

Studies on Skewness and Kurtosis of Brinjal (Solanum melongena L.) Germplasm for Yield and its Contributing Traits

Praveen P. Yankanchi¹, Dhanalakshmi, T.N.^{2*}, Lakshmana, D.¹, Shashidhara, N.³, Prakash, K.⁴ and Onkarappa, S.⁴

¹Department of Genetics and Plant breeding, College of Horticulture, Mudigere, UAHS, Shivamogga, India ²Department of Genetics and Plant breeding, College of Horticulture, Hiriyur, UAHS, Shivamogga, India ³Department of Genetics and Plant Breeding, University of Agricultural Sciences, Dharwad, India ⁴Indian Council of Agricultural Research – Krishi Vigyan Kendra, Babbur Farm, Hiriyur, Chitradurga, India

*Corresponding author: dhanugpb@gmail.com (ORCID ID: 0000-0002-4041-422X)

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ABSTRACT

The aim of the present experiment was to investigate the phenotypic and genotypic variance among different varieties of brinjal (Solanum melongena L.), as well as three check varieties, using a randomized complete block design with two replications. The focus of the study was on yield-related traits, including fruit length, girth, and weight. The results showed that the phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) was high for these traits, with values above 20%, indicating the presence of high variability within the population. This suggests that there is significant potential for improvement through selection. Additionally, positive skewness and high values of kurtosis were observed for several traits, including several clusters per plant, days to first picking, fruit weight, fruit length, fruit girth, yield per plant, and plant height. This suggests that these traits usually are generally distributed within the population and are likely influenced by complementary gene action. Overall, this study's results suggest considerable potential for improving yield in brinjal through selective breeding efforts.

HIGHLIGHTS

- The information found from the analysis of skewness and kurtosis can be used to form a breeding program.
- Effectively identifying the dominant gene action.

Keywords: Skewness, Kurtosis, Phenotypic variance, Genotypic variance

Brinjal, also known as eggplant or Solanum melongena L., is a popular vegetable crop belonging to the Solanaceae family. It is native to India, where it is widely cultivated and considered to be the primary center of origin (Santosh et al. 2017). The Solanaceae family also includes several other important crop species, including potato, tomato, chili, and tobacco. In India, brinjal is grown in an area of 7.3 lakh hectares, with a production of 128.01 lakh tonnes and a productivity of 17.54 tonnes per hectare (NHB, 2018).

One of the critical characteristics of brinjal is alarge

amount of variability within the population, which offers the potential for producing new forms through selective breeding. Estimation of the coefficient of variation (CV) is a valuable tool for assessing the level of variability in a population. Additionally, understanding the relationship between phenotypic

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and genotypic variability parameters for various characters is essential for formulating an appropriate breeding strategy. Third and fourth-degree statistics, such as skewness and kurtosis, can provide insight into the genetics of different traits. Skewness is a measure of the asymmetry of a distribution, while kurtosis is a measure of the peakedness or flatness of the tails of a distribution.

The present study aimed to assess the phenotypic and genotypic variance among different brinjal germplasm, along with three check varieties, using a randomized complete block design with two replications. The focus of the study was on yield-related traits, including fruit length, girth, and weight. It also used skewness and kurtosis to evaluate the distribution of these traits within the population and to understand better the genetics underlying them. The aim was to identify potential avenues for improving yield in brinjal through selective breeding efforts.

MATERIALS AND METHODS

The present investigation was conducted at the College of Horticulture in Hiriyur during the kharif season of 2019-20. A total of 30 brinjal genotypes were evaluated, along with three check varieties, using a randomized complete block design (RCBD) with two replications. All recommended cultural practices were followed during the study, including proper irrigation, fertilization, and pest management. Observations were recorded for various yield-related traits, including plant height (cm), number of primary and secondary branches per plant, days to 50% flowering, number of flowers per cluster, number of clusters per plant, days first to pick, number of fruits per plant, fruit length (cm), fruit girth (cm), fruit weight (g) and fruit yield per plant (kg). All measurements were taken at the appropriate stages of plant development, and all data were recorded in a standardized format. Data analysis was performed using appropriate statistical software, and all results were subjected to appropriate statistical tests to ensure their validity and reliability.

Statistical analysis: Phenotypic and genotypic coefficient of variance was calculated using the formulae suggested by Burton De Vane (1952). Broad sense of heritability was calculated, and genetic advance and as percent over mean were

estimated by the method suggested by Johnsons *et al.* (1955).

The distribution study using skewness and kurtosis provides information about the nature of gene action (Fisher *et al.* 1932) and the number of genes controlling the traits (Robson, 1956), respectively. Skewness and kurtosis are calculated using the frequency distribution of the characters mentioned (Kapur, 1981). β 1 = Skewness and β 2 = Kurtosis

If, $\beta 1 > 0$, then positively skewed

- β 1 < 0, then negatively skewed
- $\beta 1 = 0,$

then symmetric distribution for a normal distribution, skewness is equal to zero in the absence of gene interaction; it is greater and smaller than zero in the presence of average complementary and duplicate interactions, respectively

If, $\beta 2 > 1$, then leptokurtic

- β 2 < 1, then platykurtic
- β 2 = 0, then mesokurtic

RESULTS AND DISCUSSION

The present study of skewness and kurtosis aimed at evaluating the 33 brinjal germplasm for 13 quantitative traits. The estimate of PCV was higher than GCV for all characters and is due to the interaction of genotypes with the environment. The estimate of the phenotypic coefficient of variation (PCV) was high (>20%) whereas the genotypic coefficient of variation (GCV) was high (>20%) for fruit length (30.31%), fruit girth (26.55%) and fruit weight (20.07%) indicating high variability in the genotypes used for natural selection.

The skewness values for most of the quantitative traits studied in the germplasm were between -0.5 and 0.5, except the trait "Number of clusters per plant," which had a value of 0.735, indicating a normal distribution in the population. Additionally, all the quantitative traits had kurtosis values greater than zero, indicating that the distribution of these traits had leptokurtic tails with a relatively peaked shape.

Skewness and kurtosis estimates are highly optimistic for Fruit weight (1.057) followed by the number of clusters per plant (0.735), Fruit yield per plant (0.457), days to first picking (0.445), Fruit girth (0.426), Fruit length (0.373) and Plant height (0.046)

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Sl. No.	Characters	Mean	Range		PCV			<u></u>	
			Max.	Min.	(%)	(%)	t-Statistics	Skewness	Kurto

140.			iviax.	IVIIII.	(70)	(70)			
01	Plant height (cm)	51.20	61.53	41.42	11.30	9.16	-0.133	0.046039	2.1009
02	No. of primary branches/plant	4.70	6.10	3.13	15.45	12.0	1.434	-0.15774	2.78912
03	No. of secondary branches/plant	12.22	15.24	8.10	17.18	14.20	1.377	-0.36482	2.26444
04	Days to 50 % flowering	58.69	67.50	470	9.28	7.27	2.185	-0.59896	2.78386
05	Number of flowers per cluster	2.89	4.22	1.71	21.42	17.87	-2.160	-0.037722	2.59317
06	Number of clusters per plant	6.58	9.51	4.45	19.22	17.82	-0.717	0.73575	3.28585
07	Days to first picking	85.64	102.40	73.95	8.71	6.82	0.901	0.44539	2.77388
08	Number of fruits per plant	11.29	14.77	6.17	19.57	17.11	-0.281	-0.80198	3.13263
09	Fruit length (cm)	10.64	17.59	4.45	31.36	30.31	0.470	0.37310	2.46968
10	Fruit girth (cm)	8.711	13.53	4.76	27.87	26.55	0.445	0.4267	2.29324
11	Fruit weight (g)	55.48	84.67	39.81	21.68	20.07	0.482	1.0577	3.34928
12	Fruit yield per plant (g)	593.18	796.01	454.37	18.39	15.17	-0.461	0.45725	2.0653
13	Fruit yield per hectare (t)	21.97	29.48	16.82	18.39	15.17	-0.461	0.45725	2.0653

which means that more germplasms are below the mean than expected in a normal distribution. Distribution was negatively skewed for the traits, number of fruits per plant (-0.801), days to 50% flowering (-0.598), number of secondary branches per plant (-0.364), number of primary branches per plant (-0.157) and number of flowers per cluster (-0.037) which means that more germplasms are above the mean than expected in a normal distribution. High value of kurtosis was observed for the traits like Fruit weight (3.349) followed by the number of clusters per plant (3.285), number of fruits per plant (3.132), number of primary branches per plant (2.789), days to first picking (2.773), days to 50% flowering (2.783), number of flowers per cluster (2.593), fruit length (2.469), fruit girth (2.293), number of secondary branches per plant (2.264), plant height (2.100) and yield per plant (2.06) showing leptokurtic distribution that indicates average complementary gene action.

CONCLUSION

In conclusion, this study's results suggest significant variability among different brinjal genotypes, with high values of phenotypic and genotypic coefficient of variation recorded for several yield-related traits, including a number of flowers per cluster, fruit length, fruit girth, and fruit weight. This indicates the presence of high variability within the population and suggests significant potential for improvement through selective breeding. High heritability coupled with high genetic advance as a percent of the mean was estimated for several traits, including the number of secondary branches per plant, number of flowers per cluster, number of clusters per plant, number of fruits per plant, fruit length, fruit girth, fruit weight and fruit yield per plant. This suggests that these traits are influenced by additive gene action and that direct selection could effectively improve these traits. Overall, the results of this study highlight the importance of understanding the genetics of different traits in brinjal and the patterns of gene expression within the population. Through a better understanding of these factors, it may be possible to identify key traits that can be targeted through breeding efforts in order to improve the productivity and quality of brinjal.

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