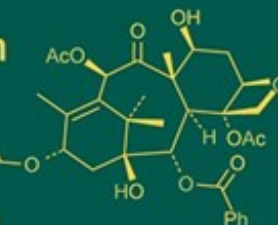


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Vijayashree

Ph.D. Scholar, Department of Horticulture, Pandit Jawaharlal Nehru College of Agriculture and Research Institute, Karaikal, Puducherry, India

A Shanthi

Professor, Department of Horticulture, Pandit Jawaharlal Nehru College of Agriculture and Research Institute, Karaikal, Puducherry, India

V Sundaram

Professor, Department of Horticulture, Pandit Jawaharlal Nehru College of Agriculture and Research Institute, Karaikal, Puducherry, India

V Vengadessan

Professor, Department of Genetics and Plant Breeding, Pandit Jawaharlal Nehru College of Agriculture and Research Institute, Karaikal, Puducherry, India

S Nadaradjan

Professor, Department of Genetics and Plant Breeding, Pandit Jawaharlal Nehru College of Agriculture and Research Institute, Karaikal, Puducherry, India

M Manikandan

Assistant Professor, Department of Horticulture, Pandit Jawaharlal Nehru College of Agriculture and Research Institute, Karaikal, Puducherry, India

Corresponding Author:**Vijayashree**

Ph.D. Scholar, Department of Horticulture, Pandit Jawaharlal Nehru College of Agriculture and Research Institute, Karaikal, Puducherry, India

Assessment of morphological diversity in brinjal (*Solanum melongena* L.) genotypes using qualitative descriptors and the Shannon-Wiener diversity index

Vijayashree¹, A Shanthi², V Sundaram³, V Vengadessan⁴, S Nadaradjan⁵, M Manikandan⁶

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ABSTRACT

Brinjal (*Solanum melongena* L.) is one of the most important solanaceous vegetables of South and South-East Asia and India is recognized as its primary centre of diversity. However, the continued use of a limited number of released varieties has weakened the genetic base available to breeders, so it has become essential to systematically characterize the genotypes that are locally available to aid future improvement programmes. The present investigation was undertaken to assess the extent of morphological diversity among 45 brinjal genotypes evaluated at the Pandit Jawaharlal Nehru College of Agriculture and Research Institute, Karaikal, Puducherry. Twenty qualitative descriptors covering vegetative, floral and fruit characters were scored using IBPGR descriptors for eggplant and the Shannon-Wiener diversity index (H') was computed for each trait. The Shannon diversity index across the 20 traits ranged from 0.393 (fruit curvature) to 1.606 (fruit colour at commercial ripeness), with a mean H' of 0.884 and a mean normalized diversity index ($H'n$) of 0.789, indicating a broad and even spread of phenotypic classes among the genotypes evaluated. Fruit colour at commercial ripeness, fruit length-to-breadth ratio, fruit shape and corolla colour were the most polymorphic traits ($H' > 1.0$). In contrast, fruit curvature, leaf blade length and calyx colour showed comparatively low diversity, reflecting the predominance of a few descriptor classes for these characters in the germplasm evaluated. Ward's hierarchical clustering grouped the genotypes into four morphologically distinct clusters (6, 13, 17 and 9 genotypes respectively). The results confirm that considerable exploitable variability exists among the 45 genotypes for fruit-related traits and the diversity estimates generated can guide the choice of morphologically divergent parents for future hybridization and varietal improvement programmes in brinjal.

Keywords: *Solanum melongena*, Morphological diversity, Qualitative descriptors, Shannon-Wiener diversity index

Introduction

Brinjal (*Solanum melongena* L.) is one of the most widely grown and economically important vegetable crop of the family Solanaceae, with a diploid chromosome number of $2n = 2x = 24$. It is cultivated extensively across the tropical and sub-tropical regions of Asia and Africa and is often described as the 'King of vegetables' on account of its versatility and usage in different culinary purposes (Choudhary *et al.*, 2009) [1]. India, together with the wider Indo-Burma region, is known as the primary centre of origin and diversity of the crop (Kousalya *et al.*, 2024) [2] and this rich native variability in terms of fruit size, shape, color, growth habit, yield, pest and disease resistance, climate adaptability and quality attributes has historically formed the foundation for varietal improvement through selection and hybridization.

Brinjal is valued not only as an inexpensive source of dietary fibre, minerals and phenolic antioxidants, but also for its wide-ranging culinary uses and its role in the livelihoods of resource-poor farmers who grow numerous local landraces alongside a limited number of improved cultivars and hybrids. However, the increasing popularity of a small set of high-yielding hybrids has progressively narrowed the genetic base under commercial cultivation, while a very large reservoir of morphologically distinct landraces, traditional types and locally adapted genotypes continues to be maintained on-farm or in institutional germplasm collections without adequate characterization. Systematic documentation of this variability is therefore a prerequisite for its conservation and effective utilization in breeding programmes.

Morphological characterization using standard, internationally accepted descriptors is the first and most accessible step in germplasm evaluation, since qualitative traits of plant growth habit, leaf, flower and fruit are largely under simple genetic control and are unaffected by most environmental fluctuations. Frequency distribution of genotypes across the classes of a qualitative descriptor can be summarized using diversity indices originally developed in information theory and later adapted for the analysis of biological and genetic variation. Among these, the Shannon-Wiener (also referred to as the Shannon-Weaver) diversity index has

become one of the most widely used tools for quantifying phenotypic diversity in plant genetic resources, since it simultaneously reflects both the number of classes present (richness) and the evenness with which genotypes are distributed among them (Shannon *et al.*, 1949) [3].

A higher value of H' for a given trait indicates a more even spread of genotypes across a greater number of descriptor classes, whereas a low value points to the dominance of one or a few classes and hence limited exploitable variability for that character. Since the index compresses a full frequency distribution into a single number (Zeven *et al.*, 1991) [4], a recommendation has been followed in the present study by reporting the complete descriptor-class distribution together with the H' values. The Shannon-Wiener index has been successfully applied to describe morphological diversity in brinjal germplasm collections of varying size and origin, including large national gene bank holdings profiled with the help of DIVA-GIS (Gangopadhyay *et al.*, 2013) [5] and regional landrace collections from Eastern India (Tripathy *et al.*, 2025) [6], providing a useful basis for comparison with the present set of genotypes.

Although several studies have documented quantitative genetic divergence in brinjal using Mahalanobis' D^2 statistics and principal component analysis (Anbarasi *et al.*, 2021; Lintu *et al.*, 2023; Zabbar *et al.*, 2024) [7, 8, 9], comparatively fewer reports combine a complete set of qualitative descriptor traits with Shannon-Wiener diversity estimation for germplasm maintained under the coastal, deltaic agro-climatic conditions of Puducherry. In view of this, the present study was undertaken with the specific objective of characterizing 45 brinjal genotypes based on twenty qualitative morphological descriptors of plant, leaf, flower and fruit characters, and of quantifying the extent and pattern of diversity for each trait using the Shannon-Wiener diversity index, to identify the most polymorphic characters and to generate baseline information useful for parental selection in future brinjal breeding programmes.

2. Materials and Methods

The present investigation was carried out at the Department of Horticulture, Pandit Jawaharlal Nehru College of Agriculture and Research Institute, Karaikal, Union Territory of Puducherry, India (10.9522° N, 79.7825° E), which lies in the coastal, deltaic tract of the Cauvery river basin characterized by a warm, humid tropical climate. Forty-five brinjal genotypes, comprising released varieties and local/regional collections, were raised in the field following the recommended agronomic package of practices, with observations recorded from five randomly tagged, representative plants of each genotype at the appropriate vegetative, flowering and fruiting stages. Morphological descriptors covering vegetative, floral and fruit characters were recorded for each genotype by following the descriptor states standardized for brinjal germplasm characterization by IBPGR Descriptors for eggplant (1990) [10], except two traits (Calyx color and fruit shape), which were recorded as per Tripathy *et al.* (2025) [6]. Each trait was scored on the internationally used 0-9 (or 1-9) class scale appropriate to that descriptor.

The frequency of genotypes falling in each descriptor class was computed for every trait and the percentage distribution was worked out. Phenotypic diversity for each was quantified using the Shannon-Wiener diversity index (H'), calculated from the class-frequency distribution as follows (Shannon *et al.*, 1949) [3]:

$$H' = - \sum_{i=1}^s P_i \times \ln P_i$$

Where, P_i is the proportion of the total 45 genotypes falling in the i^{th} descriptor class of a given trait, and s is the number of descriptor classes actually represented (*i.e.*, classes with a non-zero frequency). The maximum possible value of the index for a trait, H_{max} , is given by $\ln(s)$ and the normalized Shannon diversity index, $H'n = H'/H_{\text{max}}$, was additionally computed to allow direct comparison of relative diversity across traits differing in their number of descriptor classes; $H'n$ ranges from 0 (complete uniformity) to 1 (genotypes distributed with perfect evenness across all observed classes) (Zeven *et al.*, 1991) [4].

Agglomerative hierarchical cluster analysis was performed based on the Gower dissimilarity matrix using Ward's minimum-variance method (Ward, 1963; implemented as *ward.D2*, which operates directly on the dissimilarity matrix rather than on squared Euclidean distances). Basic statistical analysis, such as frequency distribution, was carried out in Microsoft Excel and the Shannon-Wiener diversity index and cluster analysis were carried out using R software version 4.4.2.

3. Results and Discussion

The 45 brinjal genotypes evaluated in the present study displayed a wide range of phenotypic variation for the majority of the 20 qualitative descriptors recorded, confirming the presence of substantial exploitable morphological diversity in the germplasm. The complete frequency distribution of genotypes across descriptor classes, together with the trait-wise Shannon-Wiener diversity index (H'), its theoretical maximum (H_{max}) and the normalized index ($H'n$), is presented in Table 1.

Vegetative and floral traits

Among the vegetative descriptors, plant growth habit showed a predominance of the intermediate class (53.33% of genotypes), followed by the upright (37.78%) and prostrate (8.89%) classes, giving a moderately high H' of 0.918 ($H'n = 0.836$), indicating that although one class was numerically dominant, all three growth-habit classes were reasonably well represented. Plant height was overwhelmingly skewed towards the tall class (64.44%), with the remainder intermediate (35.56%) and no genotypes in the very short, short or very tall classes; the resulting H' of 0.651 was nevertheless associated with the highest normalized diversity recorded among all vegetative traits ($H'n = 0.939$), because only two classes were actually present and the genotypes were divided between them in a near-even 64:36 ratio.



Figure 1. Descriptor-class distribution (%) and Shannon-Wiener Diversity index (H') for 20 morphological traits across 45 brinjal genotypes.

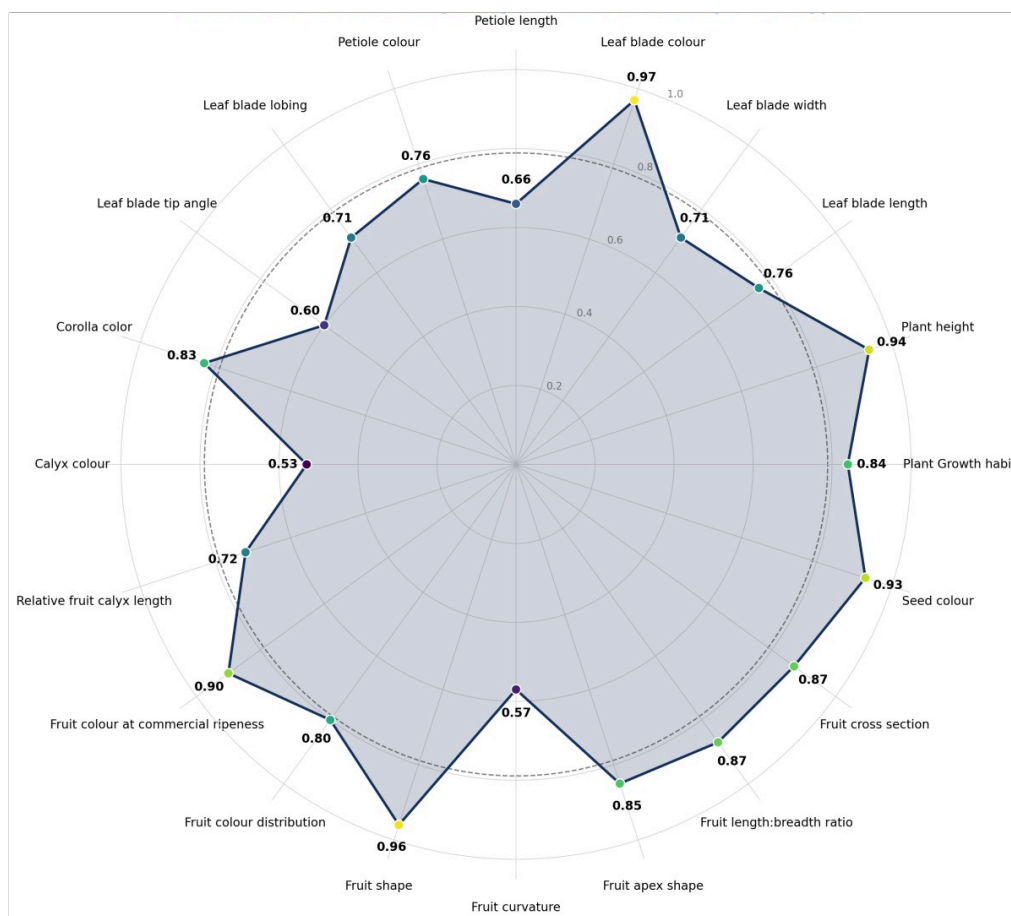


Figure 2. Radar profile of normalized Shannon-Wiener Diversity Index ($H'n$) across 20 qualitative Morphological traits in 45 brinjal genotypes.

Leaf-related descriptors (leaf blade length, leaf blade width, leaf blade lobing, leaf blade tip angle, petiole length and petiole colour) each

produced moderate H' values in the range of 0.53-0.83, with leaf blade colour recording the highest diversity among leaf traits ($H' =$

1.072, $H'n = 0.975$) owing to a fairly even three-way split among light green (26.67%), green (44.44%) and dark green (28.89%) genotypes. Leaf blade tip angle showed the lowest normalized diversity among the vegetative traits ($H'n = 0.597$), reflecting the marked dominance of the intermediate class (73.33%). Among floral descriptors, corolla colour was moderately diverse ($H' = 1.157$, four classes repre-

sented, $H'n = 0.835$) with pale violet corollas predominating (53.33%), while calyx colour was comparatively uniform, with green calyces recorded in 82.22% of genotypes and a correspondingly low $H'n$ of 0.533, the lowest normalized diversity recorded for any trait in the study.



Figure 3. Variation in leaf, flower and fruit morphology among evaluated brinjal genotypes.

Fruit and seed traits

Fruit-related descriptors consistently returned the highest Shannon diversity values in the present study. Fruit colour at commercial ripeness was the single most polymorphic trait overall ($H' = 1.606$, six of the nine possible descriptor classes represented, $H'n = 0.896$), with genotypes distributed among green (26.67%), milky white (11.11%), lilac grey (8.89%), purple (33.33%), purple-black (15.56%) and black (4.44%) fruited types, and none scored as deep yellow, fire red or scarlet red. Fruit length-to-breadth ratio was the second most diverse character ($H' = 1.398$, five classes, $H'n = 0.869$), reflecting the co-existence of round/as-long-as-broad, slightly longer, and markedly elongated fruit types in the genotype set, while fruit shape ($H' =$

1.325, four classes: long 24.44%, round 24.44%, oblong 37.78%, oval 13.33%; $H'n = 0.956$) recorded the highest normalized diversity of any trait studied, indicating an almost even spread of genotypes across all four observed fruit-shape classes.

Seed colour ($H' = 1.016$, $H'n = 0.925$) and fruit cross-section ($H' = 0.958$, $H'n = 0.872$) also showed relatively high diversity, whereas fruit colour distribution ($H' = 0.556$, uniform fruits predominating in 75.56% of genotypes) and, most notably, fruit curvature ($H' = 0.393$, $H'n = 0.567$, with 86.67% of genotypes bearing straight fruits and only 13.33% slightly curved) were the least diverse of the fruit descriptors. Fruit apex shape, with genotypes distributed among pro-truded (11.11%), rounded (33.33%) and depressed (55.56%) classes, recorded intermediate diversity ($H' = 0.937$, $H'n = 0.853$).

Table 1. Frequency distribution of 45 brinjal genotypes across descriptor classes and Shannon-Wiener diversity index (H') for 20 qualitative traits.

S. No.	Trait	Descriptor class	No. of genotypes	Distribution (%)	H'	Hmax	$H'n$
1.	Plant Growth habit	3 - Upright	17	37.78	0.918	1.099	0.836
		5 - Intermediate	24	53.33			
		7 - Prostrate	4	8.89			
2.	Plant height	1 - Very short	0	0.00	0.651	0.693	0.939
		3 - Short	0	0.00			
		5 - Intermediate	16	35.56			
		7 - Tall	29	64.44			
		9 - Very tall	0	0.00			
3.	Leaf blade length	3 - Short	35	77.78	0.530	0.693	0.764
		5 - Intermediate	10	22.22			
		7 - Long	0	0.00			
4.	Leaf blade width	3 - Narrow	9	20.00	0.779	1.099	0.710
		5 - Intermediate	32	71.11			
		7 - Wide	4	8.89			
5.	Leaf blade lobing	1 - Very weak	0	0.00	0.780	1.099	0.710
		3 - Weak	1	2.22			
		5 - Intermediate	24	53.33			
		7 - Strong	20	44.44			
		9 - Very strong	0	0.00			
6.	Leaf blade tip angle	1 - Very acute	0	0.00	0.656	1.099	0.597
		3 - Acute	11	24.44			
		5 - Intermediate	33	73.33			
		7 - Obtuse	1	2.22			
		9 - Very obtuse	0	0.00			

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7.	Petiole length	0 - None	0	0.00	0.730	1.099	0.664
		1 - Very short	0	0.00			
		3 - Short	3	6.67			
		5 - Intermediate	33	73.33			
		7 - Long	9	20.00			
8.	Petiole colour	9 - Very long	0	0.00	0.830	1.099	0.755
		1 - Green	30	66.67			
		3 - Greenish violet	11	24.44			
		5 - Violet	4	8.89			
		7 - Dark violet	0	0.00			
9.	Leaf blade colour	9 - Dark brown	0	0.00	1.072	1.099	0.975
		1 - Light green	12	26.67			
		3 - Green	20	44.44			
		5 - Dark green	13	28.89			
		7 - Greenish violet	0	0.00			
10.	Corolla color	9 - Violet	0	0.00	1.157	1.386	0.835
		1 - Greenish white	0	0.00			
		3 - White	10	22.22			
		5 - Pale violet	24	53.33			
		7 - Light violet	3	6.67			
11.	Calyx colour	9 - Bluish violet	8	17.78	0.586	1.099	0.533
		1 - Green	37	82.22			
		2 - Light purple	3	6.67			
12.	Relative fruit calyx length	3 - Dark Purple	5	11.11	0.794	1.099	0.722
		1 - Very short	5	11.11			
		3 - Short	32	71.11			
		5 - Intermediate	8	17.78			
		7 - Long	0	0.00			
13.	Fruit apex shape	9 - Very long	0	0.00	0.937	1.099	0.853
		3 - Protruded	5	11.11			
		5 - Rounded	15	33.33			
14.	Fruit colour at commercial ripeness	7 - Depressed	25	55.56	1.606	1.792	0.896
		1 - Green	12	26.67			
		2 - Milky white	5	11.11			
		3 - Deep yellow	0	0.00			
		4 - Fire red	0	0.00			
		5 - Scarlet red	0	0.00			
		6 - Lilac grey	4	8.89			
		7 - Purple	15	33.33			
		8 - Purple black	7	15.56			
15.	Fruit colour distribution	9 - Black	2	4.44	0.556	0.693	0.802
		1 - Uniform	34	75.56			
		3 - Mottled	0	0.00			
		5 - Netted	0	0.00			
16.	Fruit shape	7 - Stripes	11	24.44	1.325	1.386	0.956
		3 - Long	11	24.44			
		5 - Round	11	24.44			
		7 - Oblong	17	37.78			
17.	Fruit curvature	9 - Oval	6	13.33	0.393	0.693	0.567
		1 - None	39	86.67			
		3 - Slightly curved	6	13.33			
		5 - Curved	0	0.00			
		7 - Snake shaped	0	0.00			
		8 - Sickle shaped	0	0.00			
		9 - U shaped	0	0.00			

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18.	Fruits length: breadth ratio	1 - Broader than long	0	0.00	1.398 1.609 0.869
		3 - As long as broad	11	24.44	
		5 - Slightly longer	19	42.22	
		7 - Twice as long as broad	2	4.44	
		8 - Three times as long as broad	8	17.78	
		9 - Several times as long as broader	5	11.11	
19.	Fruit cross section	1 - Circular, no grooves	14	31.11	0.958 1.099 0.872
		3 - Elliptic, no grooves	25	55.56	
		5 - Few grooves (~4)	6	13.33	
		7 - Many grooves (~8)	0	0.00	
		9 - Very irregular	0	0.00	
20.	Seed colour	1 - White	0	0.00	1.016 1.099 0.925
		2 - Light yellow	18	40.00	
		3 - Grey yellow	0	0.00	
		4 - Brownish yellow	20	44.44	
		5 - Brown	7	15.56	
		7 - Brown black	0	0.00	
		9 - Black	0	0.00	

Hierarchical cluster analysis (Ward's method on Gower's dissimilarity)

Agglomerative hierarchical clustering of the 45 genotypes on their Gower dissimilarity matrix, using Ward's minimum-variance method, produced a dendrogram (Fig 4) that grouped the genotypes into four major clusters at a dissimilarity height of approximately 0.9-1.0, well above the height of most of the internal branching within each cluster. Cluster III was the largest (17 genotypes), followed by Cluster II (13 genotypes), Cluster IV (9 genotypes) and Cluster I (6 genotypes; Table 2).

Cross-tabulation of cluster membership against the original descriptor states (Table 3) showed that the four clusters were morphologically interpretable rather than arbitrary statistical groupings. Cluster I was uniformly tall (100%), predominantly upright in growth habit (83.3%) with a white corolla (83.3%) and was the only cluster fixed for green fruit colour at commercial ripeness (100%) combined with a markedly elongated fruit (several times as long as broad in 66.7% of genotypes) and slightly curved fruit shape (83.3%) - a combination consistent with the long, green-fruited genotypes (e.g., Brinjal Green

Long, Haritha, Arka Kusumakar and Arka Shirish) that dominate this group. Cluster II was dominated by tall plants (84.6%) with dark green leaves (61.5%), bluish-violet corollas (53.8%) and distinctively, purple-black fruit at commercial ripeness (53.8%) with round-to-oblong, perfectly straight fruit (100% non-curved) - the classic profile of popular purple round-oblong table varieties such as *Pusa Krishna*, *Pusa Uttam* and Black Brinjal types. Cluster III, the largest and most heterogeneous group, was characterized by intermediate plant height (58.8%) and growth habit (64.7%), a pale violet corolla (70.6%) and comparatively even representation across several fruit colours (milky white, purple and lilac grey together accounting for most genotypes), indicating that this cluster brings together a morphologically diverse assemblage of landraces and breeding lines that did not align closely with either of the more distinctive Clusters I or II. Cluster IV combined intermediate growth habit (66.7%) and light green leaves (66.7%) with a pale violet corolla (88.9%) and a high proportion of oblong-fruited genotypes (77.8%), distinguishing it from the predominantly round-fruited Cluster II despite sharing purple fruit pigmentation in most genotypes (55.6%).

Table 2. Grouping of 45 brinjal genotypes into four clusters by Ward's minimum-variance hierarchical clustering on Gower's dissimilarity matrix

Cluster	No. of Genotypes	List of Genotypes
I	6	Haritha, Arka Kusumakar, Arka Shirish, Brinjal Green Long, Devanahalli Local and BR-5
II	13	Arka Nidhi, Arka Keshav, <i>Pusa Krishna</i> , <i>Pusa Uttam</i> , Kashi Uttam, Black Brinjal Round, Black Brinjal Long, Brinjal Banarasi, Purple line brinjal, Sevanthampatti Local, Poyyur Local, Purple Cluster and BR-8
III	17	Arka Avinash, Arka Harshita, VRM-2, <i>Pusa Safed Baingan</i> -1, Kashi Taru, Mannapari Brinjal, Black Beauty, Long Bhavani, Round Bhavani, Thoppi Brinjal, Kulasai Brinjal, White Long Brinjal, Kamudhi Brinjal, Graffity, BR-2, BR-3 and BR-4
IV	9	CO-2, Brinjal Kateri, Green Oval, Round Gujarat, Purple Striped Brinjal, BR-1, BR-6, BR-7 and BR-9

Overall pattern of diversity and comparison with earlier reports

Averaged across all 20 descriptors, the mean H' was 0.884 and the mean normalized diversity index ($H'n$) was 0.789, indicating that, on the whole, the 45 genotypes evaluated were distributed evenly across the descriptor classes actually expressed in this germplasm set, with diversity being concentrated disproportionately in fruit-related traits. This pattern - higher Shannon diversity for fruit colour, fruit shape and fruit length-to-breadth ratio relative to vegetative and floral traits - is consistent with several earlier reports on brinjal. Working with 48 landraces from *Odisha*, Tripathy *et al.* (2025) [6] reported an overall mean Shannon-Wiener index of 0.733 with the greatest variation ob-

served for fruit length-to-breadth ratio, leaf blade colour, fruit shape and petiole colour, while a large-scale characterization of 622 indigenous and exotic NBPGR accessions using DIVA-GIS reported Shannon diversity values ranging from as low as 0.01 for fruit position and 0.20 for fruit curvature up to 1.51 for fruit colour, with fruit shape (1.30) and fruit length-to-breadth ratio (1.40) again ranking among the most diverse traits (Gangopadhyay *et al.*, 2013) [5]. The concordance between the ranking of highly diverse traits in the present study and in these two independent germplasm sets - despite differences in genotype origin, sample size and geography - suggests that fruit colour, fruit shape and fruit elongation are traits that have been subjected to comparatively less selection pressure, or have diversified more readily under farmer and breeder selection for market

preference, than characters such as fruit curvature and calyx colour, which remain comparatively conserved across brinjal germplasm.

Table 3. Most frequent descriptor state of each Ward-Gower cluster for nine key morphological traits

Trait	Cluster I (n = 6)	Cluster II (n = 13)	Cluster III (n = 17)	Cluster IV (n = 9)
Plant growth habit	Upright (83.3%)	Intermediate (46.2%)	Intermediate (64.7%)	Intermediate (66.7%)
Plant height	Tall (100.0%)	Tall (84.6%)	Intermediate (58.8%)	Tall (55.6%)
Leaf blade colour	Green (50.0%)	Dark green (61.5%)	Green (58.8%)	Light green (66.7%)
Corolla colour	White (83.3%)	Bluish violet (53.8%)	Pale violet (70.6%)	Pale violet (88.9%)
Fruit colour at ripeness	Green (100.0%)	Purple black (53.8%)	Milky white (29.4%)	Purple (55.6%)
Fruit shape	Long (66.7%)	Round (38.5%)	Round (29.4%)	Oblong (77.8%)
Fruit curvature	Slightly curved (83.3%)	None / straight (100.0%)	None / straight (94.1%)	None / straight (100.0%)
Fruit length:breadth ratio	Several times as long as broad (66.7%)	As long as broad (46.2%)	Slightly longer (52.9%)	Slightly longer (55.6%)
Seed colour	Brownish yellow (66.7%)	Brownish yellow (46.2%)	Light yellow (41.2%)	Brownish yellow (44.4%)

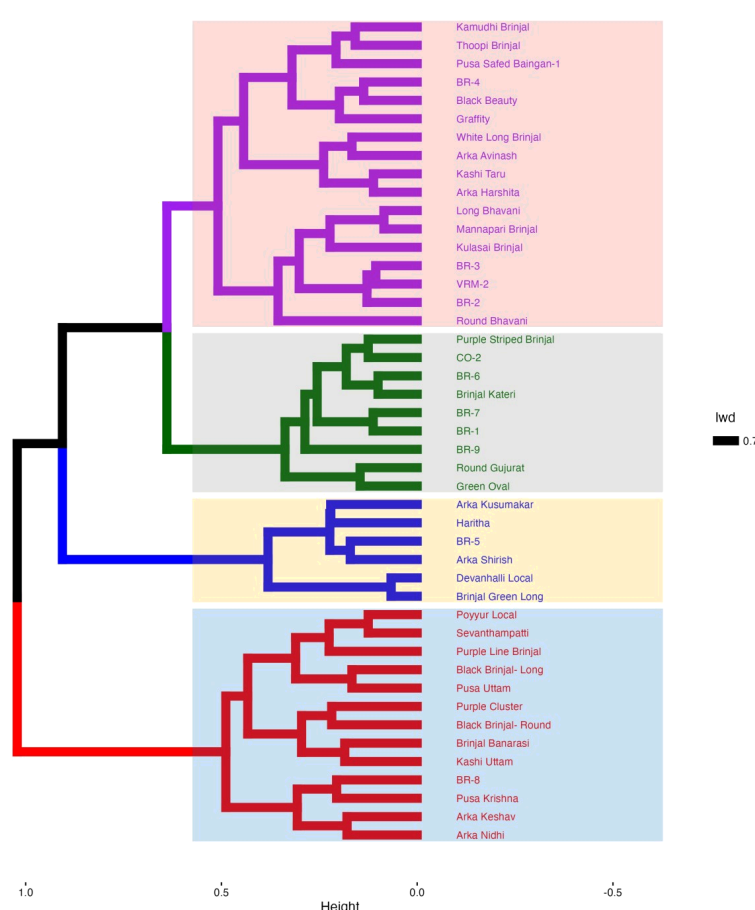


Figure 4. Dendrogram of 45 brinjal genotypes based on Ward's minimum-variance hierarchical clustering of Gower's dissimilarity matrix computed from 20 qualitative morphological descriptors, with the four resolved clusters.

A morphological survey specifically conducted on brinjal germplasm from the coastal Karaikal region reported similarly wide variation for fruit and plant traits among locally available genotypes (Bharathi *et al.*, 2024) [11], supporting the observation that the coastal, deltaic tract in which the present genotypes were evaluated genuinely diverse brinjal material rather than a narrow, closely related set of types. Likewise, multivariate divergence studies employing Mahalanobis'

D^2 statistics on other brinjal collections have consistently identified fruit size, fruit shape and fruit colour as major contributors to overall genetic divergence (Anbarasi *et al.*, 2021; Younas *et al.*, 2022; Zabbar *et al.*, 2024) [7, 12, 9], and divergence analysis including wild and semi-wild relatives has shown that fruit and flowering characters differentiate cultivated types most sharply (Lintu *et al.*, 2023) [8], further corroborating the trait-wise pattern of diversity recorded here.

The comparatively low diversity recorded for calyx colour, fruit curvature, leaf blade length and leaf blade tip angle indicates that these characters are close to fixation in the present genotype set, with one descriptor class accounting for more than 70-85% of genotypes in each case; such traits are of limited direct value for distinguishing genotypes or for use as morphological markers in this particular collection, although they may still be diagnostic when this material is compared against germplasm from other agro-ecological regions. In contrast, the pronounced diversity for fruit colour, fruit shape, fruit length-to-breadth ratio and corolla colour identifies these as the descriptors of greatest immediate value for distinguishing among the 45 genotypes and, more importantly, for guiding the choice of morphologically divergent parents in future hybridization programmes aimed at combining desirable fruit-quality attributes, since genetic divergence for fruit traits translates directly into scope for heterosis and transgressive segregation for yield- and quality-related characters in the F_1 and subsequent generations (Anbarasi *et al.*, 2021; Tripathy *et al.*, 2025) [7, 6].

4. Conclusion

The present study demonstrates that considerable and unevenly distributed morphological diversity exists among the 45 brinjal genotypes evaluated at PAJANCOA & RI, Karaikal, with the Shannon-Wiener diversity index ranging from 0.393 for fruit curvature to 1.606 for fruit colour at commercial ripeness across the 20 qualitative descriptors examined (mean $H' = 0.884$; mean $H'n = 0.789$). Fruit-related traits - fruit colour, fruit shape, fruit length-to-breadth ratio and fruit cross-section - together with corolla colour, contributed disproportionately to the overall diversity recorded, while calyx colour, fruit curvature and certain leaf descriptors were comparatively uniform across the genotype set. Ward's hierarchical clustering of Gower's dissimilarity matrix grouped the 45 brinjal genotypes into four morphologically divergent clusters distinguished mainly by fruit colour, fruit shape and plant stature. Cluster analysis separated a distinctive group of tall, green, long-fruited genotypes (Cluster I) from the remaining, more variable purple- and oblong-fruited genotypes. These findings confirm that the germplasm assembled for this study, comprising released varieties, landraces and breeding lines, constitutes a genetically diverse working collection that can be profitably exploited for the selection of morphologically divergent parents in brinjal hybridization programmes, for the construction of representative core or working collections, and for descriptor-based documentation and varietal identification. Fruit colour and fruit shape-related descriptors, in particular, merit priority attention in future characterization and breeding efforts targeting fruit-quality improvement in brinjal and crosses between Cluster I and Cluster II genotypes, in particular, they are recommended as a priority for future hybridization work aimed at maximizing heterosis and transgressive segregation for fruit traits.

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