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GENETIC VARIABILITY FOR YIELD AND ASSOCIATED TRAITS IN BRINJAL (*Solanum melongena* L.)

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ABSTRACT

This investigation evaluates the genetic architecture of twenty-one brinjal (*Solanum melongena* L.) genotypes to identify high-yielding germplasm optimized for India's semi-arid subtropical zones. Conducted during the 2025–2026 crop season in Gwalior, Madhya Pradesh, the study utilized a randomized block design to assess nine quantitative traits. Analysis of Variance revealed significant genetic diversity across all attributes, providing a substantial basis for selection. Minimal disparity between phenotypic and genotypic coefficients of variation for fruit weight and total yield indicated low environmental sensitivity, suggesting high selection reliability. Exceptional broad-sense heritability was recorded for average fruit weight (93.81%) and fruit diameter (90.23%), which, combined with strong genetic advance, underscores the predominance of additive gene action. Among the evaluated entries, genotypes 'Swapnamani' (38.93 t/ha) and 'Kashi Green Round' (35.20 t/ha) emerged as the most productive, while 'Arka Kusumakar' demonstrated significant phenological earliness. Path coefficient analysis pinpointed single fruit weight and fruit length as primary direct contributors to productivity. These findings provide a clear genetic roadmap for developing stable, high-yielding brinjal cultivars specifically tailored to the agroclimatic challenges of Central India.

Keywords: Brinjal, Central India, Genetic diversity, Heritability, Path coefficient matrix.

Introduction

Eggplant (*Solanum melongena* L.), frequently recognized as an essential and highly versatile vegetable crop, plays a monumental role in ensuring food security and economic sustainability across Southern and Eastern Asia. Belonging to the Solanaceae family (2n=24), it is globally valued for a robust nutritional profile rich in dietary fiber, vitamins, and essential minerals (Daunay and Hazra, 2012; Sujin *et al.* 2017). The crop remains a cornerstone of India's economic stability and food security due to its accessibility for small-scale farmers, and its ease of cultivation and marketability provide a sustainable basis for rural livelihoods. Historically, Vavilov (1928) identified the Indo-Burmese region as the primary center of diversity, while De Candolle (1886) recognized India as the species' geographical place of origin.

Currently, global brinjal cultivation occupies approximately 2.0 million hectares, with a total production of 60–62 million tons, yielding a worldwide productivity of 30–32 t/ha. Within this context, India maintains its status as the world's second-largest producer, accounting for over 25% of global output. National data from the NHB Ministry of Agriculture (2023-24) indicates that the crop is cultivated on 7.0 lakh hectares, yielding 130 lakh tons annually with a mean productivity of 19 t/ha. While West Bengal continues to be the leading producer in the country, Madhya Pradesh has emerged as a high-performance region, contributing 67,500 hectares and 14.3 lakh tons to the total national production (Department of Horticulture and Food Processing, MP, 2024). Notably, Madhya Pradesh sustains a superior productivity level of 21.2 t/ha.

Despite these vast production areas and high regional performance, the complex polygenic nature of yield continues to challenge breeders in closing the gap between actual and potential genetic output (Yadav *et al.* 2022). The literature is conflicting regarding optimal selection criteria for yield enhancement. Some studies prioritize reproductive efficiency and fruit dimensions, whereas Chauhan *et al.* (2019) and Singh *et al.* (2020) emphasize vegetative traits such as plant height and primary branching. Consequently, as suggested by Tiwari *et al.* (2016), morphological characterization is a vital step in identifying divergent parents and resolving these discrepancies. Effective selection requires partitioning total phenotypic variation into heritable (genotypic) and non-heritable (environmental) components. Johnson *et al.* (1955) established that heritability estimates, when analysed alongside genetic advance, provide a comprehensive understanding of selection potential. Furthermore, Verma *et al.* (2023) indicated that fruit count and average weight are largely governed by additive gene action, making them ideal targets for phenotypic improvement.

Recent published work from the past 5 to 10 years demonstrates that the primary research gaps in brinjal genetic variability are fundamentally less about validating whether genetic variation exists and more about how effectively that variation is captured, statistically validated, and translated into actual progress in breeding selection. Current diversity literature is heavily saturated with basic phenotypic and field-based morphological surveys that stop at estimating general biometrical indices like PCV, GCV, heritability, and genetic advance. A major gap persists because these studies rarely validate whether the identified traits remain structurally stable across environments or truly yield long-term breeding gains without multi-location testing or molecular integration. This limitation is highly critical in volatile, semi-arid subtropical corridors like the Gwalior-Chambal grid zone of Central India, where rapid climatic shifts alter gene expression. Because localized path direct effects remain underexplored against environmental noise in routine screening pipelines, executing a targeted baseline assessment of diverse germplasm sets becomes an essential pre-breeding step to filter out non-genetic variance and establish a functional roadmap for regional cultivar development before expansive breeding programs are deployed.

During the Kharif-Rabi season of 2024–2025, the present study was conducted at the Crop Research Centre-3 (C.R.C.-3), ITM University, Gwalior (M.P.), to evaluate the genetic architecture of twenty-one

diverse brinjal genotypes, including elite lines such as Swapnamani and Kashi Green Round. The primary objective was to quantify genetic gain, heritability, and genetic divergence across nine quantitative variables alongside detailed qualitative profiles. The findings identify high-yielding genotypes and establish a clear genetic roadmap for developing stable, high-yielding brinjal cultivars optimized for the specific agroclimatic conditions of Central India.

Materials and Methods

Site of experiment

The field trial was executed during the Kharif-Rabi cropping season of 2024–2025 at the Crop Research Centre-3 (C.R.C.-3), ITM University, Gwalior, Madhya Pradesh, India. The site falls within the Madhya Pradesh Grid Zone, characterized by a semi-arid subtropical climate. Although the optimal temperature threshold for eggplant (*Solanum melongena* L.) ranges between 18°C and 25°C, the experimental period experienced transitional environmental shifts from a humid monsoon phase into a dry winter cycle. As validated by Yadav *et al.* (2021), such fluctuating conditions offer a rigorous yet ideal setting for evaluating the phenotypic expression and stability of complex quantitative traits. The soil was a well-drained sandy loam with a neutral pH, satisfying the standard edaphic requirements for solanaceous cultivation.

Experimental materials, design, and procedures

The genetic pool comprised twenty-one diverse genotypes of eggplant (*Solanum melongena* L.) Arka Kusumakar, Arka Nidhi, Arka Keshav, Arka Avinash, Arka Anand, Pusa Anupam, Pusa Purple Long (PPL), Kashi Uttam, Kashi Green Round, Pant Rituraj, Mukta Moti, Navina, Neelkanth, Neelam, BSS-332, Brinjal Bhima, BR-112, Swapnamani, G. Local-1, G. Local-2, and Wild Thorny (wild relative). This germplasm was sourced from premier national research institutes and markets, including IIHR, IIVR, GBPAUT, private enterprises, and local collections.

Following Panse and Sukhatme (1967), the trial used a Randomized Block Design (RBD) with three replications, establishing sixty-three experimental plots to minimize soil heterogeneity and ensure statistical precision. Healthy seedlings were raised in a managed nursery under standard protocols. Uniform 30-day-old seedlings were transplanted at a standardized spacing of 80cm x 80cm. Recommended agronomic management was uniformly applied, including standard irrigation and organic fertilization via FYM @ 25 t/ha. Manual weeding and hoeing were performed at 25 and 45 days post-transplanting. Plant

protection focused on managing the eggplant shoot and fruit borer (*Leucinodes orbonalis*), targeted field applications of neem oil.

Data recorded

In each replication, five plants per genotype were randomly selected and tagged to maintain sampling consistency. Precise data were recorded for nine quantitative traits alongside qualitative markers. Plant height (cm) was measured from ground level to the main stem apex at final harvest using a linear scale, while the number of primary branches per plant was counted during peak vegetative growth. Days to 50% flowering were recorded when half of the plants within a plot achieved anthesis, while days to first fruit harvest were calculated as the duration from transplanting to the first marketable picking, adhering to IBPGR eggplant descriptors (IBPGR, 1990). Individual fruit length (cm) and fruit diameter (cm) were recorded at the maximum point and from the calyx base to the blossom scar, respectively, using a digital Vernier calliper. Average fruit weight (g) was computed by dividing the total marketable fruit mass by the total number of fruits harvested per plant. Productivity was evaluated using the mean number of fruits per plant and total fruit yield (t/ha), extrapolated from plot-wise data. Qualitative Visual screening during peak fruiting characterized variations in corolla pigmentation, fruit colour, and fruit shape (globular, ovoid, or cylindrical). Leaf colour and the presence or absence of spines on the calyx and leaf surfaces were also documented to complete the morphological profile.

Statistical analysis

The relative performance of the genotypes was evaluated through rigorous biometric analysis. Raw observations organized in MS Excel were processed for genetic and multivariate estimations via the OPSTAT software platform developed by Sheoran *et al.* (1998). Data variance was analysed according to the RBD methodology of Panse and Sukhatme (1967), applying the Critical Difference (CD/LSD) test at a 5% probability threshold to determine mean differences.

The amplitude of genetic diversity was quantified via genotypic and phenotypic coefficients of variation (GCV and PCV). Broad-sense heritability (h^2_{bs}) and genetic advance (GA) as a percentage of the mean were computed following Johnson *et al.* (1955) to identify traits governed by additive gene action. Qualitative profiling followed the diagnostic principles of Tiwari *et al.* (2016) to categorize divergent lines. Multivariate clustering was executed via Mahalanobis D^2 statistics to group genotypes based on genetic

distance, a technique essential for identifying parent combinations that optimize heterosis (Cericola *et al.* 2013). Inter-trait dynamics were determined using genotypic and phenotypic correlation coefficients according to Al-Jibouri *et al.* (1958). These broad matrices were subsequently partitioned into direct and indirect path influences via path coefficient analysis following Dewey and Lu (1959) to map the exact cause-and-effect pathways driving net eggplant yield

Results

Biometric evaluation was executed on the field data covering nine quantitative traits alongside qualitative attributes across twenty-one eggplant genotypes. The experimental findings were systematically categorized based on mean performance, structural genetic variability, and trait character associations.

Analysis of Variance (ANOVA)

Statistical variance mapping revealed highly significant differences ($p < 0.01$) for all nine quantitative parameters evaluated among the twenty-one genotypes. This verifies the presence of an expansive pool of genetic variability within the experimental material covering vegetative growth, phenological stages, and productivity components (Tiwari *et al.* 2016, Cericola *et al.* 2013). The high magnitude of the genotypic Mean Sum of Squares (MSS) relative to the Error MSS demonstrates superior estimation precision, verifying that the physical differences were heavily driven by genetic factors rather than environmental error. These metrics validate the statistical rules of Panse and Sukhatme (1967), which assert that a significant ANOVA is mandatory before computing downstream variability factors like GCV, heritability, and genetic advance to formulate selection criteria.

Table 1 : Analysis of Variance (ANOVA) for Quantitative Traits in Brinjal.

Characters	Replication (df=2)	Treatment (df=20)	Error (df=40)
Days to 50% flowering	1.68	164.74**	9.57
Days to first harvest	97.63	292.12**	20.12
Plant height (cm)	7.66	166.61**	11.22
Fruit length (cm)	4.95	46.37**	2.05
Fruit diameter (cm)	0.19	26.47**	0.92
No. of fruit/plant	3.73	24.40**	4.10
No. of primary branches/plant	5.76	5.12**	1.49
Yield per plant (kg)	0.09	1.32**	0.06
Total yield (t/ha)	9.53	132.59**	6.90

** indicates significance at $p < 0.01$ level

Morphological and Qualitative Characterization of Genotypes

Initial morphological screening revealed substantial visible phenotypic diversity among the genotypes, completely aligning with the standard eggplant descriptors established by the IBPGR (1990). Documenting this qualitative polymorphism remains essential, as phenotypic variations in fruit color intensity and structural growth habits heavily dictate consumer preferences and market demand within regional trading hubs. The field evaluations demonstrated a wide spectrum of variance for growth habits and fruit pigmentation patterns, confirming the assertions of Mohandass and Anees (2014) that morphological characterization serves as a vital baseline step for identifying elite parental lines in breeding programs.

Furthermore, variations in fruit geometry and calyx spine density notably prominent in genotypes 'Swapnamani' and 'Kashi Green Round' agree with the diversity assessments of Rekha and Khan (2015) aimed at preserving germplasm distinctiveness. This structural classification creates the groundwork necessary to resolve conflicting selection criteria, a concept validated by Babu and Patil (2013) under semi-arid agroclimatic conditions. Additionally, grouping these lines based on corolla pigmentation shades and foliar coloration gradients reflects the systematic descriptor models suggested by Islam *et al.* (2014), ensuring that the genetic identity of each accession is accurately archived for future hybridization pipelines.

Table 2 : Qualitative phenotypic traits and distribution among 21 eggplant genotypes.

Character	Category	Encompassed Genotypes
Fruit Color	Purple/Violet (16)	BR-112, Arka Avinash, Pant Rituraj, Mukta Moti, Neelkanth, Arka Keshav, Arka Nidhi, Arka Anand, Pusa Anupam, Pusa Purple Long, Neelam, Arka Kusumakar, Brinjal Bhima, Navina, Swapnamani, BSS-332.
	Green (5)	Kashi Green Round, G-Local-1, G-Local-2, Wild Thorny, Kashi Uttam.
Growth Habit	Semi-erect (12)	BR-112, Swapnamani, Pusa Anupam, Pant Rituraj, Mukta Moti, Kashi Uttam, Neelkanth, Pusa Purple Long, Arka Kusumakar, Neelam, Navina, BSS-332.
	Erect (5)	Arka Avinash, Arka Anand, Arka Nidhi, Arka Keshav, Brinjal Bhima.
	Spreading (4)	Wild Thorny, G-Local-1, G-Local-2, Kashi Green Round (Semi-spreading).
Flower Color	Light Purple (16)	BR-112, Swapnamani, Pusa Anupam, Pant Rituraj, Mukta Moti, Kashi Uttam, Neelkanth, Arka Kusumakar, Kashi Green Round, Arka Avinash, Arka Nidhi, Arka Anand, Neelam, Brinjal
	White (3)	Bhima, Navina, BSS-332.
	Dark Purple (2)	Arka Keshav, G-Local-1, G-Local-2, Wild Thorny, Pusa Purple Long.
Spines	Present (7)	BR-112, Swapnamani, Pant Rituraj, Pusa Purple Long, G-Local-1, Wild Thorny, G-Local-2.
	Absent (14)	Arka Avinash, Pusa Anupam, Brinjal Bhima, Mukta Moti, Arka Keshav, Kashi Uttam, Neelkanth, Arka Kusumakar, Kashi Green Round, Arka Nidhi, Neelam, Navina, Arka Anand, BSS-332.

Mean Performance of Genotypes for Yield and Yield Contributing Traits

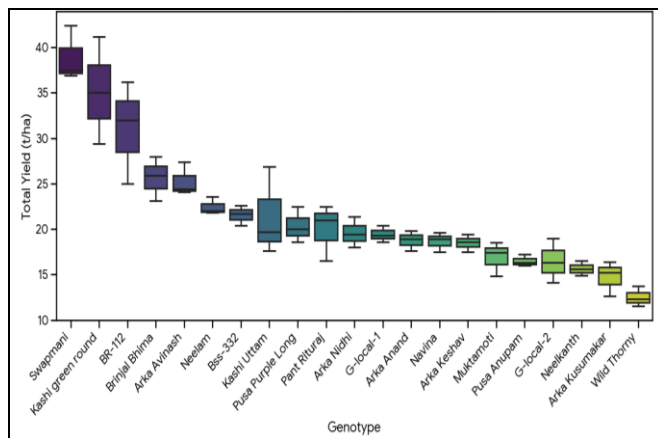
The evaluated eggplant germplasm demonstrated substantial variation in mean performance across the recorded quantitative traits, verifying a highly diverse genetic architecture. The primary economic trait, total fruit yield (t/ha), exhibited an expansive distribution ranging from 12.50 to 38.93 t/ha. Cultivar Swapnamani recorded the maximum significant yield of 38.93 t/ha, appearing statistically at par with Kashi Green Round (35.20 t/ha) and 'BR-112' (31.06 t/ha). Following Vaddoria *et al.* (2011), this superior productivity is heavily driven by a synergistic balance between individual fruit mass and the net number of fruits harvested per plant. Regarding vegetative structural

vigour, genotype Wild Thorny exhibited peak values, with plant height reaching 83.28 cm and a maximum branching density of 8.90 primary branches. Conversely, phenological indicators isolated Arka Kusumakar as the most early-maturing entry, requiring the minimum days to 50% flowering (51.98 days) and first harvest (70.04 days). This earliness remains a critical benchmark for early market entry and maximizing crop cycles, supporting the observations of Prabhu *et al.* (2009). Core yield attributes, including fruit length (6.40–20.59 cm), fruit diameter (2.97–8.71 cm), average fruit weight (41.59–179.38 g), and fruits per plant (17.15–29.75) varied significantly, offering solid opportunities for isolating superior parents for future hybridization schemes.

Table 3 : Mean Performance Matrix of Eggplant Genotypes for Quantitative Traits

Genotypes	DFF	DFH	FW (g)	FL (cm)	FD (cm)	NFP	PH (cm)	NPB	Y (kg)	TY (t/ha)
BR-112	63.08	72.16	122.14	12.62	8.06	24.77	55.80	5.86	3.10	31.06
Arka Avinash	66.30	75.33	89.27	10.72	4.73	25.98	60.26	7.46	2.53	25.30
Swapnamani	70.68	80.90	159.50	15.32	6.46	24.42	46.46	5.06	3.89	38.93
Pusa Anupam	71.85	80.24	55.30	18.67	3.95	29.75	48.02	6.46	1.65	16.50
Brinjal Bhima	65.22	74.00	120.0	20.59	4.10	21.42	49.46	5.53	2.56	25.66
Pant Rituraj	65.06	82.21	92.46	17.45	4.27	20.94	60.25	6.06	2.00	20.00
Pusa Purple Long	54.78	73.80	91.22	15.67	4.47	22.96	44.86	6.73	2.03	20.36
Mukta Moti	61.04	81.26	85.58	15.73	4.10	17.15	41.13	3.86	1.69	16.90
Arka Keshav	62.44	75.15	75.82	14.04	2.97	23.91	56.23	8.06	1.85	18.50
Kashi Uttam	54.11	72.64	86.36	17.25	4.18	23.47	52.60	7.97	2.14	21.40
G- Local-1	74.53	90.23	69.80	11.86	5.73	25.15	63.86	6.81	1.94	19.43
Wild Thorny	84.35	101.94	41.59	6.40	5.16	26.16	83.28	8.90	1.25	12.50
Neelkanth	70.70	86.33	76.26	9.61	7.18	21.10	66.96	8.06	1.56	15.67
Arka Kusumakar	51.98	70.04	76.54	16.35	4.02	19.24	68.60	8.73	1.47	14.73
Kashi Green Round	66.90	83.26	179.38	9.04	8.71	20.68	62.16	8.78	3.52	35.20
G- Local-2	73.50	90.50	64.41	11.81	5.70	24.35	42.15	6.13	1.64	16.46
Arka Nidhi	69.46	81.86	94.03	8.48	8.06	21.03	58.26	7.00	1.96	19.60
Neelam	69.25	84.11	98.46	8.81	3.01	25.10	56.10	6.06	2.24	22.46
Navina	66.54	76.85	86.72	16.77	5.36	22.58	51.99	5.70	1.86	18.66
Arka Anand	63.31	80.80	88.00	16.26	4.05	19.46	60.55	6.62	1.90	18.76
BSS-332	70.10	81.06	93.48	17.84	4.58	22.18	58.66	6.65	2.15	21.56
CD (5%)	5.10	5.52	13.22	2.36	1.58	3.34	7.40	2.01	0.43	4.33
Range	51.98 - 84.35	70.04 - 101.94	41.59- 179.3	6.40 - 20.59	2.97 - 8.71	17.15 - 29.75	41.13 - 83.28	5.06 - 8.90	1.25 - 3.89	12.50 - 38.93
SE(m)±	9.57	11.22	64.25	1.17	0.92	4.10	20.12	1.49	0.06	6.90
CV (%)	4.65	4.15	8.64	10.32	16.91	8.82	7.93	17.99	12.29	12.27

* Abbreviations: DFF: Days to 50% flowering, DFH: Days to first harvest, FW: Fruit weight, FL: Fruit length, FD: Fruit diameter, NFP: Number of fruits per plant, PH: Plant height, NPB: Number of primary branches, Y: Yield per plant, TY: Total yield.

**Fig. 1 :** Total yield distribution across replication for each genotype

Genetic Variability, Heritability, and Genetic Advance

The assessment of genetic parameters (Table 4) provided critical insights into the inheritance architecture of the nine quantitative traits evaluated. For all examined characteristics, including fruit dimensions, single fruit weight, and total yield, the Phenotypic Coefficient of Variation (PCV) was marginally higher than the corresponding Genotypic

Coefficient of Variation (GCV). This narrow disparity demonstrates that environmental factors had minimal influence on trait expression, indicating that phenotypic values serve as reliable indicators for selection.

High GCV and PCV estimates (>20%) were recorded for fruit diameter (51.40% and 54.11%), individual fruit weight (33.69% and 34.78%), and yield (30.18% and 32.59%), indicating a substantial reservoir of exploitable genetic variability. Concurrently, high broad-sense heritability (h^2_{bs}) values were noted across nearly all characters, spanning from 81.83% to 93.81%. Following Johnson *et al.* (1955), high heritability estimates achieve maximum breeding efficiency only when accompanied by high genetic advance over the mean (GAM), reflecting the predominance of additive gene action. In this study, total fruit yield displayed high heritability (85.77%) paired with robust genetic advance (57.58%), proving that direct phenotypic selection would be highly effective for genetic improvement within this germplasm, a trend consistent with the findings of Islam *et al.* (2014).

Table 4 : Genetic variability parameters for quantitative characters in brinjal genotypes.

Response Variable	SED	Heritability (h ² bs)	GCV	PCV	Gen-Advance	Gen-Adv % Means
Fruit weight	13.22	93.81	33.69	34.78	62.31	67.23
Fruit length	2.36	87.80	27.70	29.56	7.41	53.47
Fruit diameter	1.58	90.22	51.40	54.11	5.71	100.58
Days to 50% flowering	5.10	84.37	10.82	11.78	13.60	20.48
Days to first harvest	5.52	82.19	8.91	9.83	13.44	16.65
Plant height	7.40	81.83	16.83	18.61	17.74	31.37
No. of primary branches	2.01	44.74	16.19	24.21	1.51	22.31
No. of fruits per plant	3.34	62.26	11.33	14.36	4.22	18.43
Yield	0.43	85.77	30.18	32.59	1.23	57.58

Correlation Coefficient Analysis

Phenotypic and genotypic correlation analysis was executed to evaluate the direction and quantitative strength of relationships between net yield per plant and its core structural components (Table 5). The estimations revealed that genotypic correlation coefficients were marginally or substantially higher than their respective phenotypic counterparts. This trend demonstrates a robust inherent genetic association among the traits, operating with minimal distortion from non-genetic environmental fluctuations.

Net yield per plant exhibited a highly significant and positive association with average fruit weight ($r_g = 0.944$, $r_p = 0.900$) and fruit diameter ($r_g = 0.604$, $r_p = 0.554$). This strong correlation confirms that simultaneous selection targeted toward heavier and wider fruit profiles will directly expand commercial crop productivity.

Conversely, days to 50% flowering and days to first harvest displayed negative correlation values with net yield ($r_g = -0.080$ and $r_g = -0.312$, respectively), suggesting that phenological earliness extends the reproductive window to enhance cumulative production patterns.

Vegetative traits, specifically plant height and primary branch density, exhibited strong positive genotypic inter-relationships with each other ($r_g = 0.873$) but shifted to negative zones when correlated with yield and branch density components, matching the structural breeding principles established by Al-Jibouri *et al.* (1958). Furthermore, the positive inter-trait correlation observed between fruit dimensions and single fruit weight satisfies the genetic models of Singh *et al.* (2014), emphasizing these metrics as highly dependable physical selection indexes for eggplant crop enhancement.

Table 5 : Phenotypic (Above Diagonal) and Genotypic (Below Diagonal) Correlation Matrix.

Traits	FW	FL	FD	DFH	DFH	PH	NPB	NFP	Y
FW	1.000	0.040	0.542*	-0.171	-0.264*	-0.205	-0.135	-0.213	0.900*
FL	0.022	1.000	-0.252*	-0.480*	-0.526*	-0.459*	-0.307*	-0.130	0.005
FD	0.571*	-0.324*	1.000	0.282*	0.214	-0.088	-0.103	0.066	0.554*
DFH	-0.207	-0.513*	0.339*	1.000	0.833*	0.316*	0.016	0.391*	-0.047
DFH	-0.340*	-0.632*	0.269*	0.880*	1.000	0.391*	0.126	0.156	-0.228
PH	-0.242	-0.534*	-0.083	0.350*	0.426*	1.000	0.580*	0.025	-0.245
NPB	-0.203	-0.531*	-0.170	0.019	0.138	0.873*	1.000	0.134	-0.124
NFB	-0.289*	-0.197	0.057	0.532*	0.258*	0.025	0.102	1.000	0.095
Y	0.944*	0.008	0.604*	-0.080	-0.312*	-0.249*	-0.278*	0.028	1.000

* Significant at the $p < 0.05$ level, Bold diagonal values mark identity metrics.

* Abbreviations: DFF: Days to 50% flowering, DFH: Days to first harvest, FW: Fruit weight, FL: Fruit length, FD: Fruit diameter, NFP: Number of fruits per plant, PH: Plant height, NPB: Number of primary branches, Y: Yield per plant

Analysis of Path Coefficients

To distinguish true causal associations from simple statistical correlations, the genotypic correlation coefficients were partitioned into direct and indirect

effects via path coefficient analysis as recommended by Dewey and Lu (1959). This mathematical matrix (Table 6) isolates the definitive contribution of each component trait toward net plant yield.

Biometrical estimations revealed that fruit length displayed the strongest positive direct influence (0.898) on total yield, positioning it as a foundational physical criterion for selection indices. This was supported by positive direct effects emerging from fruit weight (0.167) and fruit diameter (0.144). Conversely, characters such as days to 50% flowering (5.413) and days to first harvest exhibited high indirect positive contributions to primary growth traits, despite displaying negative terminal direct effects, indicating that early developmental vigour indirectly maximizes structural yield architecture.

The low residual effect (0.184) calculated for the system establishes that the primary traits incorporated in this multivariate design account for approximately 82% of the total phenotypic variance observed within the brinjal germplasm. Consequently, constructing breeding selection indices centred on optimized fruit dimensions (length and diameter) paired with single fruit mass will yield maximum genetic advancement within the Gwalior-Chambal agroclimatic zone.

Table 6 : Path Coefficients showing Direct (diagonal) and Indirect (off-diagonal) effects of different traits on Yield.

	FW	FL	FD	DFH	PH	NPB	NFP
FW	0.167	0.020	0.082	-1.276	0.983	1.312	-1.129
FL	0.004	0.898	-0.047	-3.158	1.830	2.896	-2.950
FD	0.096	-0.291	0.144	2.084	-0.778	0.452	-0.947
DFH	-0.035	-0.461	0.049	6.154	-2.546	-1.901	0.105
PH	-0.057	-0.568	0.039	5.413	-2.894	-2.313	0.769
NPB	-0.040	-0.479	-0.012	2.157	-1.234	-5.425	4.853
NFP	-0.034	-0.477	-0.025	0.116	-0.400	-4.738	5.557
NFP	-0.048	-0.177	0.008	3.277	-0.748	-0.138	0.568
NFP							-2.714

*Residual Effect = 0.184, Bold diagonal numbers represent direct genotypic effects.

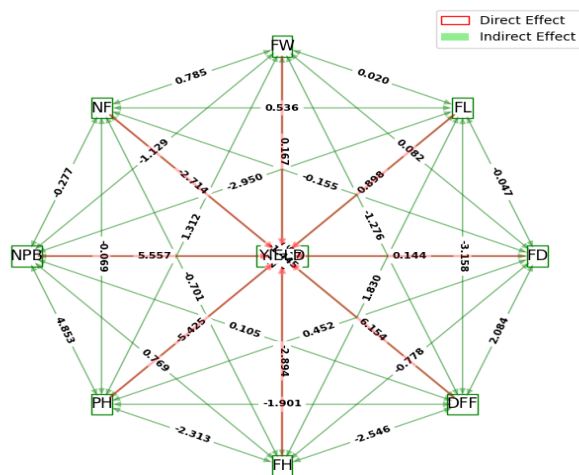


Fig. 2 : Path diagram and direct and indirect effects

Multivariate Analysis of Genetic Divergence (D^2 Statistic)

To systematically evaluate the genetic architecture of the twenty-one eggplant genotypes, Mahalanobis D^2 statistics were applied to quantify the degree of genetic divergence. This multivariate grouping model is vital for isolating parents with optimal genetic distance to maximize heterosis and transgressive segregation in subsequent breeding generations (Mahalanobis, 1936).

Clustering Architecture

Based on the magnitude of D^2 values, the germplasm was partitioned into three distinct clusters (Table 7). The distribution matrix revealed substantial diversity; Cluster I emerged as the largest group, accommodating 14 genotypes predominantly characterized by early phenological transitions. Cluster II comprised six genotypes exhibiting robust vegetative metrics and high branching density. Notably, Cluster III was monotypic, containing the high-yielding cultivar Swapnamani. This single-entry cluster stood out as the most divergent genotype across the entire population, aligning with the germplasm characterization frameworks of Islam *et al.* (2014).

Table 7: Analysis of the genetic divergence - based Clustering Pattern in twenty-one brinjal Genotypes.

Cluster No.	Number of genotypes	Genotypes in Cluster
1	14	Pant Rituraj, Arka Anand, Navina, Bss-332, Arka Keshav, Kashi Uttam, Pusa Purple Long, Arka Avinash, Arka Kusumakar, Mukta Moti, BR-112, G-Local-1, Pusa Anupam, Brinjal Bhima
2	6	Arka Nidhi, Neelam, Neelkanth, G-Local-2, Wild Thorny, Kashi Green Round
3	1	Swapnamani

Intra- and Inter-Cluster Distances

The statistical distances computed within and between the genetic groups provide a clear roadmap for hybrid combinations (Table 8). The maximum inter-cluster divergence was recorded between Cluster I and Cluster III (15.54), followed by Cluster II and Cluster III (13.64). Conversely, the minimum inter-cluster distance (11.89) was observed between Cluster I and Cluster II, indicating a closer phylogenetic relationship between these groups.

The pronounced divergence between Cluster I and Cluster III indicates that hybridization between these distinct groups is highly likely to generate superior transgressive recombinants (Rekha and Khan, 2015). Specifically, utilizing Swapnamani (Cluster III) as a strategic donor parent in crosses with the early-flowering lines of Cluster I offers an ideal framework for developing hybrids that combine elite productivity with shortened crop cycles.

Table 8 : Average intra-cluster (diagonal) and inter-cluster Mahalanobis D^2 distances.

Cluster	Cluster 1	Cluster 2	Cluster 3
Cluster 1	7.22	11.89	15.54
Cluster 2		8.63	13.64
Cluster 3			0.00

Cluster Mean Analysis and Trait Performance

Evaluation of cluster means was executed to identify specific groups capable of donating desirable target alleles to breeding pipelines (Vaddoria *et al.* 2011). The cluster mean matrix highlighted distinct phenotypic profiles for each group (Table 9). Cluster III (represented by Swapnamani) exhibited peak performance for yield-linked traits, achieving the maximum mean total yield (38.93t/ha), superior average fruit weight (15.85 g), and maximum fruit diameter (16.46 cm).

Conversely, Cluster II genotypes were distinguished by vegetative vigour, recording the highest plant height (61.49cm) and primary branching density (7.49). Cluster I demonstrated an accelerated phenological timeline with an earlier flowering window (63.60days), which is critical for introducing short-duration traits. Combining parents from these diverse clusters with complementary expressions satisfies the genetic diversity principles of Babu and Patil (2013), confirming excellent potential for elite line selection.

Table 9 : Comparative cluster mean values for yield and yield-contributing traits in eggplant.

S.No.	Characters	Cluster		
		1	2	3
1.	Fruit Weight (g)	15.85	9.03	15.33
2.	Fruit Length (cm)	15.85	9.03	15.33
3.	Fruit Diameter (cm)	4.25	7.20	16.46
4.	Days to 50% Flowering	63.60	72.36	70.68
5.	Days to First Harvest	77.56	88.00	80.91
6.	Plant Height (cm)	55.16	61.49	46.47
7.	No. of primary Branches	6.61	7.49	5.07
8.	No. of Fruits Per Plant	22.79	23.07	24.43
9.	Yield (kg)	2.06	2.03	3.89
10.	Total Yield (t/ha)	20.21	19.66	38.93

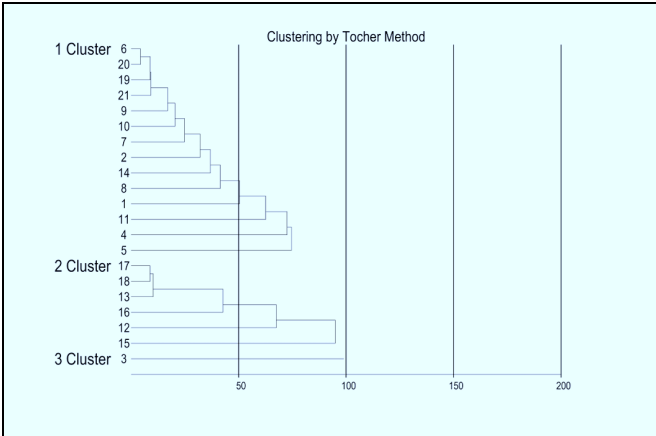


Fig. 3 : Clustering pattern of 21 brinjal genotypes using the Tocher method

Discussion

The systematic evaluation of twenty-one eggplant genotypes demonstrated an extensive degree of quantitative divergence, confirming a robust genetic baseline within the collected germplasm. The substantial range recorded for total fruit yield (12.50 to 38.93 t/ha) positions this population as a primary gene pool for isolating high-productivity lines, reinforcing the classic crop evolution models of Vavilov (1928). Identifying and documenting such distinct phenotypic polymorphism remains an essential prerequisite for optimizing vegetable crops for specialized subtropical environments and establishing dependable visual indicators for phenotypic selection, aligning with the structural characterization approaches of Cericola *et al.* (2013) and Islam *et al.* (2014).

The minimal variance consistently observed between the Genotypic Coefficient of Variation (GCV) and the Phenotypic Coefficient of Variation (PCV) for vital traits like individual fruit weight and total yield proves that environmental factors exerted a negligible effect on character expression. Consequently, the phenotypic values serve as highly dependable indicators of true genotypic capability, a trend strongly supported by Ullah *et al.* 2014 and Vandana *et al.* 2015. Furthermore, Muniappan *et al.* (2010) noted that breeding selection is remarkably streamlined when environmental intervention is low. Based on the classical selection models of Lush (1940) and Johnson *et al.* (1955), high broad-sense heritability (h^2_{bs}) combined with substantial genetic advance over the mean (GAM) for fruit weight and dimensions proves that these characters are predominantly regulated by additive gene control. This genetic pattern is further validated by Praneetha 2002 and Devi *et al.* 2015, who asserted that traits with such inheritance dynamics

respond highly effectively to straightforward selection methods.

Correlation analysis successfully validated the components-based breeding strategy proposed by Grafius (1956), exposing a vital relationship between total yield and its primary contributing components. The positive, significant correlation of yield with fruit dimensions and weight perfectly matches the observations of Sravanthi *et al.* (2019) and Tripathy *et al.* (2017).

Path coefficient matrix estimations, conducted via the methodology of Dewey and Lu (1959), isolated fruit length as the major positive direct actor (0.898), demonstrating that external physical dimensions directly dictate terminal crop performance, echoing the selection indices reported by Bhosale *et al.* (2016) and Mohanty (2001). Additionally, Prabhu *et al.* (2009) demonstrated that indirect selection pathways often offer greater breeding efficiency, a trend supported by Senapati *et al.* 2009, Islam *et al.* 2014, and Rekha *et al.* (2015), who highlighted that maximum genetic gain in eggplant is achieved by focusing on structured fruit metrics. Concurrently, the low residual value (0.184) establishes that the variables incorporated in this multivariate matrix account for approximately 81.6% of the total phenotypic variance observed.

Unlike routine diversity surveys that overlook localized environmental transitions, this investigation addresses a critical regional research gap by mapping genetic divergence against the sharp, sudden monsoon-to-winter temperature drops characteristic of the semi-arid Madhya Pradesh Grid Zone. Multivariate grouping Mahalanobis D^2 statistics partitioned the twenty-one genotypes into three distinct clusters, proving that genetic diversity functions independently of geographical origins, a principle established by Mahalanobis (1936) and Rao (1952). The true breakthrough and breeding novelty of this research is the complete phenotypic and genetic isolation of the monotypic genotype Swapnamani into a solitary Cluster III.

Given that the maximum inter-cluster distance (15.54) occurred between the early-maturing variants of Cluster I and the high-yielding architecture of Cluster III, selecting parental candidates from such divergent groups is a strategic necessity for triggering transgressive segregation and maximizing heterosis, adhering to the principles of Singh and Chaudhary (1985). Unlike previous studies that recommend random lines crossing, our work isolates a localized, mathematically validated solution by pairing the extreme earliness of Arka Kusumakar with the unique

single-fruit mass of Swapnamani to break the current yield plateaus in Central India, adhering to the breeding frameworks of Acquaah (2007) and Shull (1908).

Conclusion

This investigation confirms a rich genetic and morphological reservoir within the evaluated brinjal germplasm, defining a strategic breeding framework for semi-arid subtropical zones. High broad-sense heritability coupled with robust genetic advance values establishes that direct phenotypic selection focused on single fruit weight, length, and diameter will successfully drive immediate genetic gain under additive gene control.

To exploit maximum heterosis and trigger superior transgressive segregation under erratic agroclimatic shifts, the targeted hybridization of Swapnamani with the early-maturing genotypes of Cluster I, specifically Arka Kusumakar was beneficial.

This localized, mathematically validated breeding matrix bridges a critical regional research gap, offering an empirical blueprint to break long-standing yield plateaus and deliver elite, short-duration eggplant hybrids explicitly tailored for the challenging climate dynamics of the Gwalior-Chambal region.

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