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RESEARCH ARTICLE

Characterization of native eggplant (*Solanum melongena* L.) germplasm of India for economic traits and variation assessment using SSR markers

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Abstract

Characterization and periodic multiplication of germplasm collections conserved in gene banks are essential for their effective use in crop improvement. In this study, 404 eggplant accessions of Indian origin, conserved at the National Gene Bank, New Delhi, were characterized for nineteen agro-morphological traits of economic importance at ICAR-IIVR, Varanasi, and molecular diversity was evaluated using microsatellite markers. Substantial variability was observed for the number of fruits per plant (1–57.3), fruit weight (6.9–274.0 g), fruit yield (0–1976.2 g), fruit length (4.5–30.5 cm), fruit width (2.3–9.9 cm), and plant height (47.8–112.8 cm). Accessions with desirable traits across different fruit shapes were identified. Agglomerative hierarchical clustering revealed three major clusters based on fruit shape: long, oval/round, and oblong. The first five principal components explained 50% of the observed variance. Leaf length, leaf width, and fruit weight contributed most to Principal Component 1, while fruit curvature, fruit length, fruit shape, and fruit width were key for Principal Component 2. A diverse subset of 81 accessions (20% of the total) representing maximum allelic diversity was identified for practical field maintenance. SSR markers were effective in diversity assessment with an average PIC value of 0.425, and cluster analysis grouped accessions primarily by collection region. Combined morphological and molecular variation assessment supports the effective use of diverse eggplant accessions in future breeding programs.

Keywords: Brinjal, Characterization, Eggplant, SSR, *Solanum melongena*.

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Introduction

Brinjal (*Solanum melongena* L.), also called eggplant/ aubergine, is an important vegetable crop of the Solanaceae family, cultivated in tropical and subtropical regions of the world. During 2022, the global production of brinjal fruits was 59.3 million tonnes with a gross value of 30.8 billion US dollars (http://faostat.fao.org/). China is the lead producer, followed by India, contributing to 64.5 and 21.6% of global production, respectively. In India, it is cultivated in 6.75 lakh hectares and contributes to 9% of the total vegetables produced in the country. India is one of the domestication centres of brinjal or eggplant (Meyer et al., 2012). A large diversity of landraces exists in the country, and the wild relatives such as *S. incanum,* which is the direct progenitor of cultivated *S. melongena,* are commonly found (de Candolle, 1886; Karihaloo and Gotlieb, 1995; Kumar et al., 2008; Tiwari et al., 2016). There is a large variation in fruit shape, *viz*., long, round, oval, oblong, club shape, fruit size, fruit skin colour, *viz*., green, different shades of purple, white, with or without stripes and patches. As modern cultivars are replacing diverse landraces, there is a risk of increased vulnerability to abiotic and biotic stresses owing to climate change. Thus,

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extensive characterization and utilization of germplasm conserved in the National Gene Bank (NGB) at ICAR-National Bureau of Plant Genetic Resources (ICAR-NBPGR), New Delhi, collected at different times, representing diverse ecological regions of the country, would help in breeding programmes and broaden the genetic base. Brinjal germplasm evaluation is reported from India and other parts of the world (Kumar et al., 2008; Palignano et al., 2010; Adeniji et al., 2012; Cericola et al., 2013; Tiwari et al., 2016). Although, part of brinjal germplasm from NBPGR, New Delhi were morphologically characterised by Kumar et al. (2008) and Tiwari et al. (2016), the present study included characterization of large brinjal germplasm predominantly of Indian origin/indigenous collections (IC) with aim to assess the variability using Multivariate analysis, identify promising accessions for important yield related traits, identify minimum germplasm size with maximum genetic diversity for practical field maintenance and assessment of molecular diversity with simple sequence repeat(SSR) markers.

Materials and Methods

Plant materials and field experiment

A total of 404 brinjal accessions, including landraces (47%), elite/breeding lines and released varieties (18%), unknown genetic background (35%) collected from 25 states and 3 union territories of India (Indigenous collection, IC), two exotic collections (EC) conserved at National Gene Bank, New Delhi, were evaluated during 2023-24 (main kharif)**.** One-month-old seedlings were transplanted to the field on 18 August 2023 at ICAR- Indian Institute of Vegetable Research, Varanasi, located at a latitude of 25.10˚N, longitude of 82.52˚E, altitude of 128.93 m AMSL, receiving average annual rainfall of 1115 mm and experiencing a humid subtropical climate. The farm has sandy loam soil with a pH of 7.7. Each accession was grown in a single row with 8 plants, 75 cm between rows, and 60 cm between plants in an Augmented Block Design (Federer 1956) in 6 blocks. Five check varieties representing round fruit shape: Kashi Uttam, long fruit shape: Arka Shirish, Kashi Prakash, Arka Nidhi, and Kashi Taru were replicated randomly in each block. Recommended agronomic practices were followed to raise a healthy crop. Four fruit pickings were taken up at the commercial fruit harvest stage with a 15-20-day interval. The diverse eighty-one accessions identified were re-evaluated in the field in an augmented design in four blocks using the same five checks during the main growing season 2024 for qualitative traits.

Phenotyping of agro-morphological and phenological traits

The data was recorded on 19 traits including 10 quantitative *viz*., days to 50% flowering (dff), plant height (ph; cm), primary branches (pb), leaf length (ll; cm), leaf width (lw; cm), fruit length (fl; cm), fruit width (fw; cm), number of fruits (nf; No.), fruit weight (fwt, g) and fruit yield (fy, g) and 9 qualitative traits namely growth habit (gh), leaf lobbing (lb), corolla color (cc), pigmentation of leaves (pig), calyx thorn (ct), fruit curvature (fc), fruit shape (fs), fruit colour (fclr) and fruit colour distribution (fcd) as per the descriptors for eggplant (IBPGR, 1990).

Molecular characterization using SSR markers

Sixty-one SSR markers from the sequence information obtained from transcriptome analysis (Mishra et al, 2020) were used in the study. Genomic DNA was extracted from leaves of 81 morphologically diverse genotypes obtained using a modified cetyl trimethylammonium bromide (CTAB) method as described by Doyle and Doyle (1987). Polymerase chain reaction (PCR) was performed in a 10 µL volume consisting of 2x ready-to-use PCR master mix (Helix), 5pmol of each primer, and 50 ng template DNA. PCR protocol consisting of a 94°C/5 min initial denaturation, 36 cycles of thermal profile with:94°C/1 min denaturation, marker-specific annealing temperature/1 min, and 72°C/2 min extension. The final extension was carried out at 72°C for 10 min. The amplicons were separated on 3% high-resolution agarose gel stained with ethidium bromide and visualized on the ChemiDOCTM Imaging System (BIO RAD, California, USA).

Statistical analysis

Morphological quality traits were analyzed for frequency distribution using Microsoft Excel. Quantitative traits were subjected to ANOVA under an augmented randomized block design (Federer, 1956), and adjusted means were generated in R (R Core Team, 2019) via the *augmentedRCBD* package (Aravind et al., 2019). Genetic variability parameters—PCV, GCV (Burton, 1952), broad-sense heritability (Lush, 1940), and genetic advance (Johnson et al., 1955)—were estimated for each trait. Cluster analysis based on the Gower distance matrix was performed using the *cluster* package, employing Ward's method (agglomerative coefficient = 0.95). Principal Component Analysis (PCA) using *FactoMineR* and *factoextra* identified key traits contributing to multivariate variation. A representative diverse subset was selected using the Gower matrix in the R front-end for Core Hunter 3 (De Beukelaer et al., 2018). The Shannon–Weaver diversity index (H') and evenness (Shannon and Weaver, 1949) were computed for phenotypic frequency classes in both full and representative sets. SSR data were processed in DARwin 6.0.21 (Perrier and Jacquemoud-Collet, 2006) using the simple matching coefficient and Ward's clustering method. Polymorphic information content (PIC) and expected heterozygosity were calculated via Polypicker (Botstein et al., 1980).

Results and Discussion

Frequency distribution of qualitative traits

The frequency distribution of nine qualitative traits is presented in Figure 1. Leaf blade lobbing showed four

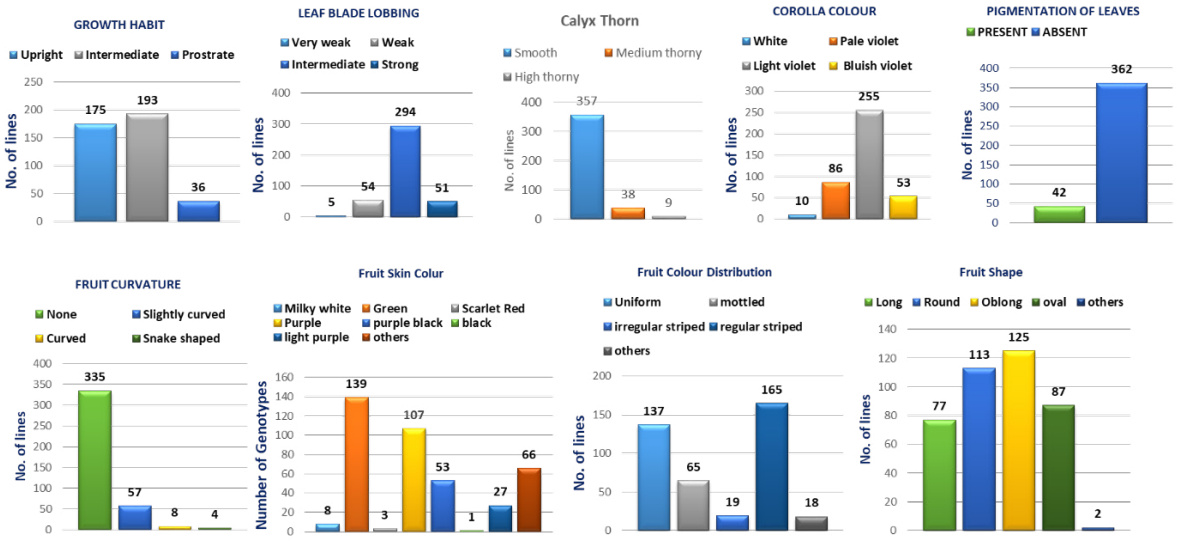

Figure 1: Frequency distribution of brinjal germplasm for qualitative traits

categories, with 73% exhibiting the intermediate type. Thornless calyx occurred in 88% of accessions, while only 2% were highly thorny. Corolla colour varied in four shades, predominantly light violet (63%), and anthocyanin pigmentation in leaves appeared in 10% of accessions. Eight fruit skin colours were recorded at commercial maturity—green (34%) and purple (26%) were most frequent, while eight accessions showed white fruit and one (IC0573431) exhibited a rare black skin. Fruit colour pattern was mainly striped (41%) or uniform (34%), and shape ranged from oblong (31%) and round (28%) to oval (21.5%) and long (19.1%) (Figure 2). Green fruit types were common in southern India, while both green and purple types appeared in eastern states; long and oblong fruits dominated in the North East.

The wide variation in fruit traits underscores adaptation to diverse agro-climatic regions and culinary preferences across India. Although high-yielding hybrids dominate markets, traditional landraces with distinct flavour, shape, and colour are declining, warranting conservation. Several regional types, such as *Udupi Mattu Gulla* (Karnataka), *Vellore Spiny* (Tamil Nadu), *Ramnagar Bhanta* (Uttar Pradesh), *Jalgaon Bharit* (Maharashtra), and *Nayagarh Kanteimundi* (Odisha), already hold Geographical Indication (GI) status. Community-level seed multiplication and biochemical characterization of unique landraces can enhance conservation and nutritional understanding. Upright and intermediate growth habits are favoured for high-density cultivation. While wild relatives of brinjal (Leptostamineae) are thorny, domestication has selected for thornless genotypes preferred for ease of harvest. Nevertheless, prickliness may have a role in pest resistance, meriting further study in breeding programs.

Figure 2: Variability in fruit colour, shape, size among brinjal accessions

Descriptive statistics pertaining to quantitative traits

All quantitative traits, except primary branches, exhibited wide variability (Table 1). Accession IC601469 was the earliest to flower (60 days), with 53% of accessions classified as medium (60–80 days) and the remainder as late (>80 days), averaging 81 days. Most genotypes were tall (60–100 cm), while four accessions (IC261793, IC446672, IC344749, IC427021) exceeded 100 cm. The majority of accessions had intermediate leaf length (10–20 cm, mean 13.4 cm) and leaf width (5–10 cm, 79% of genotypes). Fruit length varied from 4.19 to 30.49 cm, while fruit width ranged from 2.3 to 9.9 cm. Fruit yield per plant exceeded 1 kg in 128 accessions. The number of fruits per plant ranged from 1 (IC 345291) to 57.32 (IC 594923), with a mean value of 12.

Both GCV and PCV were low for dff, pb, and lw, medium GCV and PCV for ph and ll. All other 14 traits had high GCV and PCV values. Heritability in the broad sense was high for all traits, except pb (low) and lw (medium). Genetic advance over per cent mean was high (>20) for all traits, except pb (low), dff (medium), and lw (medium). High GCV coupled with high heritability and genetic advance for a trait indicates its high reliability based on phenotypic selection (Johnson et al. 1955). Fruit traits with economic relevance, namely fruit length, fruit width, number of fruits per plant, average fruit weight and fruit yield, were found to have high GCV with high heritability and genetic advance. Thus, accessions identified as promising for these traits can be reliably selected for future breeding programmes. Traits viz., dff, pb, and lw with low GCV indicate governance by non-additive genes and are significantly influenced by the environment, which is in concurrence with reports by Sulaiman et al. 2020.

Agronomically superior accessions across fruit shape identified

Identifying accessions as potential donors is essential for effective utilization of genetic resources in breeding programs. Accordingly, promising accessions for key economic traits such as minimum dff, intermediate plant height with erect growth habit, fruit length more than 25 cm in long fruit shape, fruit width with more than 9 cm in round fruited ones, average fruit weight more than 100g in all four fruit shapes (long, round, oblong, oval), fruit yield per plant more than 1.5 kg and average fruit number/plant more than 30 were identified (Table 2).

Cluster categories of the germplasm based on morphological attributes

Hierarchical clustering based on genetic distance using both quantitative and qualitative traits identified three major groups (Figure 3). Cluster I (177 accessions) primarily comprised oblong genotypes, Cluster II (64 accessions) included long-fruited genotypes, and Cluster III (164 accessions) contained mostly oval and round genotypes. Similar grouping was also reported by Cericola et al. 2013 among 'Oriental' and 'Occidental' eggplant germplasm represented from diverse regions of the world. Fruit shape is also greatly influenced by traits like fruit length, fruit width and fruit weight, which contribute to genetic distance used for grouping. Thus, different-shaped fruits should be considered for representative samples in brinjal.

Principal component analysis of agro-morphological characteristics

Principal component analysis helps to understand the major combination of variables influencing directions of the coordinate system, called principal components, in the total variance observed. In the present study, PCA based on singular value decomposition of both quantitative and qualitative traits depicted that the first two PCs explained 33% of the total variance, whereas the first nine principal components were responsible for 77% of the variance. Traits, namely ll, lw, and fwt, were major influencing traits for PC 1, whereas fc, fl, fs, and fw contributed to PC 2, fy and nf were positively influencing PC 3, lb ratio for PC 4. Since 50% of the total variance is contributed by first four factors, it can be considered that leaf dimension traits (ll, lw) and fruit traits

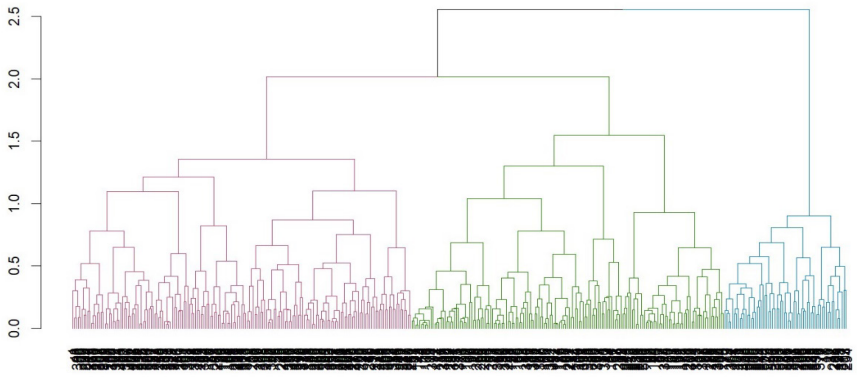

Figure 3: Hierarchical Cluster grouping of brinjal germplasm based on agro-morphological traits

Table 1: Descriptive Statistics and estimates of genetic variability in brinjal germpalsm

Trait	*Mean ± SE*	*Min*	*Max*	*GCV*	*PCV*	*h2(bs)*	*GA*	*GAM*
DFF	80.91 ± 0.26	60.47	94.83	5.9	6.4	85.8	9.25	11.43
PH	76.40 ± 0.51	47.84	112.86	12.5	13.8	83.4	18.13	23.73
PB	5.62 ± 0.06	2.80	9.97	6.0	21.5	7.9	0.20	3.50
LL	13.43 ± 0.10	4.99	20.01	12.1	14.4	70.2	2.81	20.90
LW	8.90 ± 0.07	3.99	14.56	9.2	15.8	34.2	0.99	11.13
FL	10.48 ± 0.22	4.19	30.49	35.8	39.3	83.2	7.06	67.38
FW	5.30 ± 0.08	2.30	9.90	29.3	30.4	92.9	3.09	58.36
NF	12.23 ± 0.38	1.00	57.32	59.9	62.8	90.7	14.39	117.66
FWT	78.32 ± 2.13	6.91	274.05	42.6	49.4	74.1	59.24	75.64
FY	823.14 ± 20.28	0.00a	1976.19	42.66	51.0	69.8	605.44	73.55

DFF: days to fifty percent flowering; PH: plant height (cm); PB: number of primary branches; LL: leaf length(cm); LW: leaf width(cm); FL: fruit length(cm); FW: fruit width(cm); NF: number of fruits; FWT: average fruit weight (g); FY: fruit yield per plant (g). [a]Negative adjusted mean value considered as zero

Table 2: Superior accessions identified for different yield related traits

S. No.	*Trait*	*Fruit shape*	*Accessions*	*Superior check*
1	Days to fifty percent flowering	Long	IC0601469 ≤60 days	Kashi Taru (74.6)
		Round/ oblong/ oval	-	
2	Plant height (60-80 cm) with erect growth habit	Long	IC0394872, IC0381562, IC0590818, IC0398175, IC0585689, IC0594923	Kashi Prakash (76.5)
		Round	IC0545860, IC0427015, IC0427012, IC0545876, IC0446676	
		Oblong	IC0545863, IC0427011, IC0527009, IC0261845, IC0545857	
		Oval	IC0439266, IC0439307, IC0439249, IC0439277, IC0439280	
3	Fruit length (≥25 cm)	Long	IC0553604, IC0636524, IC0585689, IC0345746, IC0610392	Arka Shirish (26.4)
4	Fruit width (≥9.0 cm)	Round	IC0285126, IC0555949, IC0585690, IC0343007, IC0526173	Kashi Uttam (8.2)
5	Average Fruit weight(g) >100g	Long	IC0398175, IC0636522, IC0642079, EC0169089, IC0345746	
		Round	IC0594916, IC0285126, IC0594906, IC0526173, IC0427009	
		Oblong	IC0639101, IC0594907, IC0411486, IC0261840, IC0555931	
		Oval	IC0594920, IC0523083, IC0594929, IC0644920, IC0439280	
6	Fruit yield/plant(g) >1500g	Long	IC0644922, IC0585689, IC0573430, IC0642079	Kashi Uttam (1476.81)
		Round	IC0218975(g326), IC0644912(g384), IC0604991(g272), IC0265252 (g43)	
		Oblong	IC0594922, IC0594914, IC0555927, IC0523081, IC0644893	
		Oval	IC0644919	
7	Number of fruits >30 No	Long	IC0594923, IC0345758, IC0573430, IC0636532, IC0090947, IC0523082	Arka Nidhi (16.2)
		Round	IC0265247, IC0112927, IC0343009	
		Oblong	IC0638176, IC0555927, IC0636518	
		Oval	IC0641521, IC0607223, IC0636532, IC0427025	

mainly fruit curvature and fruit shape among qualitative traits, fruit length, fruit width, lb ratio, fruit weight, number of fruits and fruit yield among quantitative traits contribute to most variability in the brinjal germplasm. (Figures 4 and Table 3). Since none of the principal components account for more than 25% of the total variance, the dataset reflects high multidimensional diversity. Similar contribution of PCs to total variance using phenotyping traits was reported in eggplant landraces of Spain by Martínez-Ispizua et al. (2021).

Comparative evaluation of representative and whole germplasm set

For effective resource management, identification of a diverse set with reduced and optimum accession number from a large germplasm set is an important strategy for practical utility in breeding programmes (Marita et al., 2000). A representative set comprising 81 accessions was identified, with 20% of the entire set of accessions. The Shannon-Weaver diversity index and evenness value between the whole germplasm set and the representative set were compared for qualitative traits (Table 4). The 20% of the germplasm was selected for optimum size for allele diversity representation in maize by Franco-Duran et al. 2019, in radish by Li et al. (2023). The increased H'value and evenness for the representative set depicted maximization and effective representation of diversity for all the traits evaluated from the germplasm set. Similar criteria were applied to evaluate a core set from the entire barley germplasm using qualitative traits by Kaur et al. (2022).

Analysing the molecular diversity present in a set characterized by morphological diversity

Morphologically diverse set of 81 accessions identified from the whole germplasm set (404 accessions) was analysed for molecular diversity using SSR primers. Among the 61 SSR primers employed to analyse genetic diversity, 34 were found to be polymorphic and their allelic variation is presented in Table 5. A gel picture of polymorphic marker Si_1126 is presented in Figure 5. A total of 114 alleles were amplified, with an average of 3.35 alleles per marker, wherein the number of alleles varied from 2 to 7. A maximum number of 7 alleles was detected in marker 146- Si_323. Major allelic frequency varied from 0.271605 (146-Si_323) to 0.975309 (190-Si-815). The expected heterozygosity varied from 0.0198 to 0.8036 with a mean value of 0.4945. PIC varied from 0.0196 to 0.7756 with a mean value of 0.425. Twenty-one rare alleles with less than 5% allelic frequency were identified. Also, eight unique alleles were identified.

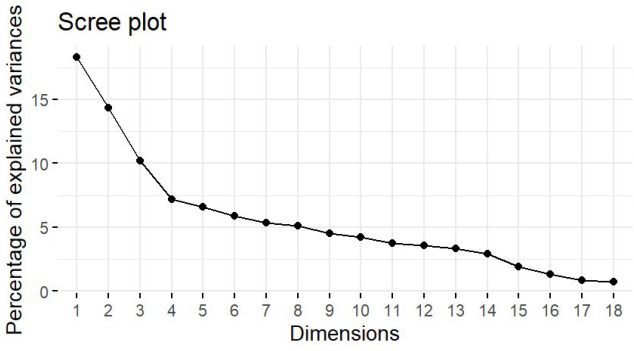

Figure 4: Percentage contribution of variables to total variance

Table 3: Contribution of principal components to total variance observed in brinjal germplasm

PC	*eigenvalue*	*percentage of variance*	*cumulative percentage of variance*
PC1	3.30	18.34	18.34
PC2	2.58	14.34	32.69
PC3	1.84	10.21	42.89
PC4	1.29	7.19	50.09
PC5	1.19	6.60	56.69
PC6	1.06	5.86	62.55
PC7	0.96	5.32	67.87
PC8	0.91	5.08	72.95
PC9	0.81	4.52	77.47
PC10	0.76	4.23	81.70
PC11	0.67	3.72	85.42
PC12	0.64	3.56	88.98
PC13	0.59	3.30	92.28
PC14	0.53	2.94	95.22
PC15	0.34	1.90	97.12
PC16	0.24	1.33	98.45
PC17	0.15	0.86	99.31
PC18	0.12	0.69	100.00

Table 4: Shannon-Weaver diversity index (H') of qualitative traits in population and corset of brinjal germplasm

Traits	*H' index*		*Evenness*	
	population	*coreset*	*population*	*coreset*
Growth habit	0.93	0.99	0.85	0.91
Leaf blade lobbing	0.82	1.09	0.59	0.79
Corolla colour	0.98	1.18	0.71	0.85
Pigmentation of leaves	0.33	0.46	0.48	0.66
Calyx thorn	0.42	0.71	0.38	0.65
Fruit curvature	0.55	0.88	0.40	0.63
Fruit shape	1.39	1.41	0.86	0.87
Fruit colour	1.59	1.71	0.77	0.82
Fruit colour distribution	1.31	1.41	0.81	0.88

Table 5: List of microsatellite primers used along with their alleles no, expected heterozygosity (%) and PIC

	Sn	*Primer ID*	*Forward sequence (5'-3')*	*Reverse Sequence (5'-3')*	*No. of alleles*	*Expected heterozygosity (%)*	*PIC*
1	145	Si_303	GGAATCAAAATAATCAATCA	GAGAAGACATCGAACTGATA	3	0.2986	0.2596
2	146	Si_323	GAGAAGACATCGAACTGATA	TTTTGTGAATCTGAACTTTT	7	0.8036	0.7756
3	147	Si_333	GCTTGTGAATTAAGTTTGAC	TATCTATTGTTTGCAATCCT	6	0.7418	0.7024
4	149	Si_351	CGCAAATTATTAATCAAAGA	TAATGCTTATGACATCTTCC	6	0.6264	0.5807
5	150	Si_355	ATACTTGTTTCCAATGTCAG	ATTAGTCGGGACTCTAAGAC	5	0.6662	0.6142
6	152	Si_362	TTGAAAATTTGGAGAACTAA	AGGAGCAATACAATAAAACA	5	0.5979	0.5172
7	153	Si_365	ACGGGTTAGATAGATACTCC	AAAAACCATAAAACTGTGG	6	0.7536	0.7146
8	154	Si_373	CAAAGAATGTCATGTAAGGT	ATTCAGTCTTGGAGATCTTT	4	0.5244	0.4213
9	155	Si_374	ACAAAGAATGTCATGTAAGG	CATCTTCTCACCTTGATAGA	4	0.5322	0.436
10	157	Si_401	AGACCCCTTATAAGAAGAAA	CATCCACAACACTAGCTAAC	3	0.4842	0.3789
11	158	Si_449	AAATTTCTTGCTACCCTAAT	GGGTTATAGCTAAGGATTTC	2	0.2861	0.2452
12	159	Si_456	CTTCTCTATATTCAAATCGAAG	GCTTTGTATTTCAACTTCAC	3	0.6494	0.5743
13	161	Si_490	CATTCATCTGTGGTAAAACT	CAGACTTAAAAGAAGGCATA	4	0.4386	0.4092
14	162	Si_515	CAATGGTTTTAGAGAAACTG	ATAGTGGCTAATCAAATGAA	2	0.3942	0.3165
15	163	Si_546	CTTCTACATGCGTACCTAAC	TATTTGACATTCTTCTCCAC	5	0.653	0.6054
16	164	Si_557	CACGGCCATTGGAGTATC	GATCTTAGCAACAGATATGC	3	0.4394	0.3821
17	165	Si_562	AAATTGTCAGAAAACAAGAA	TCATAAAACTCAATGTACCC	2	0.4422	0.3444
18	167	Si_600	AATCAAAATGGTAATGAATG	ACAATCAAAACAAACACAGT	3	0.5058	0.3876
19	168	Si_608	ACATTACAAAAGCACAAAAT	GAATGGAAGAATTGACATAA	3	0.427	0.383
20	169	Si_611	TTTTTAATTGTCACCACTTT	ATCAATCAATCACATCATTT	3	0.6478	0.5744
21	190	Si_815	TGACAAATCCTCTTTCATAC	ACAATCCATGTAATCTACCA	3	0.0485	0.0479
22	191	Si_816	GATTAAAGCAACTTCACAAC	CGATCCTCTATCACTCATAA	3	0.5665	0.4918
23	192	Si_830	CAAATACCCTCTTTCTCTCT	ATCTTCTCTCTTTCTCCAAC	3	0.6383	0.5615
24	193	Si_839	TTACTACTACAAAACCCCAA	GTCATCCCTACTAAAATTCC	2	0.4671	0.358
25	194	Si_843	TATTCTACCAGACACACACC	ACCAATTTCTTTTCTTTCTT	2	0.499	0.375
26	195	Si_846	TTATCACCAACTACCAAGAC	TGTTAAAGATGAAGATGAGG	3	0.5557	0.4556
27	196	Si_849	CTGGAAAGAATTTAAACAAA	ATATTATGAAATCATGGCAA	5	0.7684	0.7314
28	197	Si_853	ATTTGGATGATACCAGCTAC	TCACCTTCTCTATCTTGATG	2	0.2952	0.2516
29	201	Si_1054	CCACTTATTCCAAACAGTAA	GTTCTGCAAGTTTTATATGG	2	0.3942	0.3165
30	207	Si_1108	AATATCGATGGGTAAGAAAT	TGACCTTCATGAGTTATACAG	2	0.3318	0.2768
31	211	Si_1126	TAGTTTCCAAGAAAGAAACC	TCTCAATCATTCAACTTTGT	2	0.4928	0.3714
32	212	Si_1141	GTCTGAACATGGAAGAATAA	GGAATTATCAATCAAGTCAA	2	0.4838	0.3668
33	210	Si_1114	ATACCTCACCATTCTCATCT	ATGAGGTTCATTATTCACAA	2	0.4928	0.3714
34	200	Si_1053	GAACTAGCCTCAAGTCAAA	TTGACATTGAAAACCTCTAC	2	0.0198	0.0196
				Average	3.35	0.4945	0.425561

The cluster analysis of the molecular data grouped the representative diverse 81 accessions into five groups. The number of genotypes varied from 21 in group I to 11 in group IV. Though markers used in the study did not clearly differentiate genotypes for fruit shape/colour, they mostly correlated with the geographical location of their collection. Group I included landraces mostly from southern states *viz*., Karnataka, Andhra Pradesh, Telangana and Tamil Nadu, Group II included 20 landraces mostly from North eastern/Hilly states *viz*., Assam, Tripura, Jharkhand, Himachal

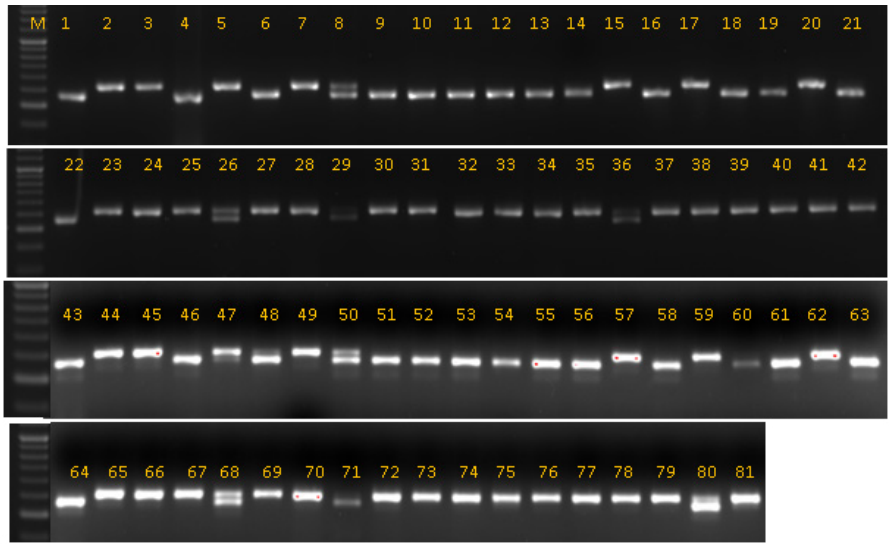

Figure 5: Allelic variation of SSR Marker Si_1126 run in 81 corset brinjal accessions. Genotypes are labelled 1-81, M: Marker (50 bp)

Pradesh, Group III included 15 released varieties/advanced breeding lines for Eastern states mainly Uttar Pradesh and Jharkhand, Group IV included 11 accessions mostly from West Bengal, Group V included 13 landraces from different regions. In addition to morphological diversity, assessment of diversity at the molecular level is important to appreciate allelic diversity in the germplasm set. Molecular markers, mainly SSRs, are commonly used in diversity assessment due to their abundance, reproducibility, codominant and polyallelic nature. Brinjal molecular diversity with genome-wide SSR primers from Nunome et al. (2009) has been reported **(**Miyatake et al. 2019, Mangal et al., 2016). In the present study, a new set of SSR primers reported from transcriptome studies from our previous work (Mishra et al., 2016) was found to be effective in diversity analysis in brinjal. Interestingly, allelic diversity was depicted across geographical regions, showing different selection pressures in the evolution of landraces. The markers in the future can be utilised in fingerprinting studies as well. The morpho and molecular characterization of brinjal germplasm in the study clearly depicts the large variation present and the importance of their conservation and utilization for broadening sthe genetic base in breeding programmes.

Conclusion

This study characterized 404 brinjal accessions, including landraces, advanced breeding lines, and released varieties, primarily from India and conserved at the National Gene Bank, New Delhi, using agro-morphological traits and SSR markers. Substantial variation was observed in the corolla colour, fruit skin colour, colour distribution, fruit shape, number of fruits per plant, fruit weight, fruit yield, plant height, fruit length, and fruit width. Promising accessions for key agro-morphological traits across major fruit shapes were identified for potential use in future breeding programs. Three major cluster groups corresponded to distinct fruit shapes, which significantly influenced crop variability. Principal component analysis highlighted fruit weight, fruit curvature, fruit length, fruit shape, and fruit width as major contributing traits. The representative set of 81 accessions captured maximum germplasm diversity, supporting efficient resource management, field conservation, and further evaluation for abiotic and biotic stress tolerance.

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सारांश

फसल सुधार में, जीन बैंकों में संरक्षित जर्मप्लाज्म के लक्षण-निर्धारण और आवधिक गुणन, उनके प्रभावी उपयोग के लिए आवश्यक है। इस अध्ययन में, राष्ट्रीय जीन बैंक, नई दिल्ली में संरक्षित भारतीय मूल के 404 बैंगन परिग्रहणों का, आईसीएआर-आईआईवीआर, वाराणसी में आर्थिक महत्व के उन्नीस कृषि-आकृति विज्ञान संबंधी लक्षणों के लिए लक्षण-निर्धारण किया गया और माइक्रो-सैटिलाइट) एसएसआर(चिह्नकों का उपयोग कर आणविक विविधता का मूल्यांकन किया गया। प्रति पौध फलों की संख्या (1-57.3), फल का वजन (6.9-274.0 ग्राम), फल उपज (0-1976.2 ग्राम), फल की लंबाई (4.5-30.5 सेमी), फल की चौड़ाई (2.3-9.9 सेमी), और पौधे की ऊँचाई (47.8-112.8 सेमी) में पर्याप्त भिन्नता देखी गई। विभिन्न फलों के आकार में वांछनीय गुणों वाले अभिगमों की पहचान की गई। समूहात्मक पदानुक्रमित क्लस्टरिंग ने फलों के आकार के आधार पर तीन प्रमुख समूहों का पता लगायाबलं :, अंडाकारलोग/, और आयताकार। पहले पाँच प्रमुख घटकों ने प्रेक्षित विचरण के 05% भागीदारी का निर्धारण कर पाया। पत्ती की लंबाई, पत्ती की चौड़ाई और फल के वजन ने मुख्य घटक-1 में सर्वाधिक योगदान दिया, जबकि फल की वक्रता, फल की लंबाई, फल का आकार और फल की चौड़ाई मुख्य घटक-थे र्णपूत्वहम एलकै 2। व्यावहारिक क्षेत्र रखरखाव के लिए अधिकतम ऐलीलिक विविधता दर्शाने वाले 02 ाक लकु) ोंमगभअि 18%) के एक विविध उप-समूह की पहचान की गई। विविधता आकलन में एसएसआर चिह्नक प्रभावी रहे, जिनका औसत पीआईसी मान 0.ाथ 524, और क्लस्टर विश्लेषण ने अभिगमों को मुख्य रूप से संग्रहण क्षेत्र के आधार पर समूहीकृत किया। संयुक्त रूपात्मक और आणविक विविधता आकलन भविष्य के प्रजनन कार्यक्रमों में विविध बैंगन अभिगमों के प्रभावी उपयोग में सहायक रहेगा।