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Genetic variability studies on physiological and yield related traits in mungbean (*Vigna radiata* (L.) Wilczek)

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ABSTRACT

Thirty five genotypes of mungbean were evaluated in randomized block design for fourteen physiological and yield related traits to estimate genetic variability, heritability and genetic advance as a percentage of mean. High PCV and GCV were observed for net assimilation rate, number of pods per plant and leaf area duration. High heritability was observed for all the characters studied except days to 50% flowering. High estimates of heritability coupled with high genetic advance as per cent of mean was registered for number of clusters per plant, number of pods per cluster, number of pods per plant, 100 seed weight, harvest index, net assimilation rate, leaf area duration, chlorophyll content and seed yield per plant indicating that the genetic variances for these traits are probably owing to their high additive gene effects.

Key words: Variability, Heritability, Genetic advance, Mungbean.

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INTRODUCTION

Mungbean is the third most important pulse crop after chickpea and redgram in India. It is a short duration crop and is grown mainly in arid and semi arid situations across the country during *kharif* season and contributes nearly 15% of the total pulse production. Nutritionally, mungbean is a protein rich staple food containing about 20-25 per cent protein content besides rich in aminoacids particularly with lysine, minerals and vitamins, thus meeting the dietary needs of the vegetarian population of the country.

Though, mungbean is considered to be an important pulse crop in India and also in Andhra Pradesh, the production and productivity levels are low to meet the nutrient status of the people. The per capita availability of pulses has declined from 22.1 kg/capita/year in 1951 to 15 kg/capita/year currently and is anticipated to fall further due to decline in their production and continuously rising prices. The low yields may be attributable to different factors such as lack of high yielding varieties suitable for different niches and susceptibility of existing local varieties to various biotic and abiotic stresses. Hence, based on the above reasons the production and productivity potential of pulses has to be increased substantially. Therefore, there is an immediate need to breed stable mungbean cultivars with high yielding ability.

To initiate any breeding programme aiming for varietal improvement, the knowledge of genetic variability existing among different parameters is a prerequisite. The nature and extent of variability forms the basis for all crop improvement programmes. Estimation of genetic variability in conjuction with the estimates of heritability and genetic advance indicates the possible improvement achieved through selection. The degree of success depends on the magnitude of heritability which measures the relative amount of the heritable portion of total variation and aids in selection. Similarly, genetic advance (GA) under selection gives an idea about how much of the genetic gain was obtained due to selection. Hence, the estimates of genetic variability, heritability and genetic advance will be of immense value in selection and breeding for high yielding strains.

MATERIAL AND METHODS

Thirty five genotypes of mungbean were grown in randomized block design with three replications during *kharif*, 2015 at Sri Venkateswara Agricultural College dry land farm, Tirupati. Each treatment was sown in three rows of 3m length with a spacing of 30 cm between rows and 10 cm between plants within

rows. The data were recorded on five competitive plants taken from each replication for plant height, number of clusters per plant, number of pods per cluster, number of seeds per pod, number of pods per plant, hundred seed weight, harvest index, seed yield per plant, net assimilation rate, leaf area duration, SPAD Chlorophyll meter reading (SCMR) and chlorophyll content. The characters *viz.*, days to 50% flowering and days to maturity were recorded on per plot basis. Means were computed and data were analysed for variances and coefficient of variation as suggested by Burton (1952) and heritability (broad sense) as the ratio of genotypic to phenotypic variance. The procedure of Johnson *et al.* (1955) was followed for calculating the expected genetic advance and genetic advance as per cent of mean.

RESULTS AND DISCUSSION

In the present study the analysis of variance revealed highly significant differences for all the fourteen characters among the genotypes, indicating a good deal of variation among thirty five genotypes of mungbean (Table. 1). Maximum range of variation was observed for leaf area duration followed by number of pods per plant, plant height, harvest index, SCMR and days to maturity.

The results of variability, heritability and genetic advance as percentage of mean are presented in Table 2. In the present study, phenotypic co-efficient of variation was of high magnitude than the genotypic coefficient of variation for all the characters indicating the influence of environment in the expression of these traits. The estimates of PCV and GCV were high for net assimilation rate (GCV=23.52; PCV=24.56), number of pods per plant (GCV=23.16; PCV=23.74) and leaf area duration (GCV=20.80; PCV= 20.95). Similar kind of estimates was also reported by Patel et al. (2014) and Aparna et al. (2015) for number of pods per plant. Moderate co-efficient of variation was observed for chlorophyll content (GCV=18.24; PCV=18.58), 100 seed weight (GCV= 16.38; PCV=17.22), seed yield per plant (GCV=15.83; PCV=17.09), number of clusters per plant (GCV=12.74; PCV=14.82), number of pods per cluster (GCV=11.97; PCV=13.00) and harvest index (GCV=11.73; PCV=13.01). Similar kind of estimates were also reported by Hozayn et al. (2013), Reddy et al. (2014) for seed yield per plant, number of clusters per plant and number of pods per plant and Aparna et al. (2015) and Devendra (2015) for 100 seed weight. On contrary, low estimate of coefficient of variation was observed for the remaining characters viz., plant height (GCV=6.49; PCV=8.01), days to maturity (GCV=3.81; PCV=4.46), SCMR (GCV=3.67; PCV=4.45), number of seeds per pod (GCV=3.45; PCV=4.31) and days to 50% flowering (GCV=2.91; PCV= 3.96). Similar kind of findings were also reported by Hemanth et al. (2014) for days to 50% flowering, days to maturity and 100 seed weight; Patel et al. (2014) for days to 50% flowering and days to maturity.

High heritability estimates were recorded for all the traits *viz.*, leaf area duration (98.64%), chlorophyll content (96.43%), number of pods per plant (95.11%), net assimilation rate (91.72%), 100 seed weight (90.56%), seed yield per plant (85.84%), number of pods per cluster (84.68%), harvest index (81.30%), number of clusters per plant (73.80%), days to maturity (72.77%), SCMR (67.98%), plant height (65.71%) and number of seeds per pod (63.97%) except for days to 50% flowering. Similar results were also observed by Devendra (2015) for days to maturity, plant height, seed yield per plant and 100 seed weight and Aparna *et al.* (2015) for pods per plant and seed yield per plant. The high heritability observed for these traits in the present investigation indicated that the influence of environment on expression of these traits is relatively low. Therefore, for improving these traits the selection would be more effective in early generations on the basis of *per se* performance of these traits. These traits may be improved by mass or progeny selection.

The maximum genetic advance as per cent of mean was registered for number of pods per plant (46.52), net assimilation rate (46.41), leaf area duration (42.56), chlorophyll content (36.90), 100 seed weight (32.12), seed yield per plant (30.22), number of pods per cluster (22.68), number of clusters per plant (22.54) and harvest index (21.78). This was in conformity with the findings of Mehandi *et al.* (2014) for number of clusters per plant and number of pods per plant; Omvir and Singh (2016) for seed yield per plant, 100 seed weight, number of pods per plant and number of pods per cluster.

In the present investigation, high heritability coupled with high genetic advance as per cent of mean was recorded for number of clusters per plant, number of pods per cluster, number of pods per plant, 100 seed weight, harvest index, net assimilation rate, leaf area duration, chlorophyll content and seed yield per plant indicating the preponderance of additive gene action and hence simple selection would be more effective for improvement of these characters. Similarly, high heritability coupled with moderate genetic advance as per cent of mean was recorded for plant height, which might be controlled by both additive and non-additive gene effects. Recurrent selection would be more effective to improve this trait.

Considering the mean performance the genotypes GVIT-203, AKM-9904, WGG-37, KM-122 and LM-95 recorded the highest per se performance for seed yield per plant (Table 3). Similarly, the genotypes GVIT-203, WGG-37 and KM-122 showed better performance for the yield contributing traits *viz.*, number of clusters per plant and number of pods per plant. Hence, these genotypes could be exploited in breeding

programmes for improvement of yield and other yield contributing traits. In the present investigation, among thirty five genotypes studied, the genotypes KM-122 recorded high seed yield coupled with high chlorophyll content high net assimilation rate. Similarly, the genotype WGG-37 recorded high seed yield coupled with high leaf area duration. The genotypes GVIT-203 and LM-95 recorded high seed yield coupled with high chlorophyll content. Hence, these genotypes could be exploited in the breeding programmes to develop varieties with high yield and increased physiological efficiency.

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S. No.	Characters	Mean sum of squares					
		Replications (df: 2)	Treatments (df: 34)	Error (df: 68)			
1.	Days to 50% flowering	4.20	5.68**	2.60			
2.	Days to maturity	8.68	22.82**	6.21			
3.	Plant height (cm)	5.00	63.23**	21.68			
4.	No. of clusters per plant	4.50	10.16**	2.66			
5.	No. of pods per cluster	0.18	0.80**	0.12			
6.	No. of seeds per pod	1.64	0.77**	0.28			
7.	No. of pods per plant	0.01	345.72**	16.89			
8.	100 seed weight (g)	0.10	1.45**	0.13			
9.	Harvest index (%)	70.52	99.11**	18.53			
10.	Net assimilation rate (g dm ⁻² w ⁻¹)	0.003	0.0147**	0.0013			
11.	Leaf area duration	2.47	650.43**	8.87			
12.	SPAD Chlorophyll meter reading	40.47	16.31**	5.22			
13.	Chlorophyll content (mg g ⁻¹)	0.05	1.51**	0.05			
14.	Seed yield per plant (g)	10.15	17.52**	2.48			

Table. 1 Analysis of variance for fourteen quantitative characters in thirty five genotypes of mungbean

** Significant at 1% level

	r			urteen					an genotype		r
S. No	Character	Mean	Range		Variance		Coefficient of Variation		Heritability (Broad sense) (%)	Genetic advanc e (GA)	Genetic advance as percent of
•			Min.	Max.	Genoty pic	Phenot ypic	Genot ypic	Phen otypi c	Sensey (70)	c (un)	mean (%)
1.	Days to 50% flowering	34.77	31.00	37.33	1.03	1.89	2.91	3.96	54.21	1.53	4.42
2.	Days to maturity	61.74	56.67	68.33	5.53	7.61	3.81	4.46	72.77	4.13	6.70
3.	Plant height (cm)	57.32	45.73	71.93	13.85	21.08	6.49	8.01	65.71	6.21	10.84
4.	No. of Clusters per plant	12.42	9.24	17.07	2.50	3.39	12.74	14.82	73.80	2.80	22.54
5.	No. of Pods per cluster	3.98	2.76	4.65	0.23	0.27	11.97	13.00	84.68	0.90	22.68
6.	No. of Seeds per pod	11.80	10.88	13.81	0.17	0.26	3.45	4.31	63.97	0.67	5.68
7.	No. of Pods per plant	45.21	17.47	64.33	109.61	115.24	23.16	23.74	95.11	21.03	46.52
8.	100 seed weight (g)	4.05	2.58	6.03	0.44	0.49	16.38	17.22	90.56	1.30	32.12
9.	Harvest index (%)	44.20	32.35	55.72	26.86	33.04	11.73	13.01	81.30	9.63	21.78
10.	Net assimilation rate	0.29	0.14	0.46	0.01	0.01	23.52	24.56	91.72	0.13	46.41
11.	Leaf area duration	70.29	40.27	93.27	213.85	216.81	20.80	20.95	98.64	29.92	42.56
12.	SPAD chlorophyll meter reading	52.45	45.73	58.20	3.70	5.44	3.67	4.45	67.98	3.27	6.23
13.	Chlorophyll content (mg g-1)	3.82	1.93	5.22	0.49	0.50	18.24	18.58	96.43	1.41	36.90
14.	Seed yield per plant (g)	14.15	10.96	20.25	5.01	5.84	15.83	17.09	85.84	4.27	30.22

Table. 2Mean, coefficient of variability, heritability (broad sense) and genetic advance as per cent of mean for fourteen characters in thirty five mungbean genotypes

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