Studies on Genetic Parameters for Seed Yield and its Components in Greengram (*Vigna radiata* L.) Germplasm

V. Sridhar, A. Sriram, S. Srinivasa Rao, G. Venu Gopal

ABSTRACT

The studies were conducted at the PJTSAU, Agricultural Research Station, Madhira to evaluate thirty nine genotypes of greengram during *rabi*, 2017-18. The experiments were laid out in RBD with two replications to determine the variability, heritability, genotypic and phenotypic coefficient of variation, correlation and path coefficients among seven quantitative traits viz., days to 50% flowering, days to maturity, plant height (cm), number of clusters/plant, number of pods/plant, 100 seed weight (g) and seed yield/plant (g). Results revealed that magnitude of the phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation (GCV) for all the traits, indicating the interaction of genotype with the environment. Phenotypic coefficient of variation and genotypic coefficient of variation was found to be high for the plant height, seed yield per plant, number of clusters per plant and the number of pods per plant. Heritability estimates ranged from to 75% (number of clusters and pods per plant) to 96.80% (Plant height). The genetic advance was found to be very high for the plant height and number of pods per plant. In the present study all the characters have recorded high heritability coupled with high genetic gain as per cent of mean. Genotypic (rg) correlation coefficients were higher than the Phenotypic (rp) correlation coefficients for all the traits. Character association studies revealed that the single plant yield was significantly correlated with number of clusters and pods per plant (0.919), 100 seed weight (0.5111), plant height (0.489). Path analysis revealed that the number of clusters per plant (1.561), 100 seed weight (0.349) had a high positive and direct effect on seed yield. Phenotypic selection of traits contributing to grain yield exhibiting high heritability coupled with genetic advance would help in the selection of superior genotypes for the improvement of seed yield in greengram. The present findings could be suggested that on the basis of genetic parameter correlation and path analysis, number of clusters per plant, number of pods per plant and 100 seed weight should be given

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topmost priority while formulating a selection strategy for improvement of yield in greengram.

INTRODUCTION

Greengram is a self pollinated diploid grain legume (2n=2x=22) crop with cheap and rich source of vegetable protein (22-24%) and commonly used as supplement to the normal diet. Greengram is accentuated due to its nutritional value. Hundred grams of greengram seeds contains carbohydrates (57.5%), protein (24.6%), fat (1.0%), energy (234 cal), calcium (0.08 g), phosphorus (0.045 g), iron (5.7 mg), fiber (2.2 g), thiamin (0.525 mg) and vitamin B (300 mg) (Srivastava and Ali 2004). It is rich in lysine, an essential amino acid, which is deficient in most of the cereal grains. This crop plays an important role in crop rotation due the ability to restore the seed fertility through symbiotic nitrogen fixation (Malik 1994). Seed yield in greengram is a complex character and determined by various components. The selection simply based on yield is not effective. The presence of genetic variability existing among different parameters is important in crop improvement, as it provides a source for the breeders to develop new varieties. Knowledge of heritability and genetic advance of the trait indicate the scope for improvement of a character through selection. Genetic gain under selection can be effectively predicted with the estimates of heritability along with genetic advances.

Correlation coefficient analysis is a complex technique, which elaborates the degree and extent of relationship among important plant characters and it provides basic criteria for selection and leads to directional model based on yield and its components in the field experiments but, the results seems to be often incomplete about the nature of association among the traits. Path coefficient analysis is an efficient statistical technique specially designed to quantify the interrelationship among different components traits and their direct and indirect effects on seed yield (Hemavathy *et al*. 2015).

Through this technique yield attributing traits can be ranked and specific traits producing a given correlation can be progressed (Rao *et al*. 2006). Correlation studies and path analysis gives an idea about the contribution of different characters to seed yield (Vandana and Dubey 1993). The results of earlier workers pertaining to correlation and path coefficient studies in greengram have been found to be non-consistent and varied with the materials and environments used (Yaqoob 1997). Therefore, the present study was undertaken to estimate the genetic variability, heritability, genetic advance, along with the correlation and path analysis to understand the mode of inheritance, degree and direction of association of different yield attributing traits with the seed yield in thirty genotypes of greengram.

MATERIALS AND METHODS

The present study was carried out at PJTSAU, Agricultural Research Station, Madhira during *rabi* season (October to December) 2017-18. The farm is geographically located at 17°- 58' North Latitude, 78°-44' East Longitude and at an elevation of 189 m AMSL. The experimental material comprised of thirty nine diverse germplasm accessions which are being maintained at the research station. The greengram germplasm lines were evaluated in a Randomized Block Design replicated twice. Each entry was planted in 2 rows of 4 m length with 30 x 10 cm spacing between and within rows. The recommended fertilizers doses of 16:50 kg ha^{-1} of N:P were applied. Observations on seven quantitative traits viz., plant height (cm), number of clusters/plant, number of pods/plant, 100 seed weight (g) and seed yield/plant (g) were recorded following standard procedures on randomly selected five plants per replication but with respect to the traits of days to 50% flowering and days to maturity the observations are noted on plot basis and the data was subjected to statistical analysis. The statistical analysis for variance was worked out as per Panse and Sukhatme (1961). The genotypic and phenotypic coefficients of variance were calculated based on the method suggested by Burton (1952). Heritability (broad sense), genetic advance and genetic gain were calculated according to the formula given by Johnson *et al*. (1955). The phenotypic and genotypic correlation coefficients were calculated from phenotypic and genotypic variances and co variances and path

Table 1. Analysis of variance for seed yield and yield components of greengram. ** Significant at 1% level of significance.

Source of variation	df	Mean sum of squares						
		Days to 50% flowering	Days to maturity	Plant height (cm)	Number of clusters/plant	Number of pods/plant	100 seed weight (g)	Seed yield/plant
Replications	1	0.05	0.32	25.16	0.01	0.12	0.20	2.73
Genotypes	38	14.39**	15.12**	482.97**	8.09**	72.81**	0.55**	13.74**
Error	38	0.79	0.79	7.79	1.14	10.26	0.07	1.69

coefficients analyses were worked out as suggested by Dewey and Lu (1959).

RESULTS AND DISCUSSION

Significant differences among the genotypes for all the morphological traits such as days to 50% flowering, days to maturity, plant height (cm), number of clusters/plant, number of pods/plant, 100 seed weight (g) and seed yield/plant (g) were revealed by analysis of variance (Table 1), which gives the evidence of sufficient variability among the genotypes. The results are accordance with Venkateswarlu and Jayamani (2001), Sathya (2011), Dhoot *et al*. (2017), Reshmi Jahan *et al*. (2020) and Salman *et al*. (2021) in greengram.

The substantial improvement of this crop is possible because of the presence of broad variability among the genotypes. Extent of variability was measured in terms of range, genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) along with per cent heritability (h^2), genetic advance and genetic advance over per cent mean and is presented in Table 2. The mean data exhibited a wide range of variations among the characters studied (Table 2). Plant height ranged from 11 to 76 cm, number of clusters/plant (4.20 to 15.75), number of pods/plant ranged from 12.60 to 47.25, for hundred seed weight the range is in between 2.63-5.35 g. Days to 50 % flowering and days to maturity recorded (32.50 to 44.50) and (57 to 69.50) days respectively. Single plant yield had a range of 4.80 grams for the genotype IC-436634 and the genotype IC-261272 recorded highest contribution of 17.20 grams.

The estimates of the phenotypic coefficient of variation (PCV) was found higher than that of genotypic coefficient of variation (GCV) for all the traits, indicating the influence of the environment in governing the characters or expression of genotypes, also suggested by Khajudparn and Tantasawat (2011), Reshmi Jahan *et al*. (2020), Salman *et al*. (2021) (Table 2). Phenotypic coefficient of variation and genotypic coefficient of variation was found to be high (>20%) for the plant height (51.69 %, 50.86 %) seed yield per plant (33.81%, 29.88 %) number of clusters per plant and the number of pods per plant each (30.12 %, 26.14 %) respectively, indicating the presence of sufficient variability for these traits. Moderate PCV

Table 2. Genetic variability parameters for different quantitative traits in greengram.

Sl. No.	Character	Mean	Range		GCV (%)	PCV (%)	Heritability (Broad sense) (%)	Genetic advance (GA) @ 1%	GA as percent of mean (%)
			Min.	Max					
1	Days to 50% flowering	39.21	32.50	44.50	6.65	7.02	89.60	6.52	16.62
2	Days to maturity	64.42	57.00	69.50	4.15	4.37	90.00	6.70	10.41
3	Plant height (cm)	30.30	11.00	76.00	50.86	51.69	96.80	40.04	132.14
4	Number of clusters/plant	7.13	4.20	15.75	26.14	30.12	75.00	4.27	59.88
5	Number of pods/plant	21.39	12.60	47.25	26.14	30.12	75.00	12.81	59.88
6	100 seed weight (g)	3.51	2.63	5.35	14.03	15.08	78.90	1.16	32.93
7	Seed yield/plant (g)	8.21	4.80	17.20	29.88	33.81	78.00	5.73	69.71

(15.08 %) and GCV (14.03 %) was recorded for 100 seed weight and low estimates of the phenotypic coefficient of variation were recorded for days to maturity (4.37 %, 4.15 %) as proposed by Sivasubramanian and Madhava Menon (1973). Similar results were reported by Tabasum *et al*. (2010), Payasi (2015), Raturi *et al*. (2015), Anand *et al*. (2016) and Garg *et al*. (2017), Jagdhane *et al*. (2017), Rasal and Parhe, (2017) and Yadav *et al*. (2017); Reshmi Jahan *et al*. (2020), Sineka *et al*. (2021) for the number of clusters per plant; number of pods per plant; seed yield per plant. Baisakh *et al*. (2016) and Sunayana *et al*. (2017), Reshmi Jahan *et al*. (2020) for plant height. In the present study, PCV and GCV were found to be low for days to maturity. This is in accordance with Makeen *et al*. (2007), Nand and Anuradha (2013), Sunayana *et al*. (2017) Zuge *et al*.(2019) and Asari *et al*. (2019), Reshmi Jahan *et al*. (2020), Sineka *et al*. (2021) in greengram.

Heritability (in broad sense) estimates ranged from to 75 % (number of clusters and pods per plant) to 96.80 % (Plant height) (Table 2). All the other traits had heritability estimates of more than 70%. Indicates preponderance of additive gene action in the expression of these traits and they can be improved through individual plant selection. These findings are in agreement with the findings Makeen *et al*. (2007), Rahim *et al*. (2010), Kumar *et al*. (2013), Hemavathy *et al*. (2015), Garg *et al*. (2017), Mehendi *et al*. (2018), Zuge *et al*. (2019), Reshmi Jahan

et al. (2020), Sineka *et al*. (2021) for plant height, for number of clusters/plant, number of pods/plant, 100 seed weight, seed yield /plant. Payasi (2015) and Reshmi Jahan *et al*. (2020) for days to 50% flowering and days to maturity.

The heritability value alone, however, does not provide any indication of the amount of genetic improvement that would results from selecting the best individuals. Limitations of heritability in broad sense include both the additive and non additive gene effects, which become reliable for selection if, coupled with high genetic advance (Ramanujan and Tirumalachar 1967). The genetic advance was found to be very high for the plant height (40.04) followed by number of pods per plant (12.81). The highest genetic advance was obtained for plant height, and number of pods/plant, days to maturity, days to 50% flowering, seed yield/plant whereas, lowest was observed for 100 seed weight. Results are in accordance with the earlier researchers viz., Pandiyan *et al*. (2006), Gul *et al*. (2007), Rehman *et al*. (2009), Rahim *et al*. (2010) and Payasi (2015).

High heritability accompanied with high genetic advance as per cent of mean was recorded for the plant height, number of clusters per plant and the number of pods per plant, seed yield per plant, 100 seed weight. This suggests that most likely the heritability is due to additive gene effects and hence the selection may be effective for these characters and

Table 3. Genotypic (rg) and Phenotypic (rp) correlation coefficients among the yield attributing characters in greengram.

Characters	Correlation coefficients	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of clusters/plant	Number of pods/plant	100 seed weight (g)	Seed yield/plant (g)
Days to 50% flowering	rg	**1.000**	0.832**	-0.126	0.002	0.002	0.116	0.082
	rp	**1.000**	0.750**	-0.136	-0.056	-0.056	0.090	0.009
Days to maturity	rg		**1.000**	-0.020	0.032	0.032	-0.127	0.033
	rp		**1.000**	-0.019	-0.003	-0.003	-0.093	0.009
Plant height (cm)	rg			**1.000**	0.693**	0.693**	-0.061	0.489**
	rp			**1.000**	0.623**	0.623**	-0.048	0.461**
Number of clusters/plant	rg				**1.000**	1.000	0.174	0.919**
	rp				**1.000**	1.000	0.083	0.903**
Number of pods/plant	rg					**1.000**	0.174	0.919**
	rp					**1.000**	0.083	0.903**
100 seed weight (g)	rg						**1.000**	0.511**
	rp						**1.000**	0.462**
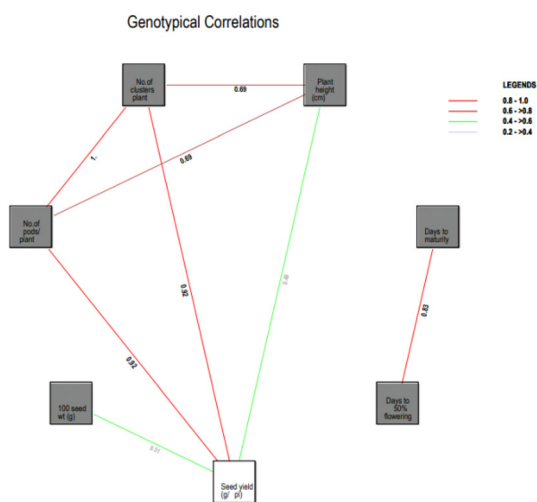
Fig. 1. Genotypic correlations for seed yield and yield components in greengram.

The degree of correlation, observable among attributes will depend on the development relations between them and on genes which contribute to the variation. Positive correlation is due to changes of genes supplying precursors. Genotypic correlations were higher than the phenotypic correlations (Table 3 and Fig. 1) for most of the characters, which can be explained due to the masking or modifying effects of the environment on the genetic association between characters. In the present investigation, seed yield per plant was positive and significantly correlated with the number of cluster and number of pods per plant each (rg = 0.919 and rp = 0.903), followed by 100 seed weight (rg = 0.511 and rp = 0.462), plant height (rg = 0.489 and rp = 0.461). These results are in accordance with Baisakh *et al*. (2016), Kate *et al*. (2017), Sandhiya and Saravanan (2018), Sandhiya and Shanmugavel (2018), Ramakrishnan *et al*. (2018), Reshmi Jahan *et al*. (2020), Sineka *et al*. (2021) for the traits like number of clusters per plant, number of pods per plant, plant height, 100 seed weight. Hence, these characters can be utilized in direct selection so as to improve the seed yield per plant. Among the inter correlation of different traits, days to 50% flowering showed positive significant association with days to maturity. Plant height showed positive significant association with number of clusters per plant and

pedigree or modified pedigree method of selection may be followed. Similar findings were obtained for Ghimire *et al*. (2017) for seed yield per plant; Makeen *et al*. (2007), Baisakh *et al*. (2016), Muthuswamy *et al*. (2019), Pavan *et al*. (2019), Asari *et al*. (2019) for plant height, for the number of pods per plant, seed yield per plant. Kumar *et al*. (2013) for 100 seed weight. Moderate GAM was observed days to 50% flowering and days to maturity.
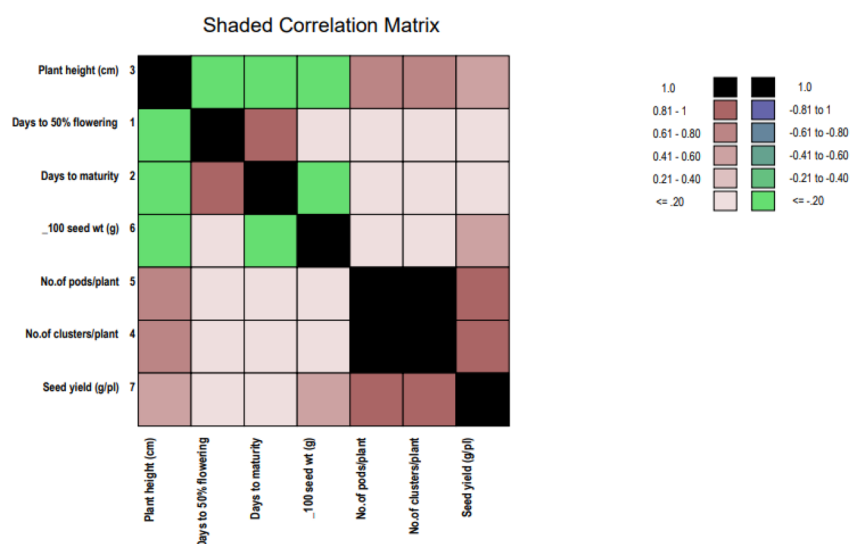

Fig. 2. Shaded correlation matrix for seed yield and yield components in greengram.

Table 4. Direct and indirect effects of yield component characters on seed yield in greengram. ** Significant at 1% level of significance. Diagonal indicates direct effects. Residual effect:, Genotypic = 0.112, Phenotypic = 0.154.

Characters		Days to 50% flowering	Days to maturity	Plant height (cm)	Number of clusters/plant	Number of pods/plant	100 seed weight (g)	Seed yield/plant (g)
Days to 50% flowering	G	**-0.053**	-0.044	0.007	0.000	0.000	-0.006	0.082
	P	**-0.054**	-0.041	0.007	0.003	0.003	-0.005	0.009
Days to maturity	G	0.072	**0.086**	-0.002	0.003	0.003	-0.011	0.033
	P	0.065	**0.087**	-0.002	0.000	0.000	-0.008	0.009
Plant height (cm)	G	0.021	0.003	**-0.167**	-0.116	-0.116	0.010	0.489**
	P	0.015	0.002	**-0.109**	-0.068	-0.068	0.005	0.461**
Number of clusters/plant	G	0.003	0.050	1.081	**1.561**	1.561	0.271	0.919**
	P	-0.080	-0.004	0.884	**1.419**	1.419	0.118	0.903**
Number of pods/plant	G	-0.001	-0.019	-0.409	-0.590	**-0.590**	-0.103	0.919**
	P	0.027	0.001	-0.301	-0.483	**-0.483**	-0.040	0.903**
100 seed weight (g)	G	0.040	-0.044	-0.021	0.061	0.061	**0.349**	0.511**
	P	0.035	-0.037	-0.019	0.033	0.033	**0.392**	0.462**

number of pods per plant (Fig. 2). The inter correlation between yield contributing traits may affect the selection for component traits either in favorable or unfavorable direction. Hence, the knowledge on inter-relationship between yield and yield component traits may facilitate breeders to decide upon the intensity and direction of selection pressure to be given on related characters for the simultaneous improvement of these traits.

The estimates of correlation coefficients revealed only the relationship between yield components, but did not show the direct and indirect effects of different traits on yield, because the attributes which are in association do not exist by themselves, but are linked to be with other components. In order to get exact information of yield components on yield, the direct and indirect effects were investigated through path coefficient analysis which are presented in Table 4 and
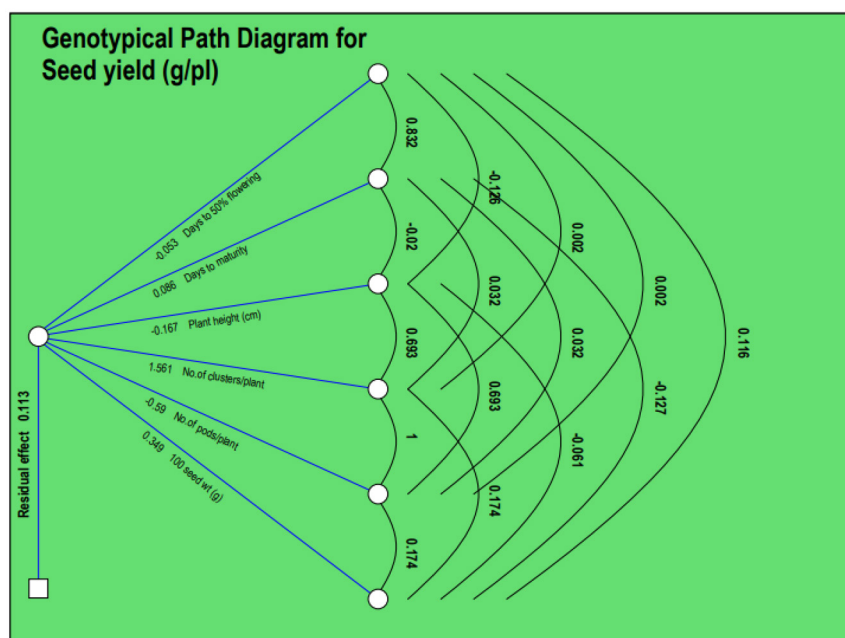
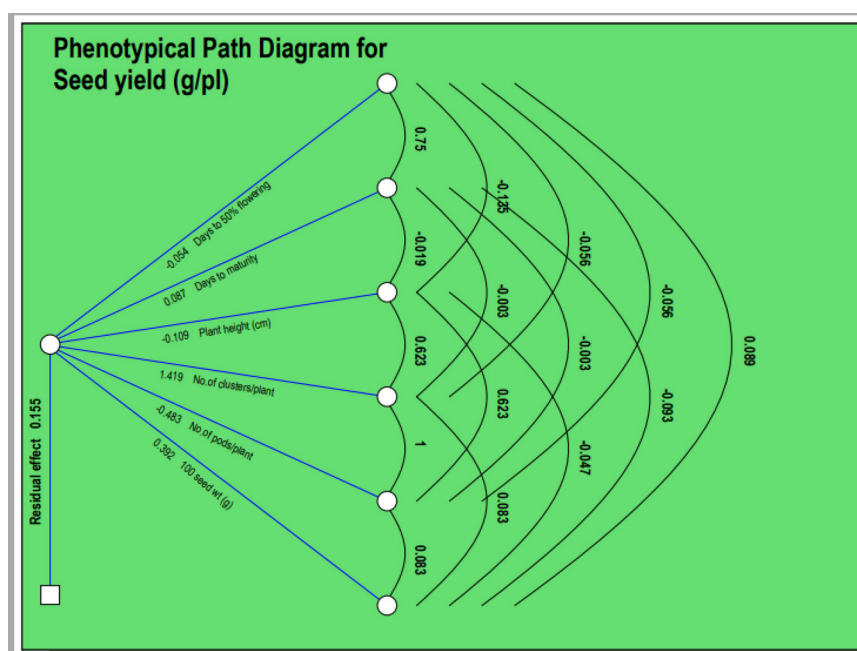**Fig. 3.** Genotypic path diagram for seed yield and yield components in greengram.

Fig. 4. Phenotypic path diagram for seed yield and yield components in greengram.

depicted in Figs. 3 - 4. The residual effect (0.155) indicated that most (84.5%) of the characters related to seed yield per plant were accounted for path analysis. Path coefficient analysis revealed that days to maturity (G= 0.086, P= 0.087), number of clusters/plant (G=1.561, P= 1.419) and 100 seed weight G=0.349, P=0.392) showed positive direct effect coupled with positive indirect effects through number of clusters/plant, number of pods per plant and 100 seed weight resulting in a true relationship with seed yield per plant by plant establishing significant and positive direct effects both at the genotypic and phenotypic levels. Similar findings were obtained by Thippani *et al.* (2013), Reshmi Jahan *et al.* (2020), Gadakh *et al.*(2013), Degefa *et al.*(2014) Thanga Hemavathy *et al.* (2015). Direct and indirect matrix revealed that negative direct effect of plant height on seed yield per plant as well as negative indirect effects via number of clusters per plant, number of pods per plant. This indicated that plant height is not directly associated with yield as a result less importance is given during the selection process. These findings are in accordance with the Rohman and Hussain (2003) and Thanga Hemavathy *et al.* (2015) For path analysis it may be concluded that number of clusters per

plant followed by 100 seed weight may be given due weightage during selection to increase the seed yield of greengram in the present material under study.

CONCLUSION

It is suggested that on the basis of genetic parameters, correlation and path analysis, number of clusters per plant, number of pods per plant and 100 seed weight should be given topmost priority while formulating a selection strategy for improvement of seed yield in greengram.

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