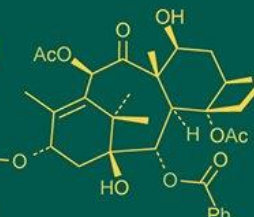
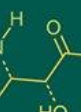
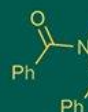
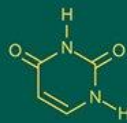
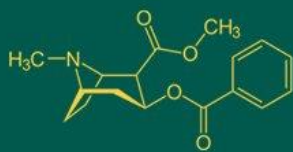


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Studies on genetic variability, heritability and genetic advance in Brinjal (*Solanum melongena* L.)

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Abstract

The current study was conducted in a Randomized Block Design with three replications at the Crop Research Center-1, School of Agriculture, ITM University Gwalior (Madhya Pradesh), during the Rabi season of 2022–2023. Fourteen quantitative characters from 18 brinjal genotypes were assessed, and it was discovered that there were substantial differences in all the features examined. All of the genotypes and characters under examination showed highly significant differences, showing that each character had a considerable level of variability. For every character analyzed, PCV estimates were greater than their matching GCV. Fruit width (41.29% and 41.2%), average fruit weight (36.44% and 35.89%), fruit production per plant (32.15% and 31.88%), flower count per cluster (31.17% and 27.93%), and days to first flowering (25.24% and 24.65%) all had high PCV and GCV values. Fruit width (83.94 and.), average fruit weight (72.80%), fruit output per plant (65.11%), number of flowers in cluster (51.57%), and days to first blossom (49.58%) were all found to have high heritability along with high genetic progress.

Keywords: Brinjal, genotype, variability, heritability and genetic advance

Introduction

Brinjal (*Solanum melongena* L.), an Indian native, is a nightshade and a member of the Solanaceae family. It is one of the most common, well-liked, and substantial vegetable crops in India and other nations across the globe. All 22 of the species of brinjal that have been identified in India belong to the comparatively large genus *Solanum*, which has a somatic chromosomal number of $2n = 2x = 24$. Given its high productivity, it is frequently referred to as the poor man's crop. In spite of the fact that heterostyly primarily self-pollinates, it has been shown to cause up to 29% of cross-pollination, which qualifies it as usually cross-pollinated or facultatively cross-pollinated.

The crop has a vast genetic variability and provides the opportunity to enhance a number of horticultural aspects. Heritability is the heritable component of a phenotypic variation. Using heritability estimates, the plant breeder can select superior genotypes from a variety of genetic subgroups. Heritability does not describe expected genetic development over the course of a selection cycle; rather, it only describes how successfully a genotype can be selected based on phenotypic performance. Heritable variation can be used more precisely and productively when heritability and genetic development are addressed jointly (Johnson *et al.*, 1955) [8]. Genetic advance, which helps breeders select offspring in the first generation, is the rise in mean genotypic values of selected families relative to the base population. To boost the yield and quality of brinjal, hybridization or the selection of genotypes with a desirable trait combination naturally occurring in nature are frequently employed techniques. The current study, which used brinjal germplasm, had this as its goal.

To produce high-yielding brinjal kinds, it is essential to fully comprehend and be aware of the following. The genetic diversity of the population, the potency of trait correlations between yield-enhancing variables, and the variety of readily available germplasm are all important. Understanding genetic diversity, the connections between traits that affect yield, and genetic divergence are necessary for designing an effective breeding program for any crop. Utilizing one of the many biometric methods developed to measure genetic divergence, genetically dissimilar parents can be separated in order to successfully carry out a hybridization plant (Uddin *et al.*, 2014) [14].

As a result, an evaluation of genetic variety is necessary to decide which genetic resources should be used in the hybridization project (Amin *et al.*, 2014) ^[1]. The large genetic diversity of the material provides better chances for obtaining different traits in the segregating generations and contributes to the improvement of the crop.

Materials and Methods

The Department of Horticulture at ITM University in Gwalior, Madhya Pradesh, conducted the current examination into the genetic variability of brinjal (*Solanum melongena* L.). The experiment was place between the rabbis of 2022 and 2023. Five check varieties and 18 genotypes total made up the experimental material. Five randomly chosen plants were examined for various traits, including days to first flowering, days to 50% flowering, days to first fruit setting, days to first fruit harvesting, number of flowers per cluster, number of fruits per cluster, average fruit weight (g), average fruit length (cm), average fruit width (cm), number of primary branches per plant, plant height (cm), and fruit yield (g/plot). According to Panse and Sukhatme (1985) ^[11], each character underwent an analysis of variance for the randomized block design (RBD). According to the formula proposed by Burton and De Vane (1952) ^[15], phenotypic co-efficient variation (PCV) and genotypic co-efficient variation (GCV) were determined. Using the formula proposed by Allard (1960) ^[2], heritability and genetic advancement were observed. Eighteen brinjal genotypes with tropical and subtropical ancestry made up the experimental components of the current studies. The list of the genotypes that were tested at the Horticulture Research Farm-I of the Department of Horticulture, ITM University Gwalior in India after being acquired from the ICAR-Indian Institute of Vegetable Research (IIVR), Varanasi, (U.P.), has been provided. In an experimental field that was repeated three times and set up in a randomized block design with 18 genotypes, each block was divided into 18 unit plots. The 18 unit plots in each block were assigned one of the eighteen genotypes. Thus, there were a total of 54 plots, each measuring 2.40 m by 1.80 m. The distances between the plants and the rows were 50 cm by 50 cm, respectively. To prevent water logging, the plots were elevated from the ground by 15 cm. The total number of plants maintained in the cultivated area is 864 plants. Each plot is divided into four rows, each of which has four plants. Applying farmyard manure (FYM) 150 q/ha and adding nitrogen, phosphate, and potash.

Results and Discussions

Analysis of variance and mean performance of genotypes

The analysis of variance was displayed in Table 1 for a number of characters. The genotype-related mean squares for each character were statistically significant. In other words, the genotypes' performances in terms of these characteristics were statistically varied, showing that there is a lot of potential for selection to improve brinjal in a number of attributes. For each of the examined characters, a very wide range of variations in genotype mean performance was found. In order to assess the given genotypes, Table 2 shows the mean of 18 genotypes, including checks for 14 characters. The following observations were made: the number of flowers per cluster, the number of fruits per

cluster, the number of fruits per plant, the fruit length (cm), the fruit width (cm), the average fruit weight (g), the plant height (cm), the number of primary branches per plant, the fruit yield per plant (g), and the total fruit yield (g/plot).

Table 2 displays the value for the coefficient of variation. The individual genotypic coefficient of variation (GCV) underperformed the phenotypic coefficient of variation (PCV) for every characteristic under investigation. Jyoti *et al.* (2019) ^[9] discovered that the fruit output per plant (74395.04-73142.61) showed the greatest range, followed by fruit width (1033.60-1020.06), average fruit weight (882.13-855.39), days to first fruit harvesting (273.43-237.45), and days to 50% flowering (188.75-181.73).

All the genotypes and characters under study showed highly significant differences, proving that each character had a considerable level of variability. For every character examined, PCV estimates were larger than their matching GCV. PCV along with GCV were highest for the phenotypic coefficient of variation was recorded in fruit width (41.29% and 41.2%) and followed by average fruit weight (36.44% and 35.89%), fruit yield per plant (32.15% and 31.88%), number of flower per cluster (31.17% and 27.93%) and days to first flowering (25.24% and 24.65%), days to first flowering (25.24% and 24.65%) days to 50% flowering (22.72% and 22.29%) fruit length (22.28% and 21.87%) and days to first fruit setting (20.87% and 20.39%) whereas, moderate estimated of GCV along with PCV was found in days to first fruit harvesting (19.1% and 17.72%), number of fruit per cluster (18.59% and 17.27%), number of fruit per plant (18.52% and 17.08%), no. of primary branches per plant (15.06% and 13.32%) and plant height (13.46% and 12.94%), Similar results were reported by Golani *et al.*, (2007) ^[7] in brinjal.

Estimates of broad sense heritability and genetic advance in per cent of mean for thirteen characters in brinjal genotypes are depicted in Table 2.

Highest estimates of heritability fruit width (98.69%), fruit yield per plant (98.32%), average fruit weight (96.97%), fruit length (96.38%), and days to 50% flowering (96.28%), days to first fruit setting (95.46%), days to first flowering (95.38%) and plant height (92.49%). However, days to first fruit harvesting (86.84%) number of fruit per cluster (86.84%), fruit length (85.38%) and number of flower per cluster (80.33%) had moderate heritability. the lowest heritability (78.15%). Tirpathi *et al.*, (2009) ^[13], Ravali *et al.*, (2017) ^[12], Divya and sharma (2018) ^[6] and Bende *et al.*, (2019) ^[4] all made similar discoveries.

The traits with the highest genetic advance in per cent of mean were fruit width (83.94%), average fruit weight (72.80%), fruit yield per plant (65.11%) and number of flowers in cluster (51.57%). Moderate gene advance was estimated for days to first flowering (49.58%), days to 50% flowering (45.05%), fruit length (44.23%), days to first fruit setting (41.05%), days to first fruit harvesting (34.01%), number of fruits per cluster (33.06%), number of fruit per plant (32.46%) and plant height (25.64%). The parameters with the lowest genetic advance in per cent of mean were number of primary branches per plant (24.25%). These findings are largely supported by the findings of Tripathi *et al.*, (2009) ^[13], Muniappan *et al.*, (2017) ^[10], Ravali *et al.*, (2017) ^[12], Divya and Sharma (2018) ^[6], Bende *et al.*, (2019) ^[4] and Balas *et al.*, (2019) ^[3].

Table 1: Analysis of variance showing mean squares for 14 characters in 18 genotypes of brinjal

Source of variation	DF	Days to first flowering	Days to 50% flowering	Days to first fruit setting	Days to first fruit harvesting	Number of flower per cluster	Number of fruit per cluster	Number of fruit per plant
Replication	2	7.57	30.57	0.72	10.91	0.30	0.033	0.52
Treatment	17	309.87**	552.20**	529.11**	748.33**	6.01**	0.786**	10.47**
Error	34	4.93	7.03	8.25	35.99	0.45	0.039	0.58
Total	53	102.84	182.78	175.03	263.53	2.23	0.279	3.75

Cont....

Source of variation	DF	Fruit length(cm)	Fruit width (cm)	Average fruit weight (g)	Plant height (cm)	No. Of primary branches per plant	Fruit yield per plant (g)	Total fruit yield (g/plot)
Replication	2	0.45	3.56	2.81	5.06	0.049	287.3	73545.7
Treatment	17	30.44**	3073.72**	2592.91**	221.46**	0.595**	220680.3**	56494146.2**
Error	34	0.38	13.54	26.74	5.84	0.051	1252.4	320621.2
Total	53	10.02	994.73	848.95	74.97	0.225	71598.5	18329220.7

Table 2: Estimation of mean, range, Phenotypic variance (PV), genotypic variance (GV), phenotypic coefficient of variance (PCV) genotypic coefficient of variance (GCV), heritability (h²), genetic advance (GA) and genetic advance as per cent of mean (GAM) for 13 characters of brinjal genotypes

Genotypes	Mean	Min.	Max.	Var (g)	Var (p)	Heritability (%)	GA	GA% mean	GCV (%)	PCV (%)
Days to first flowering	40.91	28.00	57.33	101.65	106.58	95.38	20.28	49.58	24.65	25.24
Days to 50% flowering	60.48	41.67	86.00	181.73	188.75	96.28	27.25	45.05	22.29	22.72
Days to first fruit setting	64.61	44.67	82.67	173.62	181.87	95.46	26.52	41.05	20.39	20.87
Days to first fruit harvesting	86.98	58.00	108.67	237.45	273.43	86.84	29.58	34.01	17.72	19.01
Number of flower per cluster	4.87	2.33	8.67	1.85	2.30	80.33	2.51	51.57	27.93	31.17
Number of fruit per cluster	2.89	2.20	4.27	0.25	0.29	86.30	0.95	33.06	17.27	18.59
Number of fruit per plant	10.63	6.67	13.33	3.30	3.87	85.10	3.45	32.46	17.08	18.52
Fruit length(cm)	14.48	9.23	22.13	10.02	10.40	96.38	6.40	44.23	21.87	22.28
Fruit width (cm)	77.87	19.83	152.93	1020.06	1033.60	98.69	65.36	83.94	41.02	41.29
Average fruit weight (g)	81.50	56.03	152.93	855.39	882.13	96.97	59.33	72.80	35.89	36.44
Plant height (cm)	65.50	44.33	82.00	71.87	77.71	92.49	16.80	25.64	12.94	13.46
No. of primary branches per plant	3.20	2.37	4.47	0.18	0.23	78.15	0.78	24.25	13.32	15.06
Fruit yield per plant (g)	848.45	546.13	1630.23	73142.61	74395.04	98.32	552.42	65.11	31.88	32.15

Conclusion

Based on the overall results of the study, it was concluded that there was significant room for improving brinjal cultivars through selections because there was a broad range of variance across the germplasm lines for all the traits. Genetic factors and a correlation research showed that, out of the eighteen genotypes, superior genotypes should be selected with the greatest priority. For yield Swarnamani, Kashi Taru, Kashi Utam, Punjab Barsati, and Navina from ITM University, Gwalior, (M.P.) was found to be superior, and these germplasms may be recommended for widespread cultivation among farmers after careful testing in multi-locational trials and the use of these superior genotypes in breeding programmes.

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