



Genotypic and phenotypic variances among different quantitative characters in green gram genotypes

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ABSTRACT

Present study was carried out at National Bureau of Plant Genetic Resources, Regional Station, Rajendranagar, Hyderabad during the year 2014-15. Seventy six green gram accessions were characterized for nine quantitative characters. Based on the correlation coefficients, plant height showed highly significant and positive correlation with number of branches plant⁻¹ and clusters plant⁻¹. Pod length was positively and significantly correlated with 100 seed weight; Seed yield plant⁻¹ was positively and highly significantly correlated with number of branches plant⁻¹, clusters plant⁻¹ and pods plant⁻¹; pods plant⁻¹ was positively and highly significantly correlated with clusters plant⁻¹. Pod length was positively and highly significantly correlated with number of seeds pod⁻¹. On the basis of cluster analysis, the seventy six accessions were grouped into three main clusters with several sub-clusters. Cluster 1 had 59 accessions further distributed into 6 sub-clusters. The three control varieties were in Cluster I but in two separate sub-clusters. The Cluster II had 16 accessions distributed in three sub-clusters (KARS-177, KARS-212, SKN-139, KARS-30, KARS-44, clustered together in sub-cluster I; KARS-47, KARS-53, KARS-51, KARS-191, KSAS-06/91, KARS-295, KVSA-1761, KVSA-1779, SK-37 clustered together in sub-cluster II and KVSA-1760, KVSA-1762 clustered together in sub-cluster III. Cluster III had one accessions CN-9074.

Received 29.07.2017

Revised 09.08.2017

Accepted 27.08.2017

INTRODUCTION

Green gram is one of the most important short duration pulse crop grown in the subcontinent. It ranks third among all pulse crops grown in India after chickpea and pigeonpea. India is the largest producer and consumer of pulses in the world accounting for 33 per cent of world's area and 22 per cent of world's production of pulses. In India, green gram is grown on an area of 34.4 lakh ha, with a production of 14 lakh tonnes and a productivity of 406.98 kg ha⁻¹ (2011). In Andhra Pradesh, mung bean is grown on an area of 4.40 lakh ha, with a production of 2.17 lakh tonnes, and productivity of 493.18 kg ha⁻¹ (<http://agropedia.iitk.ac.in> 2011).

In any crop, yield is a complex trait, depending on various component agro-morphological characters some of which are highly influenced by the environment, while others are quantitatively inherited. In most of the breeding programmes, major emphasis is given to the improvement of yield *via* agro-morphological traits. Hence, knowledge of the nature and extent of the diversity present in germplasm collections is of utmost importance. The primary objective of any breeding programme is to identify superior genotypes on the basis of expression of multiple traits over a wide range of environments for a targeted location. Recognition and exploitation of variation among genetically diverse groups of germplasm are therefore fundamental to plant breeding and genetic engineering. Consequently, the assessment of genetic diversity within and among germplasm accessions including landraces has assumed high priority in recent times. At the same time, technological advances have provided contemporary plant breeders with efficient and high precision laboratory equipment and rapid data collection and computation systems for data storage and retrieval. This has led to development of better methods of characterization and evaluation of germplasm collections to improve strategies for

conservation and increase the utilization of the collections. Smith and Smith (1989) considered morphological characterization as an important step in description and classification of crop germplasm as a breeding programme mainly depends on magnitude of genetic variability (Smith *et al.*, 1991). With morphological characters alone it is difficult to fully characterize and evaluate individual genotypes as they are highly influenced by the environment. Hence, an assessment of the genetic variation and trait relationships could lead to better understanding of yield components and yield potential for improvement of green gram.

MATERIALS AND METHODS

Studies on characterization of green gram genotypes were taken up at NBPGR, Regional Station, Rajendranagar, Hyderabad. Seventy three accessions of green gram collected from different sources were studied for nine quantitative characters *viz.*, days to 50 % flowering, plant height, number of branches plant⁻¹, number of clusters plant⁻¹, number of pods plant⁻¹, pod length, seeds pod⁻¹, seed size and seed yield plant⁻¹. Three control varieties *viz.*, ML-267, LGG-460 and K-851 were also grown along with the germplasm for comparison.

The experiment was laid out in a randomized block design with two replications. Each accession was grown in three rows of 3 m length each with a spacing of 30 × 10 cm. Recommended package of practices were followed to raise a healthy crop. Observations on quantitative characters were recorded on three plants in each accession in each replication for all traits except for days to 50 per cent flowering and 100 seed weight. The mean values of three plants were averaged and expressed as mean of the respective characters. The data was statistically analyzed using RCBD (Snedecor and Cochran, 1965). Genetic parameters (heritability by Allard (1960), genetic and phenotypic variance and genetic and phenotypic coefficients of variation as per Falconer, 1960 were estimated. Phenotypic and genotypic correlation coefficients between different variables were calculated by using covariance technique (Al-Jibouri *et al.*, 1958). Phenotypic inter-relationships among accessions were assessed using Euclidean distance (Sneath and Sokal, 1973). The resulting phenotypic distance matrix was hierarchically represented in a dendrogram by subjecting the distance matrix to cluster analysis using the average linkage algorithm. Principal Coordinate Analysis was also done to visualize the clustering of accessions in two-dimensional space (Sneath and Sokal, 1973).

RESULTS AND DISCUSSION

Wide range of variation was observed in the nine quantitative traits among the 76 accessions as summarized by mean, range and CV estimates (Table 1). High and significant differences were observed among the accessions for characters days to 50 % flowering, plant height, clusters plant⁻¹, pod length and 100 seed weight indicating the presence of great amount of variability for the characters studied.

Days to 50 % flowering ranged from 34.5 to 43.0 days with a mean of 36.9 days. Highly significant differences were observed for days to 50 % flowering among the accessions studied. NSKMS-91 was the earliest to flower in 34.5 days. Several accessions flowered significantly later than the control varieties grown including NSKMS-177 (40.5 days), KSAS-06/91 (43.0 days), KARS-295 (40.0 days) and KARS-191 (41.5 days).

Plant height ranged from 21.7 cm to 48.3 cm with a total mean of 36.65 cm. Highly significant differences were observed among the accessions for plant height. Based on LSD of 3.45, two accessions were taller KARS-53 (48.3 cm) followed by KSAS-06/287 (48.2 cm) than the control varieties grown for comparison. These accessions were the tallest plants. Variety K-851 was observed to be the tallest under the conditions grown with a height of 44.2 cm. Varieties ML-267 and LGG-460 were 33.6 cm and 35.7 cm tall, respectively. Accessions NSKMS-72, KDRS-226 and KVSA-1790 were among the shortest plants with heights ranging from 24.5 cm to 26.8 cm.

Number of branches plant⁻¹ ranged from 3.0 to 5.5 with a mean of 3.85. Maximum number of branches plant⁻¹ was observed in KVSA-1762 with 5.5 branches followed by KVSA-1760 (5.2) as compared to LGG-460 which had 3.8 branches plant⁻¹. ML-267 and K-851 had 3.5 and 3.3 branches plant⁻¹. Several accessions had more number of branches plant⁻¹ than the check varieties although not significantly higher. These included KARS-51 (4.7), KVSA-1761 (4.5), KARS-191 (4.5), KSAS-06/91 (4.3) and KVSA-1784 (4.3).

Number of pods plant⁻¹ ranged from 9.2 to 166.3 with a mean of 49.59. Accession CN-9074 (166.3) was observed to be the only accession with significantly higher pods plant⁻¹ as compared to the best check variety LGG-460 (67.2) for the trait. However, there were several accessions on par with the three control varieties including KARS-295 (101.5), SK-57 (93.2), KVSA-1761 (82) and KVSA-1779 (79.5). This trait had a very high CV percentage (45.35).

Number of clusters plant⁻¹ ranged from 4.5 to 31.5 with a mean of 12.36. Significant differences were observed for this trait among all the accessions. LSD was 8.89 based on which differences between best control variety K-851 (14.7) were computed. One accession CN-9074 with 31.5 clusters plant⁻¹ was significantly better than variety K-851. However, several accessions were on par with the control varieties including KVSA-1761 (21.5), KARS-295 (20.8), KARS-240 (19.5) and SK-37 (18.8).

Pod length ranged from 6.2 to 9.1 cm with a mean of 7.08 cm; Highly significant differences were observed for this trait among all the accessions studied. Among the control varieties, K-851 performed the best with a pod length of 7.5 cm. Four accessions had significantly longer pods than this control variety. These included KARS-51 (9.1 cm), KARS-30 (8.9 cm), SKN-139 (8.8 cm) and KARS-44 (8.7 cm). Several accessions were on par with the control varieties including KARS-53 (8.6 cm), KARS-212 (8.3 cm)

Seeds pod⁻¹ ranged from 7.1 to 12.9 with a mean of 10.74. Although there were no significant differences among the accessions for this trait, several accessions were on par with the three control varieties ML-267 (10.8), LGG-460 (11.1) and K-851 (11.1). Accessions with slightly higher number of seeds pod⁻¹ included KARS-44 (12.9), KARS-51 (12.6), KARS-177 (12.6), KARS-191 (12.5), KARS-30 (12.3) and KARS-53 (12). Accessions NSKMS-177 (7.1), NSKMS-48 (8.9) and SKN-137 (9.4) had the least number of seeds pod⁻¹.

100 seed weight ranged from 1.8 to 4.4 g. Highly significant differences were observed for this trait with seeds of control variety ML-267 weighing 3.00 g per 100 seeds. Accessions NSKMS-72 (4.4 g), KARS-177 (4.1 g), CN-8027 (4.1 g) and NSKMS-91 (4.0 g) were significantly superior to the best control variety ML-267, while the accessions with least weight were KARS-226 (1.8 g), SKN-137 (2.2 g) and KARS-135 (2.4 g).

Seed yield plant⁻¹ ranged from 2.7 g to 44.2 g. Significant differences were observed among all the accessions for seed yield plant⁻¹. Accession CN-9074 was the highest seed yielder with 44.2 g plant⁻¹. This was significantly higher as compared to the best control variety LGG-460 with 23.8 g plant⁻¹. Lowest seed yield was observed in accessions NSKMS-177 (2.7 g), KDRS-226 (4.6 g), NSKMS48 (5.1 g) KARS-147 (5.6 g).

Heritability, Phenotypic and Genotypic Variance : Heritability in broad sense is the ratio of genotypic variance to the phenotypic variance and is expressed in percentage. The results with regard to mean, genotypic variance (σ^2g), phenotypic variance (σ^2p), phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV) and heritability in broad sense (h^2b) for nine characters were furnished in Table 2. In general PCV was more than GCV for all the characters indicating the influence of environment in expression of characters. Plant height, days to 50 % flowering, pod length and 100 seed weight showed high to moderate heritability of 91 %, 56 %, 48 %, and 47 %, respectively. The combination of high to moderate heritability for the above mentioned traits along with genetic coefficient of variance suggests that selection for these characters would be effective for further selection and improvement in green gram. As in the present study high heritability estimates were observed for plant height, pod length and 100 seed weight by Natarajan *et al.* (1988) also. Low heritability was obtained for seed yield plant⁻¹ which suggests that yield is a product of several complex characters. So, direct selection for yield for improvement may not be possible. Traits such as clusters plant⁻¹, pods plant⁻¹, seeds pod⁻¹ and 100 seed weight were observed to have lower genetic coefficient of variance combined with higher phenotypic coefficient of variance. This indicates the lack of sufficient variability for these traits in the set of germplasm investigated in the present study.

Correlation Coefficient Analysis: Correlation coefficient analysis reveals the association of characters *i.e.*, a change in one character brought about by a change in the other character (Table 2). Plant height showed highly significant and positive correlation with number of branches plant⁻¹ and clusters plant⁻¹. However, plant height was negatively correlated with 100 seed weight. Similar results were reported by Rahman *et al.* (2002) who also observed that plant height was negatively correlated with 100 seed weight. Pod length was positively and significantly correlated with 100 seed weight; Seed yield plant⁻¹ was positively and highly significantly correlated with number of branches plant⁻¹, clusters plant⁻¹ and pods plant⁻¹; pods plant⁻¹ was positively and highly significantly correlated with clusters plant⁻¹. Similar results were reported by Sharma (1999) and Gill *et al.* (1995). Number of seeds pod⁻¹ was positively and highly significantly correlated with pod length. Hakim (2008) also mentioned that yield had significant positive correlation with number of pods plant⁻¹. Strong negative association was observed between pods plant⁻¹ and 100 seed weight. Positive correlation of plant height with clusters plant⁻¹ and branches plant⁻¹ indicates that the taller the plant more the branches and consequently the number of clusters plant⁻¹ also increase and hence final grain yield increases as compared to vegetative growth. This study indicates that accessions having both more pods plant⁻¹ and taller plant height potentially produce higher yield.

Inter relationships among 76 accessions: The dendrogram/cluster analysis (Fig. 1) of the 76 accessions using average linkage algorithm on Euclidean distance for the nine quantitative traits revealed three main clusters with several sub-clusters. Cluster 1 had 59 accessions further distributed into 6 sub-clusters. The three control varieties were in Cluster I but in two separate sub-clusters. The Cluster II had 16 accessions distributed in three sub-clusters (KARS-177, KARS-212, SKN-139, KARS-30, KARS-44 clustered together in sub-cluster 1; KARS-47, KARS-53, KARS-51, KARS-191, KSAS-06/91, KARS-295, KVSA-1761, KVSA-1779, SK-37 clustered together in sub-cluster II and KVSA-1760, KVSA-1762 clustered together in sub-cluster III). Cluster III had one accessions CN-9074. The principal coordinated analysis (Fig. 2) revealed clustering similar to the dendrogram. The first coordinate explained 75 % of the variation while the second explained 25 %.

On the basis of results obtained in the present study it can be suggested that the accessions NSKMS-91, KARS-53, KSAS-06/287, KVSA-1762, KVSA-1760, CN-9074, KARS-53, KARS-30, SKN-139, KARS-44, KARS-51, KARS-177, KARS-191, KARS-53, NSKMS-72, CN-8027 NSKMS-91 could be utilized in the future mung bean breeding programs. On the basis of high heritability, plant height, pod length and seeds pod⁻¹ could be used as selection criteria in future breeding programs. On the basis of correlation, characters such as plant height, pods plant⁻¹, pod length and 100 seed weight could be a better index for increasing yield in green gram.

For selection of genetically diverse parents from the germplasm, it is essential that the collection should be systematically characterized using descriptors encompassing both quantitative and qualitative traits. Qualitative characters are important for plant description and are influenced by consumer's preference, socio-economic scenario and natural selection.

Systematic characterization and evaluation of plant genetic resources are necessary for the efficient use of the material through conventional methods or modern techniques. Analysis of genetic diversity is also a prerequisite to monitor genetic erosion, guidance for collection priorities, to investigate the evolutionary history of crops to support breeding strategies and methodologies, and to guide the management of germplasm collections (Engels and Vissor, 2003).

The importance for studying characterization traits in the collection of plant genetic resources becomes more relevant in the changing scenario of plant genetic resources (Rao, 2004). Characterization of gene pool is an important aspect for the management of germplasm collected for the future use. Many social and ethical issues are also associated with the characterization of accessions for their proper management, as it is the only way to stop biopiracy (Esquinas-Alcazar, 2005).

These accessions of green gram studied could be an important source of genetic variability particularly to develop new varieties suitable for sustainable agriculture, crop diversification, and varieties fitting into the changing cropping pattern and for efficient use of marginal land. This justifies the continued characterization and evaluation of different collections. In the present study we focused on the characterization of important pulse crop *i.e.* green gram. The major advantages of phenotypic characterization data are easy scoring, less time consuming and cost effectiveness. The present study revealed the overall picture at a glance of the variability pattern for these characterization traits in a collection of green gram accessions. The importance for studying characterization traits in the collection of plant genetic resources becomes more relevant in the changing scenario of plant genetic resources regime where we can act on "The Protection of Plant Varieties and Farmer's Rights, 2001". According to this act a registrable variety must confirm the criteria of novelty, distinctiveness, uniformity and stability. Presently, DUS criteria can be justified by specifying a combination of characterization (qualitative) traits (Ramanna, 2003). Thus the importance of accessions and to promote their utilization in crop improvement programs may be facilitated by assessing the genetic (morphological and molecular) diversity for different traits of agronomic importance.

REFERENCES

1. Allard, R.W. 1960. *Principles of Plant Breeding*. John Wiley Sons Inc. New York. 485.
2. Al-Jibouri, H. A., Miller, P. A and Robinson, H. F. 1958. Genetic and environmental variances and covariances in upland cotton cross of inter-specific origin. *Agron. J.*, 50(10): 633-637.
3. Engels, J. M. M and Vissor, L. 2003. *A guide to effective management of germplasm collections*. IPGRI Series Handbook for Genebanks No. 6. IPGRI, Rome, Italy.
4. Esquinas-Alcazar, J. 2005. Protecting crop genetic diversity for food security: political, ethical and technical challenges, *Nature Reviews Genetics*. 6: 946-953.
5. Falconer, D. S. 1960. *Introduction to quantitative genetics*. Oliver and notes. Iowa State University, Ames, IA. Boyd, Edinburgh/London. 364.
6. Gill, J. S., Verma, M. M., Gumber, R. K and Singh, B. 1995. Character association in mung bean lines derived from three intervarietal crosses in mung bean. *Crop Improvement*. 22: 255-260.

7. Hakim, L. 2008. Variability and correlation of agronomic characters of mung bean germplasm and their utilization for variety improvement program. *Indonesian Journal of Agricultural Science*. 9: 24-28.
8. <http://agropedia.iitk.ac.in/content/area-production-and-productivity-major-pulses>.
9. Natarajan, C., Thyagarajan, K and Rathnaswamy, R. 1988. Association and genetic diversity studies in green gram. *Madras Agricultural Journal*. 75:238-245.
10. Protection of Plant Varieties & Farmer's Rights. 2001. Protection of Plant Varieties and Farmer's Right Act (No. 53 of 2001). Dept. of Agriculture and Cooperation, Ministry of Agriculture, Govt. of India, Krishi Bhavan, New Delhi.
11. Rahman, A. K. M., Nag, B. L., Uddin, M. S and Miah, M. A. 2002. Correlation and path analysis of seed yield in mung bean. *Bangladesh Journal of Agricultural Research*. 27: 305-308.
12. Ramanna, A. 2003. *Indian Plant Variety and Farmer's Rights Legislation: Potential impact on stakeholder access to genetic resources*, Environment and production technology Division, International Food Policy Research Institute. 96.
13. Rao, N. K. 2004. Plant genetic resources: Advancing conservation and use through biotechnology. *African Journal of Biotechnology*. 3(2): 136- 145.
14. Sharma, R. N. 1999. Heritability and character association in non segregating populations of mung bean (*Vigna radiata* L. Wilczek). *Journal of Interacademia*. 3: 5-10.
15. Smith, J. S. C and Smith, O. S. 1989. The description and assessment of distances between inbred lines of maize: the utility of morphological, biochemical and genetic descriptors and a scheme for the testing of distinctiveness between inbred lines. *Maydica*. 34: 151-161.
16. Smith, S. E., Doss, A. A and Warburton, M. 1991. Morphological and agronomic variation in North African and Arabian alfalfa. *Crop Science*. 31: 1159-1163.
17. Sneath, P. H. A and Sokal, R. R. 1973. *Numerical Taxonomy*. Freeman and Co., San Francisco, California. 573.
18. Snedecor, G. W and Cochran, W. G. 1967. *Statistical Methods*. Calcutta Oxford and IBH. 296.

Table 1 Quantitative traits in different accessions of green gram (contd.)

S. No.	Cultivars	Days to 50 % flowering	Plant height (cm)	No. of branches plant ⁻¹ (No.)	Pods plant ⁻¹ (No.)	Clusters plant ⁻¹ (No.)	Pod length (cm)	Seeds pod ⁻¹ (No.)	100 seed weight (g)	Seed yield plant ⁻¹ (g)
1	CN-8016	35.0	38.1	3.7	37.2	9.67	6.2	9.7	2.6	10.9
2	CN-8027	37.0	34.9	4.2	59.7	12.17	7.5	10.3	4.1	22.3
3	CN-8067	37.0	42.4	3.8	49.7	15.83	7.7	11.3	3.0	17.0
4	CN-9042	35.0	42.2	3.8	34.2	8.83	6.9	10.7	2.8	9.7
5	CN-9074	37.0	38.4	4.0	166.3	31.5	6.8	11.1	2.7	44.2
6	KARS-104	37.0	32.2	3.7	44.5	11.83	6.2	9.9	2.8	12.3
7	KARS-107	35.0	37.6	4.3	33.3	9.33	6.5	10.1	2.7	8.8
8	KARS-110	35.0	36.2	3.5	24.7	9.5	6.5	9.6	2.6	7.0
9	KARS-118	37.0	36.8	4.0	70.8	10	7.1	11.3	3.0	24.4
10	KARS-125	36.0	36.0	4.2	51.3	9.33	6.2	10.2	3.3	17.7
11	KARS-131	35.0	39.5	4.2	52.7	13	7.3	10.2	3.3	17.4
12	KARS-132	38.0	33.1	3.8	39.8	8.5	7.5	10.3	2.7	11.0
13	KARS-135	36.0	36.3	3.2	41.2	9	6.3	10.7	2.4	10.4
14	KARS-137	36.0	38.9	3.7	78.7	15	7.0	10.7	2.7	20.6
15	KARS-138	37.0	27.6	3.5	61.7	11.17	6.6	10.1	2.6	16.2
16	KARS-147	37.0	33.5	3.3	21.3	8.17	6.5	9.7	2.7	5.6
17	KARS-149	37.0	37.6	3.8	59.2	13.5	6.5	10.3	2.6	16.0
18	KARS-169	37.0	39.0	3.5	38.8	10.67	7.2	11.2	3.1	12.9
19	KARS-173	36.0	37.5	4.2	27.2	9.83	7.1	10.2	3.2	8.5
20	KARS-177	37.0	35.0	3.7	22.8	5.5	7.7	12.6	4.1	11.6
21	KARS-191	41.5	36.5	4.5	70.0	16.33	7.9	12.5	2.7	24.0
22	KARS-212	35.0	36.2	3.7	38.7	9.17	8.3	11.4	3.6	15.5
23	KARS-222	39.0	28.9	3.7	77.0	15.67	6.9	9.9	2.9	19.9
24	KARS-24	36.0	36.4	3.5	40.7	9.67	7.3	9.7	3.1	12.2
25	KARS-240	38.0	42.1	4.3	53.5	19.5	6.4	10.4	2.8	15.8
26	KARS-263	36.0	36.7	3.7	27.5	7.83	7.2	11.3	3.5	10.9
27	KARS-279	38.0	35.6	3.7	25.0	6.67	6.7	10.9	2.6	6.7
28	KARS-295	40.0	42.1	3.7	101.5	20.83	7.2	11.0	3.0	33.6
29	KARS-30	39.0	33.5	3.7	37.7	12.5	8.9	12.3	3.5	17.3
30	KARS-39	37.0	28.0	3.5	38.5	12.83	7.3	10.8	3.2	13.1
S. No.	Cultivars	Days to 50 % flowering	Plant height (cm)	No. of branches plant ⁻¹ (No.)	Pods plant ⁻¹ (No.)	Clusters plant ⁻¹ (No.)	Pod length (cm)	Seeds pod ⁻¹ (No.)	100 seed weight (g)	Seed yield plant ⁻¹ (g)
31	KARS-44	38.0	34.4	3.2	39.2	12.67	8.7	12.9	3.7	18.8
32	KARS-47	39.0	45.2	4.2	30.5	8.83	7.4	11.9	3.2	11.7
33	KARS-51	36.0	38.8	4.7	52.7	11.33	9.1	12.6	3.3	24.4
34	KARS-53	37.0	48.3	4.2	33.3	9.83	8.6	12.0	3.7	14.9

35	KARS-69	37.0	39.4	4.0	57.0	13.5	7.1	11.0	2.8	17.3
36	KARS-72	38.0	39.8	3.8	63.0	14.67	6.2	10.9	2.6	18.4
37	KARS-74	36.0	46.9	3.8	44.5	11	6.8	10.5	3.0	13.9
38	KARS-77	37.0	35.1	3.7	40.5	11	6.5	10.6	2.6	11.3
39	KARS-84	37.5	32.5	3.3	48.7	11	7.4	11.2	2.7	14.5
40	KARS-96	36.0	41.3	3.3	54.5	10.83	7.0	10.8	2.5	14.3
41	KDRS-226	37.0	26.4	3.5	25.8	8.67	6.4	9.7	1.8	4.6
42	KSAS-06/140	36.0	40.9	3.8	60.2	18.33	6.7	10.5	2.9	18.5
43	KSAS-06/235	37.0	36.4	4.3	62.5	16.83	7.5	11.5	2.8	19.4
44	KSAS-06/287	36.0	48.2	4.2	59.8	13	6.8	10.8	3.0	19.6
45	KSAS-06/319	37.0	34.6	3.8	51.8	10.5	6.6	9.7	3.0	16.0
46	KSAS-06/359	36.0	28.7	3.8	50.0	11.5	6.5	11.1	2.7	15.8
47	KSAS-06/91	43.0	46.7	4.3	48.5	15.5	7.3	11.4	2.7	14.5
48	KVSA-1738	39.0	30.6	4.2	37.7	12.83	6.2	10.3	2.5	9.5
49	KVSA-1741	36.0	38.1	3.7	44.5	12	6.6	10.9	2.5	12.3
50	KVSA-1748	35.5	37.5	4.5	67.3	14.33	7.1	10.4	2.8	19.1
51	KVSA-1760	38.0	43.2	5.2	58.7	17.17	7.5	11.3	3.0	19.9
52	KVSA-1761	39.0	41.8	4.5	82.0	21.5	7.6	11.1	2.8	23.9
53	KVSA-1762	38.5	35.1	5.5	65.2	14.5	7.0	11.1	2.4	18.1
54	KVSA-1779	38.0	44.2	4.3	79.5	17.33	7.0	11.7	2.6	23.8
55	KVSA-1784	37.0	46.6	4.3	57.3	17.17	7.1	11.4	2.7	17.5
56	KVSA-1787	35.0	38.6	3.5	63.3	15.67	6.9	10.8	2.7	19.6
S. No.	Cultivars	Days to 50 % flowering	Plant height (cm)	No. of branches plant⁻¹ (No.)	Pods plant⁻¹ (No.)	Clusters plant⁻¹ (No.)	Pod length (cm)	Seeds pod⁻¹ (No.)	100 seed weight (g)	Seed yield plant⁻¹ (g)
57	KVSA-1789	35.0	39.8	3.7	49.3	11.67	6.8	9.8	3.0	14.3
58	KVSA-1790	35.0	26.8	3.7	22.8	6.5	7.0	10.3	3.2	7.1
59	NSKMS-111	35.0	27.2	3.8	56.3	11.33	7.1	10.3	3.6	21.3
60	NSKMS-148	38.0	34.3	3.5	73.7	14.83	7.0	9.9	2.8	17.9
61	NSKMS-161	37.0	39.2	3.8	37.2	9.83	7.7	10.5	3.5	13.5
62	NSKMS-177	40.5	21.7	3.0	9.2	4.5	7.7	7.1	3.6	2.7
63	NSKMS-72	37.0	24.5	3.7	24.2	9.17	7.2	10.4	4.4	11.2
64	NSKMS-91	34.5	28.5	3.0	20.0	8.83	7.0	11.7	4.0	9.1
65	NSKMS48	39.0	37.8	3.5	18.5	7	6.5	8.9	3.2	5.1
66	SK-41	37.0	42.2	3.8	61.7	16.17	7.0	11.3	2.4	16.9
67	SK-11	35.0	31.4	3.2	35.3	12.17	6.8	11.0	2.6	10.0
68	SK-37	37.0	44.7	4.3	93.2	18.83	7.0	11.6	2.7	29.1
69	SKN-137	38.0	30.0	4.3	63.8	9.83	6.6	9.4	2.2	12.4
70	SKN-139	37.0	39.3	3.8	32.7	11.33	8.8	11.9	3.7	14.5
71	SKN-155	35.0	32.6	3.3	33.7	8.67	6.6	11.1	2.7	10.1
72	SKN-61	35.0	29.9	3.0	50.0	12.17	6.5	10.0	2.6	12.9
73	VKAP-39	37.0	38.0	3.8	35.5	11.67	7.1	10.9	2.8	10.7
74	ML-267 (C)	35.0	33.6	3.5	62.2	12.5	7.3	10.8	3.0	20.6
75	LGG-460 (C)	37.0	35.7	3.8	67.2	14.33	6.5	11.1	2.8	23.8
76	K-851 (C)	36.0	44.2	3.3	58.7	14.67	7.5	11.1	2.9	18.9
	General Mean	36.92	36.69	3.84	50.11	12.36	7.08	10.73	2.95	15.61
	C.D.	1.60	5.73	0.46	22.72	4.14	0.64	0.91	0.46	6.64
	CV %	4.32	15.62	11.95	45.35	33.49	9.06	8.47	15.74	42.56

Table 2 Heritability, genotypic and phenotypic variances among different quantitative traits of green gram accessions

Traits	Genetic variance (σ^2_g)	Phenotypic variance (σ^2_p)	Mean	Heritability (h^2)	GCV	PCV
Days to 50 % flowering	1.81	3.24	36.958	0.56	22.16	29.60
Plant height (cm)	31.13	34.17	36.657	0.91	92.18	96.57
Branches plant ⁻¹ (No)	0.04	0.38	3.847	0.11	10.51	31.68
Pods plant ⁻¹ (No)	144.60	878.80	49.593	0.16	169.91	418.86
Clusters plant ⁻¹ (No)	7.19	27.12	12.319	0.27	76.27	148.13
Pod length (cm)	0.29	0.60	7.0876	0.48	20.13	29.10
Seeds pod ⁻¹ (No)	0.33	1.48	10.747	0.22	17.42	37.06
100 seed weight (g)	0.14	0.29	2.9575	0.47	21.55	31.41
Seed yield plant ⁻¹ (g)	12.82	74.34	15.395	0.17	90.65	218.30

