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Study of genetic variability in brinjal under Balaghat region

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Abstract

This study aimed to explore the genetic diversity among different brinjal varieties and their characteristics. Conducted at the Horticulture Department's field within the School of Agriculture Research and Technology at Sardar Patel University in Balaghat, Madhya Pradesh, during the rabi season of 2023, the experiment utilized a Randomized Block Design (RBD) featuring 20 varieties, each replicated three times. The findings indicated significant differences among the various rice genotypes for all traits assessed, as revealed by the analysis of variance. For traits such as the number of branches per plant, fruit length, total soluble solids (TSS), fruit weight, and fruit girth, moderate levels of both the Phenotypic Coefficient of Variation (PCV) and the Genotypic Coefficient of Variation (GCV) were observed. Specifically, fruit length, fruit girth, and TSS showed a moderate GCV, high heritability, and a notable genetic advance as a percentage of the mean. Conversely, the number of branches per plant exhibited a moderate GCV with moderate heritability and a significant yet moderate genetic advance. Furthermore, fruit girth also demonstrated a moderate GCV, moderate heritability, and a substantial genetic advance as a percentage of the mean. These findings indicate that these traits possess significant genetic potential and are less influenced by environmental factors, making them strong candidates for breeding selection.

Keywords: Brinjal, GCV, Genetic Advance, Heritability, PCV

Introduction

Brinjal, commonly referred to as eggplant or aubergine in French, is scientifically classified as *Solanum melongena* (L.). Aubergine or Brinjal are horticulture crop belongs to the family Solanaceae bearing chromosome number $2n=2X=24$ (Choudhary, 2013) ^[6]. It originated from India (Zeven and Zhukovsky, 1975) ^[29]. This vegetable is among the most widely cultivated and favoured crops throughout India. It serves as a significant source of vitamins, vegetable proteins, and minerals. In India, it is popularly known as baingan and holds a notable position in Ayurvedic medicine, particularly in the management of diabetes. Aubergines are frequently utilized in the preparation of pickles and stews. Their pulp and seeds are recognized for being easily digestible and act as a mild aperitif, gastric secretagogue, and blood purifier. The medicinal properties attributed to brinjal in Ayurveda make it beneficial for individuals with diabetes, and it is also recommended as a valuable treatment for liver-related ailments (Sailesh *et al.*, 2023) ^[24]. Aubergine is significant in human nutrition, as its fruit is rich in nutrients, containing approximately 6.4% carbohydrates, 1.3% protein, 0.3% fat, 0.02% calcium, 0.02% phosphorus, 0.0013% iron, and various other minerals. Additionally, it provides B-carotene (34 mg), riboflavin (0.05 mg), thiamine (0.05 mg), niacin (0.5 mg), and ascorbic acid (0.9 mg) per 100 grams of fruit (Choudhary, 2013) ^[6]. Brinjal is also a source of valuable vitamins and acts as a cholesterol-lowering agent due to the presence of polyunsaturated fatty acids (linoleic and linolenic acids), which constitute 65.1% of the pulp and seeds. The glycoalkaloid content in brinjal varies, with Indian commercial cultivars containing approximately 0.37 mg per 100 grams of fruit. In the 2021-22 period, the area dedicated to Brinjal cultivation in India was 7.62 lakh hectares, yielding 11.15 million metric tonnes. West Bengal led in both area and production of Brinjal during this period, followed by Odisha, Gujarat, and Bihar. In Uttar Pradesh, the area under Brinjal production was 6.20 lakh hectares, with an estimated production of 31.29 million metric tonnes for the same year (NHB, 2022).

The information on coefficients of variation at genotypic, phenotypic, and environmental level provides clear understanding of existing variability in a crop and relative importance of genetic and environmental components. The presence of high magnitude of variability in the germplasm or breeding materials only indicates the greater possibility of improvement through selection but the existence of high transmissibility is an important pre-requisite for realization of such possibility (Singh *et al.*, 2019) ^[25]. Effective selection occurs when there is a significant level of genetic variation among the breeding materials' individuals (Sumanth *et al.*, 2017) ^[27]. Heritability quantifies the extent to which a trait is inherited by future generations, while genetic advance illustrates the variance between the average genotypic values of the chosen group and the initial population. When heritability estimates are coupled with genetic advances, they provide a more precise prediction of the genetic progress achievable through selection compared to relying solely on heritability measurements (Demeke *et al.* 2023) ^[7]. The rising population of country demands the supply of foodgrains, vegetables and fruits for dietary need. Not standing at par to rising population (1.48 billion in 2023), high demand makes India to depend on import of grains. And the vision to become developed nation till 2047 will be a procrastinate if we don't achieve self-reliance in grain production. Therefore, it becomes a necessity to develop high yielding varieties along with stress tolerant features for which study of variability and character for yield and yield attributing traits becomes a logistic tool in field of plant breeding to serve the need. By conducting thorough evaluations, researchers can identify superior genetic traits that can withstand local challenges such as drought, pests, and diseases. This process aids in developing improved varieties tailored to Balaghat specific requirements, ensuring sustainable crop production and food security. Varietal evaluation of brinjal genotypes in the Balaghat region of Madhya Pradesh is essential due to the region's unique agro-climatic conditions, which influence crop performance. Brinjal, a heat-tolerant crop, requires region-specific genotypes that can adapt to local soil types, temperature fluctuations, and rainfall patterns for optimal yield and quality. Balaghat's climate and soil fertility vary from other regions, necessitating the identification of high-

yielding, pest- and disease-resistant varieties suitable for the area. Moreover, evaluating different genotypes can uncover varieties with improved fruit quality traits, including size, shape, color, and nutritional content, aligning with market preferences. Such evaluation also supports sustainable agricultural practices by identifying varieties with better input use efficiency and stress tolerance, thus contributing to enhanced productivity and income for farmers in the region. Ultimately, the development of region-specific brinjal varieties ensures the crop's resilience and profitability under local conditions.

Materials and Methods

The present investigation was done to understand the genetic variation, heritability among various morphological characters and varieties of brinjal suited under Balaghat region. The details of the materials used, and the procedures adopted in the investigation, which was carried out at Field of Horticulture Department, School of Agriculture Research and Technology, Sardar Patel University, Balaghat, (M.P.) during the *rabi* season of 2023. Balaghat District is located the south-eastern portion of the Satpura Range and the upper valley of the Wainganga River. The Fisher and Yates, 1963 ^[8] method was used to statistically analyse the data. Johnson *et al.*, (1955) ^[13] formulae was used to calculate GCV and PCV. Heritability (in the broad sense) was eliminated by the formula deduced by Burton and Devane (1953) ^[4]. The details of genotype used in experiment has been enlisted below in table 1. The height of five randomly selected grafted plants from each plot was measured in cm with help of a meter scale from ground level to tip of the shoot at harvest stage. The average of plant height of each replication was recorded and subjected to statistical analysis. The number of days taken from transplanting to days to 50% flowering in experimental plots was observed as days to 50% flowering. The number of days taken from transplanting to days to maturity in experimental plots was observed as days to maturity. The data were recorded, averaged, and analysed for all replications. The fresh fruit which was harvested from the plants from randomly selected five plants were measured for length individually treatment wise and replication wise, calculated, then averaged and subjected to analysis.

Table 1: Genotypes details

Sl. No.	Symbol	Varieties
1	V ₁	Kavya
2	V ₂	VNR-218
3	V ₃	Kashi Taru
4	V ₄	Sweta-12
5	V ₅	NBH-1156
6	V ₆	Ankur Sachin
7	V ₇	VNR-60
8	V ₈	Ankur-786
9	V ₉	Niranjan Baigan
10	V ₁₀	Ankur Vinayak
11	V ₁₁	Sehore Selection 1
12	V ₁₂	Punjab Nagina
13	V ₁₃	Green round
14	V ₁₄	White round
15	V ₁₅	DBL-24
16	V ₁₆	Pant Rituraj
17	V ₁₇	Kashi Komal
18	V ₁₈	Phule Harit
19	V ₁₉	Pusa Purple Long
20	V ₂₀	Kashi Sandesh (Check)

Results and Discussion

Variability refers to the presence of difference among the individuals of a population. The components of variability include phenotypic variation, genotypic variation, environmental variation, heritability, genetic advance etc. It is a known fact that genotypes within the species exhibit variation in different metric traits and components of yield. The genetic variation can only be useful for crop improvement with the help of partitioning variances. Plant breeders should be able to determine the relative importance or magnitude of genetic and environmental variances. Genetic variability is the existence of differences among individuals due to differences in their genetic composition and/or the environment in which they are raised (Allard 1960; Falconer and Mackay 1996) ^[2, 8]. Genetic variability is considered as important aspect which considered before planning for any breeding program.

Analysis of Variance

ANOVA enables researchers to assess whether significant differences exist among various genotypes or treatments and to measure the amount of variation attributable to different factors. This method compares the variability between groups (often called "treatments" or "factors") to the variability within each group. When the variability between groups is substantially greater than that within groups, it indicates that the traits under analysis significantly affect brinjal yield. ANOVA results highlight which traits contribute most to variations in grain yield, offering crucial insights for refining cultivation practices, breeding programs, and selecting the most promising genotypes to enhance overall yield and quality. An analysis of variance (table 2) was performed on the mean sum of squares data across 11 traits to structure the experiment. The findings from this analysis unveiled substantial genetic variation among the 20 brinjal genotypes, with highly significant differences ($\alpha=0.05$) detected for all traits examined. These results underscore a considerable potential for genetic enhancement in brinjal through the process of selection. These findings align with the research conducted by Tasing *et al.*, (2019) and Soumya *et al.*, (2023) ^[26, 28].

Genetic Variability Heritability and Genetic Advance

To assess genetic variability (table 3 and figure 1), several key metrics are employed: the genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), broad-sense heritability (h^2), genetic advance (GA), and genetic advance as a percentage of the mean (GAM). These parameters help quantify genetic variability and are crucial for evaluating how environmental factors influence genotype expression. By analyzing these biometric parameters, breeders can better estimate variability and make informed decisions in their selection processes, ultimately enhancing crop plants' genetic makeup for human benefit. The conservation of germplasm is vital to preserve genetic diversity in crop species. A broader genetic base in breeding materials increases the likelihood of developing crops with desirable traits. Consequently, the primary goal of germplasm conservation is to collect and safeguard this genetic variability, ensuring its availability for current and future agricultural advancements (Maurya *et al.*, 2022) ^[14]. Genetic Advance (GA) represents the expected improvement in the mean value of a trait based on selection.

Genetic Advance as a Percentage of the Mean (GAM) provides a relative measure of genetic improvement.

The Genotypic Coefficient of Variation (GCV) in the study varied significantly across traits, ranging 5.94% (days to 50% flowering) to 14.74% (number of branches per plant), suggesting a significant degree of genotype variability. Phenotypic Coefficient of Variation (PCV) in the study varied significantly across traits, ranging days to 50% flowering (6.53%) to number of branches per plant (19.82%). Traits number of branches per plant, fruit length, fruit yield per plant and fruit girth exhibited a notable disparity between their Genotypic Coefficient of Variation (GCV) and Phenotypic Coefficient of Variation (PCV) values. This suggests a significant environmental influence on these traits' expression relative to their genetic potential. Conversely, other traits displayed a smaller difference between GCV and PCV, indicating a lesser impact of environmental factors on their expression. Previous studies by Sailesh *et al.*, (2022) ^[24] have reported similar findings, confirming the substantial role of environmental factors in the phenotypic expression of certain traits.

Moderate values for both Phenotypic Coefficient of Variation (PCV) and Genotypic Coefficient of Variation (GCV) were observed for number of branches per plant, fruit length, TSS, fruit weight and fruit girth, consistent with findings reported by Pandey and Singh (2022), Sahu *et al.*, (2022) and Soumya *et al.*, (2023) ^[18, 22, 25, 26]. These results suggest significant potential for further improvement of these traits through hybridization followed by targeted selection. Genetic variability serves as the foundation upon which selection operates to enhance the genetic makeup of plants. Key indicators for direct selection, such as broad-sense heritability and genetic advance as a percentage of the mean, offer insights into the transmissibility of traits and the effectiveness of selection in improving these characteristics (Gupta *et al.*, 2022) ^[11]. Genetic variability research offers essential insights into the genetic characteristics of a population, forming the basis for developing breeding strategies to enhance the crop further. These studies are also valuable in understanding the nature and extent of variability arising from various factors, the crop's responsiveness to its environment, the heritability of traits, and the potential for genetic advancement (Chavan *et al.*, 2022) ^[5].

Environmental factors play a significant role in shaping the phenotypic expression of a genotype at various developmental stages, underscoring the importance of heritability estimates for quantitative traits in plant breeding. Heritability essentially measures the proportion of phenotypic variation attributable to genotypic differences, providing a vital tool for breeders in the selection process. When heritability is high, it indicates that the trait is predominantly controlled by genetic factors, with minimal influence from the environment. This close alignment between genotype and phenotype makes selection more straightforward and effective, as the observed traits reliably reflect the underlying genetic potential. On the other hand, traits with low heritability are more prone to environmental influences, which can obscure the genotypic effects and complicate selection efforts. Therefore, focusing on traits with high heritability can significantly enhance the efficiency and success of breeding programs. According to Panse and Sukhatme (1957) ^[19], traits with high to moderate heritability are often governed by additive gene action,

making them particularly amenable to improvement through individual plant selection.

Similar findings for high heritability in plant height, fruit girth, fruit weight, fruit yield per hectare, TSS have been reported by Soumya *et al.*, (2023) [26]. Likewise, high heritability for days to 50% flowering, fruit weight was earlier concluded by Gazala *et al.*, (2020) [10]. Days to maturity, number of fruits per plant, fruit length exhibited high heritability, with comparable results documented by Alamaet *et al.*, (2021) [1] and Pandey and Singh (2022) [18] in their studies. Additionally, traits such as the fruit yield per plant and number of branches per plant were found to have moderate heritability, consistent with the investigations of Barik *et al.*, (2021) [3].

The estimation of genetic advance enhances our comprehension of the type of gene action underlying the expression of various traits. The genetic advance ranged from 0.28 (fruit yield per plant) to 26.99 (fruit weight). Notably, traits such as the fruit yield per plant exhibited a high genetic advance (>20). Days to maturity demonstrated a moderate genetic advance (10-20), whereas remaining characters displayed a low genetic advance (<10). A high genetic advance suggests the predominance of additive gene action, while a low value points to non-additive gene action. Similar findings were reported by Prajapati *et al.*, (2021) [20]. Heritability and genetic advancement are additional crucial factors for selection. Heritability estimations aid plant breeders in identifying which traits would be beneficial for selection and the degree of transmissibility of traits of interest (Sabesan *et al.*, 2009) [21]. Breeders aim to choose superior genotypes based on their observable characteristics (Paikhombaet *et al.*, 2014) [17]. The traits that are considered for further breeding are determined based on the estimates of heritability. Heritability quantifies the extent to which a trait is inherited by future generations, while genetic advance illustrates the variance between the average genotypic values of the chosen group and the initial population. When heritability estimates are coupled with genetic advance as percent of mean, they provide a more precise prediction of the genetic progress achievable through selection compared to relying solely on heritability measurements. When high heritability is observed along with a substantial genetic advance, it suggests the influence of additive gene action whereas high heritability with low genetic advance indicates non additive gene action of the concerned traits. When there's a combination of high genetic advance and high heritability estimations, it presents

breeders with the optimal circumstances to swiftly identify and promote desirable characteristics within a population (Gupta *et al.*, 2018) [12]. Consequently, making selections based on these parameters would result in more reliable outcomes (Johnson *et al.*, 1955) [13].

In the current study, moderate genotypic coefficient of variation (GCV), coupled with high heritability and significant high genetic advance as a percentage of the mean, was observed for traits such as fruit length, fruit girth and TSS while moderate genotypic coefficient of variation (GCV), coupled with moderate heritability and significant moderate genetic advance as a percentage of the mean, was observed for traits such as number of branches per plant. Fruit girth showed moderate genotypic coefficient of variation (GCV), coupled with moderate heritability and significant high genetic advance as a percentage of the mean. These traits, governed by additive gene effects, show promising potential for improvement through direct selection. These findings align with earlier research, such as Prajapati *et al.*, (2021) [20, 23] for the fruit girth, and Saikia *et al.*, (2021) for fruit length and fruit weight. Additionally, studies by Mohanty *et al.*, (2022) [15], Sahu *et al.*, (2022) [22] provide support for similar conclusions regarding TSS, number of branches per plant further validating the results of this study.

Conclusion

The investigation concluded that the analysis of variance demonstrated significant variation among different rice genotypes for all studied traits. Moderate values for both Phenotypic Coefficient of Variation (PCV) and Genotypic Coefficient of Variation (GCV) were observed for number of branches per plant, fruit length, TSS, fruit weight and fruit girth. Moderate genotypic coefficient of variation (GCV), coupled with high heritability and significant high genetic advance as a percentage of the mean, was observed for traits such as fruit length, fruit girth and TSS while moderate genotypic coefficient of variation (GCV), coupled with moderate heritability and significant moderate genetic advance as a percentage of the mean, was observed for traits such as number of branches per plant. Fruit girth showed moderate genotypic coefficient of variation (GCV), coupled with moderate heritability and significant high genetic advance as a percentage of the mean. This indicates that these traits possess significant genetic potential and are less influenced by environmental factors, making them highly suitable for straightforward selection in breeding programs.

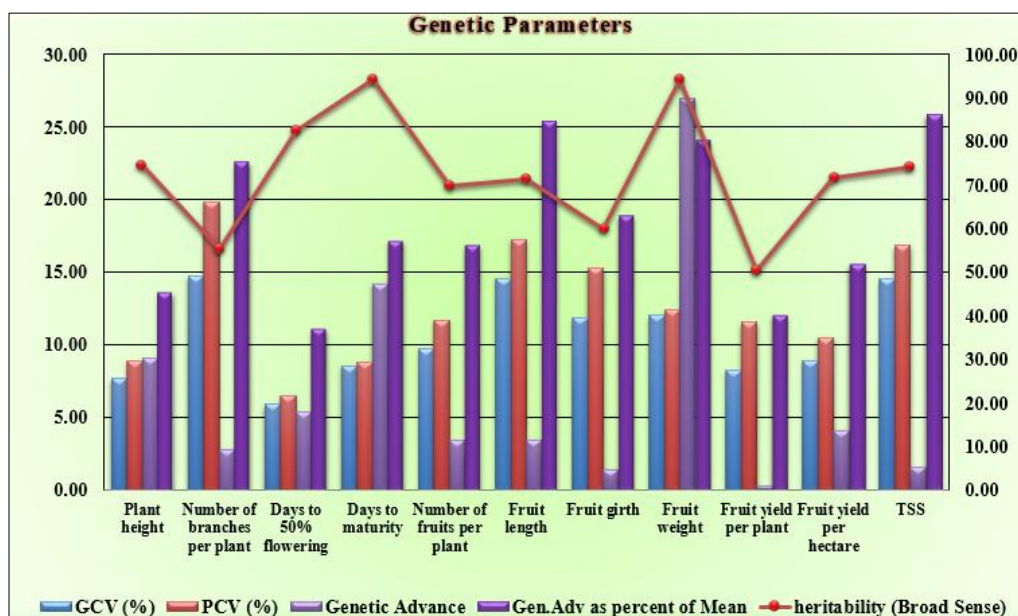
Table 2: Analysis of Variance (ANOVA) for 13 characters in brinjal

Mean Sum of Squares				
Sl. No.	Source of variation	Replication (df=2)	Varieties (df=19)	Error (df=38)
1	Plant height	13.19	86.54**	8.83
2	Number of branches per plant	6.16	12.70**	2.70
3	Days to 50% flowering	2.90	26.94*	1.77
4	Days to maturity	29.12	154.85**	3.10
5	Number of fruits per plant	4.44	13.63*	1.71
6	Fruit length	1.00	13.60*	1.60
7	Fruit girth	0.64	2.95**	0.54
8	Fruit weight	7.03	558.31**	11.38
9	Fruit yield per plant	0.10	0.14**	0.03
10	Fruit yield per hectare	0.25	18.81*	2.18
11	TSS	0.12	2.64**	0.27

*, ** at 5% and 1% level of significance respectively.

Table 3: Genetic Parameters for 11 characters of 20 brinjal varieties

Sl. No.	Characters	Range	GCV (%)	PCV (%)	h^2 (%) [broad sense]	Genetic Advance	Genetic Advance as percent of Mean (%)
1	Plant height	55.14-74.58 cm	7.66	8.87	74.58	9.05	13.63
2	Number of branches per plant	8.85-16.48 branches	14.74	19.82	55.29	2.80	22.57
3	Days to 50% flowering	43.81-55.42 days	5.94	6.53	82.58	5.42	11.12
4	Days to maturity	75.43-97.76 days	8.55	8.80	94.22	14.22	17.09
5	Number of fruits per plant	16.27-24.07 fruits	9.77	11.68	69.91	3.43	16.82
6	Fruit length	9.24-16.59 cm	14.58	17.25	71.42	3.48	25.39
7	Fruit girth	5.79-9.92 cm	11.84	15.28	60.03	1.43	18.89
8	Fruit weight	84.32-136.25 grams	12.04	12.41	94.13	26.99	24.06
9	Fruit yield per plant	1.84-2.58 kg	8.22	11.57	50.52	0.28	12.04
10	Fruit yield per hectare	23.09-30.41 tons/hectare	8.92	10.52	71.83	4.11	15.57
11	TSS	4.50-8.46 °Brix	14.53	16.87	74.21	1.57	25.79

GCV : Genotypic Coefficient of Variation**GA** : Genetic Advance**PCV** : Phenotypic Coefficient of Variation**GAM** : Genetic Advancement as percent of Mean (5%) **h^2** : Heritability (Broad sense)**Fig 1:** Histogram representing the relationship among the GCV, PCV, Heritability, Genetic Advance and Genetic Advance as percent of mean in brinjal

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