



E-ISSN: 2278-4136
P-ISSN: 2349-8234
JPP 2017; 6(4): 119-122
Received: 27-07-2017
Accepted: 28-08-2017

Ch Himabindu

Department of Genetics and Plant breeding, Naini Agricultural Institute, Sam Higginbottom University of Agriculture Technology and Sciences, Allahabad, Uttar Pradesh, India

G Roopa Lavanya

Department of Genetics and Plant breeding, Naini Agricultural Institute, Sam Higginbottom University of Agriculture Technology and Sciences, Allahabad, Uttar Pradesh, India

Character association among yield component characters and with seed yield in greengram (*Vigna radiata* (L.) Wilczek)

Ch Himabindu and G Roopa Lavanya

Abstract

The experimental material comprised 22 greengram genotypes. The Observations were recorded on five randomly selected plants of each treatment and replication for 12 quantitative characters viz., days to 50% flowering, plant height (cm), number of branches per plant, number of clusters per plant, number of pods per plant, pod length (cm), number of seeds per pod, days to maturity, biological yield (g), harvest index, seed index (g), seed yield per plant (g) to estimate the genetic variability, heritability and correlations among yield and its related traits. Maximum GCV and PCV were recorded for no of branches/plant, pod length and harvest index. High heritability coupled with high genetic advance was registered for harvest index, pod length and seeds/pod. Correlation coefficient analysis revealed that seed yield per plant exhibited significant and positive correlation both at genotypic and phenotypic level with harvest index and biological yield/plant. Based on the results, KM 11-583XKM11-587 cross showed high mean performance for seed yield per plant. Heritability, genetic advance and correlation coefficient analysis indicated that these traits may be used for the development of higher grain yielding chickpea genotypes to improve yield of greengram. Hence, direct selection for these traits could be helpful in the improvement of greengram breeding.

Keywords: Greengram, Variability, Heritability, Genetic advance, GCV, PCV, Correlation

1. Introduction

Greengram (*Vigna radiata* L.) ($2n=2x=22$) is third important pulse after chickpea and Pigeon pea. The creation of variability is difficult through hybridization due to its high self-pollination and flower droop (Deepalakshmi and Anandakumar, 2004) [4]. Besides the major constrains in achieving higher yield of greengram is absence of suitable ideotypes for different cropping system, poor harvest index and susceptibility to disease (Subramanien and Gopalakrishnan, 2004) [13]. In order to improve yield and other polygenetic characters, mutation breeding can also be effectively utilized (Deepalakshmi and Anandakumar, 2004) [4]. Therefore, genetic variability is the basic requirement for making progress in crop breeding (Appalaswamy and Reddy, 2004) [2].

However, it is only genetic variation which is heritable and hence important in any selection programme. Correlation coefficient gives an ideal about the various associations existing between yield components. As yield is a complex character direct selection for this character as such becomes a difficult task without knowledge of relationship between yield and its various components. Since all these characters are correlated the change in one of the character may cause a series of a change in other characters. Therefore, to bring a change in yield or other characters to a desired level proper understanding of association between yield and yield contributing characters is must. The approach might be useful in selection of traits associated with highest expression of yield and improvement of the characters (Singh *et al.*, 2009) [14].

Materials and Methods

The present investigation was carried out at the Field Experimentation Centre, Department of Genetics and Plant Breeding, Naini Agricultural Institute, Sam Higginbottom University of Agriculture, Technology and Sciences, Allahabad, U.P. (India) during *Rabi*-2016. The experimental materials consist of 22 genotypes obtained from AICRIP on MULLaRP crops, Dept. of GPB, SHUATS. The experiment was laid out in Randomized Complete Block Design with 3 replications. The genotypes were sown by hand dibbling in each plot by imposing randomization in each replication along with check Samrat. The spacing of row to row 30cm and plant to plant 10cm. The fertilizer dose of 20:40:40 NPK kg/ha is applied as Nitrogen as two splits, phosphorus and potassium as basal dose. All recommended package of practices was followed during the cropping period to raise a good crop.

Correspondence**Ch Himabindu**

Department of Genetics and Plant breeding, Naini Agricultural Institute, Sam Higginbottom University of Agriculture Technology and Sciences, Allahabad, Uttar Pradesh, India

Observations were recorded in each plot and replication by taking five plants randomly for 12 quantitative characters *viz.* Mean data for 12 characters *viz.*, days to 50% flowering, plant height, number of branches per plant, days to maturity, number of clusters per plant, number of pod per plant, pod length, number of seed per pod, biological yield, harvest index, seed index and seed yield per plant. The data was subjected to the statistical analysis the correlation coefficients are estimated as suggested by Al Jibouri *et al.* (1958) ^[1].

Results and Discussion

The analysis of variance revealed highly significant differences among the genotypes for all the twelve characters studied (Table 1). In the present study variation among the characters are estimated by Genotypic Coefficient of Variation (GCV) and Phenotypic Coefficient of Variation (PCV). The PCV was slightly higher than the GCV for few characters indicates the interaction of genotypes with the environment (Table 2). High GCV and PCV were recorded for harvest index (24.74 and 25.9) followed by a number of primary branches per plant (14.14 and 19.74). Estimates of heritability is a good index for predicting the transmission of

characters from parents to their offspring (Falconer, 1981) ^[5]. High heritability (broad sense) was recorded for characters *i.e.*, harvest index (91 %) followed by clusters per plant (65 %) pod length (63%), plant height (63 %). High heritability alone may not lead to valid conclusions unless it is accompanied with the Genetic advance as percent mean (Johnson and Robinson, 1955) ^[6]. High heritability coupled with high genetic advance as percent of the mean was recorded for harvest index and biological yield per plant.

The genotypic and phenotypic correlation coefficients were computed among 13 characters (Table 3). The Seed index, clusters per plant, biological yield and harvest index showed highly significant positive association with seed yield at both genotypic and phenotypic levels. Therefore, these characters appeared as greatest important associates of seed yield per plant and have also been observed by preceding workers (Kumar *et al.*, 2005; and Verma, 2001).

By considering the nature and extent of correlation coefficients it can be concluded that improvement of Greengram seed yield is brought through simultaneous selection Seed index, clusters per plant, biological yield and harvest index.

Table 1: Analysis of variance for seed yield & its contributing characters in Greengram genotypes (Mean squares)

Source of Variation	d.f.	Days to 50% flowering	Plant height(cm)	Primary branches/plant	Clusters/plant	Pods/plant	Pod length(cm)	Seeds/pod	Days to maturity	Seed index(gm)	Biological yield(gm)	Harvest index (%)	Seed yield/plant (gm)
Replications	2	13.37	4.1	0.02	0.09	1.59	1.59	0.49	8.9	0.02	4.76	5.13	0.35
Genotypes	29	23.5**	164.59**	0.27**	2.80**	3.76**	3.76**	6.52**	75.56**	3.84**	15.19**	756.44**	0.29**
Error	58	8.1	27.23	0.06	0.42	0.61	0.61	1.4	20.34	0.06	5.98	23.45	1.24

**Significant at 1% level and *Significant at 5% level.

Table 2: Estimates of variability, heritability and genetic advance as per cent of mean for seed yield and yield components in Greengram genotypes.

Sl. No.	Characters	Range		Grand Mean	Genotypic Coefficient of variance (GCV)	Phenotypic coefficient of variance (PCV)	Heritability(in broadsense) (%)	Genetic Advance as percent mean
		Minimum	Maximum					
1	Days to 50 % flowering	32.66	42.66	37.93	5.96	9.61	2.88	7.6
2	Height of Genotypes	47.6	75.06	65.88	10.27	12.97	11.04	16.75
3	Number of primary Branches	1.4	2.46	1.86	14.14	19.74	0.51	1.88
4	Cluster/plant	5.06	8.46	7.33	12.13	15.06	0.65	7.33
5	Pods/plant	14.13	22.6	17.13	12.22	17.31	0.5	17.14
6	Length of pods	6.69	11.626	8.2	12.45	15.72	0.63	8.21
7	Seeds/pod	8	12.86	11.3	11.56	15.6	0.55	11.3
8	Days to maturity	47.66	68.66	59.43	5.96	10.47	0.47	10.25
9	Seed index	3.16	4.12	3.64	7.62	10.29	0.55	3.64
10	Biological yield	18.66	30.45	24.86	7.05	12.1	0.34	24.86
11	Harvest index %	33.95	86.27	63.18	24.74	25.9	0.91	63.19
12	Seed yield/plant	6.93	11.51	9	10.33	16.14	0.41	9.01

Table 3: Genotypic and Phenotypic correlation coefficients of Greengram genotype.

Characters		Plant height	Primary branches/plant	Clusters/plant	Pods/plant	Pod length	Seeds/pod	Days to maturity	Seed index	Biological yield	Harvest index	Seed yield/plant
Days to 50% flowering	G	0.497**	-0.020	-0.119	-0.157	0.500**	-0.235	0.792**	-0.226	0.067	-0.088	0.009
	P	-0.0667	0.0394	0.2736	-0.2651	-0.1836	-0.0766	0.1317	0.2081	-0.1913	-0.0725	-0.0164
Plant height	G	1.000	-0.240	-0.369*	-0.398*	0.088	0.665**	0.809**	-0.266	0.358*	0.044	0.044
	P	1.0000	-0.0734	-0.0267	0.2189	0.0454	0.1264	-0.0847	-0.0991	0.0788	-0.0399	-0.339
Primary branches/plant	G		1.000	-0.253	0.166	-0.027	0.180	-0.204	-0.363*	0.228	-0.178	-0.178
	P		1.0000	-0.1994	0.0689	-0.1530	0.2830	-0.0637	0.1221	0.2145	-0.0948	-0.0948
Clusters/plant	G			1.000	-0.377**	0.649**	0.751*	0.472**	0.356*	0.120	0.519**	0.519**
	P			1.0000	-0.4087	-0.0610	-0.0964	0.0692	0.1927	-0.2528	0.0454	0.0454
Pods/plant	G				1.000	0.079	0.636*	0.864**	0.295	-0.344*	0.056	0.056
	P				1.000	0.1757	-0.0096		-0.2249	0.0556	0.1783	-0.0309
Pod length	G					1.000			0.362*	0.030	0.270	0.236
	P					1.0000			-0.0106	0.2329	-0.1599	-0.1438
Seeds/pod	G						1.000		0.799**	-0.167	0.292	0.133
	P						1.000		0.0147	-0.0107	0.2494	-0.0153
Days to maturity	G	-0.220	0.087	0.016	-0.114	-0.215	0.065	1.000	0.091	0.202	-0.0120	0.190
	P	0.3423	0.0728	0.0404	0.0796	-0.0338	0.1208	1.0000	-0.0583	0.0385	-0.2257	-0.1096
Seed index	G								1.000			0.397*
	P								1.0000			-0.0007
Biological yield	G								0.007	1.000	-0.44**	0.611**
	P								-0.1188	1.0000	-0.0491	-0.0224
Harvest index	G								0.465**		1.000	0.426**
	P								-0.0613		1.0000	0.0573

G = Genotypic correlation coefficient. P = Phenotypic correlation coefficient. *Significant at 5% level, **Significant at 1% level.

Conclusion

The results from present study entitled “character association among yield component characters and with seed yield in greengram (*Vigna radiata* (L.) Wilczek)” concludes that among 22 genotypes of greengram KM 11-583XKM11-587 was found to be superior for seed yield per plant. High heritability and genetic advance were observed for harvest index, plant height, days to maturity, seed/pod, number of branches/plant and seed yield/plant hence these parameters could be used as for selection. Correlation coefficient analysis revealed that seed yield per plant exhibited significant and positive correlation both at genotypic and phenotypic level with harvest index and biological yield/plant, Hence, direct selection for these traits could be helpful in the improvement of greengram breeding.

References

1. Al-Jibouri HA, Mullar PA, Rabinsion HF. Genetic and environmental variances and co-variances in an upland cotton cross of inter specific origin. *Journal of Agronomy*. 1958; 50:633-636.
2. Appalaswamy A, Reddy M. Genetic divergence and heterosis studies of mungbean (*Vigna radiata* L. Wilczek). *Legume Research*, 2004; 21:115-118.
3. Burton GW. Quantitative inheritance in grass. Proc. 6th Int. Grassland Cong. 1952; 1:227-83.
4. Deepalakshmi AJ, Anandakumar CK. Creation of genetic variability for different polygenic traits in blackgram (*Vigna mungo* L. Hepper) through induced mutagenesis, *Legume Research*. 2004; 3:188-192.
5. Falconer DS. Introduction to Quantitative genetics, 3rd ed. Longman, New York. 1981, 340.
6. Johnson HW, Robinson HF, Comstock RE. Estimates of genetic and environmental variability in soybean, *Agronomy Journal*. 1955; 47:314-318.
7. Karpechenko GD. Chromosomes of phaseolinae. *Bulletin Application of Botany*. 1925; 14:143-148.
8. Konda CR, Salimath PM, Mishra MN. Genetic variability studies for productivity and its components in blackgram (*vigna mungo* L. Hepper). *Indian journal Genetics*. 2009; 62(4):345-346.
9. Lush K. Inter- se correlation and regression of characters proceeding of American Society of Animal Production. 1949; 33:293-301.
10. Mishra DK, Khan RA. Stability analysis in urdbean for grain yield and associated traits, *Indian Journal of Pulses Research*. 2001; 14(2):145-147.
11. Neelavati, Sand Govindarasu R. Studied on Analysis of Variability and diversity in rice fallow blackgram (*Vigna mungo* L. Hepper), *Legume Research*. 2010; 33(3):206-210.
12. Sarkar G, Panda S, Senapati BK. Genetic variability and characterassociation in blackgram (*Vigna mungo* L. Hepper), *Journal of Arid Legumes*. 2006; 3(1):44-46.
13. Souframanien J, Goplalakrishnan T. A comparative analysis of genetic diversity of blackgram genotype using RAPD and ISSR markers. *Theor Applied Genetics*. 2004; 109: 1687-1693.
14. Singh Tejbir, Sharma A, Alie FA. Morpho-physiological traits as selection criteria for yield improvement in mungbean [*Vigna radiata* (L.) Wilczek]. *Legume Research*. 2009; 32(1):36-40.