

RESEARCH ARTICLE

Quantitative Genetic Analysis of Yield and Associated Traits in Brinjal under Sub-Tropical Conditions of Srinagar Garhwal

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ABSTRACT

This study evaluated genetic variability, heritability, and genetic advance for yield and associated traits among 21 brinjal (*Solanum melongena* L.) genotypes under sub-tropical conditions at Srinagar Garhwal, Uttarakhand, during the summer-rainy season of 2025. The experiment was assessed in a randomized complete block design with three replications, measuring traits including plant height at 30, 60, and 90 DAT, primary and secondary branches per plant, fruit length, diameter, weight, yield per plant, total soluble solids (TSS), ascorbic acid, and ash content. Analysis of variance revealed highly significant genotypic differences across all traits, confirming substantial variability. High genotypic and phenotypic coefficient of variation were recorded for fruit weight (GCV 26.94%, PCV 26.97%), fruit length (25.03%, 27.18%), and fruit diameter (26.01%, 30.48%). High broad-sense heritability and high genetic advance as a percentage of the mean were observed in plant height at 30 DAT (93.18% h², 23.27% GA%) and secondary branches per plant (69.75% h², 21.73% GA%). Moderate values were observed for yield per plant (GCV 14.92%, PCV 27.84%, h² 28.72%, GA% 16.47%), while low values prevailed for ascorbic acid, ash content, and primary branches. Traits with high heritability and high genetic advance, particularly fruit morphology parameters, indicate predominant additive gene action, enabling effective phenotypic selection for yield improvement in brinjal breeding programs under subtropical conditions.

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INTRODUCTION

Fruits and vegetables constitute indispensable components of a balanced human diet, supplying essential vitamins, minerals, antioxidants, and dietary fiber that contribute to the prevention of chronic diseases (Slavin and Lloyd, 2012). Recent nutritional evaluations further emphasize the functional role of vegetable-derived phytochemicals in promoting metabolic and cardiovascular health. Among vegetable

crops, brinjal (*Solanum melongena* L.), commonly known as eggplant or aubergine, is valued for its nutritional richness and phytochemical composition.

Brinjal is one of the oldest domesticated vegetable crops, originating in Southeast Asia, and exhibits extensive morphological and genetic diversity. The crop shows remarkable variation in fruit shape, size, pigmentation, and plant architecture, making it an

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important model for genetic improvement studies. Modern diversity assessments have confirmed substantial variability among cultivated genotypes for yield and component traits (Perumalu Bhuvanewari *et al.*, 2023). India remains one of the largest producers of brinjal globally, with widespread cultivation across diverse agro-climatic regions. The different biological and climatic factors are accountable for decreasing the yield of eggplant in India (Singh *et al.*, 2025). However, average productivity remains below potential levels due to limited exploitation of genetic variability and vulnerability to biotic and abiotic stresses. Contemporary studies have reported significant phenotypic variability among genotypes for growth, yield, and quality attributes, emphasizing the need for systematic evaluation under field conditions (Perumalu Bhuvanewari *et al.*, 2023).

The strains of cross-pollinated crops are very valuable because they play a crucial role in the launch and development of new varieties that can survive in the present-day scenario, as well as in showing resistance against various animate and inanimate factors. So, there is a serious requirement to preserve and explore these strains through various breeding programmes. These strains provide the flexibility of a breeder to create economically and climate-resilient varieties. The magnitude of variability components defines the crop effectiveness in a breeding programme. From a plant breeding perspective, assessment of inherent parameters such as phenotypic and genotypic coefficient of variation, heritability, and genetic advance remains fundamental.

The researcher can determine the degree to which environmental (abiotic) factors impact yield and yield-related traits by assessing genotypic and phenotypic variation in yield across various crop strains (Ullah *et al.*, 2012). Heritability estimates are very useful for breeders to allocate resources effectively to identify desirable traits and to achieve the highest genetic gain in a timely and cost-effective manner (Smalley *et al.*, 2004). Traits with high heritability can be rapidly improved through simple selection. Heritability, as a genetic component, holds no practical value on its own without accompanying genetic progress. The amount of heritable genetic variation accumulated in a trait under selection pressure is referred to as genetic progress (Bello *et al.*, 2012). The coefficient of variation indicates the extent of genetic variability in various economic traits, but it does not account for

the heritable portion. Classical quantitative genetic principles (Johnson *et al.*, 1955) continue to underpin modern variability analysis, while recent empirical evaluations confirm that heritability, coupled with genetic advance, provides reliable prediction of the selection response (Pradhan *et al.*, 2024).

MATERIALS AND METHODS

The experiment was carried out at the Horticultural Research Centre, Chauras Campus, Department of Horticulture, H.N.B. Garhwal University, Srinagar (Garhwal), Uttarakhand. Twenty-one genotypes-Black Long, Green Brinjal (Round), Light Green, Long Cover Purple, Manipur Local, Odisha local-1, Odisha local-2, Rajasthan Local 1, Rajasthan Local 2, Rajasthan Local 3, Rajasthan Local 4, Rajasthan Local 5, Rajasthan Local 6, Srinagar Local, Thorny Brinjal, Tripura Local-1, Tripura Local-2, Tripura Local-3, Uttar Pradesh Local-1, Uttar Pradesh Local-2, and Pant Samrat were evaluated in a randomized complete block design (RCBD) with three replications during the summer-rainy season of 2025.

Treated seeds were sown in raised seedbeds under a polyhouse at the end of May and transplanted in the first week of July at 60 cm × 60 cm spacing. Farmyard manure (FYM) was applied at 25 t/ha during final ploughing. The recommended NPK dose (100:75:50 kg/ha) was supplied via urea, single superphosphate (SSP), and muriate of potash (MOP). Full doses of P and K, along with half of N, were incorporated before transplanting; the remaining N was top-dressed at 30 days after transplanting (DAT).

All recommended cultural practices were followed under scientific management. Observations recorded included plant height (cm) at 30, 60, and 90 DAT; number of primary and secondary branches per plant; fruit length (cm), weight (g), and diameter; yield per plant; total soluble solids (TSS, °Brix); ascorbic acid (mg/100 g); and ash content (%). Five randomly selected and tagged plants per treatment were used for data collection. Quality parameters were analyzed following Ranganna (2015).

Statistical analysis of each trait was performed using MS-Excel and OPSTAT. Genotypic and phenotypic coefficients of variation were calculated as per Johnson *et al.*, (1955); heritability, following Lush (1940); and expected genetic advance, according to Lush (1949) and Johnson *et al.*, (1955).



RESULTS AND DISCUSSION

Analysis of variance indicated significant differences in almost all the 21 genotypes for yield and yield-related traits, confirming the reliability of the experimental design. Highly significant variations were evident across growth, yield, and quality attributes. Genotypic comparisons of the 12 traits revealed substantial differences, indicating strong potential for selection. Table 1 summarizes variability metrics: GCV, PCV, heritability, and genetic advance, expressed as a percentage of the mean. Genotypic coefficient of variation was high (>20%) for fruit weight (26.94%), fruit length (25.03%), and fruit diameter (26.01%), consistent with findings by Barik *et al.*, (2021) and Shilpa *et al.*, (2018) in brinjal. Moderate GCV (10-20%) occurred for yield per plant (14.92%), secondary branches per plant (12.63%), plant height at 30 DAT (11.70%), and TSS (11.07%), aligning with Chaudhary *et al.* (2023). GCV remained low (<10%) for ascorbic acid (8.48%), ash content (7.34%), primary branches per plant (4.04%), plant height at 60 DAT (3.74%), and plant height at 90 DAT (4.64%). Similar findings were also reported by Thomas *et al.*, (2022),

Chaudhary *et al.*, (2023), and Sangam *et al.*, (2020). Such patterns indicate strong genetic control for fruit traits and greater environmental influence on growth parameters in brinjal.

High phenotypic coefficient of variation (PCV >20%) was observed for fruit diameter (30.48%), yield per plant (27.84%), fruit length (27.18%), fruit weight (26.97%), TSS (24.20%), and ascorbic acid (22.63%), consistent with findings by Chaudhary *et al.* (2023). Moderate PCV (10-20%) characterized secondary branches per plant (15.12%), primary branches per plant (13.35%), plant height at 30 DAT (12.12%), and ash content (11.14%), aligning with results from Shruti *et al.*, (2019) and Mishra *et al.*, (2024). Low PCV (<10%) was observed for plant height at 60 DAT (5.01%) and 90 DAT (5.36%), similar observations were also recorded by Tripathi *et al.*, (2025).

Heritability estimates indicate the proportion of observed phenotypic variation attributable to additive genetic effects. Following the classification by Johnson *et al.*, (1955), heritability values are deemed low (<30%), moderate (30-60%), or high (>60%), a framework applied in this study. High heritability was

Table 1: Genetic variability parameters for different characters in brinjal genotypes

Sr. No.	Characters	Genotypic Coefficient of Variations (%)	Phenotypic Coefficient of Variations (%)	Heritability (%)	Genetic Advance	Genetic Advance value % means
1	Plant Height (30 DAT)	11.704	12.125	93.188	6.748	23.275
2	Plant Height (60 DAT)	3.746	5.011	55.877	4.116	5.768
3	Plant Height (90 DAT)	4.646	5.369	74.887	6.472	8.283
4	Number of primary branches/plants	4.043	13.357	9.163	0.156	2.521
5	Number of secondary branches/plants	12.633	15.126	69.757	2.654	21.736
6	Fruit weight (g)	26.945	26.972	99.803	59.207	55.453
7	Fruit diameter (cm)	26.011	30.481	72.821	2.599	45.725
8	Fruit Length (cm)	25.035	27.185	84.803	4.968	47.491
9	Total soluble solids (°Brix)	11.017	24.205	20.715	0.346	10.329
10	Ascorbic acid (mg/100g)	8.488	22.637	14.058	0.219	6.556
11	Ash content (%)	7.342	11.148	43.373	1.14	9.961
12	Yield per plant (kg)	14.921	27.841	28.724	0.132	16.474

observed for fruit weight (99.80%), plant height at 30 DAT (93.18%), fruit length (84.80%), plant height at 90 DAT (74.88%), fruit diameter (72.82%), and secondary branches per plant (69.75%), consistent with findings by Shruti *et al.*, (2019). Moderate heritability was observed for plant height at 60 DAT (55.87%) and ash content (43.37%), aligning with reports by Rameshkumar *et al.*, (2022). Low heritability was observed for yield per plant (28.72%), TSS (20.71%), ascorbic acid (14.05%), and primary branches per plant (9.16%), corroborating results from Vankalas *et al.*, (2024) and Shruti *et al.*, (2019).

Genetic advance represents expected genetic improvement from selection and relies directly on a population's genetic variability, whereas genetic advance expressed as a percentage of the mean provides an estimate of anticipated progress. Johnson *et al.*, (1955) classified genetic advance as a percentage of the mean into low (<10%), moderate (10-20%), and high (>20%) categories. Genetic advance as a percent of mean was high (>20%) for fruit weight (55.45%), fruit length (47.49%), fruit diameter (45.72%), plant height at 30 DAT (23.27%), and secondary branches per plant (21.73%), consistent with findings by Shruti *et al.*, (2019), Siva *et al.*, (2020) and Kuswaha *et al.*, (2023). Moderate genetic advance (10-20%) occurred for yield per plant (16.47%) and TSS (10.32%), aligning with Shruti *et al.* (2019) and Kuswaha *et al.* (2023). Low genetic advance (<10%) was observed for ash content (9.96%), plant height at 90 DAT (8.28%), ascorbic acid (6.55%), plant height at 60 DAT (5.76%), and primary branches per plant (2.52%), matching Kuswaha *et al.*, (2023). High genetic advance as a percentage of the mean (59.20%) was observed for fruit weight, consistent with findings from Kuswaha *et al.*, (2023). In contrast, low genetic advance (<10%) prevailed for plant height at 30 DAT (6.74%), 60 DAT (4.11%), and 90 DAT (6.47%), along with fruit length (4.96%), fruit diameter (2.59%), secondary branches per plant (2.65%), primary branches per plant (0.15%), ash content (1.14%), TSS (0.34%), ascorbic acid (0.21%), and yield per plant (0.13%), corroborating reports by Shah *et al.*, (2024) and Vasa *et al.*, (2025). Evaluating both heritability and genetic advance enhances the reliability of selection in brinjal breeding. When high heritability coincides with high genetic advance, it signals dominant additive gene effects, ideal for efficient selection. Conversely, low values of both suggest heavy environmental influence,

making selection unreliable; high heritability paired with low genetic advance (from non-additive effects) may deceive initial decisions; and low heritability with high genetic advance indicates environmental effects overriding additive gene action. Traits with high heritability often show considerable genetic progress, making them top priorities for selection.

CONCLUSION

Substantial variability was observed in brinjal for morphological, yield, and quality traits. High genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability, and genetic advance as a percentage of the mean were observed for key traits such as fruit weight, fruit length, fruit diameter, plant height at 30 DAT, and secondary branches per plant. Moderate levels were observed in yield per plant, TSS, plant height at 60 DAT, and ash content, whereas low values were observed for ascorbic acid, primary branches per plant, and plant height at later stages. Consequently, direct selection on fruit traits will effectively improve high-yielding genotypes, whereas indirect selection is recommended for traits with low heritability.

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Conflict of Interests

There is no conflict of interest disclosed by the authors.

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Ethics Statement

This study did not require ethical approval because it did not contain sensitive data, animal subjects, or human volunteers.

Originality and Plagiarism

The authors confirm that this work is original, hasn't been published anywhere, and isn't being reviewed by any other journal. Every relevant work has been properly cited.

Consent for Publication

The final manuscript has been reviewed and approved by all writers, who also grant permission for publication.

Competing Interests

There are no conflicting interests disclosed by the authors.

Data Availability

The accompanying author can provide the data that supports the study's conclusions upon reasonable request.

Author Contributions

This manuscript's inception, technique, analysis, and writing were all equally contributed by each author. The final version was examined and approved by all authors.

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