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Genetic Diversity of Brinjal (*Solanum melongena* L.) in the Foot Hills of Himalaya

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A B S T R A C T

Brinjal (*Solanum melongena* L.) is an important solanaceous vegetable crop cultivated throughout the world. Thirty eight genotypes were evaluated in RBD with 3 replications in GBPUA&T, Pantnagar for the analysis of genetic divergence. The present study evaluated genetic diversity of accessions through genetic components analyses, and genetic divergence by multivariate and principal component analysis (PCA). Thirty eight genotypes were meaningfully grouped into seven clusters. Cluster III was the largest having fourteen genotypes followed by cluster I, cluster II, cluster IV, cluster V, cluster VI and cluster VII had minimum genotypes. There is no direct relationship between geographical distribution and genetic distance. Among the seven clusters, cluster III showed maximum intra-cluster distance followed by cluster II. Based on inter-cluster distances, the maximum divergence was observed between cluster IV and cluster VII indicating that the genotypes in these clusters could be utilized as parents in hybridization programme to develop high heterotic hybrids and to identify transgressive segregant in F_2 generation. Among the studied characters number fruit per plants showed maximum contribution towards the diversity. On the basis of principal component analysis and average values, genotypes 'Pusa Kaushal', 'PB-70' and 'Niranjan' possessed optimum combinations of all variables and could be utilized as donor parents in breeding of eggplant.

Introduction

Brinjal (*Solanum melongena* L.) is the most popular and widely cultivated vegetable crop grown in India due to its high productivity, round the year availability, better transport qualities and good storability. It is extremely variable in habit and appearance (Cericola *et al.*, 2013). According to Vavilov (1928), its center of origin was in the Indo-Burma region. In China, brinjal has been known for the last 1,500 years. According to Zeven and Zhukovsky (1975), brinjal is originated from India, and China is believed to be the secondary centre of origin. Knowledge on genetic divergence among the breeding materials is very essential to a plant breeder for an efficient choice of parents for crossing programme. The proper choice of parents is a prerequisite in sound breeding. Genetic diversity is one important criterion for selection of parents in production of a hybrid.

Crossing involving parents selected based on genetic divergence may likely produce transgressive segregates. It usually occurs that genetically diverse parents are likely to contribute desirable segregants or to produce high heterotic hybrids. Mahalanobis D^2 techniques appears to be a fruitful approach which is based on multivariate analysis and serves to be a good index of genetic diversity. The present study was planned to generate information on genetic diversity present in thirty eight diverse genotypes of brinjal in the foot hills of Himalaya so as to help the breeder in selecting promising and genetically diverse parents for bringing the desired improvement.

Materials and Methods

Thirty eight genotypes of brinjal, collected from different sources, were tested and evaluated at the Vegetable Research Centre, Govind Ballabh Pant University of Agriculture and Technology, Pantnagar, India (29.50° N latitude and 79.30° E longitude at a distance above mean sea level of 243.84 m).

Seed beds were prepared in a sandy loam soil, pH 7.3, and were 20 cm high and 1.0 m wide. Weathered cowdung manure at 4 $kg \cdot m^{-2}$ was mixed into the beds. The soil was drenched with 0.2% chlorothalonil and 0.1% carbendazim to avoid damping off disease. Seed, after treatment with Thiram® (3 $g \cdot kg^{-1}$ of seed), were sown on 28 June 2016, at a depth 1 cm, at a 5 cm spacing, and covered with finely sieved well-rotted leaf mold (leaves left to decompose for 2 years) to add organic matter and prevent the soil from drying. After sowing, beds were covered with straw until germination which normally takes 5 to 7 days and were hand watered daily up to the 3rd week of July 2016. The beds were covered with 200 µm ultraviolet (UV)-stabilized clear polyethylene film supported by bamboo poles with open sides to protect seedlings from rain and direct sunlight. Seedlings were hardened by withholding water 4 days before transplanting. Thirty-day old seedlings were transplanted to the field on 28 July 2016. Genotypes were arranged in a randomized complete block design with 3 replications at a 75×60 cm spacing with 30 plants in each replication in a 3.75 × 3.6 m plot. Fertilizer at the rate of 75N-75P-75K $kg \cdot ha^{-1}$ was applied pre plant to the soil. Nitrogen was from urea, P was from single-super phosphate and K was from muriate of potash. Additional nitrogen at the rate of 37.5 $kg \cdot ha^{-1}$ was applied in 2 equal split doses at 30 and 55 days after transplanting. Standard agronomic practices were followed in time (Chattopadhyay *et al.*, 2007).

Fifteen plants were chosen at random from each plot for recording observations on number of branch/plant, days to 50% flowering, plant height at first harvest (cm), days to first harvest, fruit length (cm), fruit diameter (mm), number of fruit/plant, fruit weight (g), marketable yield/plant (kg) and total yield/plant (kg). The D^2 statistic (Mahalanobis, 1936) was used to assess genotype genetic divergence for quantitative traits. Grouping of populations was done using Tocher's method as described by Rao (1952). Hierarchical cluster analysis was done with the same genotypes to observe degree of association according to characteristics expressed in a dendrogram (Ward, 1963). Principal component analysis (PCA), to identify the factor dimension of the data, was used to summarize varietal information in a reduced number of factors for selection of the best performing genotypes. Statistical analyses were done using Plant Breeding Tools freely available software statistics (ver. 1.4, IRRI, Philippines, 2014).

Results and Discussion

On the basis of D^2 values the genotypes were grouped into 7 clusters by treating estimated

D^2 values as the square of the generalized distance (Table 1). The grouping pattern of genotypes was random, indicating geographical diversity, and genetic divergence, were unrelated (Mohanty and Prusti, 2001). Cluster III had 14 genotypes followed by cluster I with 12 genotypes, cluster II with 8 genotypes; clusters IV, V, VI and VII had 1 genotype. The monotypic genotypes in cluster IV, V, VI and VII indicated genotypes from these clusters might have originated across the geographical location in breeding programs.

Among the 7 clusters, cluster III with 14 genotypes had the maximum intra-cluster distance followed by cluster II and cluster I (Table 2). The clusters IV, V, VI and VII had no intra-cluster distance as they were monotypic. Maximum intra-cluster distance in cluster III indicated existence of wide genetic divergence among genotypes. A high degree of divergence among genotypes within a cluster could produce more segregating breeding material and selection within clusters can be executed based on maximum mean value for the desirable characters.

Based on inter-cluster distances the maximum divergence occurred between clusters IV and VII followed by clusters II and VII, cluster IV and VI, and cluster IV and VI. Maximum inter-cluster D^2 values occurred between clusters IV and VII indicating genotypes in these clusters can be used as parents in hybridization to identify desirable recombinants either in F_1 or subsequent generations Rathi *et al.,* (2011). Cluster V had the least inter-cluster distance with cluster VI. The least inter-cluster distance was between clusters V and VI indicating a close relationship among genotypes.

Cluster means of genotypes (Table 3) indicated mean values of clusters varied in magnitude for all characters. The maximum cluster mean was in cluster II for number of fruit/plant, marketable yield/plant and total yield/plant. This cluster could be useful sources of genes for yield component traits. The lowest cluster mean was in cluster VI for days to 50% flowering and days to first harvest. Early flowering and harvest could be helpful for breeding an early plant type. A high yielding, early flowering, type could be bred through utilizing the genotypes from cluster II and VI as parents (Das *et al.,* 2010; Kumar *et al.,* 2013 and Ravali *et al.,* 2017).

These clusters have been formed based on the contribution of different characters towards divergence. Among the characters number of fruit/plant exhibited (Table 3) the maximum contribution (31%) towards diversity followed by fruit diameter (23%), fruit weight (16%), marketable yield/plant (12%) and fruit length (11%). Other characters showed negligible contribution towards divergence.

Principal component analysis (PCA) is a standard tool in data analysis because it is a simple, non-parametric method to reduce a complex data set to a lower dimension to reveal sometimes hidden, simplified structures that often underlie it. Here the PCA was performed to obtain a simplified view of the relationship between number of fruit/plant, fruit diameter, fruit weight, marketable yield/plant and fruit length which explained 100% contribution towards divergence, and variable loadings for components PC_1 (number of fruit/plant), PC_2 (fruit diameter), PC_3 (fruit weight), PC_4 (marketable yield/plant) and PC_5 (fruit length) were determined (Table 4). These components were chosen because their eigenvalues exceeded 1.0 and explained 100% of total variance. The PC_1 explained 92.90% of total accounted for variance in which a decrease in number of fruit/plant leads to increased fruit diameter, fruit weight, and decreased marketable yield/plant and fruit length (Table 5).

Table.1 Classification of brinjal genotypes into different clusters based on D^2 value

Cluster number	Number of genotypes	Name of genotype
I	12	KS-331 (Kanpur, Uttar Pradesh), DBL-02 (New Delhi), PB-4 (Pantnagar, Uttrakhand), Tara BWX (West Bengal), Lal Teer (West Bengal), PB-6 (Pantnagar, Uttrakhand), PB-111 (Pantnagar, Uttrakhand), Pusa Anupam (New Delhi), Arka Neelkant (Bangalore, Karnataka), Pusa Bhairav (New Delhi), Pusa Purple Long (New Delhi), IBWL-2001-1 (Varanasi, Uttar Pradesh)
II	8	Pusa Purple Cluster (New Delhi), Swarna Abhinav (Ranchi, Jharkhand), BB-85 (Bhubaneswar, Orissa), PLP-1 (Varanasi, Uttar Pradesh) Pusa Shyamla (New Delhi), SMB-115 (Cuttack, Orissa), GBL-1(Gujarat), Pusa Kaushal (New Delhi)
III	14	Pusa Purple Round (New Delhi), PB-72 (Pantnagar, Uttrakhand), Muktakeshi (West Bengal), Pusa Upkar (New Delhi), WB-1(West Bengal), Green Cluster (Pantnagar, Uttrakhand), Pusa Uttam (New Delhi), Debmallika (West Bengal), PB-71 (Pantnagar, Uttrakhand), BRLVAR-11 (Varanasi, UP), Pusa Ankur (New Delhi), Pusa Bindu (New Delhi), PB-70 (Pantnagar, Uttrakhand), Pusa Kranti (New Delhi)
IV	1	White -154 (Pantnagar, Uttrakhand)
V	1	BARI (Bangladesh)
VI	1	Arka Shrish (Bangalore, Karnataka)
VII	1	Niranjan (Uttrakhand)

Table.2 Inter- and intra-cluster distances of 7 clusters of brinjal genotypes

Cluster	I	II	III	IV	V	VI	VII
I	**11.99**[a]	35.27	48.39	37.67	25.95	24.70	42.25
II		**12.56**	81.62	25.05	68.73	81.42	109.66
III			**14.97**	46.45	85.57	67.47	67.20
IV				**0.00**	99.22	86.51	110.89
V					**0.00**	17.98	26.81
VI						**0.00**	24.40
VII							**0.00**

[a]Bold diagonal values indicate intra-cluster distance; the remainder of values indicate the inter-cluster distances.

Table.3 Cluster means and percent contribution of different characters of brinjal

Character	I	II	III	IV	V	VI	VII	(%) Contribution towards divergence
Number of branch/plant	5.62	5.77	5.17	6.33	5.53	4.88	6.32	2.00
Days to 50% flowering	43.94	45.12	46.16	42.0	50.66	53.00	41.66	1.00
Plant height (cm)	81.88	78.27	85.13	80.60	90.46	97.21	117.73	1.00
Days to first harvest	64.11	64.58	66.28	64.0	70.0	69.33	62.66	1.00
Fruit length (cm)	16.81	13.87	10.33	7.16	24.95	19.21	24.76	11.00
Fruit diameter (mm)	41.32	44.47	68.42	49.74	42.34	27.55	44.57	23.00
Number of fruit/plant	19.73	38.71	13.98	31.52	15.67	6.01	11.03	31.00
Fruit weight (g)	90.73	56.95	154.26	59.21	121.30	110.64	183.96	16.00
Marketable yield/plant (kg)	1.25	1.72	1.26	1.20	1.57	0.91	1.07	12.00
Yield/plant (kg)	1.77	2.08	1.96	1.62	1.90	1.13	1.75	1.00

Table.4 Results of principal component analysis (PCA) for quantitative characters contributing to divergence

Principal component (PC)	Eigenvalue (%)	% Variance	% Cumulative variance
Eigen values and variance accounted for (%) by PCA based on correlation matrix			
PC_1	2315.31226	92.90	**92.90**
PC_2	132.92734	05.33	**98.23**
PC_3	35.63957	01.43	**99.66**
PC_4	8.36314	00.34	**1.00**
PC_5	**0.06661**	**0.00**	**1.00**

Table.5 Contribution of diverse traits in the principal components of brinjal

Variable	PC_1 [a]	PC_2	PC_3	PC_4	PC_5
Factor loadings due to PCs with eigenvalues >1					
Number of fruit/plant	-0.174388	0.293354	0.937735	-0.051699	**-0.038899**
Fruit diameter (mm)	0.238407	0.890999	-0.217058	0.319568	**-0.006721**
Fruit weight (g)	0.955232	-0.174072	0.227899	-0.072601	**-0.004711**
Marketable yield/plant (kg)	-0.001286	0.005817	0.041224	0.033744	**0.998562**
Fruit length (cm)	**-0.016769**	**-0.299549**	**0.141075**	**0.942759**	**-0.035959**

[a]PC_1-5 = Principal component 1-5.

Fig.1 Dendrogram of genotypes of brinjal following Ward's method. Genotypes are in left most column

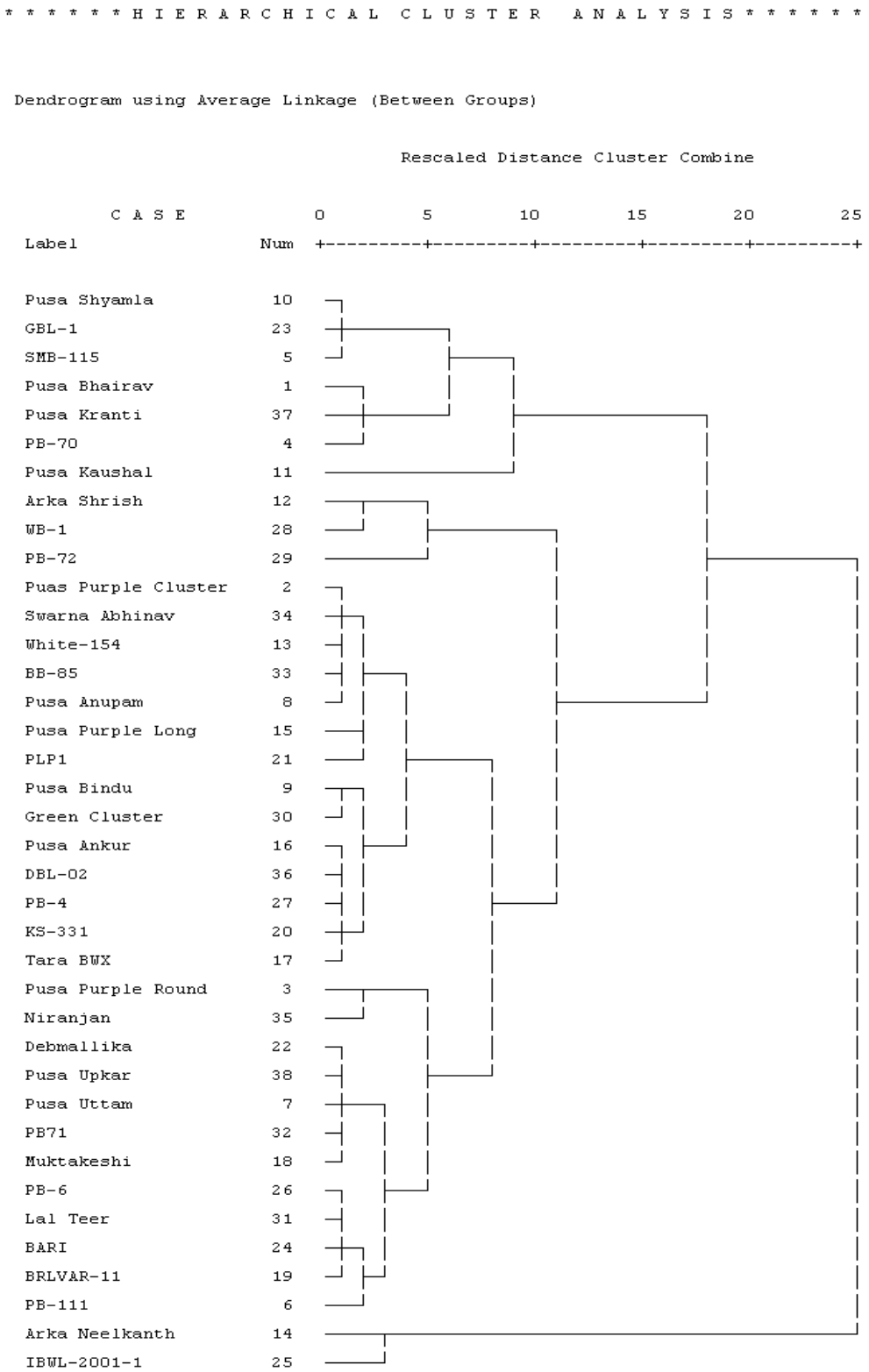


Fig.2 Scatter diagram of regression factor scores for the first and second components as determined by principal component analysis. Points in diagram closest to the intersection of 0 on the X- and Y-axes indicate similarity. Outliers on the X-axis, i.e., 35, indicate diversity. Numbers correspond to name of the genotype (see Figure 1)

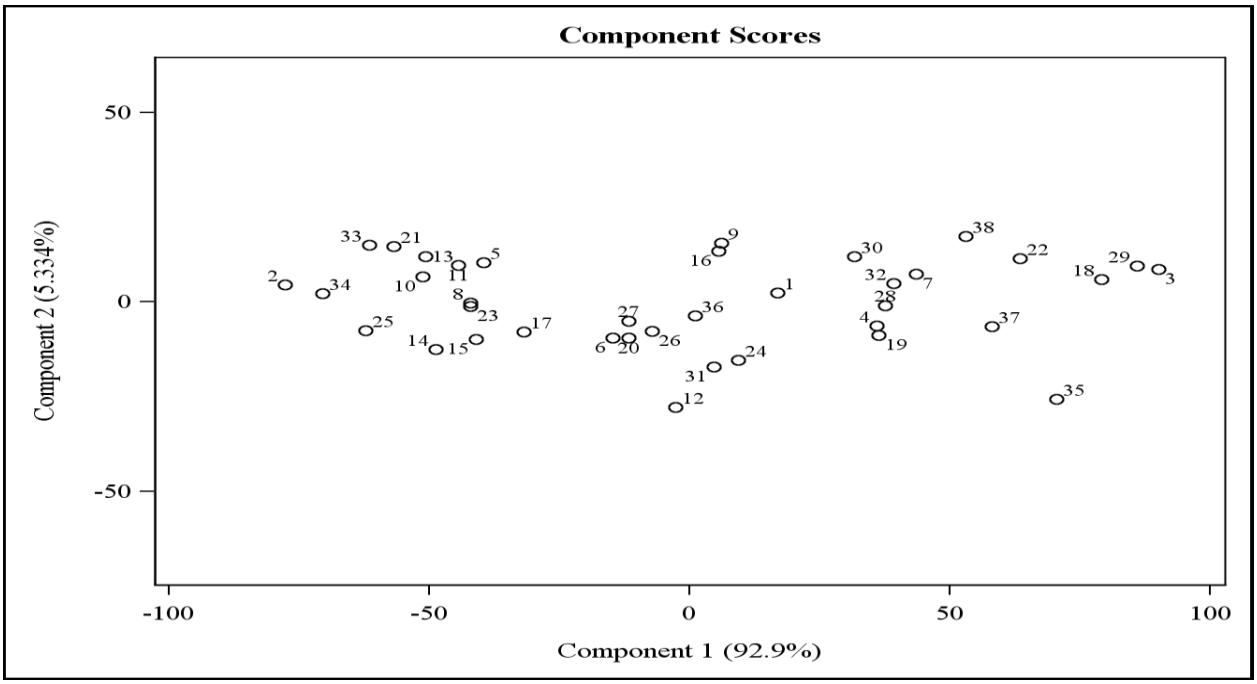


Fig.3 Scatter diagram of regression factor scores for the first and third components as determined by principal component analysis. Points in diagram closest to the intersection of 0 on the X- and Y-axes indicate similarity. Outliers on the X-axis, i.e., 4, indicate diversity. Numbers correspond to name of the genotype (see Figure 1)

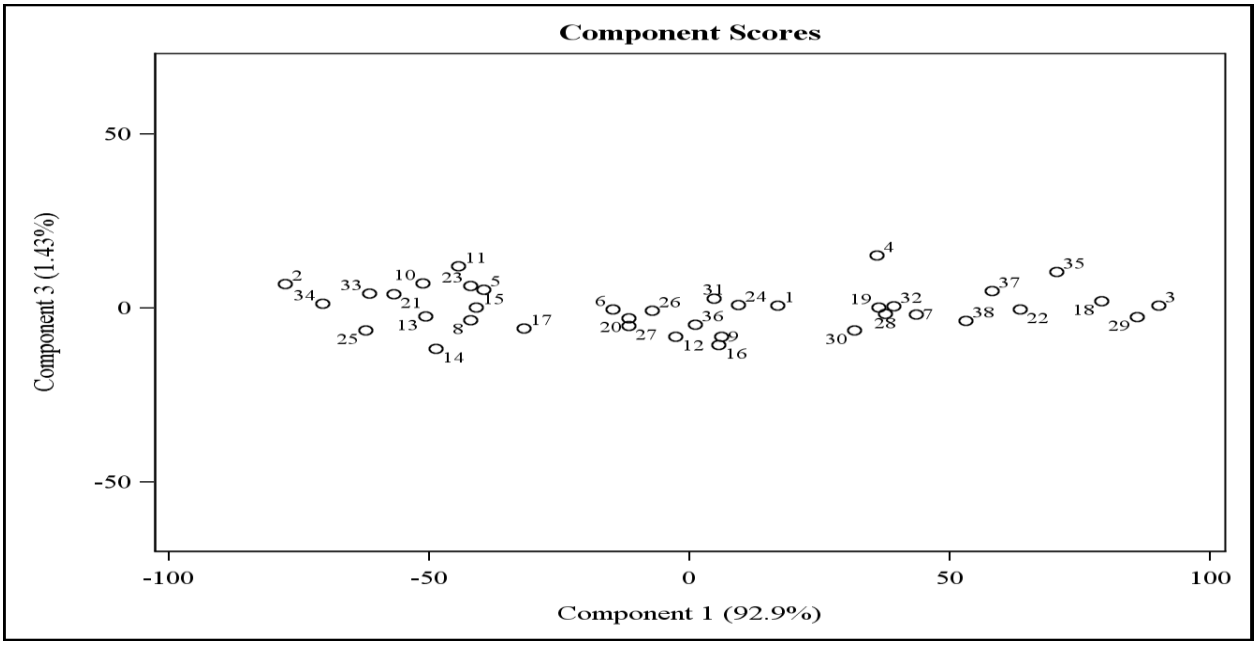
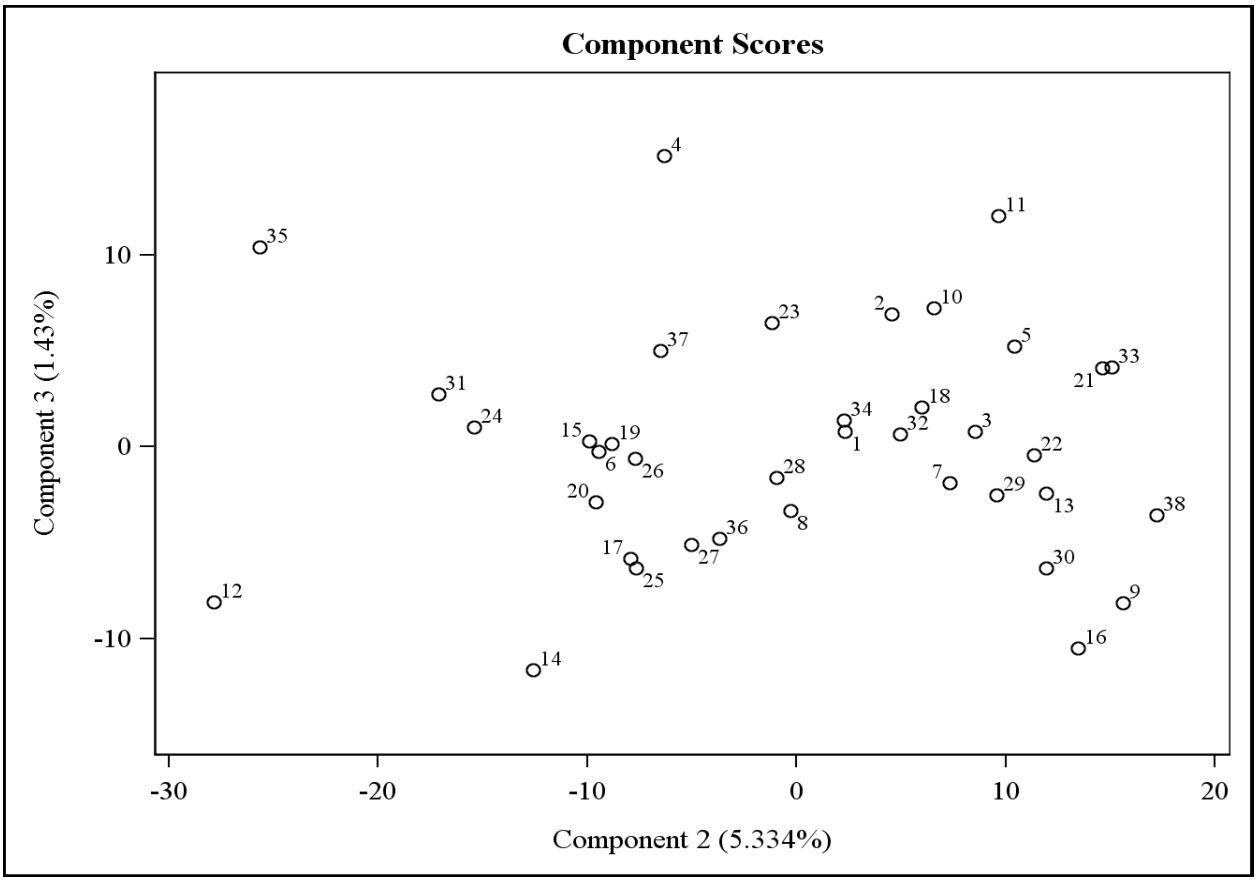


Fig.4 Scatter diagram of regression factor scores for the second and third components as determined by principal component analysis. Points in diagram closest to the intersection of 0 on the X- and Y-axes indicate similarity. Outliers on the X-axis, i.e., 4,11,12,14, and 35, indicate diversity. Numbers correspond to name of the genotype (see Figure 1)



The PC_2 explained an additional 5.33% of variance in which an increase in number of fruit/plant was associated with increased fruit diameter and marketable yield/plant and with decreased fruit weight and fruit length.

Principal component analysis (PCA) reflects importance of the largest contributor to total variation at each axis of differentiation. There are no clear-cut tests to evaluate significance of eigenvalues. Johnson and Wichern (1988) regard a coefficient greater than half of the coefficient, divided by the square root of the standard deviation of the eigenvalue of the respective principal component, as significant. Genotypes in close proximity are perceived as being similar in PCA; genotypes that are further apart are more diverse. The differences observed in the data, and summarized in the PCA, indicated genotype 'PB-70', 'Arka Neelkant', 'Pusa Kaushal', 'Arka Shirish' and 'Niranjan' were quantitatively dissimilar from others.

From the plot of PC_1 *vs.* PC_2, PC_1 *vs.* PC_3 and PC_2 *vs.* PC_3 selection may be refined considering all 3 principal components, with 'Pusa Kaushal' being the best performing cultivar having optimum combination of all variables, followed by genotypes 'PB-70' and 'Niranjan', and can be used as improved genetic material for breeding.

The Dendrogram (Figure 1) using squared Euclidean distance indicated there was high diversity among genotypes along with strong

relationships among genotypes. The scatter diagrams (Figure 2-4) indicated genotypes 'PB-70', 'Arka Neelkant', 'Pusa Kaushal', 'Arka Shirish' and 'Niranjan' have distinct differences of genotypic characters and belong to the farthest distances from other genotypes. They also possessed the optimum combination of all variables. Similar observations were reported by Rahman *et al.,* (2014) and Patel *et al.,* (2018).

Emphasis should be given on number of fruit/plant, fruit weight, and marketable yield/plant for selecting high yielding genotypes in eggplant. Based on genetic diversity, and average performance for fruit yield and other traits, genotypes 'Pusa Kaushal', 'PB-70' and 'Niranjan' are good donors for utilization in breeding. Crossing between these genotypes could produce desirable recombinants either in F_1 or segregating generations.

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