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## Research Article

### Genetic analysis of yield attributing traits in F<sub>2</sub> generation of greengram [*Vigna radiata* (L.) Wilczek]

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#### Abstract

Extensive knowledge on the variability parameters and frequency distribution of desirable traits could assist the plant breeders in formulating selection criteria for enhancing the genetic gain under selection. The F<sub>2</sub> populations of two greengram crosses viz., COGG13-39 x VGG16-058 and COGG13-39 x VGG18-002 were evaluated for nine biometrical traits during *rabi*, 2022. Magnitude of difference between PCV and GCV estimates was less than 2.50% for traits viz., pods/plant, pod length, seeds/pod and hundred seed weight in both the populations. High heritability and GAM coupled with moderate to high GCV observed for pods/cluster, pods/plant, hundred seed weight and seed yield/plant signifies the role of additive gene action. Frequency distribution results pointed out that these traits were positively skewed in both the populations. Therefore, stringent selection of segregants with desirable traits and utilizing them in yield improvement programme in greengram can be effectuated.

**Keywords:** Coefficients of variation, Frequency distribution, Genetic advance, Greengram and Heritability

#### INTRODUCTION

Population explosion and economic development has resulted in gradual shift in food consumption pattern. There is an emerging diet trend that substitutes protein rich crops over meat (Sahruzain *et al.*, 2020). For this kind, greengram (*Vigna radiata*) has become a protein alternative to animal protein source. The crop has gained significance as an affordable protein source and also its cultivation enriches soil fertility by symbiotic nitrogen fixation. However, developing a high yielding cultivar is often a challenge because of several constraints including the available variability in the breeding population. The degree of improvement relies on the variability in the breeding population. The estimates of variability helps in selection of superior genotypes from segregating generation. In addition to variability, the genetic progress is markedly influenced by the extent of heritable variation

present. Heritability extends the predictive function in plant breeding to determine the range from which a particular morphogenetic trait passes on from parent to progeny. Whereas, estimates of genetic advance reflects the gain attained by selection in a particular trait in one breeding cycle under a particular selection pressure. Assessment based on the individual sights of heritability is not credible; in turn the assessment based on both heritability and genetic advance holds significance. Therefore, an insight into the magnitude of genetic variability, the extent of heritability and genetic gain over selection is imperative to determine the progress of breeding programme. Likewise, higher order statistics viz., kurtosis and skewness helps in understanding the trait genetics by tracing out the frequency distribution pattern in F<sub>2</sub> as a reflection of variability.

## MATERIALS AND METHODS

The present investigation was carried out at the experimental farm of Department of Pulses, Centre for Plant Breeding and Genetics, Tamil Nadu Agricultural University, Coimbatore. The genetic material used for the study involved F<sub>2</sub> populations developed involving a high yielding line, COGG13-39 as female and two bold seeded donors with the test weight of >5g viz., VGG16-058 and VGG18-002 as male parents. In summer, 2022 two crosses viz., COGG13-39 x VGG16-058 and COGG13-39 x VGG18-002 were made and hybrids were evaluated during *kharif*, 2022. True hybrids were confirmed using contrasting morphological traits of the respective parents. The plants were harvested individually from each cross and forwarded to next filial generation (F<sub>2</sub>). During *rabi*, 2022, F<sub>2</sub> population of two crosses viz., COGG13-39 x VGG16-058 and COGG13-39 x VGG18-002 along with their parents were raised by adopting a spacing of 30 x 10 cm with a row length of 4 meters. All cultural practices and need based plant protection measures were followed based on the standard recommendations to maintain a healthy crop stand. Biometrical observations on nine characters recorded includes, plant height (cm), branches/plant, clusters/plant, pods/cluster, pods/ plant, pod length (cm), seeds/pod, hundred seed weight (g) and seed yield/plant (g). These observations were recorded on five random plants from the parents (COGG13-39, VGG16-058 and VGG18-002) and 76 and 81 plants in the F<sub>2</sub> populations of COGG13-39 x VGG16-058 and COGG13-39 x VGG18-002 crosses respectively.

Statistical analysis: Genetic variability parameters viz., phenotypic and genotypic coefficient of variation (PCV and GCV) for all the nine characters were estimated based on formulae of Burton, (1952). The PCV and GCV estimates were categorized as low (<10%), moderate (10-20%) and high (>20%) as per Sivasubramanian and Madhavamenon (1973). In addition, broad sense heritability in terms of the ratio of genotypic variance to total variance and other genetic advance parameters were computed in accordance to Lush, (1940) and Johnson *et al.* (1955) respectively. Based on the classifications of Johnson *et al.* (1955), heritability estimates were categorized into low (<30%), moderate (30-60%), high (>60%) and genetic advance as a per cent of mean (GAM) estimates were categorized into low (<10%), moderate (10-20%), high (>20%). To understand the distribution pattern of all the nine traits in F<sub>2</sub> population, skewness and kurtosis were computed based on reports of Snedecor and Cochran (1989) by using statistical package, SPSS version 16.0. To test the significance of skewness and kurtosis, t value was calculated by dividing the skewness and kurtosis values with the respective standard errors and compared with t-table value at n-1 degrees of freedom.

## RESULTS AND DISCUSSION

In the present study, since two F<sub>2</sub> populations were developed from high yielding female parent, COGG13-39

with two bold seeded male parents viz., VGG16-058 and VGG18-002, the mean values of hundred seed weight and seed yield/plant were duly considered. In cross I (COGG13-39 x VGG16-058), the values of seed yield/plant ranged from 10.15 g to 24.30 g and out of 76 plants in the population, 31 individual segregants surpassed the F<sub>2</sub> mean of 14.75 g. Likewise, in cross II (COGG13-39 x VGG18-002), the values of seed yield/plant ranged from 10.45 g to 38.72 g where, 32 individual segregants surpassed the F<sub>2</sub> mean of 17.95 g out of 81 plants in the population. In cross I, the values of hundred seed weight ranged from 3.00 g to 5.33 g where, 25 individual segregants surpassed the F<sub>2</sub> mean of 3.60 g. Likewise, in cross II the values of hundred seed weight ranged from 3.03 g to 5.09 g where 31 individual segregants surpassed the F<sub>2</sub> mean of 3.58 g.

Coefficients of variation: The phenotypic coefficient of variation (PCV) values were observed to be higher in magnitude when compared with genotypic coefficient of variation (GCV) values for all the nine traits examined in both the F<sub>2</sub> populations (**Table 1**). It signifies the environmental impact in the expression of traits. Meanwhile, it was ascertained that the magnitude of difference between PCV and GCV was less than 2.50% for four traits viz., pods/plant, pod length, seeds/pod and hundred seed weight in both the crosses specifying the lesser degree of environment influence on the expression of above traits. In this context, mere phenotypic selection can be duly considered. Scientific reports by Sana *et al.* (2017) have also noted narrow difference between PCV and GCV for pod length and seeds/pod in greengram.

The maximum coefficients of variation observed were 29.90% (PCV) and 28.61% (GCV) for pods/plant in cross I (COGG13-39 x VGG16-058), while in cross II (COGG13-39 x VGG18-002) were 32.47% (PCV) and 29.85% (GCV) for seed yield/plant. On the contrary, the minimum values were observed for pod length with 9.91% (PCV) and 9.65% (GCV) in cross I and 7.55% (PCV) and 7.42% (GCV) in cross II. Traits viz., pods/plant and seed yield/plant recorded high PCV and GCV (>20%) in both the crosses I and II. In addition, in cross II, plant height recorded high PCV and GCV. Magnitude of variability was found to be higher for these traits with limited environmental influence and based on the extent of heritable variation contributing to the total variability, efficient selection can be exercised. Similar results of high PCV and GCV for pods/plant and seed yield/plant was reported by Sowmini and Jayamani, (2013), Vinoth and Jayamani, (2014) in RIL population of blackgram, Garg *et al.* (2017) and Susmitha and Jayamani, (2018) in greengram. Whereas the trait branches/plant recorded high PCV and moderate GCV estimates indicating the significant environmental influence. Correspondingly, high PCV for plant height was recorded by Majhi *et al.* (2020) in F<sub>3</sub> population of greengram. Plant height in cross II and pods/cluster and hundred seed weight in

**Table 1. Mean, range, variability parameters, skewness and kurtosis for nine biometrical traits in the F<sub>2</sub> populations of two crosses**

S.No. Traits	Mean		Range		PCV (%)		GCV (%)		h <sup>2</sup> (%)		GAM (%)		Skewness		Kurtosis	
	C I	C II	C I	C II	C I	C II	C I	C II	C I	C II	C I	C II	C I	C II	C I	C II
1. Plant height (cm)	43.65	44.03	30.00 – 55.50	20.00-65.00	15.78	20.94	15.10	20.51	91.51	95.96	29.75	41.39	-0.08	0.15**	-0.96**	0.25**
2. Branches/plant	2.37	2.81	2.00-4.00	2.00-5.00	25.48	23.09	10.70	14.76	17.64	40.83	9.26	19.42	1.44**	0.76**	1.04**	1.75**
3. Clusters/plant	8.53	9.80	6.00-13.00	7.00-14.00	19.45	16.14	12.30	7.93	39.98	24.13	16.02	8.02	0.67**	0.52**	0.18**	-0.45**
4. Pods/cluster	5.06	5.45	3.67-8.33	4.00-8.00	18.32	16.95	14.77	13.65	65.03	64.87	24.54	22.65	1.36**	0.57**	2.58**	-0.22**
5. Pods/plant	36.14	45.12	18.00-71.00	26.00-88.00	29.90	27.91	28.61	27.10	91.52	94.26	56.38	54.20	0.94**	0.98**	0.88**	0.95**
6. Pod length (cm)	8.02	7.92	5.75-9.97	5.90-9.40	9.91	7.55	9.65	7.42	94.86	96.64	19.37	15.02	-0.26**	-0.24**	0.42**	0.63**
7. Seeds/pod	11.03	11.04	6.00-13.33	8.00-12.67	11.95	9.80	9.87	8.45	68.31	74.35	16.81	15.00	-1.28**	-0.95**	2.92**	0.68**
8. Hundred seed weight (g)	3.60	3.58	3.00-5.33	3.03-5.09	14.92	12.36	14.43	11.63	93.52	88.52	28.75	22.54	1.41**	1.23**	1.71**	1.65**
9. Seed yield/plant (g)	14.75	17.97	10.15-24.30	10.45-38.72	27.41	32.47	22.06	29.85	64.76	84.54	36.56	56.54	0.91**	1.22**	-0.4**	1.57**

\*\*Significance at P≤0.01. C I – Cross I (COGG13-39 x VGG16-058) C II– Cross II (COGG13-39 x VGG18-002)

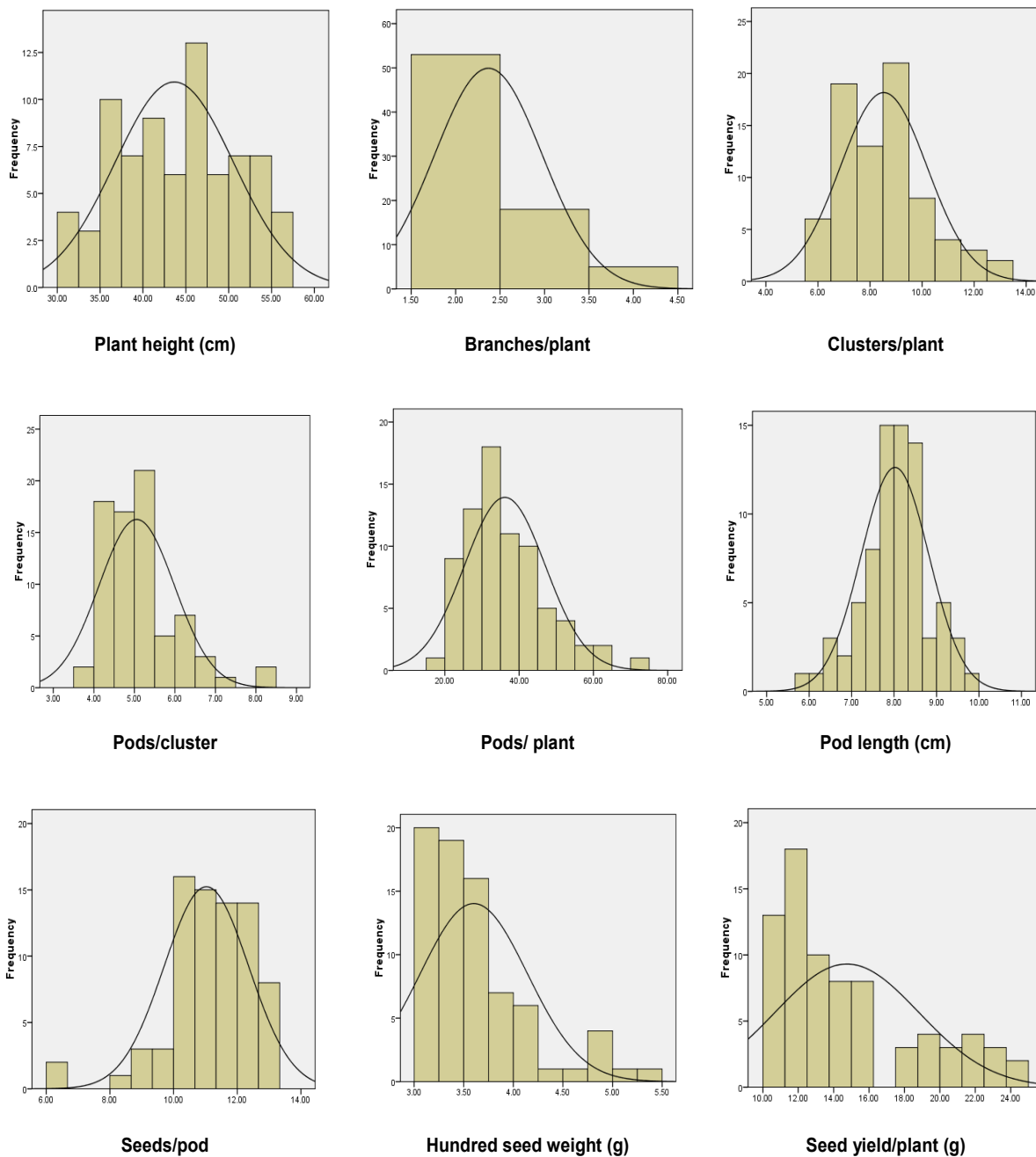
both the crosses recorded moderate PCV and GCV (10-20%). These findings were in agreement with the results of Yoseph *et al.* (2022), who observed moderate PCV and GCV for hundred seed weight in greengram. Thus, selection can be carried out based on the heritability parameters for hundred seed weight. Moreover, clusters/plant accounted for moderate PCV in both the crosses and moderate GCV in cross I and low GCV in cross II. Low PCV and GCV (<10%) estimates were observed for pod length in both the crosses. Likewise, seeds/pod recorded moderate PCV in cross I and low PCV in cross II and low GCV in both the crosses. Dhunde *et al.* (2021) also reported similar findings of low PCV and GCV for pod length and seeds/pod in greengram. In a breeding programme, the precision of a trait to be selected confides mainly on the magnitude of variations particularly GCV. In those traits with low GCV i.e., narrow range of variability, the scope of improvement by selection is confined.

Heritability and genetic advance: GCV estimates helps in figuring out only the available variability in the population. To practice selection, the prime criterion to be considered is the heritable variation that responds to selection. Heritability, being a predictive function reveals the extent to which a particular trait could be passed to successive generation. Though the highly heritable characters could be easily fixed with simple selection, heritability in a broad sense without GAM holds no practical importance. Therefore, heritability combining with genetic advance as per cent of mean (GAM) has been instrumental in determining the heritable variation with higher accuracy (Mehandi *et al.*, 2013). Broad sense heritability in cross I (COGG13-39 x VGG16-058) ranged from 17.64% (branches/plant) to 94.86% (pod length) and in cross II (COGG13-39 x VGG18-002) from 24.13% (clusters/plant) to 96.64% (pod length). GAM estimates in cross I ranged from 9.26% (no. of branches/plant) to 56.38% (pods/plant) and in cross II from 8.02% (clusters/plant) to 56.54% (seed yield/plant). In the two F<sub>2</sub> populations under study, the five traits viz., plant height, pods/cluster, pods/plant, hundred seed weight and seed yield/plant expressed high heritability coupled with high GAM substantiating the role of additive gene action. These traits also recorded moderate to high GCV. Therefore, selection for these traits can be effective. Such results of high heritability with high GAM corroborates with the findings of Sandhiya and Shanmugavel, (2018) and Bisti *et al.* (2022) for all the five traits and Garg *et al.* (2017) and Susmitha and Jayamani, (2018) for plant height and hundred seed weight and Salman *et al.* (2023) for pods/cluster, pods/plant and seed yield/plant in greengram. Though, the heritability estimates were high for pod length and seeds/pod, the GAM was moderate substantiating the role of non-fixable variation and selection is ineffective for pod length and seeds/pod. This result for pod length was in agreement with the reports of Majhi *et al.* (2020) in greengram. Inevitably, the higher heritability values were the result of environmental influence. The other two traits viz., branches/plant and clusters/plant expressed

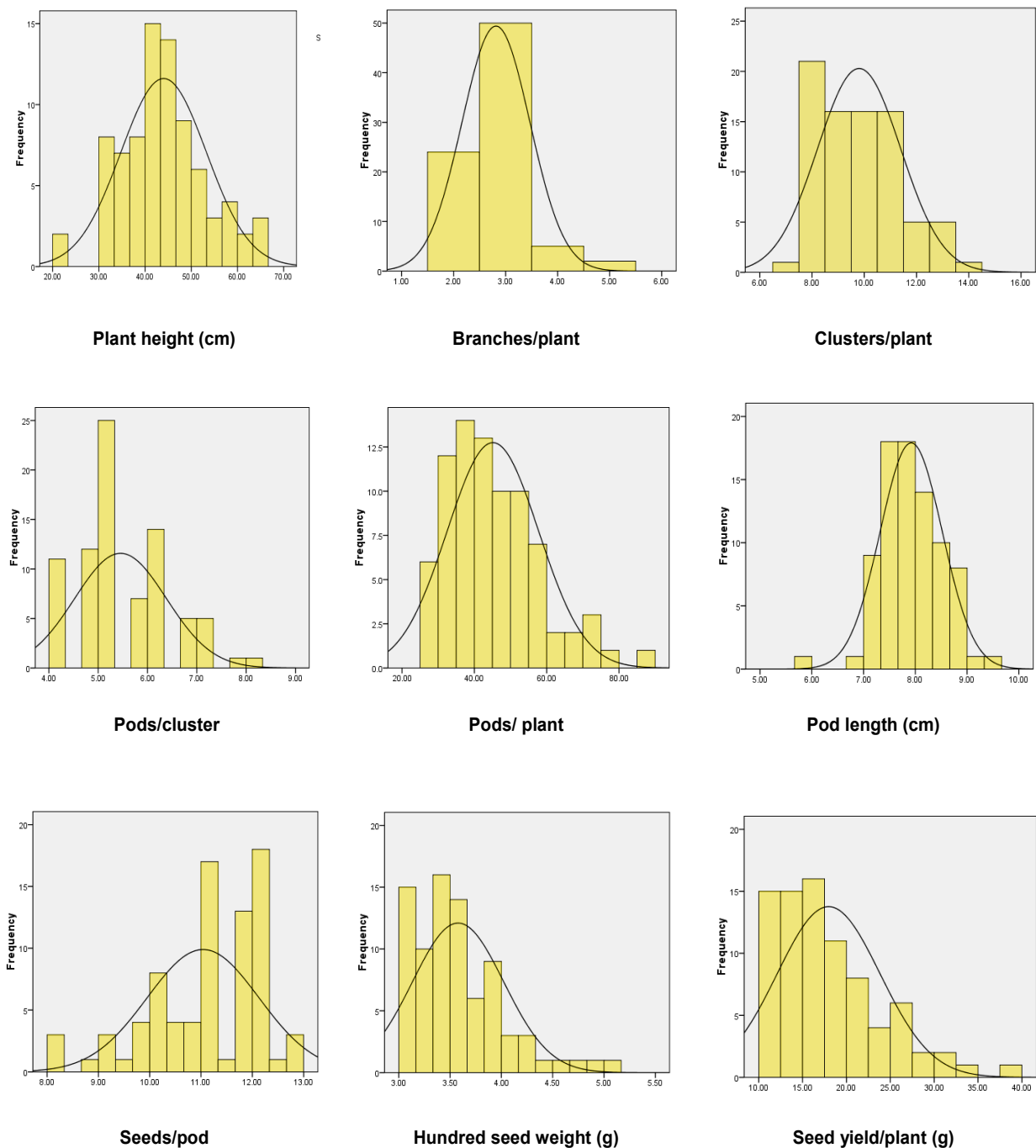
low to moderate heritability and GAM. It confronted that the traits were under the influence of non-additive gene action and selection may not be rewarding.

Frequency distribution: Nature of gene action and number of genes governing the trait can be explored by analyzing the skewness and kurtosis. Moreover, it also helps in selection of desirable segregants for the trait of interest. Frequency distribution graph of nine biometrical traits of two populations were depicted in **Fig.1 and Fig.2**. Skewness estimates in cross I (COGG13-39 x VGG16-

058) ranged from -0.08 (plant height) to 1.44 (branches/plant) and in cross II (COGG13-39 x VGG18-002) from -0.24 (pod length) to 1.23 (hundred seed weight). Significant and positive skewness was observed for traits viz., branches/plant, clusters/plant, pods/cluster, pods/plant, hundred seed weight and seed yield/plant in both the crosses and plant height only in cross II. It signifies the role of dominant and complementary gene action. The frequency distribution graph of those traits depicted that the higher frequency of segregants recorded values lesser than the mean value of the particular trait. However,



**Fig.1. Frequency distribution of nine biometrical traits in F<sub>2</sub> population of cross I: COGG 13-39 x VGG 16-058**



**Fig. 2.** Frequency distribution of nine biometrical traits in  $F_2$  population of cross II: COGG 13-39 x VGG 18-002

in both the  $F_2$  populations, among the positively skewed traits only four traits viz., pods/cluster, pods/plant, hundred seed weight and seed yield/plant recorded moderate to high GCV and high estimates of heritability and GAM. Therewith, stringent selection of segregants for the above four attributes will facilitate the population improvement. Similar findings of positive skewness were reported by Harshitha and Jayamani, (2020) for branches/plant and pods/plant and Hema *et al.* (2022) for branches/plant and

seed yield/plant in interspecific lines of greengram and Devi *et al.* (2022) for hundred seed weight and seed yield/plant in RIL population of blackgram. On the contrary, plant height in cross I, reported normal distribution with non-significant skewness. Significant and negative skewness was observed for traits viz., pod length and seeds/pod in both the crosses indicating that the pod length and seeds/pod of most of the segregants were higher than the respective mean. It signifies the role of

dominant and duplicate gene action. However, in the present population, genotypic variability was low for pod length and seeds/pod and so selection is not effective.

Kurtosis estimates in cross I (COGG13-39 x VGG16-058) ranged from -0.40 (seed yield/plant) to 2.92 (seeds/pod) and in cross II (COGG13-39 x VGG18-002) from -0.22 (pods/cluster) to 1.75 (branches/plant). Significant and leptokurtic (positive values) nature of distribution was observed for traits viz., branches/plant, pods/plant, pod length, seeds/pod and hundred seed weight in both the crosses in addition to clusters/ plant, pods/cluster in cross I and seed yield/plant in cross II. Similar findings were reported by Devi *et al.* (2022) for pod length and seeds/pod in RIL population of blackgram. Leptokurtic nature indicated the involvement of fewer genes in controlling these traits. Whereas significant and platykurtic (negative values) nature of distribution was observed for traits viz., plant height and seed yield/plant in cross I and clusters/ plant and pods/cluster in cross II. Platykurtic nature indicated the involvement of large number of genes in controlling these traits. Platykurtic nature of plant height was in consonance with the reports of Harshitha and Jayamani, (2020) in interspecific lines of greengram.

On considering the current research findings involving the two  $F_2$  populations, the traits viz., pods/cluster, pods/plant, hundred seed weight and seed yield/plant were under the influence of additive effects with discernible amount of genetic variability. Therefore, selection of these traits will be effective in enhancing the genetic gain and yield improvement. Stringent selection of segregants with desirable traits will be rewarding in the present population since the populations are positively skewed.

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