



RESEARCH ARTICLE

Genetic analysis of bold seeded greengram (*Vigna radiata* (L.) Wilczek) genotypes for yield and yield component traits

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Received: 04 March 2026; Accepted: 16 June 2026; Available online: Version 1.0: 21 July 2026

Cite this article: Mahalingam A, Manivannan N, Ragul S, Subrahmaniyan K, Sathish KR, Bharathi KK. Genetic analysis of bold seeded greengram (*Vigna radiata* (L.) Wilczek) genotypes for yield and yield component traits. Plant Science Today (Early Access). <https://doi.org/10.14719/pst.14381>

Abstract

Greengram (*Vigna radiata* (L.) Wilczek) is grown mainly in South and Southeast Asia and parts of Africa and it is cultivated during the kharif, rabi and summer seasons depending on climate and irrigation. The sprouted greengram is rich in antioxidants which helps in maintaining gut health as well as preventing cardiovascular diseases. In the present investigation, a total of 20 bold seeded accessions of greengram were evaluated for 10 quantitative traits viz., days to 50 % flowering, plant height (cm), number of branches per plant, number of clusters per plant, number of pods per cluster, number of pods per plant, pod length (cm), number of seeds per pod, 100 seed weight (g) and seed yield per plot (g). High phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) estimates were recorded for number of branches per plant (26.97, 20.97), number of pods per plant (25.66, 20.47) and seed yield per plant (27.29, 25.92). These traits also recorded high heritability (h^2) along with high genetic advance as percent of mean. The PCV was slightly higher than the GCV which indicated that the expression of these traits is less influenced by environmental fluctuations. Estimates of correlation coefficient revealed positive and significant association of seed yield per plot with the number of pods per cluster (0.49). The principal component analysis indicates that the traits viz., number of branches per plant, number of pods per cluster and number of pods per plant are the most influential principal component traits governing 84 % of variation among the bold seeded greengram genotypes. Hence, number of branches per plant, number of pods per cluster and number of pods per plant should be given due to importance in selection programme for the development of bold seeded greengram varieties.

Keywords: bold seed; character association; genetic variability; greengram; heritability; yield traits

Introduction

Pulses play a crucial role in the global food system, offering an affordable source of dietary proteins, particularly for vegetarian communities. Their protein content ranges from 20–30 %, which is about two to three times higher than the content found in cereals (1). Besides protein, pulses are also abundant in complex carbohydrates, dietary fibre, vitamins and minerals, making them valuable in combating malnutrition and micronutrient deficiencies. Among these crops, mungbean or greengram (*Vigna radiata* (L.) Wilczek) is significant in Asia, Africa and Latin America, where it is consumed as dry seeds and fresh green pods (2). This self-pollinating diploid legume ($2n = 2x = 22$) belongs to the Leguminaceae family and has a genome size of 560 mb (3). Mungbean seeds contain about 15–30 % protein (4) and 53–67 % carbohydrates (5, 6). Greengram is also rich in essential amino acids like lysine, arginine, histidine and tryptophan (7). Mungbean can enhance cereal-based diets by supplying lysine, an essential amino acid lacking in cereals, thereby improving

overall protein quality (8). When sprouted, the seeds become a source of antioxidants that support gut health and help prevent cardiovascular diseases (9). Ascorbic acid (vitamin C) is produced in sprouted mungbean seeds and the levels of riboflavin and thiamine also increase during sprouting. Agronomically, mungbean is well-suited to various environments, with rapid growth, nitrogen-fixing ability and tolerance to heat, drought and salinity, making it suitable for different cropping systems, especially those based on cereals (10).

Greengram (*V. radiata*) is an important pulse crop valued for its high protein content, short duration and adaptability to diverse agro-climatic conditions; however, its productivity remains relatively low due to limited genetic improvement in yield and its component traits. In recent years, bold-seeded genotypes have gained greater market preference because of their superior consumer acceptability and higher economic value, yet the genetic architecture governing yield and associated traits in these genotypes is not well understood. The

absence of precise information on genetic variability, gene action and trait associations limits the efficiency of breeding programmes aimed at yield enhancement. Therefore, the present study aims to assess the extent of genetic variability, estimate genetic parameters such as heritability and genetic advance, analyse the nature of gene action and determine the association among yield and its component traits to identify superior genotypes and effective selection indices (11, 12). It is hypothesised that significant genetic variability exists among bold-seeded greengram genotypes for yield and its component traits, that both additive and non-additive gene effects govern their inheritance, that yield is positively associated with key traits such as number of pods per plant, seeds per pod and 100-seed weight and that selection based on highly heritable and genetically correlated traits will facilitate the development of high-yielding bold-seeded greengram varieties.

Materials and Methods

The experimental material consisted of 20 bold seeded greengram genotypes developed from National Pulses Research Centre (NPRC), Tamil Nadu Agricultural University, Vamban, Pudukkottai, Tamil Nadu (Table 1). All the 20 genotypes were evaluated during kharif 2018 and rabi 2018–19 seasons at NPRC, Vamban. All the entries were evaluated under randomized block design (RBD) with 2 replications in the plot size of 2.4 m² with a spacing of 30 × 10 cm. The soil type was red lateritic with the pH of 6.5 with annual mean rainfall of approximately 881 mm. Recommended package of practices was adopted for the whole cropping period.

Data collected

The biometrical observations on 10 quantitative traits viz., days to 50 % flowering, plant height (cm), number of branches per plant, number of clusters per plant, number of pods per cluster, number of pods per plant, pod length (cm), number of seeds per pod, 100 seed weight (g) and seed yield per plot (g) were recorded. Five representative plants were selected randomly and tagged to collect all the under mentioned agro-morphological data for each genotype at each test environments and seed yield was estimated in (g/plot).

Days to 50 % flowering: The number of days taken from the date of sowing to the date on which 50 % of the plants in a plot started first flowering was recorded.

Plant height: The height of the plant was measured from the base of the stem to the tip of the main stem at the end of flowering and was expressed in centimetres (cm).

Number of branches per plant: The number of branches that emerged from the leaf axils of the main stem were counted and recorded.

Number of clusters per plant: The total number of clusters were counted and recorded in each plant.

Number of pods per cluster: The number of pods per cluster were counted on individual plant.

Number of pods per plant: The total number of fully matured pods were counted at the time of harvest.

Pod length (cm): The length of the pod was measured from end to end for five mature pods. The mean was calculated and expressed in cm.

Number of seeds per pod: The total number of seeds in five randomly chosen pods was counted. The mean was calculated and used.

100-seed weight (g): Hundred well filled seed were selected at random from each plant and weighed in grams.

Seed yield per plot (g/plot): All the matured pods harvested from each plot were threshed, air dried and the weight recorded in grams.

Statistical analysis

The data were analysed using STAR (version 1.4) package developed by International Rice Research Institute (IRRI), Philippines. The principal component analysis (PCA) was carried out to identify traits that contribute most of the observed variation among the genotypes (13). Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were assessed (14). Heritability and genetic advance parameters were calculated (15, 16). The PCV and GCV estimates were categorised < 10 % as low, 10–20 % as moderate and > 20 % as high as suggested by (9). Heritability per cent values were categorised as low (< 30 %), medium (30–60 %) and high (> 60 %). Genetic advance as a per cent of mean values were categorised as low (< 10), moderate (10–20) and high (> 20).

Table 1. Name and origin of genotypes

Sl. No	Genotypes	Pedigree	Origin
1	VGG 16-048	VBN (Gg) 2 × SM 47	NPRC, Vamban
2	VGG 16-058	VBN (Gg) 2 × SM 47	NPRC, Vamban
3	VGG 17-046	VBN (Gg) 2 × MH 215	NPRC, Vamban
4	VGG 17-056	EC 496839 × EC 520011	NPRC, Vamban
5	VGG 17-057	EC 496839 × EC 520011	NPRC, Vamban
6	VGG 17-076	ML 2037 × EC 496841	NPRC, Vamban
7	VGG 17-107	EC 496839 × ML 2037	NPRC, Vamban
8	VGG 17-109	EC 496839 × ML 2037	NPRC, Vamban
9	VGG 18-009	EC 496839 × IPM 409-4	NPRC, Vamban
10	VGG 18-011	EC 496839 × LGG 460	NPRC, Vamban
11	VGG 18-014	EC 496839 × LGG 460	NPRC, Vamban
12	VGG 18-016	EC 520016 × LGG 460	NPRC, Vamban
13	VGG 18-017	EC 520016 × LGG 460	NPRC, Vamban
14	VGG 18-018	EC 520016 × LGG 460	NPRC, Vamban
15	VBN 2	VGG 4 × MH 309	NPRC, Vamban
16	VBN 3	K 1 × Vellore local	NPRC, Vamban
17	VBN 4	PDM 139 × BB 2664	NPRC, Vamban
18	CO 7	MGG 336 × CoGG 902	Coimbatore
19	CO 8	COGG 923 × VC 6040A	Coimbatore
20	IPM 2-14	-	IIPR, Kanpur

NPRC: National Pulse Research Centre; IIPR: Indian Institute of Pulses Research.

Results and Discussion

A fundamental prerequisite thing is the existence of significant difference among the genotypes taken for a study. The analysis of variance (ANOVA) for the ten yield-contributing traits in greengram revealed substantial variability among the genotypes (Table 2). Highly significant differences were observed for most traits except days to 50 % flowering and number of pods per cluster, indicating the presence of considerable genetic diversity and the potential for effective selection and improvement.

The genetic variability parameters were summarised in Table 3. The PCV and GCV are vital for understanding the nature and magnitude of variability in the population, which arises from genetic and non-genetic causes. While GCV reflects the heritable portion of total variability, PCV also accounts for environmental variability, resulting in higher PCV values compared to GCV for all traits studied. The traits viz., number of branches per plant (26.97 %, 20.97 %), number of pods per plant (25.66 %, 20.47 %) and seed yield per plot (27.29 %, 25.92 %) recorded high PCV and high GCV. This result indicated the presence of substantial inherent genetic variability within the evaluated genotypes. This level of variation is desirable for selection, as it allows breeders to identify and advance superior genotypes with improved yield potential. These traits can therefore be effectively improved through direct phenotypic selection. Whereas the other traits viz., days to 50 % flowering (5.32, 4.94) and pod length (9.23 %, 8.14 %) recorded low PCV and GCV. Moderate PCV and GCV were observed for the number of clusters per plant (18.27 %, 10.23 %), number of pods per cluster (14.95 %, 11.19 %) and 100-seed weight (19.07 %, 18.98 %). High heritability coupled with high genetic advance as per cent of mean (GAM) has been recorded by the traits viz., number of branches per plant (63.60 %, 34.45 %), number of pods per plant (63.60 %, 33.62 %), 100 seed weight (99.10 %, 38.93 %) and seed yield per plot (90.25 %, 50.73 %). The PCV was slightly higher than the GCV. This combination suggests that the expression of these traits is less influenced by environmental fluctuations and that the additive genetic component plays a major role in their inheritance. Therefore, direct selection for these characters in early segregating generations is likely to be highly effective and result in substantial genetic improvement. The traits viz., plant height and number of clusters per plant recorded moderate heritability and GAM. The traits days to 50 % flowering and number of seeds per pod

revealed high heritability but low GAM. High heritability with low GAM indicates non-additive gene action and selection for these traits may not be rewarding. Similar results were recorded in the various populations of greengram (17, 18).

The correlation coefficient assesses the relationship between various plant characteristics and identifies the component traits that can be relied upon for genetic yield improvement. The estimates of correlation coefficients for yield and yield attributes were presented in Table 4. The correlation analysis provides valuable insight into the extent to which various yield-contributing traits influence seed yield, thereby assisting in the identification of reliable selection criteria. In the present study, seed yield per plot exhibited a significant and positive correlation with number of pods per cluster (0.49), indicating that genotypes producing more pods within each cluster tend to achieve higher yield. This is consistent with earlier findings in green gram, where pods per cluster were reported as a major determinant of yield performance (17). A strong and positive association was also observed between 100-seed weight and pod length as well as number of seeds per pod, suggesting that longer pods not only accommodate more seeds but also contribute to better seed development and maturity. Similar relationships have been reported in previous studies, emphasising pod size and seed traits as critical contributors to seed weight and biomass accumulation (19). The trait number of seeds per pod, which showed a significant positive correlation with pod length, reinforces the role of pod morphology in determining reproductive efficiency. Studies in mungbean or greengram have also highlighted pod length as a reliable predictor of seed filling potential (20).

Furthermore, number of pods per plant exhibited significant and positive associations with days to 50 % flowering, plant height, number of branches per plant, number of clusters per plant and number of pods per cluster, indicating that taller plants with more branches and clusters tend to produce a greater number of pods. This aligns with earlier reports where plant architecture traits such as height, branching pattern and cluster formation were shown to strongly influence pod production (21). The significant positive correlations of number of pods per cluster with days to 50 % flowering, plant height and number of branches per plant further suggest that early and vigorous vegetative growth contributes to enhanced reproductive output. Likewise, number of

Table 2. Analysis of variance for different yield contributing attributes of greengram

Source of variations	df	Days to 50 % flowering	Plant height (cm)	Number of branches per plant	Number of clusters per plant	Number of pods per cluster	Number of pods per plant	Pod length (cm)	Number of seeds per pod	100-seed weight (g)	Seed yield per plot(g)
Replicates	1	0.03	0.03	1.00	40.00	40.00	64.01	0.46	1.44	0.03	6597.19
Genotypes	19	6.78	0.36**	0.05*	0.15**	2.80	66.04**	1.14**	0.45**	1.79**	137406.31**
Error	19	0.50	0.03	0.05	2.01	38.10	14.69	0.14	0.23	0.01	7041.63

*, ** significant at 0.05 and 0.01 level of significance, respectively.

Table 3. Mean and genetic variability parameters for various yield and yield contributing traits of green gram

Characters	Mean	PCV (%)	GCV (%)	h ² (%)	GAM
Days to 50 % flowering	35.88	5.32	4.94	86.30	9.46
Plant height (cm)	37.18	13.86	9.25	44.53	12.71
Number of branches per plant	1.75	26.29	20.97	63.60	34.45
Number of clusters per plant	6.74	18.27	10.23	31.37	11.81
Number of pods per cluster	3.57	14.95	11.19	55.97	17.24
Number of pods per plant	24.76	25.66	20.47	63.60	33.62
Pod length (cm)	8.67	9.23	8.14	77.84	14.80
Number of seeds per pod	11.67	5.01	2.85	32.37	3.34
100-seed weight (g)	4.98	19.07	18.98	99.10	38.93
Seed yield per plot (g)	984.88	27.29	25.92	90.25	50.73

PCV: phenotypic coefficient of variation; GCV: genotypic coefficient of variation; h: heritability; GAM: genetic advance as per of mean.

Table 4. Correlation coefficients of grain yield and its component characters in bold seeded greengram

Characters	Plant height (cm)	Number of branches per plant	Number of clusters per plant	Number of pods per cluster	Number of pods per plant	Pod length (cm)	Number of seeds per pod	100-seed weight (g)	Seed yield per plot(g)
Days to 50 % flowering	0.81**	0.71**	0.75*	0.47*	0.77**	-0.56**	-0.51*	-0.60**	0.25
Plant height (cm)		0.72**	0.63**	0.45*	0.69**	-0.28	-0.27	-0.51*	0.39
Number of branches per plant			0.69**	0.50*	0.76**	-0.16	-0.20	-0.39	0.36
Number of clusters per plant				0.36	0.84**	-0.60**	-0.27	-0.62**	0.10
Number of pods per cluster					0.77**	-0.46*	-0.44*	-0.77**	0.49*
Number of pods per plant						-0.65**	-0.43	-0.83**	0.31
Pod length (cm)							0.69**	0.78**	-0.04
Number of seeds per pod								0.53*	-0.21
100-seed weight (g)								1.00	-0.22

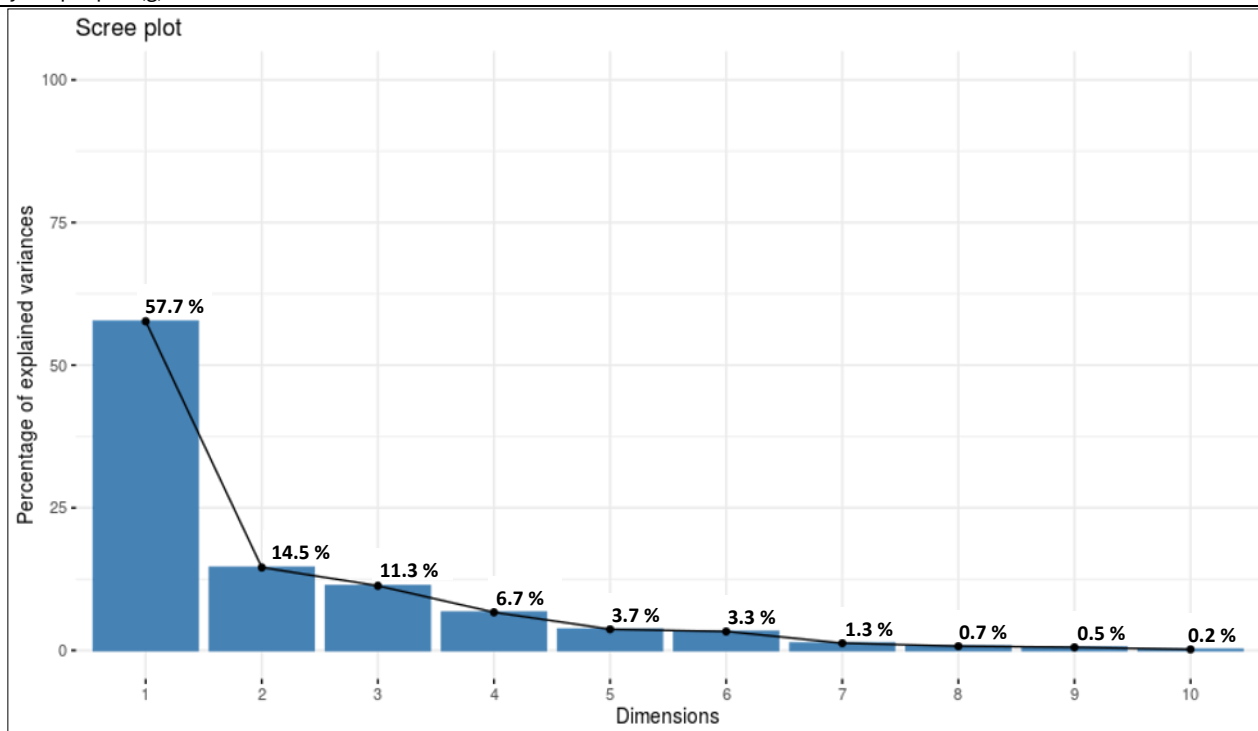
*, ** significant at 0.05 and 0.01 level of significance, respectively.

clusters per plant showed significant positive correlations with flowering time, plant height and branching, emphasising the role of plant stature and branching pattern in determining cluster formation, as previously documented in green gram (22). Additionally, number of branches per plant exhibited significant positive associations with days to 50 % flowering and plant height, indicating that plants with longer vegetative duration and greater height tend to develop more branches trait known to enhance overall pod-bearing capacity (19).

Principal component analysis is effective in evaluating genotypes by pinpointing potential traits for further genetic evaluation (23). It is the best tool for selecting promising genotypes for breeding programs based on identified traits (24). The PCA revealed that the first two components (PC1 and PC2) together explained 72.22 % of the total variation, indicating their effectiveness in capturing the major genetic variability among greengram genotypes (Table 5 and Fig 1). The PC1 alone accounted for 57.68 % of the variation and can be interpreted as a

Table 5. Cumulative variation and Eigenvalue for different principal components

Particulars	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9	PC10
Eigenvalues	5.77	1.45	1.13	0.67	0.37	0.33	0.13	0.07	0.05	0.02
Proportion of variance %	57.68	14.54	11.32	6.68	3.71	3.32	1.28	0.74	0.54	0.18
Cumulative proportion %	57.68	72.22	83.55	90.23	93.94	97.26	98.54	99.28	99.82	100.00
Days to 50 % flowering	0.36	-0.10	0.21	0.37	-0.05	0.21	-0.74	0.28	-0.08	-0.06
Plant height (cm)	0.32	-0.35	0.08	0.25	0.02	0.65	0.40	-0.33	0.00	0.09
Number of branches per plant	0.31	-0.45	0.11	0.01	-0.37	-0.46	0.08	0.03	0.55	0.17
Number of clusters per plant	0.34	-0.08	0.43	-0.11	0.38	-0.34	0.19	0.12	-0.50	0.34
Number of pods per cluster	0.31	0.05	-0.45	-0.43	-0.39	0.07	-0.23	-0.23	-0.32	0.39
Number of pods per plant	0.40	-0.03	0.06	-0.28	-0.04	-0.14	0.03	-0.24	-0.14	-0.81
Pod length (cm)	-0.29	-0.53	-0.10	-0.04	-0.36	0.06	0.17	0.49	-0.44	-0.18
Number of seeds per pod	-0.24	-0.44	0.21	-0.61	0.35	0.23	-0.32	-0.09	0.21	0.04
100-seed weight(g)	-0.35	-0.29	0.07	0.35	-0.07	-0.31	-0.24	-0.65	-0.29	0.01
Seed yield per plot (g)	0.17	-0.31	-0.70	0.18	0.56	-0.18	-0.04	0.09	0.04	-0.05

**Fig. 1.** Scree plot constructed using ten principal components.

yield architecture component, as it showed high positive loadings for number of pods per plant (0.40), number of clusters per plant (0.34), days to 50 % flowering (0.36), plant height (0.32), number of branches per plant (0.31) and number of pods per cluster (0.31). In contrast, negative loadings were observed for 100-seed weight (-0.35), pod length (-0.29) and number of seeds per pod (-0.24), indicating a trade-off between yield components and seed size traits. Thus, PC1 differentiates genotypes with superior branching and pod production capacity from those emphasising seed size and pod traits. Trait grouping further supports this pattern, with yield-related traits clustering together, while seed and pod traits form a separate contrasting group and PC2 (14.54 %) contributing to the separation of reproductive efficiency traits from structural growth traits.

From a breeding perspective, the PCA provides clear selection implications. Since PC1 represents the major yield-contributing axis, genotypes with higher PC1 scores can be prioritised for selection as they possess desirable traits such as number of branches per plant, number of clusters per plant and number of pods per plant (Fig. 2). However, the negative association of seed size traits with PC1 highlights the need to balance seed size and yield, especially in bold-seeded greengram improvement programmes. The grouping of traits such as pods per plant, clusters per plant and branches per plant suggests that simultaneous improvement through indirect selection is feasible. Similar selection strategy was followed by some scientist (25). Additionally, the influence of later components, particularly PC3 on seed yield, indicates that yield is governed by multiple interacting traits; therefore, adopting a multi-trait selection index and strategic hybridisation involving genotypes from contrasting clusters would be more effective for achieving both high yield and desirable seed characteristics.

Conclusion

The study revealed significant genetic variability among bold-seeded greengram genotypes, indicating good scope for selection and improvement. Traits such as number of branches per plant, number of pods per plant, 100-seed weight and seed yield per plot exhibited high heritability along with high genetic advance, suggesting the predominance of additive gene action and the effectiveness of direct selection. In contrast, traits like days to 50 % flowering and number of seeds per pod showed high heritability but low genetic advance, indicating non-additive gene effects and limited response to selection. Correlation and principal component analysis (PCA) results identified number of pods per plant, pods per cluster and branches per plant as key yield-contributing traits, which should be emphasised in breeding programmes for developing high-yielding varieties.

Acknowledgements

The authors would like to thank the National Pulses Research Centre, Tamil Nadu Agricultural University for the support and execution of experiment.

Authors' contributions

MA, MN, RS carried out experiment, involved in analysis, writing and original draft preparation, conceptualisation, resources, validation and supervision. SK, SKR, BKK involved in reviewing and editing of final manuscript. All authors read and approved the final manuscript.

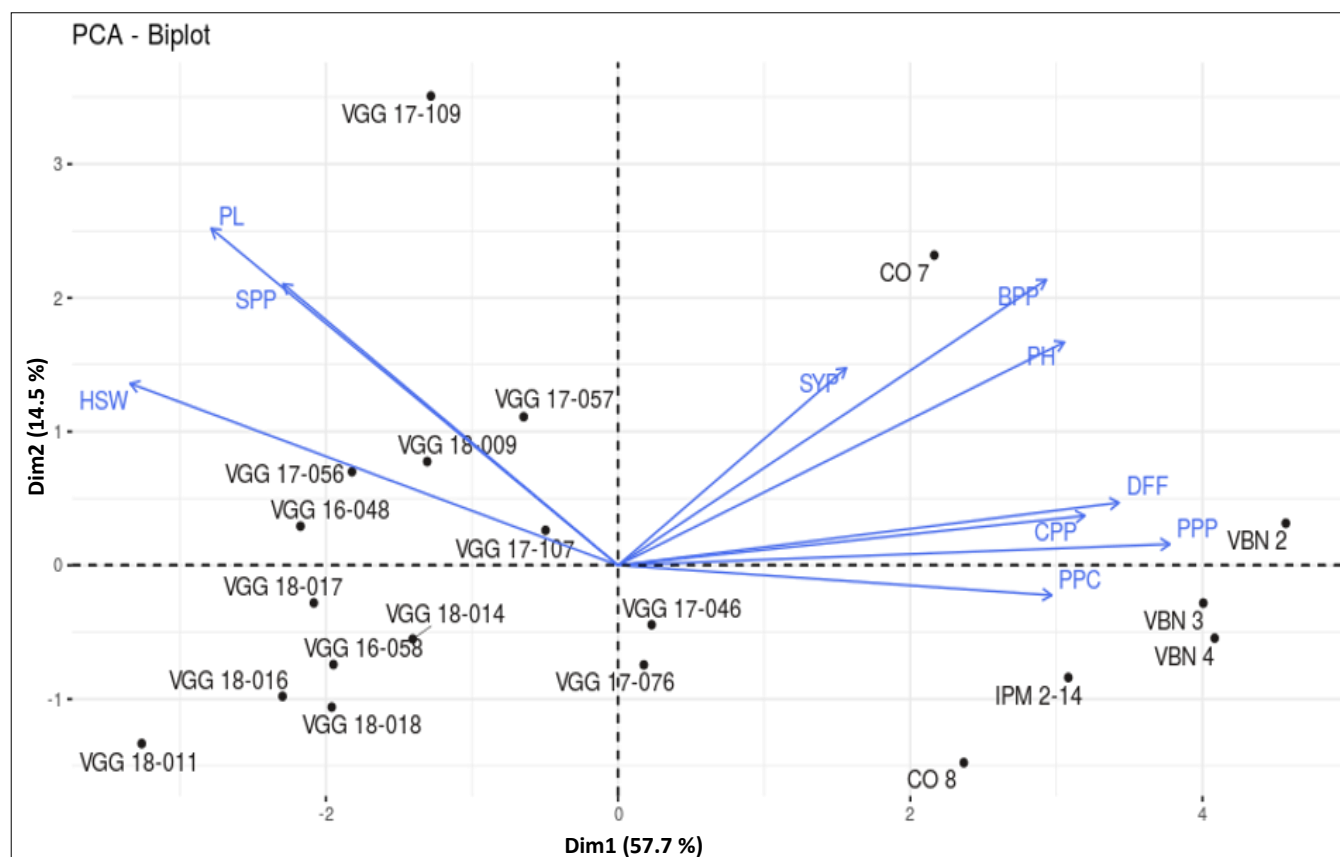


Fig. 2. Principle component analysis biplot for ten quantitative characters of bold seeded greengram genotypes.

Compliance with ethical standards

Conflict of interest: Authors do not have any conflict of interest to declare.

Ethical issues: None

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Peer review: Publisher thanks Sectional Editor and the other anonymous reviewers for their contribution to the peer review of this work.

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