Genetic Variability and Divergence of Morphological and Seed Quality Traits of Greengram (*Vigna radiata L.)* Genotypes

Abstract: Abstract in one long and continuous paragraph

Morpho-physiological and biochemical characterization of the mungbean germplasm will help to identify trait specific germplasm for crop improvement programme which will also be helpful for plant variety protection....

---Forty greengram genotypes were evaluated for their morphological traits and the extent of genetic variability. Analysis of variance revealed that the genotypes were highly significant for all the characters studied, indicating the existence of considerable magnitude of variability. High (>20%) phenotypic co-efficient of variation and high genotypic co-efficient of variation for seed yield (kg/4.05 m^2) in the present investigation was noticed and indicating the minimal influence of environment and presence of high genetic variability for the trait in the experimental material. Hence, selection on the basis of phenotype in these genotypes can also be effective for improvement of seed yield. High heritability to plant height (cm), days to 50% flowering, days to maturity, pod length, 100 seed weight, protein estimation and medium heritability to seed yield (kg/4.05 m^2). High GAM to plant height and seed yield demonstrates the presence of additive gene effect indicating effectiveness of selection for improvement of these traits. Mahalanobis D^2 analysis suggested the maximum contribution of seed yield (74.87%) towards genetic diversity followed by Plant height (8.08%), Days to Maturity (7.69%), Pod length (4.36%), Days to 50% flowering (3.59%), Seedling Dry Weight (0.64%), Protein Estimation (0.64%), 100 seed weight (0.13%). All 40 genotypes were grouped into 12 clusters, Cluster I was very large containing seventeen genotypes followed by cluster IV with ten genotypes. Clusters II, X and XI with two genotypes each and clusters II, III, V, VI, VII, VIII, IX and XII having single genotype each. The clustering pattern revealed that genetic diversity was associated with geographical diversity in the present research. Based on mean performances, out of the fifteen characters studied genotypes for seed yield was recorded highest in cluster II (MGG-512, MGG-519), highest number of clusters and highest number of seeds per pod was recorded in cluster X (IC-436557, MLGG-21-6), highest number of pods per cluster were recorded in cluster-III (RMP-21-11), Cluster XII (PUSA-9072) with maximum protein estimation (28.66) was found superior and may be used in the future breeding program. Conclusion and significance of this study

Keywords: *Vigna radiata*, Variability, Divergence, Cluster, Yield, Protein, Seed Quality

1.0 Introduction:

Greengram [*Vigna radiata* (L.)], an important food crop in developing countries of Africa, Asia and Latin America as it is an excellent source of high quality proteins (22-24%), essential aminoacids, vitamins and minerals (Panigrahi and Baisakh, 2013). Its wide adaptability to a varied soil conditions including light soils with tolerance to drought, ability to thrive well even under limited irrigation and short duration has enabled it to fit well in various multiple and intercropping systems.

In India about 35.79 lakh ha area was covered under greengram during 2020-21 as against 30.75 lakh ha during the same period in 2019-20 with the total production of 2.5 million tones and a productivity of 548 kg/ha. India contributes more than 70% of world's greengram production (Agricultural Market Intelligence Centre, PJTSAU, 2021).

Yield is a complex trait and highly influenced by the environment. The main cause of low yield in greengram is its indeterminate growth, non-synchronous maturity and losses due to pests and diseases. The breeding programmes in green gram mainly emphasize on yield improvement, hence knowledge of genetic variation and identifying agro-morphological traits associated with yield and their percent contribution will help in successful development of high yielding varieties.

Recombination breeding and trait manipulation are potential alternatives to develop high yielding varieties with determinate growth habit. In addition, variability estimation helps breeders to understand the genetic relationships among accessions and to select the superior accession in a more systemic and effective way (Lavanya *et al*., 2008). Genetic diversity is important for crop improvement as well as its conservation, evaluation and utilization (Anumalla *et al.,* 2015; Wang *et al*., 2015).

The highly self-pollinated nature of greengram reduces the natural variability which ultimately narrows down the effects of the selection process. But, the success of the selection programme in plant breeding depends on the magnitude of genetic variability in the population. Genetic variability and their quantification for qualitative and quantitative characters of economic importance are prerequisites for any crop improvement programme. Hence, the knowledge of variability, heritability and genetic advance become important for efficient breeding and it has great significance for the breeders in order to select the best genotypes for yield enhancement (Prasanta Kumar *et al*., 2020). To increase the productivity, there is a need to evaluate a large set of genotypes for their effective performance to cope up with the abiotic stresses prevalent in this area. Thus, current research aims at studying the greengram varieties for its genetic variability and to evaluate the performance of different genotypes.

2.0 Materials & Methods:

2.1 Description of the study area, 2.2 Research design, 2.3 Data collection procedures and 2.4 Data analysis

An experiment was carried out to study genotypic variability and divergence in greengram using 40 genotypes during Summer, 2022 at Research Farm, Seed Research and Technology Centre, Professor Jayashankar Telangana State Agricultural University, Rajendranagar, Hyderabad. Sixteen genotypes under study were received from Agricultural Research Station, Madhira and the remaining from Regional Agricultural Research Station, Warangal. Each genotype was sown in three rows of 3 m length at a spacing of 45 x 15 cm. The crop was raised by following all the crop management practices for effective varietal characterization of genotypes which was recommended for greengram.

The field experiment was laid out in Randomized Block Design (RBD) with three replications and forty treatment combinations. The average plant population was maintained as per DUS guidelines. Five healthy plants of each genotype were randomly selected in each replication and were labelled. Field observations at different crop growth stages i.e days to 50%

flowering, plant height (cm), days to 50% flowering, days to maturity, Pod length (cm), number of clusters per plant, number of pods per cluster, number of seeds per pod, field emergence, 100 seed weight (g), seed yield per plot (kg), the seed physiological traits viz., germination %, seedling vigour indices (I & II) and biochemical traits i.e., protein estimation were determined for all the forty genotypes. The data collected for the above mentioned characters were statistically analyzed using INDOSTAT.

3.0 Results and discussion:

Separate results from discussions

Analysis of variance (Table 1) revealed that all the quantitative traits *viz.*, days to 50% flowering, plant height (cm), days to maturity, pod length (cm), number of clusters per plant, number of pods per cluster, number of seeds per pod, seed yield per plot (kg), 100 seed weight (g), germination (%), field emergence (%), seedling vigour index-I, seedling vigour index-II and protein estimation showed significant variation among the forty genotypes. The results of present study are in line with those of Ramyashree *et al.* (2016), Arshad *et al.* (2006), Zafar *et al.* (2008), Reni and Rao (2013) in Soybean who observed a wide range of variability for traits under study.

Information on mean phenotypic coefficient of variation, genotypic coefficient of variation, heritability and genetic advance for these traits is furnished in Table 2. Under variability study, it was observed that the estimates of PCV was higher than GCV for all the parameters indicating the presence of environmental influence on expression of all the characters (Table 2) as earlier reported by Tyagi and Khan (2010) in Lentil. However, high (>20%) PCV and high GCV for seed yield (kg/4.05 m^2) in the present investigation was noticed which indicating the presence of high genetic variability for the trait and minimal influence of environment in the experimental material. Hence, selection on the basis of phenotype in these genotypes can also be effective for improvement of seed yield. Similar results were reported earlier by Mishra and Verma (2002) and Hasib *et al.* (2004) in Rice. The difference between PCV and GCV was very small for plant height, pod length, days to 50% flowering, days to maturity indicating greater role of genetic factors in expression of these characters and lower influence of environment indicating rapid progress from selection for these traits. These results are in accordance with Aditya *et al. (2011)* in Soybean. Plant height (cm), number of clusters per plant, seedling dry weight (mg), vigour index-II, 100 seed weight (g) showed moderate magnitudes of PCV and GCV, this suggests that there is a scope to enrich the variation for these characters as they possess high heritability coupled with GAM. High heritability to plant height (cm), days to 50% flowering, days to maturity, pod length, 100 seed weight, protein estimation and medium heritability to seed yield (kg/4.05 m^2). High GAM to plant height (cm) and seed yield (kg/4.05 m^2) specifies the presence of additive gene effect representing effectiveness of selection for improvement of these traits. Praveen kumar *et al*. (2005) recorded similar results for plant height, 100 seed weight and seed yield per plant in Soybean.

High heritability accompanied by moderate genetic advance as percent of mean was reported for pod length, days to 50% flowering, days to maturity, 100 seed weight, protein estimation indicating the role of both additive and non-additive gene effects for control of the characters. The results are in conformity with the reports of Seyoum *et al.* (2012) for plant height in Rice. High heritability accompanied by low genetic advance was reported for pod length, days to 50% flowering, days to maturity, 100 seed weight, protein estimation, seed yield (kg/4.05 m^2) suggesting the role of non additive gene action for the expression of these characters which are in agreement with the results of Aditya *et al.* (2011) in soybean. In the present study, high PCV coupled with high genetic advance as percent of mean were observed for seed yield (kg/4.05 m^2) indicating the pre-ponderance of additive gene action and therefore scope for the improvement of the trait through selection. Similar results were reported earlier by Mohana Krishna *et al.* (2009) in Rice.

The diversity studies based on the Mahalanobis D^2 values resulted considerable genetic diversity and grouped all the genotypes into twelve clusters. Cluster I was very large containing seventeen genotypes followed by cluster IV with ten genotypes. Clusters II, X and XI with two genotypes each and clusters II, III, V, VI, VII, VIII, IX and XII having single genotype each. The clustering pattern revealed that genetic diversity was associated with geographical diversity in the present research.

Similar results were reported by Lavanya *et al.* (2014), Patel *et al.* (2021), Kingsly *et al.* (2015), Divyaramakrishnan and Savithramma (2014) in greengram, Ramyshree *et al.* (2016) in Soybean.

Among all the cluster means, Cluster II recorded highest mean values for seed yield. Cluster III was recorded highest mean values for number of pods per cluster, germination. Cluster V was recorded highest mean values for seedling dry weight, seedling vigour index-II and field emergence. Seedling vigour index-I and hundred seed weight were recorded highest mean values in cluster VI. Cluster VII is having highest mean values for plant height and days to 50 percent flowering. Cluster X recorded highest mean values for number of clusters, number of seeds per pod, seedling vigour index-I. Cluster XII recorded highest mean values for pod length and protein estimation.

Out of the fifteen characters studied genotypes from Seed yield was recorded highest in cluster II (MGG-512, MGG-519), highest number of clusters and highest number of seeds per pod was recorded in cluster X (IC-436557, MLGG-21-6), highest number of pods per cluster were recorded in cluster-III (RMP-21-11), Cluster XII (PUSA-9072) was recorded maximum protein estimation (28.66).

The above results revealed that selection of genotypes having high values for particular character may be useful for the hybridization programme for the improvement of the trait. It is understandable that no other cluster consisted at least one genotype with all the desirable characters, there will be possibility of selecting directly one genotype for immediate use. Therefore, hybridization among the selected genotypes with the divergent clusters are important to obtain all the desired characters.

Hence the genotypes PUSA-9072, MLGG-21-2, IC-436557, MLGG-21-6, RMP-21-11, Gouri, MLGG-21-3, MGG-512, MGG-519 from these clusters can be directly used as parents in the hybridization programme.

The percentage contribution of each trait towards genetic divergence among the greengram genotypes was estimated and presented in Table 4. Among the characters, seed yield showed maximum contribution (74.87%) towards genetic diversity followed by Plant height (8.08%), Days to Maturity (7.69%), Pod length (4.36%), Days to 50% flowering (3.59%), Seedling Dry Weight (0.64%), Protein Estimation (0.64%), 100 seed weight (0.13%). Remaining quantitative characters such as Number of Clusters, Number of Pods per cluster, Number of seeds per pod, Germination, Vigour Index-I, vigour Index-II, Field Emergence have not shown any contribution towards diversity.

Conclusion:

It was concluded that the greengram germplasm under study exhibited a wide range of variability for most of the traits. Some genotypes possessed desirable genes for more than one character and hence could be utilized directly or included in hybridization programme for variety development suitable for southern zone of Telangana.

Missing; Recommendations and declaration of conflict of interest

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Table 1 Analysis of Variance for yield and laboratory parameters in Greengram

Sl.No.	Character	Mean Sum of Squares		
		Replicates (d.f=2)	**Treatments (d.f=39)**	**Error (d.f=78)**
1	Days to 50% flowering	1.075	42.735 ***	1.195
2	Days to maturity	2.158	43.596 ***	0.731
3	Plant height (cm)	4.322	152.421 ***	2.747
4	Pod length (cm)	0.959	1.172 ***	0.494
5	No.of clusters	1.913	2.966 ***	0.938
6	No.of pods per cluster	0.408	4.074 ***	1.203
7	No.of seeds per pod	1.570	2.542 ***	0.937
8	Seed yield (kg/4.05 m^2)	0.026	0.051 ***	0.009
9	100 Seed Weight (g)	0.131	0.701 ***	0.114
10	Germination	9.608	5.196*	3.334
11	Seedling dry weight (mg)	0.001	0.003 ***	0.001
12	Vigour Index-I	1118225.83	72360.949	101739.944
13	Vigour Index-II	16.249	26.453 ***	6.005
14	Field emergence	13.108	6.680	4.758
15	Protein estimation	1.131	16.987 ***	1.413

significant at 1% level　　*significant at 5% level　　* significant at 10 % level

Table 2 Genetic parameters for quantitative traits among greengram genotypes

S.No.	Character	Mean	Range		Std. Error (±)	PCV (%)	GCV (%)	h^2 (b) (%)	GA (%)	GAM (%)
			Min.	Max.						
1	Plant height(cm)	42.37	32.23	58.42	0.95	17.12	16.67	94.78	14.16	33.43
2	Pod length (cm)	7.85	6.64	9.68	0.40	8.16	7.86	92.92	1.22	15.61
3	No.of clusters (No.s)	8.01	5.93	9.46	0.55	15.85	10.26	41.90	1.09	13.68
4	No.of pods per cluster (No.s)	8.23	6.13	10.96	0.63	17.84	11.87	44.30	1.34	16.28
5	No.of seeds per pod (No.s)	10.41	8.40	13.00	0.55	12.74	6.11	23.05	0.63	6.05
6	Days to 50% flowering (days)	47.00	39.66	54.00	0.63	8.25	7.91	92.06	7.35	15.64
7	Days to maturity (days)	69.35	63.00	76.00	0.49	5.58	5.45	95.13	7.59	10.95
8	Germination (%)	96.18	93.00	98.33	1.05	2.20	0.58	7.00	0.30	0.31
9	Seedling dry weight(mg)	0.22	0.18	0.33	0.01	16.27	11.95	53.98	0.04	18.09
10	Vigour index-I	2238.59	1943.50	2575.13	184.15	10.987	3.44	9.81	49.71	2.22
11	Vigour index-II	22.06	18.16	32.13	1.41	16.22	11.83	53.16	3.92	17.77
12	Field emergence (%)	91.53	88.33	94.00	1.25	2.53	0.87	11.87	0.56	0.62
13	100 seed weight (g)	4.09	3.59	5.54	0.19	13.27	11.01	68.79	0.76	18.81
14	Protein estimation (%)	23.92	19.72	28.93	0.68	10.41	9.70	86.82	4.45	18.62
15	Yield (kgs)	0.40	0.17	0.76	0.05	37.26	28.87	60.00	0.24	59.05

PCV : Phenotypic coefficient of variation
GCV: Genotypic coefficient of variation
GA: Genetic Advance
GAM: Genetic advancement as percent of mean
h^2 (b) : Heritability in broad sense

Table 3 Distribution of greengram genotypes in different clusters based on analysis of morphological data

Cluster number	No.of genotypes	Name of the genotype
I	17	Janakalyani, RMP-20-10, RMP-20-14, RMP-21-9, RMP-20-11, RMP-20-12, RMP-21-7, RMP-21-8, Mdr-Local, PLM-858, IC-282136, TJM-03, RMP-21-4, RMP-21-5, RMP-20-5, MLGG-21-1, MGG-453.
II	2	MGG-512, MGG-519
III	1	RMP-21-11
IV	10	TARM-18, RMP-20-18, RMP-21-2, RMP-21-3, KM-17-129, RMP-20-1, RMP-21-17, MLGG-21-4, MGG-474, RMP-20-8.
V	1	Gouri
VI	1	MLGG-21-3
VII	1	MLGG-21-2
VIII	1	MH-521
IX	1	RMP-20-2
X	2	IC-436557, MLGG-21-6
XI	2	MGG-389, MLGG-21-9
XII	1	PUSA-9072

Table 4 Contribution of the different characters towards genetic divergence among forty greengram genotypes

S.No.	Characters	Times ranked first	Contribution (%)	Cumulative contribution (%)
1	Plant height (cm)	63	8.08	8.08
2	Pod length (cm)	34	4.36	12.44
3	No. of Clusters	0	0.00	12.44
4	No. of Pods per cluster	0	0.00	12.44
5	No. of seeds per pod	0	0.00	12.44
6	Days to 50% flowering	28	3.59	16.03
7	Days to Maturity	60	7.69	23.72
8	Germination %	0	0.00	23.72
9	Seedling Dry Weight (mg)	5	0.64	24.36
10	Vigour Index-I	0	0.00	24.36
11	vigour Index-II	0	0.00	24.36
12	Field Emergence	0	0.00	24.36
13	100 seed weight (g)	1	0.13	24.49
14	Protein Estimation (%)	5	0.64	25.13
15	Yield (kg/4.05 m^2)	584	74.87	100.00

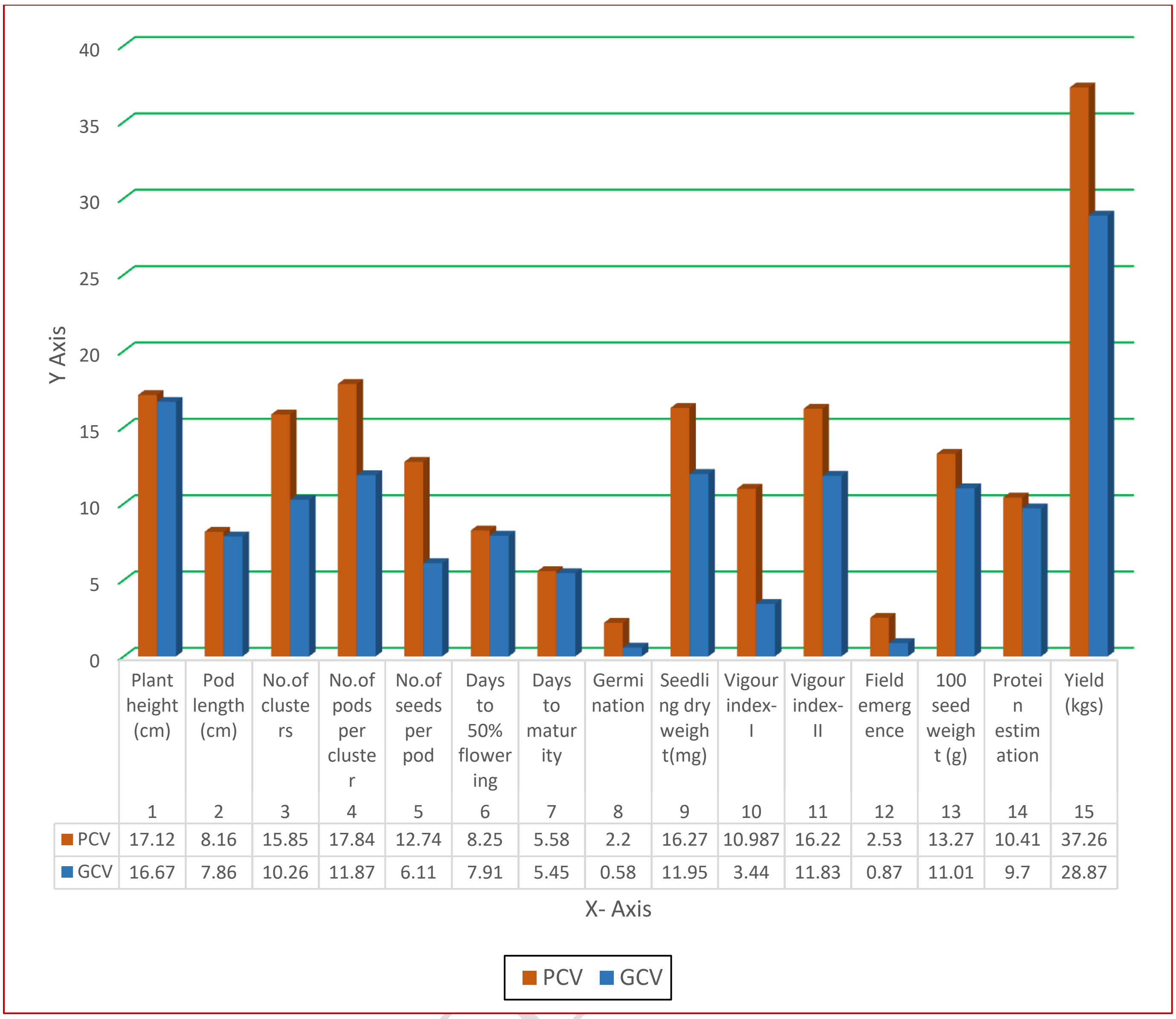

Figure 1 Graph showing the values of Phenotypic and Genotypic coefficients of variation for fifteen components in greengram.

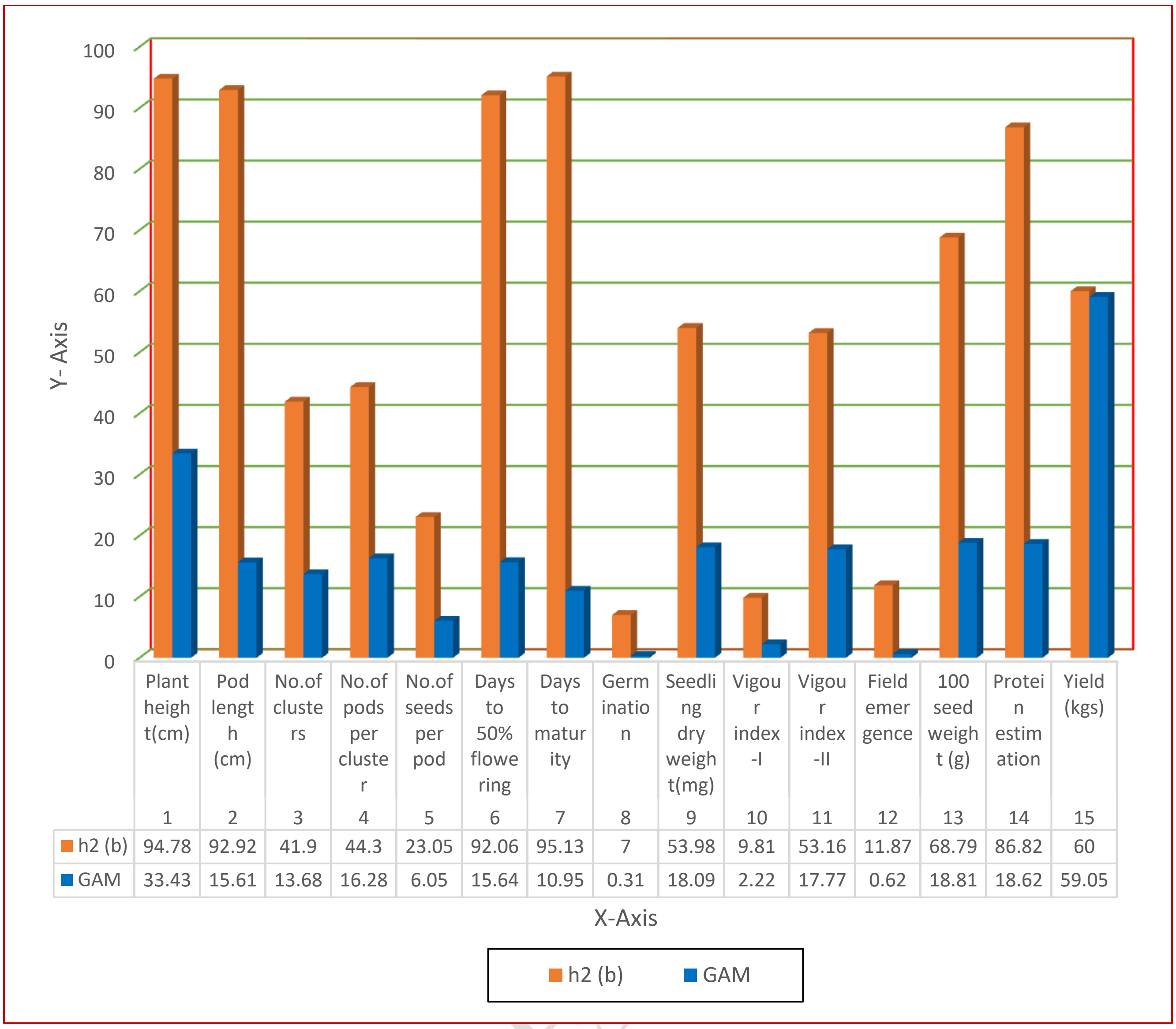

Figure 2 Graph showing the values of heritability (h^2, broad sense) and genetic advance as percent of mean (GAM) for fifteen components of greengram.