Electronic Journal of Plant Breeding, 9 (2) : 716-722 (June 2018) DOI: 10.5958/0975-928X.2018.00085.6
ISSN 0975-928X

Research Article

Genetic variability studies for yield and its contributing traits in greengram [*Vigna radiata* (L.) Wilczek]

D. Susmitha and P. Jayamani*
Department of Pulses, Centre for Plant Breeding and Genetics,Tamil Nadu Agricultural University, Coimbatore – 641 003.
*E-Mail: jayamani1108@gmail.com

(Received: 02 May 2018; Revised: 18 Jun 2018; Accepted:19 Jun 2018)

Abstract

Greengram [*Vigna radiata* (L.) Wilczek] a short duration legume crop grown throughout the year, faces biological constraints like indeterminate growth habit, YMV incidence, pod shattering and low harvest index ultimately leading to low yield. Genetic variability parameters were studied in fifty one greengram genotypes raised during *kharif* 2017 in randomised block design with two replications. Observations were made for twelve biometrical traits. The estimates of PCV was higher than GCV for all the characters. Plant height, number of primary branches per plant, number of clusters per plant, number of pods per plant and single plant yield recorded high GCV estimates. High heritability was observed for plant height and 100 seed weight where as high genetic advance as percent of mean was recorded for petiole length, peduncle length, plant height, number of primary branches per plant, number of clusters per plant, number of pods per plant, 100 seed weight and single plant yield. High heritability coupled with high genetic advance as percent of mean was observed for plant height and 100 seed weight. The high degree of variability observed among genotypes for different yield contributing traits could be utilized in the breeding program for the improvement of greengram.

Key words

Greengram, *Vigna radiata*, variability, heritability, genetic advance

Introduction

Greengram (*Vigna radiata* L. Wilczek) is an excellent source of high quality protein having high digestibility. Serves as a good source of riboflavin, thiamine and ascorbic acid. Being a short duration crop, it fits well in intensive crop rotation and also grown for improving soil fertility as it fixes atmospheric nitrogen (30-40 kg/ha) (Tak *et al.*, 2013). Mainly grown as a rainfed crop under marginal and sub marginal conditions with poor nutrient management.

The genetic improvement in production and productivity of greengram has been very slow owing to several constraints. The extent of improvement expected by selection in any population depends on the nature and amount of genetic variability present in the population. Further, yield being a complex trait is highly influenced by environmental factors, hence genetic improvement of the traits can be achieved through a clear understanding of nature and amount of variability present in the breeding material for the component traits for yield and the extent to which these traits are heritable. Therefore, information on genetic parameters such as variance, coefficient of variation and heritability of desirable traits will help the breeder to evolve suitable cultivars. Hence, the present investigation on genetic variability studies on greengram was made.

Materials and Methods

The experimental material consisting of fifty one greengram genotypes were raised during *kharif* 2017 in Randomized Block Design with two replications in the field area of Department of Pulses, Centre for Plant Breeding and Genetics, Tamil Nadu Agricultural University, Coimbatore. Row to row and plant to plant spacing were 30 cm and 10 cm with a row length of 4 metres. Normal cultural practices were carried out as per standard recommendations. Observations were made on 12 biometrical characters which includes petiole length (cm), peduncle length (cm), plant height (cm), days to 50% flowering, number of primary branches per plant, number of clusters per plant, number of pods per plant, number of seeds per pod, pod length (cm), shelling percentage (%), 100 seed weight (g) and single plant yield (g) on three plants per genotype per replication except for days to 50% flowering which was computed on row basis.
Genetic variability parameters were assessed based on the formula given by Burton (1952). Heritability and genetic advance parameters were calculated according to Lush *et al.* (1940) and Johnson *et al.* (1955).

Results and Discussion

The observations made on various yield and its attributing characters were presented on Table 1. Wide range of values were observed for plant height (20.55 – 68.06 cm), number of pods per plant (7.33 – 35.50) followed by shelling percentage (55.79 – 83.25 %) depicting the existence of maximum variability among the genotypes for these characters. The findings was in accordance with Makeen *et al*. (2007) for plant height and number of pods per plant in greengram. The petiole length varied from 7.60 -18.63 cm, peduncle length from 8.78 -19.17 cm, single plant yield from 2.8 – 10.38 g, number of clusters per plant was 3.67 – 11.33, 100 seed weight was 2.52 – 7.03 g, number of seeds per pod 7.3 – 11.6 and pod length was 5.57 – 8.95 cm indicating the presence of considerable variation. Number of primary branches per plant varied from 0.29 – 2.83 indicating narrow variation.

Genotype exhibiting maximum mean value was PLS 326 for number of primary branches per plant, LM 9 for number of clusters per plant, LM 354 for number of pods per plant, LM 179 for number of seeds per pod, PLS 294 for pod length, SML 668 for shelling percentage, PLS 294 for 100 seed weight and MS 9724 for single plant yield. LM 296, LM 272, PLS 274 and PLS 326 were early maturing genotypes as they recorded minimum days to 50% flowering (34 days). These genotypes could be utilized as parents for enriching their respective characters.

The analysis of variance (ANOVA) is useful in testing the significance as well as to estimate the different components of variance. All the genotypes exhibited significant difference ($p < 0.01$) for all the characters (Table 2).

The co efficient of variation revealed that the phenotypic coefficient of variation (PCV) is greater than the genotypic coefficient of variation (GCV) for all the characters under study indicating the environmental influence over the expression (Table 3). This finding was in accordance with Mehandi *et al*. (2013), Raturi *et al.* (2015), Hemavathy *et al.* (2015) and Anand *et al.* (2015) in greengram. Traits viz., plant height, number of primary branches per plant, number of clusters per plant, number of pods per plant and single plant yield exhibited high GCV and PCV (>20%) estimates, signifying the existence of more variability and less environmental influence on these traits. The results obtained was in agreement with Itefa *et al*. (2014) for number of primary branches per plant and number of pods per plant in greengram, Alom *et al.* (2015) and Raturi *et al.* (2015) for single plant yield in greengram and Garg *et al*. (2017) for single plant yield and number of pods per plant in greengram. High PCV and moderate GCV (10-20%) values was observed for petiole length, peduncle length and 100 seed weight indicating these characters are highly influenced by environment. Traits viz., days to 50% flowering, number of seeds per pod, pod length and single plant yield exhibited low PCV and GCV values indicating lack of variability. Similar results was reported by Mehandi *et al*. (2013) and Makeen *et al*. (2007) for days to 50% flowering and pod length in greengram.

By estimating GCV alone, it is not possible to determine the amount of variation that is heritable hence, the heritable portion was determined by using heritable estimates (Pathak *et al.,* 2011). Heritability is an index for the transmission of characters from parents to offspring. Genetic advance is the genetic gain under selection. The estimates of heritability were environment specific (Shimelis and Rhandzu, 2010). Thus, selection made on the basis of heritability alone is likely to be misleading and it becomes necessary to determine the parameters under targeted production environment. Hence, selection of traits based on heritability and genetic advance as percent of mean is of great importance (Mehandi *et al*., 2013).

High heritability (>30%) coupled with high genetic advance as percent of mean (>20%) was observed for plant height and 100 seed weight, displayed the predominance of additive gene action which could be targeted for phenotypic selection and further genetic improvement through simple selection method. The findings was in agreement with Makeen *et al*. (2007), Mehandi *et al*. (2013) and Hemavathy *et al.* (2015) for plant height in greengram, Sowmini and Jayamani (2013) for 100 seed weight in blackgram and Garg *et al*. (2017) for plant height and 100 seed weight in greengram. Traits viz., petiole length, peduncle length, number of primary branches, number of clusters per plant, number of pods per plant and single plant yield recorded moderate heritability coupled with high genetic advance which revealed additive gene effects coupled with high environmental impact. The results were in accordance with Mehandi *et al*. (2013) and Garg *et al*. (2017) for number of primary branches per plant in greengram, Sowmini and Jayamani (2013) for number of clusters per plant, number of pods per plant and single plant yield in blackgram. Moderate heritability coupled with low genetic advance was observed for days to 50% flowering, number of seeds per pod, pod length and shelling percentage indicated non additive gene action and environmental influence on the expression of characters, where selection is ineffective and could be better exploited through recombination breeding. Similar results was reported by Mehandi *et al*. (2013) for days to 50% flowering and pod length, Garg *et al*. (2017) for days to 50% flowering and Makeen *et al*. (2007) for days to 50% flowering and number of seeds per pod in greengram. Alom *et al.* (2015) reported contradictory results for pod length in greengram.

Genotypes exhibiting high mean value for yield and its component traits could be employed as parents for the development of high yielding varieties. MS 9724 genotype recorded maximum yield with significant number of primary branches per plant, number of clusters per plant, number of pods per plant and number of seeds per plant which could be utilized as one of the parent for improvement of yield.

References

Alom, K. M., Rashid, M. H. and Biswas, M. 2015. Genetic Variability, Correlation and Path Analysis in Mungbean (*Vigna radiata* L). *J. of Environmental Science and Natural Resources*, **7**(1): 131-138.

Anand, G., Anandhi, K. and Paulpandi, V.K. 2015. Genetic variability, correlation and path analysis for yield and yield components in F6 families of Greengram (*Vigna radiata* (L.) Wilczek) under rainfed condition. *Electronic J. of Plant Breeding*, **7**(2): 434-437.

Burton, G.W. 1952. Quantitative inheritance in grasses. *Proc. of the 6th Int. Grassland Cong*., 1: 24-84.

Garg, G. K., Verma, P. K. and Kesh, H. 2017. Genetic Variability, Correlation and Path Analysis in Greengram [*Vigna radiata* (L.) Wilczek]. *Int. J. Curr. Microbiol. App. Sci*., ***6***(11): 2166-2173.

Hemavathy, A. T., Shunmugavalli, N. and Anand, G. 2015. Genetic variability, correlation and path co-efficient studies on yield and its components in mungbean [*Vigna radiata* (L.) Wilczek]. *Legume Res.*, **38**(4): 442-446.

Itefa Degefa, Yohannes Petros and Mebeaselassie Andargie. 2014. Genetic variability, heritability and genetic advance in Mungbean (*Vigna radiata* L. Wilczek) accessions. *Plant Science Today*, **1**(2): 94-98

Lush, J.L.1940. Intra sire correlation and regression of offspring on dams as a method of estimating heritability of characters. *Proc. Amer. Soc. Animal Production*, **33**: 293-301.

Johnson, H. W., Robinson, H. F. and Comstock, R. E. 1955. Estimation of genotypic and environmental variability in soybean. *Agron. J.*, **47**: 314-318.

Makeen, K., Abrahim, G., Jan, A. and Singh, A. K. 2007. Genetic variability and correlations studies on yield and its components in Greengram [*Vigna radiata* (L.) Wilczek]. *Journal of Agronomy*, **6**(1): 216-218.

Mehandi Suhel, Singh, C. M. and Kushwaha, V. K. 2013. Estimates of genetic variability and heritability for yield and yield component traits in Greengram [*Vigna radiata* (L.) Wilczek]. *The Bioscan*, **8**(4): 1481-1484.

Pathak, R., Singh, M. and Henry, A. 2011. Genetic diversity and interrelationship among clusterbean (*Cyamopsis tetragonoloba*) genotypes for qualitative traits. *Indian J Agri. Sci.*, **81**: 402-406.

Raturi, A., Singh, S. K., Sharma, V. and Pathak, R. 2015. Genetic variability, heritability, genetic advance and path analysis in Greengram [*Vigna radiata* (L.) Wilczek]. *Legume Res.*, **38**(2): 157-163.

Shimelis, H. and Rhandzu, S. 2010. Variance components and heritabilities of yield and agronomic traits among cowpea genotypes. *Euphytica*, **176**: 383-389.

Sowmini, K. and Jayamani, P. 2013. Genetic variability studies for yield and its component traits in RIL population of blackgram (*Vigna mungo* (L.) Hepper). *Electronic J. of Plant Breeding*, **4**(1): 1050-1055.

Tak, S., Sharma, S. K. and Reager, M. L. 2013. Growth attributes and nutrient uptake of green gram as influenced by vermicompost and zinc in arid western Rajasthan. *Advance Res. J. of crop improvement*, **2**(1): 65-69.

Table 1. Mean table for yield and yield contributing traits in greengram

Sl. No	Genotypes	Petiole length (cm)	Peduncle length (cm)	Plant height (cm)	Days to 50% flowering	Number of primary branches per plant	Number of clusters per plant	Number of pods per plant	Number of seeds per pod	Pod length (cm)	Shelling percentage (%)	100 seed weight (g)	Single plant yield (g)
1	LM 9	15.60	18.45	63.00	35	2.33	11.33	35.50	10.80	6.87	65.56	3.36	10.19
2	LM 31	9.20	12.15	25.29	35	1.16	4.50	7.42	10.25	6.72	74.35	4.90	4.45
3	LM 38	11.72	15.08	37.04	35	1.00	6.67	18.17	10.30	6.21	71.57	3.47	5.04
4	LM 85	11.90	15.85	40.43	35	1.33	6.50	17.17	10.90	6.59	71.51	3.18	4.44
5	LM 103	14.12	18.17	48.25	37	1.67	7.25	14.17	10.45	6.78	69.23	3.35	4.70
6	LM 103/1	18.63	19.17	68.06	35	1.67	7.92	18.83	11.35	7.33	66.12	3.63	4.58
7	LM 179	14.30	17.13	53.22	35	1.67	6.00	16.42	11.60	6.57	72.76	2.52	5.55
8	LM 205	10.52	13.03	32.38	37	1.50	7.50	22.50	10.05	6.39	57.50	3.55	5.95
9	LM 216	10.58	11.02	22.53	36	1.17	7.50	14.17	9.95	6.37	73.08	3.04	4.49
10	LM 232	10.20	11.72	29.38	36	0.29	5.33	13.50	10.35	6.57	70.48	3.57	3.25
11	LM 233	11.82	13.18	29.46	38	0.55	4.75	14.67	10.40	6.77	74.13	3.25	3.79
12	LM 294	11.78	15.30	31.41	35	0.39	4.50	13.92	11.05	6.57	74.53	3.55	4.54
13	LM 296	11.10	14.80	35.25	34	1.50	9.50	26.58	10.90	6.80	71.43	2.81	6.72
14	LM 272	11.07	14.57	36.25	34	2.00	8.83	27.17	11.10	6.26	71.09	2.61	7.02
15	LM 336	9.98	12.93	30.36	37	1.33	10.42	24.42	10.65	6.28	74.49	2.94	6.26
16	LM 354	13.93	17.58	40.92	36	2.09	8.67	29.25	9.80	6.38	68.50	4.85	6.31
17	LM 399	9.70	11.43	26.53	35	1.00	6.17	11.33	9.05	6.50	75.20	4.72	4.45
18	LM 412	11.47	16.43	32.49	37	0.99	6.89	17.24	9.45	6.23	72.13	3.16	4.68
19	LM 450	13.78	15.07	34.15	39	0.38	4.50	12.50	11.10	6.65	74.58	4.08	4.10
20	PLS 239	14.28	16.35	28.47	35	1.20	6.00	13.67	10.50	6.97	66.97	3.57	3.76
21	PLS 274	15.25	13.85	36.23	34	2.17	7.67	20.50	9.85	6.33	74.96	3.89	7.84
22	PLS 282	10.65	14.70	24.68	35	0.57	4.75	8.50	9.30	5.76	77.96	3.46	2.80

23	PLS 287	11.37	13.57	28.78	36	0.50	5.50	13.83	10.85	6.69	73.60	3.12	4.81
24	PLS 294	11.55	10.98	24.30	37	0.45	4.83	9.83	10.25	8.95	73.37	7.03	6.73
25	PLS 308	12.15	14.23	35.83	36	0.40	4.67	16.17	10.00	6.43	73.86	4.00	4.88
26	PLS 318/2	12.73	17.88	51.52	36	1.50	7.23	30.57	10.65	6.46	61.00	3.43	6.67
27	PLS 326	13.68	15.55	51.43	34	2.83	10.17	21.83	10.70	6.27	71.09	3.36	4.82
28	PLA 334	10.30	10.58	25.88	36	0.94	7.50	20.33	10.60	6.53	75.90	3.72	6.26
29	ML 30	13.07	13.98	38.53	37	1.67	9.00	25.50	10.80	6.95	70.06	3.54	7.51
30	ML 131	10.90	12.62	29.62	36	0.33	6.00	14.50	10.05	6.33	74.45	3.94	5.38
31	MDU 2268	9.42	12.25	22.42	35	0.41	4.67	11.17	9.35	6.47	74.18	3.68	3.40
32	MDU 3385	10.78	11.60	34.67	36	1.00	6.50	15.50	10.45	6.47	77.09	3.46	4.89
33	MDU 3486	10.83	13.17	27.08	36	0.33	7.00	19.50	10.30	6.87	67.61	3.34	4.07
34	MDU 3485	12.40	14.80	32.23	35	0.58	5.17	14.33	10.60	6.90	71.35	3.85	5.12
35	MDU 3404/1	13.67	18.25	41.85	35	1.83	9.67	29.67	10.90	6.55	73.71	3.71	9.61
36	MS 9724	12.95	13.97	41.53	36	1.83	9.67	29.33	10.70	6.64	71.07	3.36	10.38
37	AC 147	12.67	12.92	36.93	36	0.67	5.83	16.00	10.70	6.77	74.67	3.53	4.87
38	AC 171	14.03	14.92	37.77	35	1.00	8.17	27.00	10.50	6.95	72.04	3.02	8.73
39	AC 192	9.93	9.22	23.67	37	1.14	5.50	14.50	9.25	6.19	73.88	3.68	4.31
40	AC 196	9.17	11.05	24.90	35	0.29	5.50	13.50	9.85	6.56	72.61	3.71	3.74
41	AC 198	9.92	13.27	26.38	38	0.33	4.00	11.00	8.75	5.97	75.09	3.73	3.69
42	AC 241	15.45	18.18	64.33	37	1.33	7.83	23.50	11.25	6.92	55.79	3.54	4.42
43	AC 254	10.75	14.88	25.85	37	0.67	6.33	17.17	9.70	5.95	75.38	3.61	5.74
44	G 1	15.02	18.42	42.17	38	0.75	8.17	23.33	10.45	6.25	71.71	2.86	5.44
45	CoGG 936	12.62	13.90	32.25	37	0.83	5.50	16.00	10.75	6.98	78.11	3.66	5.99
46	K 851	11.78	13.17	28.57	37	1.50	7.83	17.67	10.00	6.25	75.17	2.82	5.00
47	V 5197/1	11.73	16.24	39.78	36	1.33	7.67	20.67	10.15	5.57	65.07	3.21	3.72
48	CoGG 48	12.55	15.48	30.14	35	0.92	6.42	17.67	9.65	6.26	76.15	3.47	5.69
49	BDYR 1	9.33	10.64	24.73	38	0.88	6.17	12.33	10.75	7.81	76.15	4.71	4.29
50	SML 668	7.60	8.78	25.62	37	0.72	3.67	7.33	7.30	7.13	68.09	5.21	3.33

51	Pantmung 4	8.33	9.55	20.55	37	0.39	4.17	9.50	10.30	6.54	83.25	3.58	3.75
Mean		11.93	14.16	34.81	36	1.08	6.73	17.98	10.29	6.60	71.95	3.63	5.34
Range		7.60 - 18.63	8.78 - 19.17	20.55 - 68.06	34 - 39	0.29 - 2.83	3.67 - 11.33	7.33 - 35.50	7.30 - 11.60	5.57 - 8.95	55.79 - 83.25	2.52 - 7.03	2.80 - 10.38
SE		1.61	2.22	5.11	1.08	0.50	1.64	6.77	0.71	0.42	4.79	0.36	1.83
CD (P=0.05)		3.23	4.47	10.27	2.18	1.01	3.30	13.61	1.42	0.85	9.62	0.73	3.67

Table 2. Analysis of variance for yield and yield contributing traits in greengram

Sources of variation	**df**	**Mean sum of squares**											
		Petiole length	**Peduncle length**	**Plant height**	**Days to 50% flowering**	**Number of primary branches per plant**	**Number of clusters per plant**	**Number of pods per plant**	**Number of seeds per pod**	**Pod length**	**Shelling percentage**	**100 seed weight**	**Single plant yield**
Treatment	50	8.991*	13.432*	239.380*	2.816*	0.744*	6.722*	86.613*	1.099*	0.517*	47.869*	1.082*	7.246*
Error	50	2.588	4.942	26.134	1.174	0.252	2.695	45.871	0.501	0.179	22.954	0.133	3.340

*Significant at 1% level.

Table 3. Coefficient of variation, heritability (broad sense), genetic advance and genetic advance as percent of mean for yield and yield contributing traits in greengram

Character	Co efficient of variation (%)		Heritability (%)	Genetic advance (GA)	GA as percent of mean (%)
	PCV	GCV			
Petiole length	20.17	15.00	55.30	6.35	22.98
Peduncle length	21.51	14.62	46.21	6.51	20.48
Plant height	33.10	29.66	80.31	27.95	54.77
Days to 50% flowering	3.95	2.53	41.15	14.68	3.36
Number of primary branches/plant	63.94	44.94	49.39	0.55	65.07
Number of clusters/plant	32.16	21.03	42.77	2.88	28.34
Number of pods/plant	45.30	25.12	30.75	5.52	28.70
Number of seeds/pod	8.69	5.31	37.37	3.84	6.69
Pod length	8.94	6.23	48.52	3.20	8.94
Shelling percentage	8.2	4.90	35.18	25.31	5.99
100 seed weight	21.45	18.97	78.17	2.83	34.55
Single plant yield	42.31	25.70	36.89	2.01	32.16