

ESTIMATION OF VAIABILITY, HERITABILITY AND GENETIC ADVANCE IN GREENGRAM GENEOTYPES

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Cite This Article: Pandiyan Muthaiyan, "Estimation of Vaiability, Heritability and Genetic Advance in Greengram Geneotypes", Indo American Journal of Multidisciplinary Research and Review, Volume 6, Issue 2, Page Number 207-212, 2022.

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Abstract:

Variability assessment is to identify the most important traits in greengram. The objective of the present study was to estimate variability, heritability and genetic advance based on thirteen morphological characters of *mungbean*. The experiment was conducted with 100 genotypes of greengram at Agricultural Research Station, TNAU, Virinjipuram, Vellore, by using randomized complete block design with three replications. The analysis of variance results revealed highly significant differences ($P < 0.01$) for all characters among greengram genotypes indicated higher magnitude of variability. The characters related to phenotypic coefficient of variation (PCV) for all the characters were higher than genotypic coefficient of variation (GCV). Moderate GCV and PCV were observed for the traits plant height, number of primary branches, pod length, pod width, pod flesh thickness, number of pods / cluster, number of pods/ plant, weight of ten pods, number of root nodules/ plant, drymatter content of pods and roots. High heritability coupled with high genetic advance was recorded for maturity related traits namely days to full maturity (98.82), days to initial flowering (98.72), days to initial maturity (98.41) and days to fifty per cent flowering (98.15), seed length (97.10) and seed breadth (96.13) and highest genetic advance expressed in number of clusters per branch (78.52), length of branch (73.45) and single plant yield (71.71). It indicated the presence of additive gene effects. Thus, there is an ample scope for improving yield and quality characters in greengram bean through direct selection.

Key Words: Vaiability, PCV, GCV, Heritability and Genetic Advance

Introduction:

Vigna radiata (L.) wilczek, commonly known as greengram or mungbean or Pasipayaru in Tamil Nadu. It is the most widely distributed species among other cultivated *Vigna* species. It is one of the predominant sources of protein and certain essential amino acids in vegetarian diets. It possessed certain added features compared to other pulses. It is relatively drought tolerant and well adapted to a range of soil conditions including light soils and can thrive even under limited irrigation; moreover, it is suited for crop rotation and crop mixtures (Baldev, 1988 and Sadaphal, 1988). However, this crop is suffering from the yield advantage as realized in case of C4 cereals.

Presently, the yield level of greengram as like other pulses is well below the optimum level. The average yield of mungbean is very low. To meet out the pulses requirement we have to take challenge to increase the yield and production and productivity.

The varietal breeding program taken up in this crop had resulted only with limited success as far as yield improvement is concerned. The basic reason for limited success had been due to the limited variability prevailed among the parents used for hybridization in most of the studies. There had been always possibility of improving the crop by incorporating wild genes to the cultivated species.

Stepwise utilization of primary, secondary and tertiary gene pools of this crop can result in tremendous improvement in yield. In order to create the variability and available in the primary gene pool, secondary and tertiary gene pool to make cross between among diverse parents to get variation

For utilizing the variability available in the secondary and tertiary gene pools it is essential to attempt interspecific crosses and to develop viable hybrids. These hybrids need to be critically evaluated as such and in the segregating generations for improvement in yield and yield components. The introgressed materials developed through wide crosses can also contribute as genetic reservoirs for novel genes apart from contributing to the improvement of yield and yield components. With a view to evaluate the available germplasm using the descriptors and form the core collection and for attempting intra and interspecific hybridization to generate segregants for better yield, this study was taken up keeping the following objectives in mind.

To Study the Variability, Heritability and Genetic Advance in Greengram Genotypes:

Materials and Methods:

The experiment was conducted with 100 genotypes of greengram during kharif 2023 season Dr. M. S. Swaminathan Agricultural College & Research Institute, Tamil Nadu Agricultural University, Eachankottai, Thanjavur, Tamil Nadu- 614 902 and Moon University Western Africa by using randomized complete block design with three replications Heritability in the broad sense was calculated according to Lush (1940) and expressed in percentage.

$$\text{Heritability percent} = \frac{\text{Genotypic variance}}{\text{Phenotypic variance}} \times 100$$

The heritability percent was categorized as suggested by Robinson *et al.* (1949)

0 - 30 per cent	- Low
31 - 60 per cent	- Moderate
Above 60 per cent	- High

Genetic Advance:

This was worked out based on the formula given by Johnson *et al.* (1955).

$$\text{Genetic advance} = k \times h^2 \times \sigma_{ph}$$

h^2 = heritability in broad sense

σ_{ph} = phenotypic standard deviation

k = selection differential (at 5% selection intensity (i.e.)2.06) (Falconer,1960)

Genetic advance (GA) as percentage of mean was also calculated.

$$\text{Genetic advance as percent of mean} = \frac{\text{G.A}}{\text{Grand mean}} \times 100$$

The genetic advance as percent of mean was categorized as suggested by Johnson *et al.* (1955).

Less than 10 per cent	= Low
10-20 per cent	= Moderate
More than 20 per cent	= High

Result:

Variability Studies:

Analysis of variance for 18 traits involving 100 accessions of greengram showed significant differences among the genotypes for all the characters except seed length and seed breadth (Table 1).

Phenotypic Variance:

The maximum phenotypic variance was observed for the character dry matter production (211.94) followed by length of branches (202.61) and plant height (181.85). The minimum phenotypic variance was observed for seed length and seed breadth (Table 1)

Genotypic Variance:

The maximum genotypic variance was observed for the character length of branch (153.31) followed by plant height (147.88) while the minimum genotypic variance was observed in seed length and seed breadth (0.00) (Table 1).

Variance Components:

Coefficient of Variation:

The variability for eighteen characters, on the basis of phenotypic and genotypic coefficient of variances are furnished in Table1.

Phenotypic Coefficient of Variation:

The estimates of phenotypic co efficient revealed that maximum variation was observed in dry matter production (68.66) followed by number of clusters per branch (62.21) and single plant yield (52.72). The least phenotypic co efficient of variation was observed for the trait days to full maturity (6.15) (Table 11).

Genotypic Coefficient Of Variation:

The genotypic co efficient of variation was maximum for the character number of cluster per branch (48.69) followed by single plant yield (42.84) and length of branch (40.99). The lowest genotypic co efficient of variation observed for the character was number of seeds per pod (4.83) (Table 1).

Estimates of heritability in the broad sense, genetic advance and genetic advance as percentage of mean are furnished in Table 1.

Heritability:

The maximum heritability estimate was registered by maturity related traits namely days to full maturity (98.82), days to initial flowering (98.72), days to initial maturity (98.41) and days to fifty per cent flowering (98.15). The heritability estimates for seed dimension traits namely seed length (97.10), seed breadth (96.13) were also higher. For morphological traits namely plant height (81.32), length of branch (75.56), hundred seed weight (74.31), length of pod (73.36), number of clusters per plant (67.83), single plant yield (66.03), number of pods per plant (64.42), number of clusters per branch (61.27), number of branches per plant (58.52) and number of seeds per pod (36.00) were high to medium while for protein content (46.13) heritability was medium. The lowest heritability of 21.63 percent was registered for dry matter production (Table 1).

Genetic Advance:

The genetic advance of the characters ranged from 0.07 to 22.59 for the traits seed breadth and plant height respectively. The highest genetic advance expressed as percentage of mean was recorded by number of clusters per branch (78.52) followed by length of branch (73.45) and single plant yield (71.71) while the lowest genetic advance as percentage of mean was recorded for number of seeds per pod (5.97) (Table 1).

Discussion:

The present investigation focused on variability, heritability and genetic advance. The estimates of variability parameters namely PCV and GCV were higher for the traits namely single plant yield, number of branches per plant, number of pods per plant, number of clusters per plant, plant height and length of branch indicating that the scope of selection within the core for these traits was high. The traits, dry matter production and number of cluster per branch revealed wide differences between the estimates of PCV and GCV values indicating high influence of environmental factors while the traits, days to initial flowering, days to 50 per cent flowering, days to initial maturity, days to full maturity, hundred seed weight, seed length, seed breadth, length of pod and protein content were found less influenced by the environmental factors as the difference between the estimates of PCV and GCV were narrow. Similar results were also reported by Khan (1984), Malik and Singh (1983), Renganayaki (1985), Reddy (1997) and Venkateswarlu (2001). The wide difference between the GCV and PCV for the characters *viz.*, dry matter production and number of clusters per branch observed in this investigation were in accordance with the findings of Chandra and Nijhawa (1979), Malik and Singh (1983) Renganayaki (1985), Reddy (1997) and Venkateswarlu (2001) indicating that the expression of these traits were masked by environmental components. For the characters plant height, length of branch, days to initial flowering, days to 50 per cent flowering, days to initial maturity, days to full maturity, hundred seed weight, seed length, seed breadth, length of pod and number of clusters per plant, differences between GCV and PCV were narrow suggesting that these characters were less influenced by environmental fluctuation and similar results were reported by Malik and Singh (1983), Jain (1975), Renganayaki (1985), Reddy (1997), Venkateswarlu (2001), Chakrabarty and Parimal Barman (2003). As these traits are environmentally stable, the scope for direct selection is high.

Maturity related traits *viz.*, days to initial flowering, days to 50 per cent flowering, days to initial maturity, days to full maturity followed by seed dimension characters like seed length, seed breadth and morphological characters like plant height, length of branch, hundred seed weight and length of pods recorded high heritability values as reported by Singh and Malhotra (1970), Mansuriya (1991), Sharma (1999), Malik and Singh (1983), Dahiya and Yadav (1999), Renganayaki (1985), Venkateswarlu (2001) and Ruiz de Galarreta and Alvarez (2001).

According to Burton (1952), a character having high value of GCV coupled with high heritability would be more valuable in selection programmes. The characters *viz.*, single plant yield, number of clusters per branch, number of pods per plant, length of branch, plant height, number of cluster plant and number of branches per plant showed high GCV with high heritability indicating less influence of environment on the characters and high transmission index. This results were in accordance with the findings of Malhotra *et al.* (1974 a), Malhotra *et al.* (1974 b), Chandal *et al.* (1973), Malik and Singh (1983), Renganayaki (1985), Khorgade *et al.* (1990), Ganeshram (1993), Reddy (1997), Venkateswarlu (2001), Tefera *et al.* (1990) and Taddesse (1993).

High genetic advance as percentage of mean observed for the traits, number of clusters per branch, length of branch, single plant yield, number of pods per plant, number of clusters per plant, plant height and number of branches per plant suggesting scope for selection for these traits in the core collection. High genetic advance coupled with high heritability and GCV was observed for length of branch, number of clusters per branch, number of clusters per plant, number of pods per plant, single plant yield and plant height indicating the predominance of additive gene action for this traits. Johnson *et al.*, (1955) suggested that the heritability and genetic advance when calculated together would be more useful in predicting the effectiveness of the character for improvement. High genetic advance as per cent of mean together with high heritability and GCV was noted for length of branch, number of clusters per branch, number of clusters per plant, number of pods per plant and single plant yield. This indicated the preponderance of additive gene action. High heritability and genetic advance were also reported by Rathinasamy *et al.* (1978), Malik and Singh (1983), Renganayaki (1985), Ganesh Ram (1993), Reddy (1997) and Venkateswarlu (2001) for plant height, length of pod, number of clusters per plant and number of pods per plant. For number of branches per plant high heritability and genetic advance values were reported by Renganayaki (1985), Ganesh Ram (1993) and Reddy (1997). Therefore, simple unidirectional selection could be effective for improving the aforesaid traits. Relatively lower magnitude of genetic advance and GCV and moderate value of heritability for protein content, number of branches per plant and number of seeds per pod indicated that these characters were under the control of non additive gene effects. Similar findings in mungbean were reported by Raje and Rao (2000). Improvement for such important characters would have to be carried out by indirect selection method as suggested by Rajendrakumar *et al.* (1999) and Vikas *et al.* (1999).

The estimates of heritability in the core collection indicated that the trait days to full maturity, days to initial maturity, days to initial flowering, days to 50 per cent flowering, seed length, seed breadth, plant height, length of branch, hundred seed weight and length of pod were highly heritable. High genetic advance as percentage of mean was observed for the traits, number of clusters per branch, length of branch, single plant yield, number of pods per plant, number of clusters per plant, plant height and number of branches per plant suggesting scope for selection for these traits in the core collection. High

genetic advance coupled with high heritability and GCV was observed for length of branch, number of branches per plant, number of clusters per branch, number of clusters per plant, number of pods per plant, single plant yield and plant height indicating the predominance of additive gene action for this traits.

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Table 1: Mean, variance, co efficient of variation, heritability (broad sense), genetic advance, and genetic advances as per cent of mean for 18 characters in 65 greengram accession of core collection

Character	Mean	Variance		Co efficient of variation		Herita bility	Genetic advance	Genetic advance % of mean
		Geno typic	Pheno typic	Geno typic %	Pheno typic %			
PHT (cm)	51.53	147.88	181.85	23.60	26.16	81.32	22.59	43.84
NOB	1.93	0.27	0.46	26.98	35.27	58.52	0.82	42.52
BRL (cm)	30.20	153.31	202.61	40.99	47.12	75.56	22.18	73.45
DIF	37.58	16.64	16.85	10.85	10.92	98.72	8.34	22.21
DFF	44.25	16.86	17.18	9.27	9.36	98.15	8.38	18.93
NCB	4.53	4.86	7.94	48.69	62.21	61.27	3.55	78.52
NOC	10.29	9.71	14.32	30.28	36.77	67.83	5.28	51.38
NPP	28.48	80.63	125.18	31.52	39.27	64.42	14.84	52.12
POL (cm)	7.48	0.35	0.47	7.91	9.24	73.36	1.04	13.97
NSP	11.41	0.30	0.84	4.83	8.05	36.00	0.68	5.97
SDL (cm)	0.37	0.00	0.00	11.97	12.15	97.10	0.08	24.30
SDB (cm)	0.30	0.00	0.00	12.11	12.35	96.13	0.07	24.47
HSW (g)	3.45	0.38	0.52	18.01	20.89	74.31	1.10	31.98
SPY (g)	5.80	6.17	9.35	42.84	52.72	66.03	4.15	71.71
DMP (g)	21.20	45.83	211.94	31.92	68.66	21.63	6.48	30.58
PTC (%)	20.38	1.43	3.11	5.88	8.65	46.13	1.67	8.22
DIM	56.65	16.07	16.33	7.07	7.13	98.41	8.19	14.46
DFM	69.10	17.88	18.09	6.11	6.15	98.82	8.65	12.53