Raju Thonta
Department of Genetics and
Plant Breeding, School of
Agriculture Lovely Professional
University, Phagwara, Punjab,
India

Manoj Kumar Pandey
Department of Genetics and
Plant Breeding, School of
Agriculture Lovely Professional
University, Phagwara, Punjab,
India

Rajneesh Kumar
Department of Genetics and
Plant Breeding, School of
Agriculture Lovely Professional
University, Phagwara, Punjab,
India

Santhoshini
Department of Genetics and
Plant Breeding, School of
Agriculture Lovely Professional
University, Phagwara, Punjab,
India

Analysis of genetic variability, heritability and genetic advance for growth and yield attributes in green gram (*Vigna radiata* L. Wilczek)

Raju Thonta, Manoj Kumar Pandey, Rajneesh Kumar and Santhoshini

DOI: https://doi.org/10.22271/maths.2023.v8.i3Sa.996

Abstract
The present investigation was conducted using 20 green gram germplasm for the 13 traits studied *viz.* days to 50% flowering, days to maturity, plant height, number of primary branches, number of clusters per plant, number of pods per plant, number of pods per cluster, number of seeds per pod, pod length (cm), seed index (g), biological yield per plant (g), seed yield per plant (g) and harvest index at the agriculture research farm, Department of Genetics and Plant Breeding, School of Agriculture, Lovely Professional University, Punjab during the *kharif* season 2022. A Randomized Block Design (RBD) with three replications were used to study genotypic and phenotypic variances, heritability (H^2b), GCV, PCV and genetic advance (GA), for all the growth and yield contributing traits. Number of pods per cluster recorded highest GCV (23.93) and PCV (24.80) respectively, while biological yield had highest heritability h^2b (94.2%). However, number of spikelets per panicle (47.60), number of filled grains per panicle (30.26), plant height (25.68) had high genetic advance. Moreover, number of pods per cluster (47.61) had highest genetic advance as percent mean (GAM).

Keywords: Variability, broad sense heritability, genetic advance, green gram

Introduction

Green gram (*Vigna radiata* L. Wilczek) an important crop in the pulse category, is an annual legume belonging to Fabaceae family that is widely grown, with diploid chromosome 2n=2x=22. It can be be grown in various cropping systems. Greengram is a self-pollinated and short duration crop. It provides a high-quality protein supply (22-24%) and boosts the incomes of small-scale farmers Rahim *et al.*, (2010) [1]. Mature grain has carbohydrates (62.6g), fibre (16.3g), fat (1.2g), protein (23.9g) and 347 calories per 100 grams Majhi *et al.*, (2020) [2].

Any strategy to increase yield must begin with the choice of selecting superior parents showing higher heritability and genetic advance for specific traits. Estimation of heritability in combination with genetic advance are usually more useful than heritability alone for forecasting genetic gain under selection. However, a trait with a high heritability does not always have a high genetic advance Johnson *et al.*, (1955) [3]. Correlation reveals the degree and direction of association at phenotypic and genotypic levels btw the yield and its contributing traits. However, it should be noted that the correlation can sometimes fail to give accurate insights into the individual impact of each character on the dependent character. It is understandable that a path analysis would be necessary to determine which characters actually affect seed yield. So path analysis is used to measure the indirect and direct effects of traits Dhunde *et al.*, (2022) [4].

It is impossible to begin an effective breeding programme without first establishing genetic variability using appropriate metrics including the coefficient of variation (phenotypic and genotypic), genetic advance and broad sense heritability (h^2b) Salman *et al.*, (2021) [5]. To estimate variability for grain yield and its contributing traits, correlation between yield and its associated traits and direct and indirect contribution of different traits on grain yield.

Corresponding Author:
Manoj Kumar Pandey
Department of Genetics and
Plant Breeding, School of
Agriculture Lovely Professional
University, Phagwara, Punjab,
India

Materials and Method

The present investigation was carried out at the research farm, Department of Genetics and Plant Breeding, Lovely Professional University, Phagwara, Punjab during *Kharif* 2022. Three replications of a randomized block design (RBD) were used to raise twenty different mungbean genotypes tabulated in (Table 1). Using a 30 x 10 cm spacing, the seeds were planted and after tenth day following sowing, the crop was thinned out, leaving one healthy seedling per hill. Recommended agronomic practices and need based plant protection measures were taken. Each line was sown in two rows of 1.5 m. The information was gathered on thirteen traits where growth attributes *viz.* Days to 50% flowering, Days to maturity, Plant height (cm), Number of primary branches per plant, Clusters per plant, Pods per plant and Seed weight per pod. Additional yield-related characteristics *viz.* Biological yield, Harvesting index and Seed yield per plant (g). The mean value was then determined for analysis over three replications Figure in (Figure 1).

The recorded observations were analyzed statistically using the procedure for analysis of variance suggested by Panse and Sukhatme (1985) [6] to estimate the variability. The genotypic and phenotypic variances were calculated using the formula provided by Johnson *et al.* (1955) [3]. The genotypic and phenotypic coefficients of variation were estimated following the methods described by Burton (1952) [7] and Singh and Chaudhary (1985) [8]. The broad-sense heritability (h2b) was determined using the approach proposed by Hanson *et al.*, (1956) [9]. The estimation of genetic advance was conducted using the formulas given by Johnson *et al.*, (1955) [3] and Allard (1960) [10].

Table 1: List of 20 Genotypes of Green gram used in the experiment

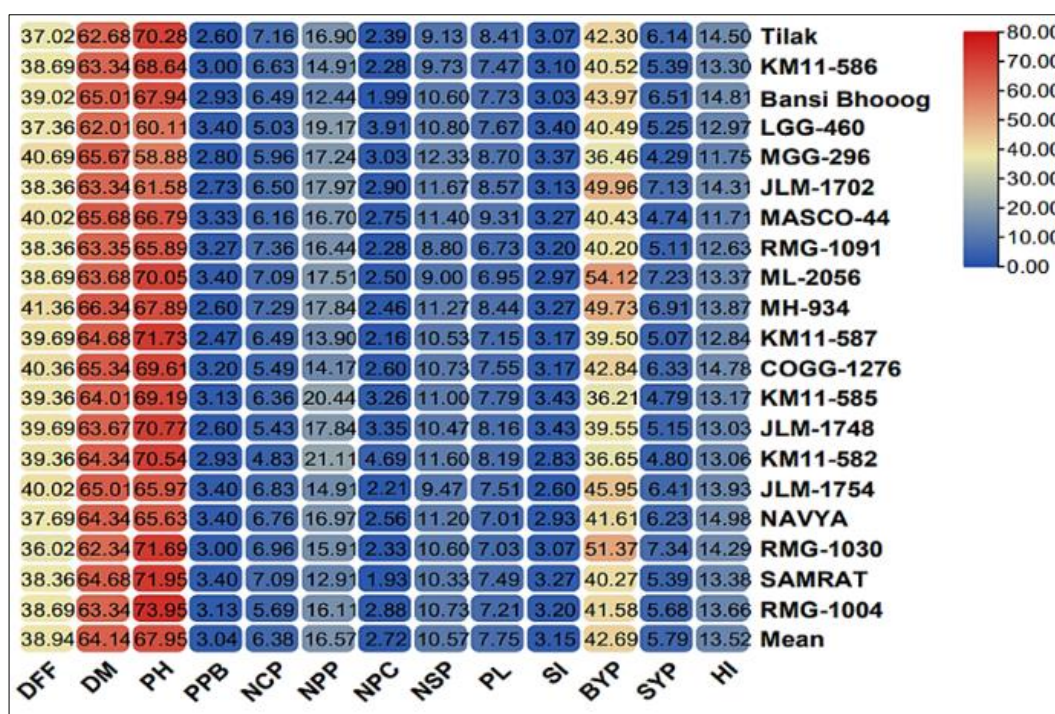| S. No	Genotypes	S. No	Genotypes
1	Tilak	11	KM11-587
2	KM11-586	12	COGG-1276
3	Bansi Bhooog	13	KM11-585
4	LGG-460	14	JLM-1748
5	MGG-296	15	KM11-582
6	JLM-1702	16	JLM-1754
7	MASCO-44	17	Navya
8	RMG-1091	18	RMG-1030
9	ML-2056	19	Samrat
10	MH-934	20	RMG-1004

Fig 1: Mean Values of green gram genotypes

Formula for GCV, PCV

$$PCV = \frac{\sqrt{\sigma 2p}}{\bar{x}} \times 100 \quad GCV = \frac{\sqrt{\sigma 2g}}{\bar{x}} \times 100$$

Where,
PCV = Phenotypic Coefficient of variation, GCV = Genotypic Coefficient of variation
σ^2g = Genotypic variance = (Mean sum of squares due to genotypes – Error mean sum of squares) ÷ Replications
σ^2p= Phenotypic variance = σ^2g + σ^2e
$\bar{x}$ = General mean

Less than 10%	Low
10-20%	Moderate
More than 20%	High

Heritability

$$h2b = \frac{\sigma 2g}{\sigma 2p} X100$$

0-30%	Low
31-60%	Medium
61% and above	High

Genetic advance

GA = K × σp × h2 (b)

Where,
K = Selection differential at 5 per cent selection intensity value 2.06
σp= Phenotypic standard deviation

Less than 10%	Low
10-20%	Moderate
More than 20%	High

Result and Discussion

ANOVA of the thirteen traits tabulated in Table 2 exhibited significant variance at 1 percent level and 5 percent respectively, indicating a substantial range of variability among the germplasm, except for number of primary branches, which showed significance at both the 5 and 1 percent level. These findings suggest that selection based on these traits can result in significant improvements, as there is a considerable degree of variability across all the characters as per Chaudhary et al., (2023) [11].

Result tabulated in Table 3 presents the genotypic and phenotypic variances, heritability, GCV, PCV, genetic advance, and genetic advance as a percentage of the mean (GAM 5%) for all the yield contributing traits represented in fig 2.

Table 2: Analysis of Variance (ANOVA) for thirteen traits in green gram

Source of Variation	Replication	Genotypes	Error
D.F.	2	19	38
Days to 50% flowering	5.028	5.08	1.77
days to maturity	0.714	4.11	0.82
plant height	56.34	48.76	14.42
primary branches	0.08	0.3	0.032
cluster per plant	1.43	1.71	0.29
pods per plant	1.14	15.57	1.45
pods per cluster	0.76	1.36	0.09
seeds per pod	0.1	2.66	0.99
pod length	1.85	1.4	0.39
seed index	0.008	0.13	0.022
Biological yield	4.45	76.95	4.46
seeds yield per plant	0.13	2.58	0.21
Harvest index	0.87	2.6	0.45

Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV)

Number of pods per cluster (23.94) recorded highest GCV. Seed yield per plant (15.35), Number of pods per plant (13.09), Biological yield (11.52), Number of clusters per plant (10.78) recorded moderate GCV. While, the traits like Number of primary branches (9.88), Pod length (7.49), Number of seeds per pod (7.05), Harvest index (6.26), Seed Index (6.04), Plant height (4.98), Days to 50% flower (2.70) and Days to maturity (1.63) recorded low GCV.

Number of pods per cluster (24.80) recorded highest PCV. Seed yield per plant (16.03), Number of pods per plant (13.75), Biological yield (11.87), Number of clusters per plant (11.84) and Number of primary branches (10.46), recorded moderate PCV. While, the traits like Number of seeds per pod (8.92), Pod length (8.84), Harvest index (6.89), Seed Index (6.64), Plant height (5.93), Days to 50% flower (3.34) and Days to maturity (1.83) recorded low GCV.

In the present study, the phenotypic coefficients of variation were slightly greater than the genotypic coefficients of variation indicated that environment had an impact on the expression of the character under study. High values for GCV and PCV were recorded for Number of pods per cluster. This suggested the possibilities for making further improvement using these traits. Table 3 indicated the genetic variability parameters such as GCV, PCV, Heritability, genetic advance and genetic advance as 5% of mean. PCV (phenotypic coefficient of variance) is higher than GCV (genotypic coefficient of variance) for all the characters; it indicates that, there is an involvement of environmental influence on traits. Number of pods per cluster recorded highest PCV and GCV. Moderate PCV and GCV is recorded for seed yield per plant followed by number of pods per plant, biological yield per plant, number of clusters per plant and estimation of PCV for number of primary branches recorded moderate with low GCV. Low PCV and GCV were recorded for number of seeds per pod followed by pod length, harvest index, seed index, plant height, days to flowering and days to maturity. Consistent with these results, comparable observations were made by (Tabasum et al., 2010) [12] for PH, NPP, PL, BYP, SYP and HI; (Sineka et al., 2021) [13] for DFF, DM, NSP, PL and SI; (Nayak et al., 2022) [14] for DFF, DM, NPP, PL, NSP.

Heritability and genetic advance

Heritability serves as a predictor of the features that parents will pass on to their offspring. (Khan et al., 2009) [15] found that selection processes become easier as heritability estimates increased. The heritability estimation reveals the extent to which quantitative traits are inherited, but it fails to disclose the extent to which genetic gain may be attained by the selection of the ideal plant from the elite populations. Therefore, the combination of heritability and genetic advance is beneficial than either factor alone (Kumar et al., 2019) [16]. Heritability is shown high for biological yield and followed by number of pods per cluster, seed yield per plant, number of pods per plant, number of primary branches, number of clusters per plant, seed index, harvest index, days to maturity, pod length and plant height. These traits exhibit a high degree of heritability, indicating that genetic factors have a strong influence on their expression.

Consequently, environmental factors are likely to have a lesser impact on the development of these traits. Medium recorded for days to 50% flowering and number of seeds per pod. Genetic advance in combination with heritability is recorded high for number of pods per cluster (47.60 and 93.2) followed by seed yield per plant (30.26 and 91.7), number of pods per plant (25.68 and 90.7), biological yield (23.02 and 94.2) and number of clusters per plant (20.21 and 82.9). Moderate genetic advance with high heritability is recorded for no. of primary branches (19.22 and 89.2) followed by pod length (13.06 and 71.8), harvest index (11.71 and 82.5) and seed index (11.31 and 82.6). Moderate genetic advance in combination with heritability is recorded for number of seeds per pod (11.49 and 62.6). Low genetic advance in relation to high heritability is noted for plant height (8.60 and 70.4) and days to maturity (3.006 and 79.9). Low genetic advance with moderate heritability is documented for days to 50% flowering (4.48 and 65.1). Comparable outcomes were noted by (Tamalapakua et al., 2021) [17] for high genetic advance in combination with high heritability for the traits viz., Seed yield per plant, biological yield, number of clusters per plant and number of pods per plant. (Salman et al., 2021) [5] also documented parallel results except for plant height and number of seeds per plant.

Conclusion

Number of pods per cluster recorded highest GCV (23.93) and PCV (24.80) respectively, while biological yield had highest heritability h^2b (94.2%). However, number of spikelets per panicle (47.60), number of filled grains per panicle (30.26), plant height (25.68) had high genetic advance. Moreover, number of pods per cluster (47.61) had highest genetic advance as percent mean (GAM).

Table 3: Genetic variability parameters *viz.* Mean, Range, GCV, PCV, H^{2}b, Genetic Advance and GAM 5%.

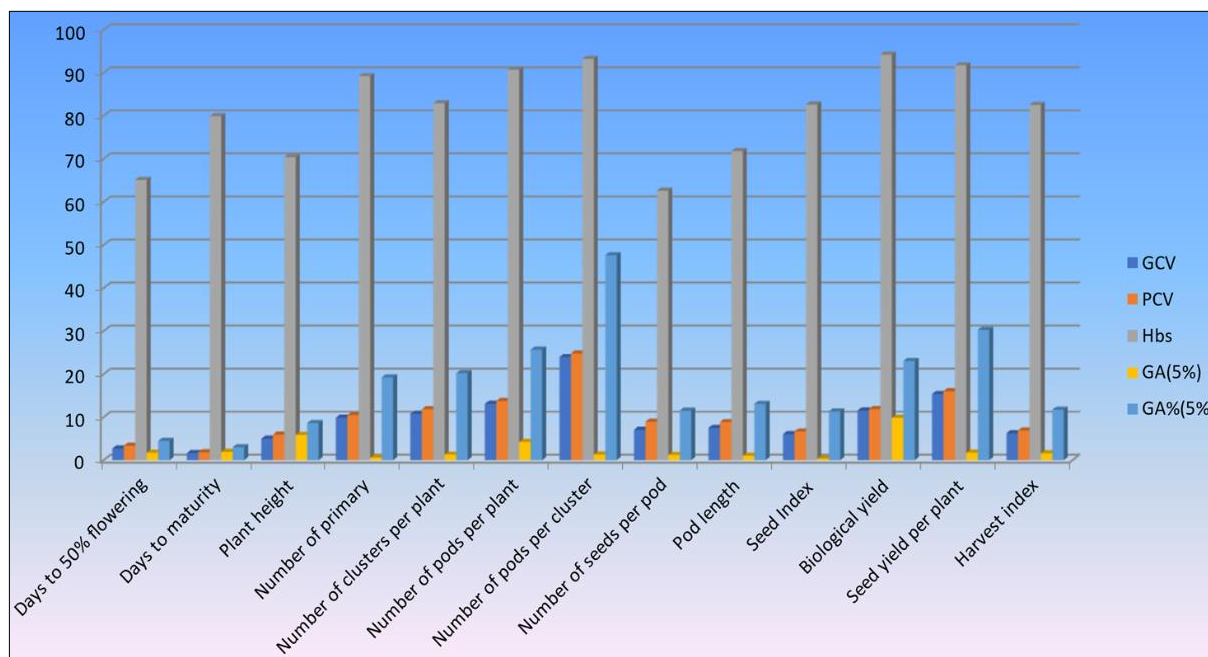| Characters	Mean	Range		GCV	PCV	Heritability (H^{2}b)%	GA (5%)	GAM (5%)
		Min	Max					
Days to 50% flower	38.94	36.02	41.36	2.70	3.34	65.1	1.75	4.48
Days to maturity	64.14	62.01	66.34	1.63	1.83	79.9	1.93	3.01
Plant height	67.95	58.88	73.95	4.98	5.93	70.4	5.85	8.61
Number of primary branches	3.04	2.47	3.40	9.88	10.46	89.2	0.58	19.22
Number of clusters per plant	6.38	4.83	7.36	10.78	11.84	82.9	1.29	20.21
Number of pods per plant	16.57	12.44	21.11	13.09	13.75	90.7	4.26	25.68
Number of pods per cluster	2.72	1.93	4.69	23.94	24.80	93.2	1.30	47.61
Number of seeds per pod	10.57	8.80	12.33	7.05	8.92	62.6	1.22	11.49
Pod length(cm)	7.75	6.73	9.31	7.49	8.84	71.8	1.01	13.07
Seed Index(g)	3.15	2.60	3.43	6.04	6.64	82.6	0.36	11.31
Biological yield(g)	42.69	36.21	54.12	11.52	11.87	94.2	9.83	23.02
seed yield per plant(g)	5.79	4.29	13.66	15.35	16.03	91.7	1.75	30.26
Harvest index	13.52	5.68	14.98	6.26	6.89	82.5	1.58	11.71

Fig 2: Genetic Variability Parameters GCV, PCV, Heritability (H^{2}b), Genetic Advance and GAM 5% of Green gram

References

1. Rahim MA, Mia AA, Mahmud F, Zeba N, Afrin KS. Genetic variability, character association and genetic divergence in Mungbean (*'Vigna radiate* 'L. Wilczek). Plant Omics. 2010;3(1):1-6.
2. Majhi PK, Mogali SC, Abhisheka L. Genetic variability, heritability, genetic advance and correlation studies for seed yield and yield components in early segregating lines (F3) of greengram [*Vigna radiata* (L.) Wilczek]. International Journal of Chemical Studies. 2020;8(4):1283-8.
3. Johnson HW, Robinson HF, Comstock RE. Estimates of genetic and environmental variability in soybeans. Agronomy journal. 1955;47(7):314-8.
4. Dhunde BB, Devmore JP, Mahadik SG, Palshetkar MG, Vanve PB, Bhave SG, *et al*. Correlation and path analysis studies on yield and its components in green gram [Vigna radiata L. Wilczek]. The Pharma Innovation Journal. 2021;10(1):727-30.
5. Salman MA, Anuradha C, Sridhar V, Babu ER, Pushpavalli SN. Genetic variability for yield and its related traits in green gram [*Vigna radiata* (L.) Wilczek]. Legume Research-An International Journal. 2021;1:5.
6. Panse VG, Sukhatme PV. Statistical Methods for Agricultural Workers. Indian Council of Agricultural Research, New Delhi; c1985.
7. Burton GW. Quantitative inheritance in grasses. Pro VI Int Grassl Cong; c1952. p. 277-83.
8. Singh RK, Choudhury BD. Biometrical method in quantitative genetic analysis. Kalyani Publishers, Ludhiana, New Delhi; c1985. p. 54-57.
9. Hanson CH, Robinson HF, Comstock RE. Biometrical studies of yield in segregating populations of Korean lespedeza 1. Agronomy journal. 1956;48(6):268-72.
10. Allard RW. Principles of plant Breeding. 1st Edn., John Wiley and Sons Inc., New York; c1960.
11. Chaudhary PL, Kumar B, Kumar R. Analysis of Heterosis and Heterobeltiosis for Earliness, Yield and Its Contributing Traits in Okra (*Abelmoschus esculentus* L. Moench). International Journal of Plant & Soil Science. 2023 May 3;35(11):84-98. https://doi.org/10.9734/ijpss/2023/v35i112949
12. Tabasum A, Saleem M, Aziz I. Genetic variability, trait association and path analysis of yield and yield components in mungbean (*Vigna radiata* (L.) Wilczek). Pak. J. Bot. 2010 Dec 1;42(6):3915-24.
13. Sineka T, Murugan E, Sheeba A, Hemalatha G, Vanniarajan C. Genetic relatedness and variability studies

in greengram (*Vigna radiata* (L.) Wilczek). Electronic Journal of Plant Breeding. 2021 Dec 29;12(4):1157-62.

14. Nayak G, Lenka D, Dash M, Tripathy SK. Genetic Diversity and Protein Analysis in Greengram. Biological Forum. 2022;14(2);994-999.

15. Khan AS, Kabir MY, Alam MM. Variability, correlation path analysis of yield and yield components of pointed gourd. Journal of Agriculture & Rural Development; c2009. p. 93-8.

16. Kumar A, Kumar M, Sharma VR, Singh MK, Singh B, Chand P. Genetic Variability, Heritability and Genetic Advance studies in Genotypes of Okra [*Abelmoschus esculentus* (L.) Moench]. Journal of Pharmacognosy and Phytochemistry. 2019;8(1):1285-90.

17. Tamalapakula TAJ, Lavanya GR, Babu VR, Krishna CNS, Sudheer RT. Genetic variability, heritability and genetic advance for yield and yield contributing traits of greengram: Variability in yield and yield contributing traits of greengram. Journal of Agri Search. 2021; 8(2):89-94.