	34.21	91.88	1.22	36.71	9.75
NPPP	48.02	48.94	96.29	180.32	654.46	9.42
PL	17.84	18.40	94.00	1.62	23.06	4.50
NSPP	23.47	24.26	93.59	5.80	57.36	6.14
HSW	41.38	41.99	97.11	2.43	65.45	7.13

Table 4. Genotypic correlation coefficients among yield components in black gram

Traits	DFF	PH	NPB	NCPP	NPPC	NPPP	PL	NSPP	HSW	SYPP
DFF	**1.000**									
PH	0.210	**1.000**								
NPB	-0.247	-0.149	**1.000**							
NCPP	0.096	-0.007	0.452**	**1.000**						
NPPC	-0.188	0.081	-0.252	-0.260	**1.000**					
NPPP	0.011	0.232	-0.151	0.413*	0.517**	**1.000**				
PL	-0.113	-0.053	0.213	-0.145	-0.124	-0.143	**1.000**			
NSPP	0.158	0.103	-0.095	0.018	-0.020	0.073	0.495**	**1.000**		
HSW	-0.318	-0.100	0.177	-0.265	0.069	-0.456**	0.585**	0.137	**1.000**	
SYPP	-0.093	-0.054	0.034	0.456**	0.479**	0.597**	0.254	0.240	0.087	**1.000**