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Research Article

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

T. Sineka[1], E.Murugan[1*], A. Sheeba[1] , G. Hemalatha[2] and C. Vanniarajan[1]

[1] Department of Plant Breeding and Genetics, Agricultural College & Research Institute, TNAU, Madurai, Tamil Nadu, India.
[2] Department of Food Science and Nutrition CSC & RI, TNAU, Madurai, Tamil Nadu, India.
***E-Mail:** siddhuhasinis2@gmail.com

Abstract

Greengram (*Vigna radiata* (L.) Wilczek) is one of the highly consumed legumes and has the ability to withstand wide environmental conditions. Sixty greengram genotypes were evaluated for genetic relatedness with 11 quantitative traits *viz.,* days to 50 per cent flowering, days to maturity, plant height, the number of primary branches per plant, the number of clusters per plant, the number of pods per cluster, the number of pods per plant, the number of seeds per pod, pod length, hundred seed weight and single plant yield. The data were subjected to variability, genetic advance, heritability, correlation and path analysis. In this study, the phenotypic coefficient of variation and genotypic coefficient of variation was found to be high for the number of clusters per pod and the number of pods per plant. High heritability was noticed for single plant yield, plant height and hundred seed weight. The genetic advance was found to be very high for the number of pods per plant. Association studies revealed that the single plant yield was significantly correlated with the number of pods per plant (0.75) followed by the number of pods per cluster (0.60), the number of clusters per plant (0.58) and the number of seeds per pod (0.49). The direct and positive effect was recorded for the traits *viz.,* days to maturity (1.44), the number of pods per cluster (0.67), pod length (0.46) and plant height (0.24). Phenotypic selection of traits contributing to grain yield exhibiting high heritability and genetic advance would help in the selection of superior genotypes for the improvement of grain yield in greengram.

Key words: Greengram, Correlation, Path analysis, Variability, GCV, PCV.

INTRODUCTION

Greengram [*Vigna radiata* (L.) Wilczek] is an annual, self pollinated crop that belongs to the family Leguminosae. It is the third most important pulse crop grown in tropical and subtropical regions. India is the leading producer of greengram with a production of 25.06 lakh tonnes (Indiastat 2019). It is a good source of protein and also containing essential amino acids *viz.,* lysine which is a limiting factor in cereals. Besides, it is also rich in protein (20-23.8 g/100g), ash (3.32 g/100g), total dietary fibre (16.3 g/100g), iron (6.74 mg/100g), zinc (2.68 mg/g), calcium (132 mg/g), magnesium (189 mg/g), phosphorus (367 mg/g) and potassium (1246 mg/g) (Kalim *et al.*, 2021). Among the pulses, greengram is generally free from antinutritional factors and less likely to cause flatulence. Hence, it is well accepted by all age groups people (Kumar Dahiya *et al*., 2014). Greengram is consumed in various forms like dhal, sprouts, *sundal*, snacks etc., The presence of genetic variability in any crop is vital for further improvement, as it provides a source for the breeders to develop new varieties. Any yield improvement programme requires superior parents with high heritability and genetic progress for the specific traits.

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Yield in greengram is a complex trait made up of several contributing characters that are interlinked. Knowledge about genetic variability is an essential pre-requisite for designing an effective selection strategy. The correlation coefficient is a promising strategy for measuring the degree of association held between two or more variables along with the yield component traits. The main objective of this study is to know about the association and variability that exist among the quantitative traits contributing for yield. Thereby, it is possible to improve grain yield in greengram by means of exploring the genetic potential that exists among the greengram genotypes.

MATERIALS AND METHODS

The research program was conducted at Agriculture College and Research Institute, Madurai during *summer,* 2021. A total of 60 greengram genotypes were collected from various centres *viz.,* Indian Institute of Pulses Research, Kanpur, National Pulses Research Centre, Vamban, Tamil Nadu and Department of Pulses, TNAU, Coimbatore. The trial was laid out in a Randomised Block Design and replicated thrice in 3 m rows with a spacing of 30 × 10 cm. Recommended agronomic practices and plant protection measures were taken up for raising the good crop. Biometric observations were recorded for eleven traits *viz.,* days to 50 per cent flowering, days to maturity, plant height, the number of primary branches per plant, the number of clusters per plant, the number of pods per cluster, the number of pods per plant, pod length, the number of seeds per pod, hundred seed weight and single plant yield. Observations were recorded in 10 randomly selected plants in each genotype and the mean value was taken for the statistical analysis. Genotypic (GCV) and phenotypic (PCV) co-efficient of variation were calculated based on the formula advocated by Burton (1952). Heritability was estimated according to Lush (1940) and classified based on Johnson *et al.* (1955). The genetic advance per cent of mean was categorized by Robinson *et al.* (1949). Analysis for correlation coefficients (Al Jibouri *et al*., 1958), path analysis (Dewey and Lu, 1959) and a direct and indirect effect by Lenka and Mishra (1973) were done for this study.

RESULTS AND DISCUSSION

The analyses of variance (ANOVA) among 60 greengram genotypes exhibited the presence of significant variability for all traits studied except the number of primary branches per plant, the number of pods per cluster, hundred seed weight and pod length (**Table 1**). This is in accordance with Venkateswarlu *et al.* (2001) and Sathya *et al.* (2011) in greengram. The mean values for all the traits exhibited a wide range of variations. Single plant yield had a range of 8.27-21.28 g, the number of pods per plant (15.53-84.13), plant height (30.39 to 59.03 cm), the number of clusters per plant (5.33 to 20.73), the number of primary branches per plant (1.27 to 3.13), days to 50 per cent flowering (27 to 39.33), days for maturity (58.33 to 72.67), the number of pods per cluster (3.10 to 5.67), pod length (5.87 to 8.89 cm), the number of seeds per pod (9.93 to 13.27) and for hundred seed weight (3.28-5.28 g).

In order to implement the appropriate breeding program, an assessment of heritable and non-heritable components to the total variability is required. When it comes to selection, information on genetic variability factors like variance and heritability, as well as genetic advance are important which provides a complete picture. Variability and heritability are said to provide better information to explore genetic improvement during selection. In the present study, the phenotypic coefficient of variation was found to be greater than the genotypic coefficient of variation, demonstrating that the environment has a major role for variation (**Table 2**). Maximum GCV and PCV was exhibited for the number of pods per plant followed by the number of clusters per plant, single plant yield and for the number of primary branches per plant. Similar results were reported by Tabasum *et al*. (2010), Raturi *et al.* (2015), Anand *et al.* (2016) and Garg *et al.* (2017) in greengram. In the present study, PCV and GCV were found to be low for days to maturity. This is in accordance with Nand and Anuradha (2013), Zuge *et al.* (2019) and Asari *et al.* (2019) in greengram. Single plant yield exhibited maximum heritability followed by plant height, hundred seed weight and the number of clusters per plant. This result is in corroboration with Mishra *et al.* (2008), Vadivel *et al.* (2020) and Salman *et al.* (2021) in greengram. The number of pods per cluster exhibited low heritability. The genetic advance varied from 6.31 - 59.22 per cent. Among eleven quantitative traits number of pods per plant had maximum genetic advance followed

Table 1. Analysis of variance for biometrical traits in greengram

	DF	DFF	DM	PH	NPB	NCP	NPC	NPP	PL	NSP	HSW	SPY
Replication	2	2.85	2.05	1.21	0.76	1.29	0.34	2.55	0.47	0.57	0.04	0.28
Treatment	59	15.86**	27.07**	98.99**	0.49	33.67**	0.85	585.01**	0.99	1.65**	0.85	25.85**
Error	118	1.05	5.56	2.50	0.09	0.99	0.19	21.28	0.04	0.12	0.01	0.28

** significant at 1%

DFF – Days to 50 per cent flowering, DM - Days to maturity, PH - Plant height, NPB - Number of primary branches per plant, NCP- Number of clusters per plant, NPC- Number of pods per cluster, NPP- Number of pods per plant, PL - Pod length, NSP - Number of seeds per pod, HSW - Hundred seed weight, SPY - Single plant yield.

Table 2. Genetic variability parameters for biometrical traits in greengram

	Range		Mean	GCV (%)	PCV (%)	h^2 (%)	GA as % of mean
	Max.	**Min.**					
DFF	39.33	27.00	33.85	6.57	7.24	82.34	12.28
DM	72.67	58.33	65.83	4.09	5.44	56.31	6.31
PH	59.03	30.39	40.06	14.37	14.73	95.19	28.88
NPB	3.13	1.27	2.24	16.24	21.43	57.45	25.36
NCP	20.73	5.33	13.57	24.34	25.42	91.67	48.00
NPC	5.67	3.10	4.42	10.70	14.54	54.13	16.22
NPP	84.13	15.53	46.40	30.28	31.88	90.17	59.22
PL	8.89	5.87	7.54	7.44	7.98	86.91	14.28
NSP	13.27	9.93	11.56	6.19	6.89	80.21	11.40
HSW	5.28	3.28	4.27	12.40	12.72	95.12	24.91
SPY	21.28	8.27	13.17	22.35	22.72	96.75	45.27

DFF – Days to 50 per cent flowering, DM - Days to maturity, PH - Plant height (cm), NPB - Number of primary branches per plant, NCP- Number of clusters per plant, NPC- Number of pods per cluster, NPP- Number of pods per plant, PL - Pod length (cm), NSP - Number of seeds per pod, HSW - Hundred seed weight (g), SPY - Single plant yield (g).

by the number of clusters per plant and single plant yield which is in accordance with Mohammed *et al*. (2020) and Sabatina *et al.* (2021) in greengram.

Grain yield is a complex trait and is influenced by various factors. The correlation coefficient is a statistical parameter that reflects the strength and direction of the relationship between yield and its component traits at both the genotypic and phenotypic levels. In the present study, single plant yield was positive and significantly correlated with the number of pods per plant (0.755) (**Table 3**). Similar findings were reported in greengram by Srivastava and Singh (2012) and Sandhiya and Shanmugavel (2018). It was followed by the number of pods per cluster (0.602), the number of clusters per plant (0.589), the number of seeds per pod (0.490) and pod length (0.442). The number of clusters per plant (0.749) and the number of pods per cluster (0.923) were significant and positively correlated with the number of pods per plant. Similar results were reported in greengram by Manivelan *et al.* (2019). The number of seeds per pod was positively correlated with pod length which is in conformation with

Table 3. Genotypic correlation estimates of eleven quantitative characters in greengram

	DFF	DM	PH	NPB	NCP	NPC	NPP	PL	NSP	HSW	SPY
DFF	1										
DM	0.925**	1									
PH	0.525**	0.327**	1								
NPB	0.443**	0.392**	0.537**	1							
NCP	0.344**	0.378**	0.420**	0.606**	1						
NPC	0.332**	0.171*	0.527**	0.303**	0.636**	1					
NPP	0.449**	0.414**	0.468**	0.394**	0.749**	0.923**	1				
PL	-0.069	-0.134	0.090	0.365**	0.109	-0.032	0.057	1			
NSP	0.263**	0.258**	0.334**	0.409**	0.262**	0.066	0.208**	0.674**	1		
HSW	-0.175*	-0.239**	-0.159*	0.210**	0.081	0.083	0.079	0.466**	0.312**	1	
SPY	0.232**	0.236**	0.345**	0.437**	0.589**	0.602**	0.755**	0.442**	0.490**	0.300**	1

*, ** significant at 5% and 1% level, respectively

DFF – Days to 50 per cent flowering, DM - Days to maturity, PH - Plant height, NPB - Number of primary branches per plant, NCP- Number of clusters per plant, NPC- Number of pods per cluster, NPP- Number of pods per plant, PL - Pod length, NSP - Number of seeds per pod, HSW - Hundred seed weight, SPY - Single plant yield.

Table 4. Path coefficient estimates of eleven quantitative characters in greengram genotypes

Characters	DFF	DM	PH	NPB	NCP	NPC	NPP	PL	NSP	HSW	Correlation with SPY
DFF	**-1.397**	1.334	0.126	-0.0002	-0.062	0.224	0.064	-0.032	0.003	-0.029	0.232**
DM	-1.292	**1.442**	0.079	-0.0002	-0.068	0.116	0.059	-0.063	0.003	-0.039	0.236**
PH	-0.734	0.472	**0.240**	-0.0003	-0.075	0.356	0.067	0.042	0.004	-0.026	0.345**
NPB	-0.619	0.566	0.129	**-0.001**	-0.108	0.204	0.056	0.171	0.005	0.035	0.437**
NCP	-0.481	0.546	0.101	-0.0003	**-0.179**	0.429	0.107	0.051	0.003	0.013	0.589**
NPC	-0.464	0.247	0.126	-0.0002	-0.114	**0.675**	0.132	-0.015	0.001	0.014	0.602**
NPP	-0.627	0.597	0.112	-0.0002	-0.134	0.622	**0.143**	0.027	0.002	0.013	0.755**
PL	0.096	-0.193	0.022	-0.0002	-0.020	-0.021	0.008	**0.467**	0.008	0.077	0.442**
NSP	-0.367	0.372	0.080	-0.0002	-0.047	0.045	0.030	0.315	**0.011**	0.051	0.490**
HSW	0.244	-0.345	-0.038	-0.0001	-0.014	0.056	0.011	0.217	0.004	**0.165**	0.300**

** significant at 1%

Diagonal and bold indicates the direct effects

Residual effect = 0.230

DFF – Days to 50 per cent flowering, DM - Days to maturity, PH - Plant height, NPB - Number of primary branches per plant, NCP- Number of clusters per plant, NPC- Number of pods per cluster, NPP- Number of pods per plant, PL - Pod length, NSP - Number of seeds per pod, HSW - Hundred seed weight, SPY - Single plant yield.

the earlier findings of Ramakrishnan *et al.* (2018) and Das *et al.* (2015) in greengram. The number of pods per plant was significant and positively correlated with all other traits except for pod length whereas hundred seed weight was negatively correlated with days to 50 per cent flowering, days to maturity and plant height.

Path analysis was performed to assess the degree of direct and indirect effect of yield-related traits on single-plant yield (**Table 4**). This will also aid in the identification of promising genotypes for the hybridization programme. The residual value of path effect was 0.230. The traits *viz.,* days to maturity (1.442), the number of pods per cluster (0.675), pod length (0.467), plant height (0.239) had registered a high positive direct effect on single plant yield. This was in accordance with Ramakrishnan *et al.* (2018), Agbeleye *et al.* (2021) and Dhunde *et al.* (2021) in greengram. The number of pods per plant exhibited a high indirect positive effect on single plant yield through the number of pods per cluster. This was in line with Ahmad *et al.* (2019) in greengram. Days to maturity and plant height showed a high negative indirect effect on single plant yield through days to 50 per cent flowering. This result is in corroboration with Thippani *et al.* (2013) and Ramakrishnan *et al.* (2018) in greengram. The number of primary branches per plant, the number of pods per plant, days to 50 per cent flowering and the number of clusters per plant showed a high indirect positive effect on single plant yield through days to maturity.

The selection of greengram genotypes for improving specific traits can be achieved by knowing the nature of gene action. In the present study, the number of pods per plant and the number of pods per cluster had registered high heritability coupled with genetic advances. These traits also had a high positive direct effect on single plant yield. Based on the result obtained from this study number of pods per plant and the number of pods per cluster were found to be the most important traits to be considered during the selection programme for improving grain yield in greengram.

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