Diversity in brinjal (*Solanum melongena* L.) landraces for morphological traits of evolutionary significance

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Abstract

India holds rich diversity of brinjal (*Solanum melongena* L.) and related species. Besides landraces, many commercial cultivars prevalent in production system also exhibit diverse range of morphological features, particularly fruit characters. We analyzed the extent of diversity among 96 accessions of brinjal with morphologically diverse characters of domestication/ evolutionary significance, representing all agro-ecological regions of the country and 19 accessions of exotic origin. The results could clearly distinguish prickly and non-prickly types of accessions, which could further be classified on the basis of growth habit and fruit characters like shape and colour. This distinctness could be due to more weightage to and high correlation among the prickliness of plant parts i.e. stem, leaves and calyx. The cluster analysis revealed low intra-cluster distances compared to the inter-cluster distances, suggesting homogenous and heterogenous nature of accessions within and between the clusters respectively. The accessions could not be classified on the basis of geographical groups probably because brinjal from India have all degree of variation and cannot be said to have any distinguishing features. The present study also supports the fact that though the brinjal germplasm shows higher morphological diversity, only a small portion of genome is variable and is responsible for such wide range of morphological diversity. This genetic difference among landraces is potentially relevant in creating variability through hybridization of the contrasting forms.

Keywords: Brinjal, evolutionary traits, genetic diversity, germplasm, principal component analysis

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Introduction

Brinjal (*Solanum melongena* L.), a member of family *Solanaceae*, is commonly grown in almost all parts of central, southern and south-eastern Asia, parts of Europe and Africa (Kalloo 1988, Karihaloo and Gottlieb 1995) throughout the year for their young, unripe fruits, which are consumed fresh, dried or pickled (Karihaloo and Gottleib 1995). It forms a major and inexpensive component of daily diet of majority of the population in the developing world especially in India and China where it is considered as the "king of vegetables". India holds rich diversity of *S. melongena* and related species. Since the crop originated and domesticated in south and south-east Asia (Zeven and Zhukovsky 1975), besides landraces, many commercial cultivars prevalent in production system also exhibit diverse range of morphological features, particularly fruit characters (Martin and Rhodes 1979).

Nature and degree of diversity is useful in selection of parents exhibiting desirable traits for a successful breeding program. Selection of parents for single attribute may not be as advantageous as the one for many important attributes collectively. The knowledge of genetic variation is therefore essential for understanding the potential use to select genotypes for breeding program, estimating loss of genetic diversity and prioritizing genotypes/ important population for conservation in traditional production systems on-farm and also in ex-situ conditions. Morphological markers were amongst the earliest markers used (by early domesticators) in selection of germplasm, which is highly influenced by the ethno-botanical use of the plant in the region. The goal of the present research was to analyze the diversity in traits of greater domestication and evolutionary significance.

Material and Methods

Experimental material: The experimental material

comprised of 96 accessions of brinjal with morphologically diverse characters of domestication/ evolutionary significance, representing all agro-ecological regions of the country and 19 accessions of exotic origin (Table 1). Accessions with morphologically diverse characters of domestication/ evolutionary significance were selected for the study. The brinjal accessions grown in augmented block design at ICAR-NBPGR Experimental Farm, Issapur, New Delhi for characterization/ evaluation. Recommended agronomic practices were followed throughout various stages of crop growth.

Observations recorded: Five competitive plants per plot were selected randomly to record observations on 4 qualitative and 16 quantitative descriptors including traits of evolutionary and economic importance. The descriptors and descriptor states were taken from the NBPGR minimal descriptors for brinjal. The qualitative traits included in the study were plant growth habit (3. Upright; 5. Intermediate; 7. Prostrate), upper leaf blade color (1. Light Green; 3. Green; 5. Dark green; 7. Greenish violet; 9. Violet), Fruit shape (1. Round; 2. Oval; 3 Oblong; 4 Long) and fruit color at marketable stage (1. Green; 2. Milky white; 3. Deep yellow; 4. Fine red; 5. Scarlet red; 6. Lilac grey; 7. Purple; 8. Purple black; 9. Black). The quantitative traits included in the study were plant height (cm) at flowering stage, spread of plant North to South (cm), spread of plant East to West (cm), stem prickle (No./10 cm); leaf lamina length (cm), leaf lamina width (cm), upper lamina prickles (No.), lower lamina prickles (No.), flowers/ inflorescence (No.), fruit length (cm), fruit breadth (cm), fruit pedicle length (cm); fruit pedicle prickle (No.), fruit calyx prickles (No.), fruits /inflorescence (No.), fruits /plants (No.).

Data analysis: For qualitative traits, the codes for different descriptor states were used for data analysis while for quantitative traits the mean values of the data was transformed into discrete classes and thus was made as if data of qualitative traits. The scores for various character states of different accessions were converted to binary codes before analyzing both qualitative and quantitative traits. The binary data was subjected to Eucledian square distance analysis. The distance matrix thus obtained was used for cluster analysis using Wards minimum variance method. Ward's method follows a series of clustering steps that begins with "t" cluster; each containing one accession, and it ends with one cluster containing all traits. At each step it makes merger of two clusters that will result in the smallest increase in value of an index E, called sum of square (SS) index, or variance. This means that at each clustering step we must try all possible mergers of two

clusters, compute value of E for each and select that one whole value of E, which is the smallest. Then we go on the next clustering step and repeat the process. For each tentative set of clusters, E is computed as follows, (i) we calculate the mean of each cluster. The cluster mean is a fictitious accession whose descriptor values are the average of traits values for the traits in the given cluster, (ii) we compute the differences between each accession in a given cluster, (iii) for each cluster we square the differences computed above. Add those for each cluster, giving a SS to each cluster. Finally, the value of E is computed by adding the SS for all clusters.

Principal component analysis (PCA): Principal components were analyzed based on binary data. Principal components W_i (i = 1, 2, 3 ——— n) were obtained as, $w = Z_x$ where Z and x are column vectors of correlation 'R' among quantitative traits. The variance of W_i is the ith characteristic root ë; of the correlation matrix 'R' with ë; obtained by solving the characteristic equation %R- ë I% = 0. For each ë, the corresponding characteristics vector is obtained by solving equation %R- ë I% = 0. Scatter plot was drawn using the first two principal components in order to identify the most distinct accessions in different clusters. The statistical analysis was carried out using INDOSTAT statistical package developed at the INDOSTAT services, Hyderabad.

Results

The dendrogram exhibited clear distinction among prickly and non-prickly types of accessions (Figure 1). The accessions of non-prickly types could further be divided into prostrate, upright and intermediate types. Further, accessions with round oval and long/oblong fruit shape formed a separate sub-cluster within prostrate and upright clusters while intermediate growth habit had mainly mixed fruit types with more number of fruits/ plants. Among the prickly accessions, round level fruit shaped and long/oblong fruit shaped form a distinct sub-cluster similar to the cluster with non-prickly accessions, green/white fruits color type accessions grouped together. Inter and intra cluster distances are shown in Table 2 and Table 3. The inter cluster distance between cluster 3 and 4 was maximum (7.522) followed by cluster 2 and 4 (6.315). The intra cluster distance was maximum for cluster 3 (5.845) followed by 4 (5.666) and cluster 1 (4.649) while cluster 2 had lowest (4.495) intra cluster distance (Table 4). The clustering pattern revealed 4 major clusters comprising of 19 accessions in cluster I, 20 in cluster II, 18 in cluster III and 39 in cluster IV.
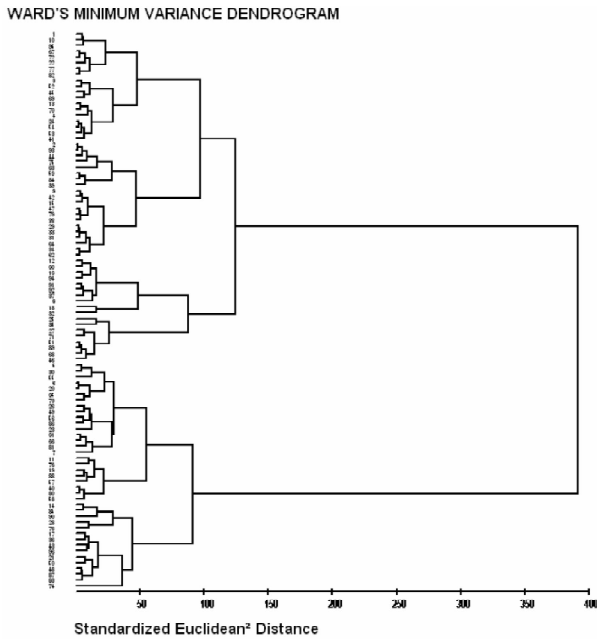
Figure 1: Clustering patter based on ward minimum varience as derived from Eucledian² distance calculated from the recorded data

PCA performed on standardized qualitative traits showed that only four most informative components accounted for 64% of the total variation. The important characters with greater weightage in principal component axes I were stem prickle number/10 cm, calyx prickle number and petiole prickle number accounting for 27.6% of variation. Important characters in principal component axes II include plant height and plant spread accounting for 14.31% of the variation. Leaf lamina length, width and number of fruits/plant had greater weightage in principal component axes III (Figure 1 and 2) with 12.54% of the total variation. The two dimensional PCO of 96 accessions could group prickly and non-prickly
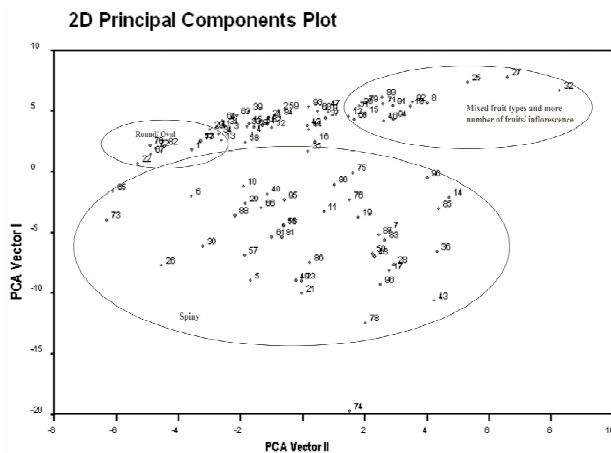

Figure 2: Two-dimension plot of Principal component analysis as derived from Eucledian² distance calculated from the recorded data

types separately, round/oval fruit types and accessions with mixed fruit types and more number of fruits/ inflorescence grouped together.

Discussion

The variation among individuals within a species is caused by the environment or by a dynamic pool of genes changing in frequency as a result of recombination, mutation, selection and chance. It is useful to classify individuals within a species as it helps in easy characterization of individuals. A simple classification of brinjal landraces into different groups is necessary for their efficient use in crop improvement.

In this study 96 germplasm accessions of *S. melongena* were characterized for 3 qualitative and 17 quantitative traits. The data were subjected to standardized Euclidean distance analysis and a dendrogram was generated using Ward's minimum variance methods. The analysis could clearly distinguish prickly and non-prickly types of accessions, which could further be classified on the basis of growth habit and fruit characters like shape and colour. All the accessions studied could be classified into 4 clusters. The details of inter and intra-cluster distance is mentioned in Table 4. Cluster I and cluster II having 19 and 20 accessions respectively had lowest intra-cluster distance suggesting close genetic make-up of accessions included amongst them. The intra-cluster distances are much low than the inter-cluster ones, suggesting homogenous and heterogenous nature of accessions within and between the clusters respectively (Table 6). Prasad and Singh (1998) also revealed high and significant differences in brinjal germplasm and suggested that biological diversity is not always related to genetic diversity and the clustering of germplasm lines depends on the directional selection pressure applied for realizing yield in different regions. Considerable variation in fruit morphology has been observed in most of the domesticated species (Harlan 1992) including brinjal. The variation in vegetative traits might be the result of accumulation of variation in neutral traits, a consequence of selection for adaptation to specific environments, or a combination of both (Prohens *et al.* 2005). In the present study, the prickly and non-prickly type accessions were clearly discriminated in the dendrogram (Table 7 and Figure 1). This distinctness could be due to more weightage to and high correlation among the prickliness of plant parts i.e. stem, leaves and calyx. The results are in congruence to Doganlar *et al.* (2002), regarding prickliness determined by a single major QTL accounting for 79% of phenotypic variation for the trait. The reduction in prickliness was favoured by the early domesticators in brinjal and thus, the cultivated alleles of the QTL favours

Table 1. *Solanum melongena* L. accessions and the available information about the source/ place of collection used for morphological characterization.

S. No.	Accessions	Source/ Place of Collection	S. No.	Accessions	Source/ Place of Collection
1	IC-90909	Coimbtore, Tamilnadu	49	IC-111070-1	India
2	IC-111021	Cooch Bihar, West Bengal	50	IC-99702	Kalahandi, Orissa
3	IC-99731	Puri, Orissa	51	EC-313524	USA
4	IC-111003	Kokrajhar, Assam	52	EC-384619	USA
5	IC-90762	APAU Hyderabad	53	IC-89847	Salem, Tamilnadu
6	IC-99658	Madhuramba, Ganjam, Orissa	54	IC-111005	India
7	IC-90869	Nowgaon, Assam	55	SN-1	India
8	IC-90987	IIHR, Banglore	56	IC-111073	Jharigaon, Orissa
9	IC-111001	Kokrajhar, Assam	57	IC-249351	India
10	IC-249296	Rayagada, Orissa	58	IC-332514	Talawan, Amritsar, Punjab
11	IC-126824	India	59	IC-111050	India
12	EC-311615	Mexico	60	IC-344646	Bogaja, Narmada, Gujrat
13	IC-11427-1	India	61	EC-305013	Jamalpur, Bangladesh
14	EC-316224	Anuradhapura, Srilanka	62	IC-126928	India
15	IC-112356	Gbpua&T, Pantnagar	63	IC-345756	Dhubri, Assam
16	IC-249297	Rayagada, Orissa	64	IC-111000	India
17	IC-127232	India	65	IC-104076	India
18	IC-219295	India	66	EC-427266	USA
19	IC-99735	Hariharpur, Nayagarh, Orissa	67	EC-316212	Srilanka
20	IC-99674	Koraput, Orissa	68	EC-305014	Jamalpur, Bangladesh
21	IC-111308	India	69	IC-9081	India
22	IC-111488	India	70	Pusa Ankur	IARI, New Delhi
23	IC-99664	Koraput, Orissa	71	EC-378820	Taiwan
24	IC-111303	India	72	IC-104088	India
25	IC-111456	India	73	IC-99748	Ghatgaon, Tamilnadu
26	IC-99666	Koraput Orissa	74	IC-336474	Bokaro, Jharkhand
27	IC-99148	India	75	IC-112327	India
28	IC-90905	Udumelpet, Tamilnadu	76	IC-127241	India
29	IC-11360	Mundra, Gujrat	77	EC-316200	Phillipines
30	IC-99614	India	78	IC-89831	Coimbtore, Tamilnadu
31	IC-99657	Madhuramba, Ganjam, Orissa	79	EC-316283	Srilanka
32	IC-90922	IIHR, Banglore	80	IC-249299	Rayagada, Orissa
33	IC-99677	Koraput, Orissa	81	IC-111067	India
34	IC-113016	India	82	EC-169079	Japan
35	IC-111601	India	83	EC-304994	Rangpur, Bangladesh
36	IC-99755	Mayurbhanj, Orissa	84	IC-111072	India
37	IC-136204	India	85	EC-169080	Japan
38	EC-144060	USSR	86	IC-1112347	India
39	IC-111018	India	87	EC-383348	Taiwan
40	IC-249309	Rayagada, Orissa	88	IC-111468	India
41	IC-90056	East Garo, Meghalaya	89	EC-383342	Taiwan
42	IC-112732	India	90	IC-336471	Chirkunda, Dhanbad, Jharkhand
43	EC-316284	Kwatara, Srilanka	91	IC-136268	India
44	IC-111013	India	92	IC-343009	Bokaro, Jharkhand
45	IC-111025	India	93	IC-111026	India
46	IC-137759	India	94	IC-137144	India
47	IC-98148	India	95	IC-111082	India
48	IC-112350	India	96	EC-316268	Srilanka

less number of prickles.

The results of the study justify usefulness of brinjal accessions in breeding program for characters of agronomic and economic importance. The results also support the suggestions of Martin and Rhodes (1979) that the grouping of accessions signifies non-random distribution of variation in the brinjal genome. The diverse geographic origin of two accessions cannot be considered as a parameter to describe genetic diversity

(Skroch *et al.* 1998). However, unlike the findings of Martin and Rhodes (1979), the accessions could not be classified on the basis of geographical groups but the results supports the view of Pramanick *et al.* (1992) and Karihaloo and Gottleib (1995) that brinjal from India cannot be said to have any distinguishing features probably because all degree of variation are found here. Kalloo and Sidhu (1980) explained the situation to be due to the difficulty in establishing actual location of

Table 2: Basic statistics of data recorded for quantitative traits in brinjal accessions.

S. No	Trait	Minimum	Maximum	Mean	SD	CV (%)	Skewness
1	Plant height (cm)	26.4	87.0	59.47	13.26	22.30	-0.16
2	Stem prickle number	0.0	13.0	1.99	2.74	137.84	1.33
3	Petiole prickle number	0.0	5.4	1.09	1.41	129.22	0.95
4	Leaf lamina length (cm)	6.8	24.4	12.88	3.54	27.48	0.45
5	Leaf lamina width (cm)	4.4	15.0	8.5.	2.45	28.81	0.40
6	Upper lamina prickle	0.0	12.2	2.23	3.03	135.93	1.26
7	Lower lamina prickle	0.0	8.2	1.01	1.66	164.52	2.03
8	Flowers/inflorescence	1.6	7.0	3.15	0.75	23.81	1.19
9	Fruit length (cm)	3.0	25.8	12.54	4.21	33.56	0.39
10	Fruit breadth (cm)	3.0	10.2	5.85	1.70	29.02	0.57
11	Pedicle prickle number	0.0	6.0	0.94	1.39	148.86	1.55
12	Calyx prickle number	0.0	13.2	2.93	3.74	127.70	0.96
13	Fruits/inflorescence	1.0	4.6	1.82	0.76	42.00	1.17
14	Fruits/plant	3.4	34.6	9.91	4.85	48.93	2.33
15	Spread (N to S) (cm)	37.2	125.0	72.51	14.96	20.64	0.24
16	Spread (E to W) (cm)	35.4	118.0	66.73	4.08	21.09	0.44

Table 3: Frequency of various descriptor states of qualitative traits observed in brinjal accessions

Qualitative trait	Descriptor state	Frequency of accessions
Plant Growth habit	3 (Upright)	41
	5 (Intermediate)	36
	7 (Prostrate)	19
Upper leaf blade colour	1 (Light green)	6
	3 (Green)	46
	5 (Dark Green)	28
	7 (Greenish violet)	15
	9 (Violet)	1
Fruit shape	1 (Round)	17
	2 (Oval)	18
	3 (Oblong)	34
	4 (Long)	27
Fruit colour at marketable stage	1 (Green)	35
	2 (Milky white)	6
	3 (Deep yellow)	0
	4 (Fire red)	0
	5 (Scarlet Red)	0
	6 (Lilac grey)	11
	7 (Purple)	26
	8 (Purple black)	14
	9 (Black)	4

Table 4: Euclidean ^{2} cluster distance (inter and intra cluster-bold underline)

	Cluster I	Cluster II	Cluster III	Cluster IV
Cluster I	**4.649**	5.460	6.296	6.513
Cluster II		**4.495**	6.143	6.815
Cluster III			**5.845**	7.522
Cluster IV				**5.666**
No. of Accessions	19	20	18	39

Table 5: Principal component analysis using 20 descriptors in brinjal accessions

	Variance explained		Characters with high weightings
	%	Cumulative	
Cluster I	27.59	27.59	Stem Prickle Number/10 cm, Calyx prickles, Petiole prickle number
Cluster II	14.31	41.90	Plant height, Spread E to W, Spread N to S
Cluster III	12.54	54.44	Leaf lamina length, Leaf lamina width, Fruits/ plant
Cluster IV	9.55	63.99	Fruit breadth, fruits/ inflorescence, Spread N to S

Table 6: Means of various characters in different clusters of 96 accessions of brinjal

Descriptors	Cluster I	Cluster II	Cluster III	Cluster IV
Plant Height	0.353	0.633	0.060	0.346
Spiny	0.931	0.165	0.023	0.058
Petiole Prickle No.	0.909	0.188	0.086	0.059
Leaf Lamina Length	0.243	0.149	0.763	0.019
Leaf Lamina Width	0.178	0.133	0.745	0.109
Upper Lamina Prickle	0.891	0.180	0.075	0.095
Lower Lamina Prickle	0.881	0.193	0.109	0.056
Flower/ Inflorescence	0.236	0.424	0.235	0.119
Fruit Length	0.303	0.516	0.345	0.155
Fruit Width	0.160	0.045	0.293	0.620
Pedicle Prickle	0.830	0.260	0.030	0.108
Calyx Prickle	0.922	0.280	0.060	0.023
Fruits/ Inflorescence	0.238	0.367	0.251	0.577
Fruits/ Plant	0.226	0.353	0.534	0.413
Spread E To W	0.104	0.631	0.492	0.447
Spread N To S	0.003	0.585	0.447	0.549
Plant Growth Height	0.306	0.460	0.377	0.130
Upper Leaf Blade Color	0.225	0.270	0.151	0.260
Fruit Shape	0.230	0.452	0.281	0.448
Fruit Color Unripe	0.110	0.458	0.193	0.183

origin of accession/genotype. The free and frequent exchange of genetic material among crop improvement programs in country before Convention on Biological Diversity makes it difficult to maintain the real identity and origin of a genotype/accession. Moreover, breeding lines/progenies incorporate genes from varied sources, thus losing the basis genetic/geographical identity.

The present study supports the fact that though the brinjal germplasm shows higher morphological diversity, but only a small portion of genome is variable and is responsible for wide range of morphological diversity. This emphasizes that DNA often changes at a different rate from the evolutionary divergence of morphological characters (Mace *et al.* 1999). This paradoxical phenomenon of high morphological diversity and low genetic diversity probably can be due to the loss, not gain of genetic control during domestication (Lester 1989).

Table 7: Pair-wise Pearson's correlation values for the quantitative traits

S. No	Traits	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
1	PlantHeight															
2	SPN	-0.245*														
3	Pet Pri No	-0.256*	0.864**													
4	LLamLeng	0.129	-0.179	-0.133												
5	LLamWidth	0.113	-0.124	-0.074	0.944**											
6	U Lam Pricles	-0.249*	0.845**	0.836**	-0.117	-0.059										
7	L Lam Pricles	-0.155	0.856**	0.818**	-0.087	-0.025	0.848**									
8	FLW/INFLO	0.265**	-0.123	-0.102	0.007	0.001	-0.144	-0.146								
9	Fruit length	0.442*	-0.206*	-0.148	0.207*	0.121	-0.146	-0.146	0.145							
10	Fruit breadth	0.087	0.110	0.180	0.134	0.204*	0.118	0.112	-0.141	0.066						
11	Pedicle Prickle	-0.108	0.806**	0.734**	-0.159	-0.133	0.701**	0.721**	-0.098	-0.064	0.040					
12	Calyx prickles	-0.134	0.880**	0.910**	-0.131	-0.091	0.847**	0.814**	-0.106	-0.109	0.138	0.878**				
13	Fruit/inflorescence	0.072	-0.116	-0.114	0.051	-0.001	-0.092	-0.131	0.390**	0.140	-0.249*	-0.088	-0.134			
14	Fruit/plant	0.019	-0.143	-0.155	-0.103	-0.126	-0.109	-0.149	0.255*	-0.006	-0.387**	-0.093	-0.145	0.573**		
15	Spread E to W	0.462**	-0.037	-0.050	-0.164	-0.125	-0.033	-0.045	0.255*	0.108	0.131	-0.016	0.032	0.152	0.378**	
16	Spread N to S	0.431**	0.051	0.031	-0.124	-0.076	0.020	0.034	0.220*	-0.004	0.154	0.067	0.113	0.012	0.306**	0.845**

The genetic differences among landraces are potentially relevant to breeding programs in that the variability created through hybridization of the contrasting forms could be exploited. Since crosses among divergent parents are likely to yield desirable recombinants, breeding programs may be initiated between the selected genotypes belonging to different clusters considering their cluster mean.

Acknowledgements

सारांश

भारत में बैंगन और संबंधित प्रजातियों की अधिक विविधता है। प्राचीन प्रजातियों के अलावा कई प्रचलित वाणिज्यिक किस्मों में भी विविध प्रकार की विशेषताएं होती हैं। हमने बैंगन के विभिन्न प्रकार की 96 जीन प्रारूपों में विविधता का विश्लेषण किया है। इनमें देश के सभी कृषि–पारिस्थितिकी क्षेत्रों और विदेशी मूल के 19 प्रवेशों का प्रतिनिधित्व है। परिणाम स्पष्ट रूप से कांटेदार और गैर–कांटेदार प्रकार के जीनद्रव्यों को स्पष्ट रूप से अलग कर सकते हैं जो आगे पौधों की वृद्धि और फल के आकार और रंग के आधार पर विभिन्न समूहों में वर्गीकृत किया जा सकता है। यह विशिष्टता पौधों के भागों में कांटे की उपस्थिति को अधिक महत्व और पौधों के भागों जैसे तना, पत्ते और पुष्पदल में उच्च सहसंबंध के कारण हो सकती है। क्लस्टर विश्लेषण ने अंतर–क्लस्टर दूरी की तुलना में कम अंतरा–क्लस्टर दूरी का पता चला है कि जो समूहों के भीतर समरूपता और समूहों के बीच विषमरूपता प्रकृति का सुझाव देते हैं। प्रविष्टियों को भौगोलिक समूहों के आधार पर शायद वर्गीकृत नहीं किया जा सकता है क्योंकि भारत में बैंगन की सभी प्रकार की भिन्नता है और कोई विशेष विशिष्टता नहीं कहा जा सकता है। वर्तमान अध्ययन इस तथ्य का समर्थन करता है कि हालांकि बैंगन जर्मप्लाज्म उच्च आकारिकी विविधता दिखाता है परंतु जीनोम का केवल एक छोटे अंश में विविधता है जो रूपात्मक विविधता की इतनी विस्तृत श्रृंखला के लिए जिम्मेदार है। स्थानीय किस्मों के बीच ये आनुवांशिक अंतर संभवत: परिवर्तनशील रूपों को संकरण के माध्यम से रूपांतरित करने में संभवत: प्रासंगिक है।

References

Doganlar S, Frary A, Daunay MC, Lester RN and Tanksley SD (2002) Conservation of gene function in the *Solanaceae* as revealed by comparative mapping of domestication traits in eggplant. Genetics 161: 1713-1726.

Harlan JR (1992) Crops and man, 2nd edition. American Society of Agronomy, Madison, Wiskinson.

Kalloo G (1988) Vegetable Breeding Vol III. CRC Press, Boca Raton, FL.

Kalloo JD and Sidhu AS (1980) Genetic divergence in muskmelon (*Cucumis Melo* L.). Genetica Agraria 36: 1-7.

Karihaloo JL and Gottlieb LD (1995). Allozyme variation in eggplant. (*Solanum, melongena* L.) (*Solanaceae*). Theor Appl Genet 90: 578-583.

Lester RN (1989). Evolution under domestication involving disturbance of geneic balance. Euphytica 44: 125-132.

Mace ES, Lester RN and Geolhardt CG (1999) AFLP analysis of genetic relationships among the cultivated eggplants, *Solanum melongena* and wild relatives (*Solanaceae*). Theor Appl Genet 99: 626-633.

Martin FW and Rhodes AM (1979) Sub-specific grouping of eggplant cultivars. Euphytica 28: 367-383.

Pramanick KK, Singh N and Kalda TS (1992) Genetic divergence in eggplant (*Solanum melangena* L.). Indian J Hort 49: 371-375.

Prasad VSRK and Singh DP (1998) Biological diversity in the landraces of eggplant (*Solanum melongena* L.) under sub-humid alfisol of Eastern India (Abstract). Silver Jubilee National Symposium Emerging Scenario in Vegetable Research and Development, PDVR, Varanasi, UP, pp 9.

Prohens J, Blanca JM and Nuez F (2005) Morphological and molecular variation in a collection of eggplants from a secondary centre of diversity: implications for conservation and breeding. J Amer Soc Hortic Sci 130: 54-63.

Skroch PW, Nienhuis J, Beebe S, Tohme J and Pedraza F (1998) Comparison of Mexican common bean (*Phaseolus vulgaris* L.) core and reserve germplasm collections. Crop Sci 38: 488-496.

Zeven AC and Zhukovsky PM (1975) Dictionary of cultivated plants and their centres of diversity. Centre for Agricultural Publishing and Documentation, Wagenngen, pp 219.