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Breeding potential of brinjal genotypes for fruit and shoot borer resistance using multivariate analysis

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Abstract
Deploying resistant varieties as a means of fruit and shoot borer **(**FSB) control in brinjal is attractive because it requires no additional cost and environment friendly. The objective of the study was to estimate genetic diversity among 27 brinjal genotypes through multivariate analysis for identifying potential donor(s) resistant preferably against FSB in future breeding. Genotypes were grouped into six distinct clusters emphasizing the relative contribution of 16 quantitative characters to total variability. Geographical diversity was not adequate as an index of genetic diversity. Fruit shape and susceptibility to FSB infestation need to be considered at the time of grouping brinjal genotypes. The principal components, fruit weight, plant height, fruit borer infestation, phenol content of shoot and shoot borer infestation, had eigenvalues >1 and together accounted for 83.33% of total variation. Based on multivariate analysis and average values, genotypes 'BCB-50, BCB-11 (Cluster VI), BCB-30, BCB-40, Garia (Cluster V), and Punjab Sadabahar (Cluster I) were identified as potential donors that could be passed on to breeders not only for FSB resistant breeding but also for improvement in yield and better fruit quality.

Keywords: Genetic diversity; principal component analysis, correlation; brinjal, fruit and shoot borer

Introduction
Among vegetables brinjal covers the largest area, depicting wide variation in size, shape, colour and striation throughout Indian subcontinent, suggesting this particular area is an important centre of variation and possible centre of origin (Vavilov, 1951) [36]. Preference of brinjal across Indian cuisine differed. Brinjal cultivation is threatened by many biotic factors including various pathogens and insect herbivores. The most extensive damage was inflicted by fruit and shoot borer (FSB) which causes colossal loss in production. Among integrated pest management strategies, host plant resistance is an important tool by saving the crop from the attack of this pest or making the crop opposing to the pest. Therefore, identification of donor parent resistant to FSB will be useful to get rid of this pest in a sustainable and eco-friendly manner.

Assessment of genetic divergence is a prerequisite for formulating an efficient breeding strategy to identify potential parents for future breeding. Genetically diverse parents may produce high heterotic crosses or transgressive segregants (Arunachalam, 1981) [1]. Assessment of genetic diversity is important for selecting breeding strategies. Quantification of genetic divergence through biometrical procedures has made it possible to choose genetically diverse parents for a successful hybridization programme. Moreover, evaluation of genetic diversity is important to know the source of genes for a particular trait within the available germplasm (Tomooka, 1991) [33].

Multivariate analysis is a powerful tool in quantifying the degree of divergence between biological populations (Genetic distance) and to assess the relative contribution of different components to the total divergence. Mahalanobis's (1936) [18] generalized distance has been used as an efficient tool in the quantitative estimation of genetic diversity and a rational choice of potential parents for a successful hybridization program.

The utility of multivariate analysis for measuring the degree of genetic divergence and for assessing the relative contribution of different characters to the total divergence in self and cross pollinated crops has been established by several workers (Kete, 2001; Hazra *et al.*, 2010;

Uddin, 2014) [17, 13, 34]. Genetic divergence of brinjal utilizing multivariate analysis for different growth, yield component and fruit quality traits was determined earlier by several workers (Hazra *et al.*, 2010; Das *et al.*, 2010; Nyadanu *et al.*, 2014; Ravali *et al.*, 2017; Nand *et al.*, 2018; Sanga *et al.*, 2018) [13, 6, 21, 26, 20, 28]. Scanty research on selection of brinjal genotypes based on genetic divergence in relation to resistance against FSB (Shukla *et al.*, 2017) [31] necessitates further study. The present investigation was undertaken to assess genetic divergence of 27 genotypes for growth, yield components, fruit quality and FSB infestation to identify potential donors for future breeding.

Materials and Methods

Plant materials and field growing

Twenty seven genotypes were evaluated during *autumn-winter* season of 2015 under the research plot of AICRP on Vegetable Crops, Bidhan Chandra Krishi Viswavidyalaya, Kalyani, West Bengal, India, situated at 23.5^0 N latitude and 89^0 E longitude at a mean sea level of 9.75m. The selfed seeds, after treatment with Thiram (3 g/kg of seed), of 27 genotypes were sown in well-prepared nursery bed to raise the seedlings during first week of July, 2016. Twenty five days old seedlings were transplanted in 3.75 m × 3.75 m plot spaced at 75 cm in both ways accommodating 25 plants in each plot for each genotype in the main field following randomized complete block design with 3 replications during end of July, 2016. Recommended dose of inorganic fertilizers @ 150:75:75 [N (urea): P (single super phosphate): K (muriate of potash)] kg/ha was applied. Agricultural practices were according to recommendations of Chattopadhyay *et al.* (2007) [5].

Data recording

Data on plant height (cm), primary branches per plant, days to first flowering, fruits length (cm), fruit girth (cm), fruits per plant, fruit weight (g), marketable fruit yield per plant (kg), shoot phenol content (mg/100 g), fruit phenol content (mg/100 g), peel anthocyanin content (mg/100 g), total sugar content (%), reducing sugar content (%), non-reducing sugar content (%), shoot borer infestation (%) and fruit borer infestation (%) were recorded. Total, reducing and non-reducing sugar contents of fruit were estimated by the method of Ranganna (1990) [24]. Anthocyanin content in the peel of fruit was estimated spectrophotometrically (Ranganna, 1990) [24]. The method of Sadasivam and Manickam (1992) [27] was used to estimate phenol content of shoot and fruit. In case of shoot and fruit borer infestation (%), number of healthy and damaged shoots and fruits was recorded and per cent damage was calculated as suggested by Mishra *et al.* (1988) [19]. Fortnightly observations were taken beginning 30 days after transplanting till the last fruit harvest. After recording the number of borer infested dead shoots, they were clipped off just above the point of insect burrow without destroying the larvae inside it. Single borer damage in fruit was also considered as infested fruit.

Statistical analyses

Data were statistically analyzed using the standard method of randomized complete block design as per Gomez and Gomez (1984) [10]. Phenotypic and genotypic correlation coefficients between different variables were calculated according to Johnson *et al.* (1955) [14]. The D^2 statistic (Mahalanobis, 1936) [18] was used to assess genetic divergence of genotypes for quantitative traits. Grouping of populations was with Tocher's method (Rao, 1952) [25]. Hierarchical cluster analysis was with the same genotypes to determine degree of association according to their characteristics and expressed in a dendrogram following Ward (1963) [37]. Principal component analysis (PCA) was used to identify factor dimension of the data, and to summarize varietal information in a reduced number of factors for selection of the best performing genotype(s). Statistical analyses were with Windostat (ver. 8.0, Indostat Services, Hyderabad, India) and SAS (ver. 9.3, SAS Inc., Cary, NC).

Results and Discussion

Grouping of genotypes

The present study aimed at determining the genetic divergence of 27 genotypes employing 16 quantitative characters employing Mahalanobis's D^2 statistics. Based on the degree of divergence (D^2 values) between any two genotypes a logical grouping of the genotypes with low D^2 value could be arrived at by Tocher's method (Rao, 1952) [25]. Genotypes could be grouped into 6 clusters (Table 1). Several earlier studies also reported that different set of genotypes were grouped under 6-10 clusters (Hazra *et al.*, 2010; Das *et al.*, 2010; Nyadanu *et al.*, 2014; Ravali *et al.*, 2017; Nand *et al.*, 2018; Sanga *et al.*, 2018) [13, 6, 21, 26, 20, 28] which agreed well to the present findings suggesting moderate biological distance among the genetic materials under study. Cluster I, III and IV contained 6 genotypes each, cluster V had 5 genotypes and 2 genotypes each grouped under cluster II and VI. Huge morphological diversity of the genotypes has not been amply reflected in their biological distance based on multivariate analysis. Geographical origin of the genotypes did not influence their clustering pattern rather, the genotypes were grouped based on the variation in different fruit yield components, quality characters and relative susceptibility to brinjal fruit and shoot borer. Genotypes bearing fruits of different shapes clustered together as for example Cluster I containing 6 genotypes (BRL VAR-2: oblong fruit; Punjab Sadabahar: long; BRLVAR-3: oblong; Kashi Taru: long; BRLVAR-6: long; SM-6-6: half-long). Genotypes bearing fruits of more or less same shape clustered together as for example Clueter V containing 5 genotypes (BRR VAR-3: round; BCB-30: round; Swarna Mani: round; BCB-40: oblong and Garia: oblong). Such clustering pattern clearly indicated that fruit shape need to be considered at the time of grouping the genotypes although its contribution might not be overwhelming in determining the clustering pattern of the genotypes. Genotypes showing least susceptibility to the infestation of brinjal fruit and shoot borer clustered together which amply suggested the applicability of multivariate analysis for the screening of genotypes for resistance to insect-pest.

Intra-and inter-cluster divergence

The intra-and inter-cluster distance based on 16 characters represent the index of genetic diversity among clusters as given in Table 2. The clustering pattern indicated that inter-cluster distance was higher than intra-cluster distance indicating wide genetic diversity among the genotypes under study. At the same time, comparatively lower intra-cluster divergence also suggested appreciable homogeneity among the genotypes which clustered together. Earlier study of Nyadanu *et al.* (2014) [21] agreed well to the present findings. Highest inter-cluster divergence was recorded between

Cluster II and VI (4064.78) followed by between cluster I and VI (3275.88) and between cluster III and VI (2933.74). The genotypes (BCB-11 and BCB-50) belonging to cluster VI appeared to be the most divergent from the rest 25 genotypes under study.

Cluster mean values for different characters

Cluster mean values for 16 characters of all genotypes belonging to 6 different clusters have been presented in Table 3. Cluster V had the highest yielding genotypes with fruits of appreciably high quality and intense anthocyanin pigmentation on the peel but the genotypes were susceptible to brinjal fruit and shoot borer (BRR VAR-3, BCB-30, Swarna Mani, BCB-40, Garia). The most diverse cluster VI had the second ranking genotypes with regard to fruit yield and quality but the fruit peel was almost devoid of anthocyanin pigment and these genotypes were most susceptible to the infestation of brinjal fruit and shoot borer (BCB-11, BCB-50). Cluster III had the lowest yielding genotypes which showed least susceptibility to the infestation of brinjal fruit and shoot borer (BRBW VAR-1, Arka Nidhi, Arka Kusumkar, BRBW VAR-2, BRBW VAR-4, BRBW VAR-3)

Contribution of different characters towards divergence

It emerged from the Table 4 that fruit weight had maximum contribution (37.32%) towards divergence of the genotypes followed by total sugar content of fruit (13.68%), anthocyanin content of fruit peel (12.25%), shoot infestation by borer (10.26%), fruit girth (9.69%), fruit infestation by borer (3.99%), fruit length (3.13%), fruits per plant (2.85%) total phenol content of shoot (1.99%), marketable fruit yield per plant (1.71%), plant height (1.42%) and total phenol content of fruit (1.14%). The top 5 characters which contributed maximum (83.20%) towards divergence viz., fruit weight, total sugar content of fruit, anthocyanin content of fruit peel, shoot infestation by borer and fruit girth, could be used to distinguish the germplasm of brinjal in this New Alluvial agro-climatic zone of West Bengal. Several earlier studies which identified different set of major contributing characters towards divergence of brinjal genotypes viz., fruits/ plant, 1000-seed weight and fruit girth (Sharma and Maurya, 2004) [29], fruit girth, fruit length and fruit weight (Golani *et al.*, 2007) [9], fruit weight and fruit yield (Das *et al.*, 2010) [6], fruit yield per plant, fruit weight (Ravali *et al.*, 2017) [26], days to first flowering, fruit set percentage and fruit girth (Nand *et al.*, 2018) [20], protein content, total carbohydrate, steroid content, total phenol content, fruit yield per plant and fruit number per plant (Sanga *et al.*, 2018) [28] agreed well to the present findings.

Principal component analysis

Principle component analysis (PCA) is a mathematical procedure that transforms a number of correlated variables into a number of uncorrelated variables called principle component (Chatfield and Collis, 1980) [4]. The first principle component accounts for as much of the variation in the data as possible, and each succeeding components depict for remaining portion of variability. The objective of PCA is to discover or to reduce the dimensionality of the data set and to identify new meaningful underline variable (Jollife, 2002) [15]. Principal component analysis explains the importance of largest contributor to the total variation at each axis of differentiation (Sharma, 1998) [30]. In the present investigation, 27 genotypes were subjected to PCA for sixteen quantitative characters. The result indicated that first principle component, PC1 (Fruit weight) explained 32.59% of variation, whereas PC2 (Plant height), PC3 (Borer infestation in fruit), PC4 (Phenol content of shoot) and PC5 (borer infestation in shoot) explained variations of 19.66%, 12.72%, 11.69% and 6.67%, respectively (Table 5). It was interesting to note that only plant height showed positive values with respect to all different principle components. The rest of the characters showed both positive and negative values among the different principle components. High diversity occurred among genotypes along with strong relationships (Figure 1). The scatter diagrams (Figures 2) indicated that the distribution of different genotypes were scattered and they were diverse in nature. Therefore, the genotype selected in the present investigation probably originated across the geographical regions of India. Similarly, Ullah *et al.* (2014) [35] used principal components with eigenvalues to explain variation among 15 accessions of brinjal. So, it can be concluded that the experimental results obtained from principle component analysis justifies the ample amount of variation present in the population and confirmed the results registered from D^2 analysis.

Selection of promising and diverse genotypes

Considering the genetic divergence of the genotypes, clustering pattern, mean performance of the genotypes for fruit yield, contributing characters and quality and relative susceptibility to the infestation of fruit and shoot borer, the following genotypes emerged as highly promising. No genotype could be selected from cluster III, being very low yielder instead, one genotype (Punjab Sadabahar) showing "Tolerant" category for borer infestation in fruit was selected as a promising parental line.

- BCB-50, BCB-11 (Cluster VI)
- BCB-30, BCB-40, Garia (Cluster V)
- Punjab Sadabahar (Cluster I)

Hybrids of these genotypes were expected to manifest considerable heterosis for different characters or to isolate desirable segregates in the advanced generation for yield, quality and tolerance to the infestation of brinjal fruit and shoot borer.

Grouping of genotypes with relation to borer infestation

The fruit and shoot borer (*Leucinodes orbonalis*) is the most serious insect-pest of eggplant throughout India causing as high as 44 % shoot and 100 % fruit damage in severe infestation. The insecticidal control is relatively ineffective because of mode of damage, high operational cost and health hazard due to lasting pesticide residue in the fruits. Consequently, plant resistance would be useful either as a complete control measure or as a part of the integrated pest management programme with limited dependence on pesticides.

According to this classification based on severity of infestation, no genotypes could be grouped under either "Immune" or "Highly resistant" category. The genotypes were placed under four severities of infestation groups. However, based on percent fruit damage 6 genotype BRBW VAR-1, BRBW VAR-3, Arka Kusumkar, Kashi Taru, SM-6-6, Arka Nidhi were grouped into moderately resistant, 11 genotypes BRL VAR-2, BRL VAR-3, BRL VAR-4, BRL VAR-5, BRR VAR-2, BRR VAR-3, BRR VAR-4, BRBW

VAR-4, Swarna Mani, BCB-30, Punjab Sadabahar were categorized as tolerant, eight genotypes BRL VAR-6, BRR VAR-1, BRR VAR-5, BRBW VAR-2, KS-224, BCB-11, BCB-40, Garia were grouped into susceptible category and 2 genotpes BRL VAR-1, BCB-50 were found highly susceptible.

From the multivariate analysis it emerged that genotypes showing least susceptibility to infestation of brinjal fruit and shoot borer clustered together (Table 1) which amply suggested the applicability of multivariate analysis for screening of genotypes for resistance to insect-pest. All the 6 genotypes under moderately resistant category were small fruited and very low yielder ranging between 0.45 kg/ plant in BRBW VAR-3 and 1.23 kg/plant in Arka Kusumkar.

From the study of correlation coefficients (Table 6), it appeared that shoot infestation by borer was uncorrelated with both fruit infestation by borer and marketable fruit yield. It was quite obvious because brinjal fruit and shoot borer bore into the shoot at the early stage of the plant before the fruits are produced. After formation of fruits, the borer preferred only the fruits for their feeding. On the other hand, fruit infestation by the borer was highly correlated with the marketable fruit yield because of the availability of more fruit biomass for their feeding. Fruit infestation by the borer was significantly and positively correlated with fruit girth (rp = 0.31), fruit weight (rp = 0.48), phenol content of fruit (rp = 0.24), total sugar (rp = 0.32), reducing sugar (rp = 0.34) and non-reducing sugar (rp = 0.23) contents of fruit but uncorrelated with fruit number plant. It appeared that the brinjal fruit and shoot borer preferred heavy, thick, plump and palatable fruits for infestation. This result amply justified the proposition of larval non-preference and antibiosis mechanisms for conferring resistance in the genotypes against this insect pest. Surprisingly, total phenol content of fruit registered significantly positive correlation (rp = 0.24) with borer infestation. This might have happened because of very low range of phenol content (2.19 - 3.52 mg /100 g fresh) in the genotypes which did not inflict any antibiosis factor in the fruits for the larvae of the borer. Total phenol content of shoot and fruit were highly correlated (rp = 0.56). Phenol content of both shoot and fruit were markedly correlated with fruit length (rp = 0.31; 0.32) and fruit number plant (rp = 0.26; 0.35). Hence, high phenol containing genotypes need to be developed / selected from genotypes bearing long and slender fruits.

Larval non-preference and antibiosis mechanisms operate in different crops for resisting the attack of many insect pests viz., shoot fly in sorghum (Dhawan *et al.*, 1993) [7], corn borer in maize (Williams *et al.*, 1997 and Kaur and Kanta, 2001) [38, 16], aphid in wheat (Havlickova, 1996) [11], brown plant hopper in rice (Soundarajan *et al.*, 2002) [32], pod borer in cowpea (Oghiakhe *et al.*, 1993) [22], aphid in mustard (Bhadauria *et al.*, 1996) [3] and brinjal (Panda and Das, 1975, Bajaj *et al.*,1989; Doshi, 2004; Hazra *et al.*, 2004) [23, 2, 8, 12]. Such resistance has reportedly been conferred on the host through over - expression of phenolic compounds and down regulation of feeding stimulants for the insect-pests like free amino acids, protein, sugar contents, etc. However, striking proper balance for these biochemical compounds is necessary to develop less susceptible genotype without hampering the organoleptic quality of fruits. It has been found that both bitterness and discolouration in fruits increase with increasing total phenol content beyond certain limit.

Table 1: Cluster classification of 27 genotypes of brinjal.

Clusters	Number of genotypes	Genotypes with sources
I	6	BRL VAR-2 (Uttar Pradesh), Punjab Sadabahar (Punjab), BRL VAR-3 (Uttar Pradesh), Kashi Taru (Uttar Pradesh), BRL VAR-6 (Uttar Pradesh), SM-6-6 (Kerala)
II	2	BRL VAR-4 (Uttar Pradesh), BRL VAR-5 (Uttar Pradesh)
III	6	BRBW VAR-1 (Uttar Pradesh), Arka Nidhi, Arka Kusumkar, BRBW VAR-2 (Uttar Pradesh), BRBW VAR-4 (Uttar Pradesh), BRBW VAR-3 (Uttar Pradesh)
IV	6	BRR VAR-1 (Uttar Pradesh), BRR VAR-2 (Uttar Pradesh), BRR VAR-5 (Uttar Pradesh), KS-224 (Uttar Pradesh), BRR VAR-4 (Uttar Pradesh), BRL VAR-1 (Uttar Pradesh)
V	5	BRR VAR-3 (Uttar Pradesh), BCB-30 (West Bengal), Swarna Mani (Jharkhand), BCB-40 (West Bengal), Garia (West Bengal)
VI	2	BCB-11 (West Bengal), BCB-50 (West Bengal)

Table 2: Intra and Inter cluster distance among the genotypes of brinjal.

Clusters	I	II	III	IV	V	VI
I	*395.141	908.559	650.626	1009.253	1958.987	3275.885
II		446.195	1603.729	1800.681	2801.088	4064.789
III			293.376	895.285	1735.713	2933.740
IV				370.819	711.461	1820.571
V					541.676	1592.961
VI						1166.426

*Bold diagonal values indicate intra-cluster distance; the remainder of values indicate the inter cluster distances.

Table 3: Cluster mean of16 characters of brinjal

Clusters	PH*	PBPP	DFF	FL	FD	NFPP	FW	MYPP	PCS	PCF	ACFP	TS	RS	NRS	SI	FI
I	79.606	3.988	31.725	14.852	5.025	16.088	83.289	1.344	3.802	2.960	90.460	2.283	1.656	0.632	0.265	24.476
II	102.172	4.508	30.812	14.685	4.552	20.038	75.073	1.508	3.405	2.715	86.377	2.497	1.783	0.715	1.110	24.797
III	78.336	3.204	33.050	17.893	3.714	8.226	80.373	0.672	3.662	2.522	88.231	1.223	0.924	0.339	0.246	22.493
IV	90.989	4.353	34.622	11.109	8.367	8.057	136.524	1.099	3.627	2.666	83.345	2.048	1.567	0.489	0.413	35.863
V	93.795	4.167	33.708	11.003	7.357	10.543	203.122	2.094	3.791	2.649	81.669	2.058	1.543	0.513	0.352	32.242
VI	106.983	4.603	29.922	14.315	6.547	10.547	195.518	1.860	4.037	2.887	3.107	1.810	1.400	0.403	0.338	39.598

*PH= Plants height (cm), PBPP= primary branches/plant, DFF= days to first flowering, FL= fruit length (cm), FD= fruit diameter (cm), NFPP=

number of fruit per plant, FW= fruit weight (g), MYPP= marketable fruit yield per plant (kg), PCS= phenol content of shoot value (µg), PCF= phenol content of fruit value (µg), ACFP= anthocyanin content of fruit peel (mg/100g), TS= total sugar content (%), RS= reducing sugar content (%), NRS= non-reducing sugar content (%), SI= shoot infestation by borer (%) and FI= fruit infestation by borer (%).

Table 4: Percentage contribution of different characters towards divergence of the genotypes.

Characters	Contribution %	Times ranked 1st
Fruit weight (g)	37.32	131.00
Total sugar content (%)	13.68	48.00
Anthocyanin content of fruit peel (mg/100g)	12.25	43.00
Shoot infestation by borer (%)	10.26	36.00
Fruit diameter (cm)	9.69	34.00
Fruit infestation by borer (%)	3.99	14.00
Fruit length (cm)	3.13	11.00
Fruits per plant	2.85	10.00
Total phenol content of shoot (mg/ 100 g)	1.99	7.00
Marketable fruit yield per plant (kg/plant)	1.71	6.00
Plant height (cm)	1.42	5.00
Total phenol content of fruit (mg/ 100 g)	1.14	4.00
Primary branches/ plant	0.28	1.00
Non-reducing sugar content (%)	0.28	1.00
Days to first flowering	0.01	0.00
Reducing sugar content (%)	0.01	0.00

Table 5: Results of principal component analysis (PCA) for quantitative characters contributing to divergence.

Principal component	Eigenevalue %	% Variance	% Cumulative variance
Eigenevalues and variance accounted for (%) by PCA based on correlation matrix			
PC1	5.22	32.60	32.60
PC2	3.15	19.66	52.26
PC3	2.04	12.73	64.98
PC4	1.87	11.67	76.66
PC5	1.07	6.68	83.33

Variables	PC1*	PC2	PC3	PC4	PC5
Factor loadings due to PCs with eigenevalues > 1					
Fruit weight (g)	0.400	0.075	0.053	0.017	0.119
Plant height (cm)	0.160	0.417	0.238	0.050	0.220
Fruit borer infestation (%)	-0.176	-0.146	0.408	-0.311	0.175
Phenol content of shoot (mg/100 g)	0.011	-0.095	-0.028	-0.622	-0.189
Shoot borer infestation (%)	0.087	0.345	-0.124	-0.105	0.629

*PC1-5 = Principal components 1-5.

Table 6: Phenotypic (P) and genotypic (G) correlation coefficients among 15 quantitative characters.

Characters		PBPP	DFF	FL	FD	FPP	FW	PCS	PCF	ACFP	TS	RS	NRS	SI	FI	MFYPP
PH[a]	P[b]	0.402**	-0.122	-0.354*	0.267*	-0.078	0.479**	-0.123	-0.046	-0.498**	0.233*	0.195	0.277*	0.331**	0.389**	0.282*
	G[c]	0.446	-0.160	-0.379	0.270	-0.080	0.494	-0.129	-0.063	-0.514	0.244	0.214	0.303	0.343	0.404	0.295
PBPP	P		-0.257*	-0.287*	0.316*	0.004	0.202	-0.135	-0.112	-0.216	0.196	0.222*	0.105	-0.059	0.010	0.118
	G		-0.323	-0.353	0.321	0.011	0.212	-0.173	-0.121	-0.234	0.210	0.233	0.137	-0.074	0.003	0.135
DFF	P			-0.164	0.236*	-0.348*	0.174	-0.120	-0.131	0.213	-0.114	-0.059	-0.224*	0.051	0.094	-0.197
	G			-0.206	0.278	-0.425	0.210	-0.156	-0.115	0.284	-0.190	-0.109	-0.308	0.051	0.085	-0.232
FL	P				-0.703**	0.285*	-0.513**	0.311*	0.312*	0.071	-0.132	-0.147	-0.068	0.004	-0.068	-0.104
	G				-0.753	0.284	-0.532	0.324	0.358	0.078	-0.155	-0.164	-0.078	-0.001	-0.070	-0.126
FD	P					-0.340*	0.620**	-0.166	-0.069	-0.125	0.177	0.250*	-0.033	0.048	0.310*	0.179
	G					-0.356	0.631	-0.173	-0.066	-0.131	0.177	0.258	-0.045	0.050	0.320	0.185
FPP	P						-0.334*	0.257*	0.345*	0.146	0.304*	0.279*	0.274*	0.407**	-0.045	0.535**
	G						-0.345	0.283	0.382	0.148	0.341	0.314	0.306	0.423	-0.048	0.518
FW	P							0.022	-0.143	-0.451**	0.164	0.205	0.013	-0.118	0.489**	0.542**
	G							0.020	-0.148	-0.457	0.171	0.218	0.009	-0.117	0.503	0.552
PCS	P								0.559**	-0.123	0.125	0.165	-0.001	0.016	0.182	0.335*
	G								0.627	-0.125	0.116	0.170	-0.018	0.012	0.212	0.370
PCF	P									-0.044	0.142	0.168	0.112	0.235*	0.243*	0.277*
	G									-0.054	0.160	0.187	0.113	0.231	0.292	0.315
ACFP	P										-0.014	-0.044	0.090	0.024	-0.345*	-0.221
	G										-0.002	-0.040	0.102	0.025	-0.361	-0.232
TS	P											0.964**	0.841**	0.205	0.325**	0.341*
	G											0.983	0.890	0.218	0.342	0.378
RS	P												0.709**	0.173	0.341*	0.350*
	G												0.793**	0.180	0.360	0.390
NRS	P													0.191	0.228*	0.219*

	G													0.220	0.265	0.245
SI	P														0.180	0.195
	G														0.192	0.206
FI	P															0.444**
	G															0.463

*, ** significant at $P = 0.05$ and $P = 0.01$, respectively.

[a]PH= Plants height (cm), PBPP= primary branches/plant, DFF= days to first flowering, FL= fruit length (cm), FD= fruit diameter (cm), NFPP= number of fruit per plant, FW= fruit weight (g), MYPP= marketable fruit yield per plant (kg), PCS= phenol content of shoot value (µg), PCF= phenol content of fruit value (µg), ACFP= anthocyanin content of fruit peel (mg/100g), TS= total sugar content (%), RS= reducing sugar content (%), NRS= non-reducing sugar content (%), SI= shoot infestation by borer (%) and FI= fruit infestation by borer (%).

[b]P = Phenotypic correlation coefficient.

[c]G = Genotypic correlation coefficient.

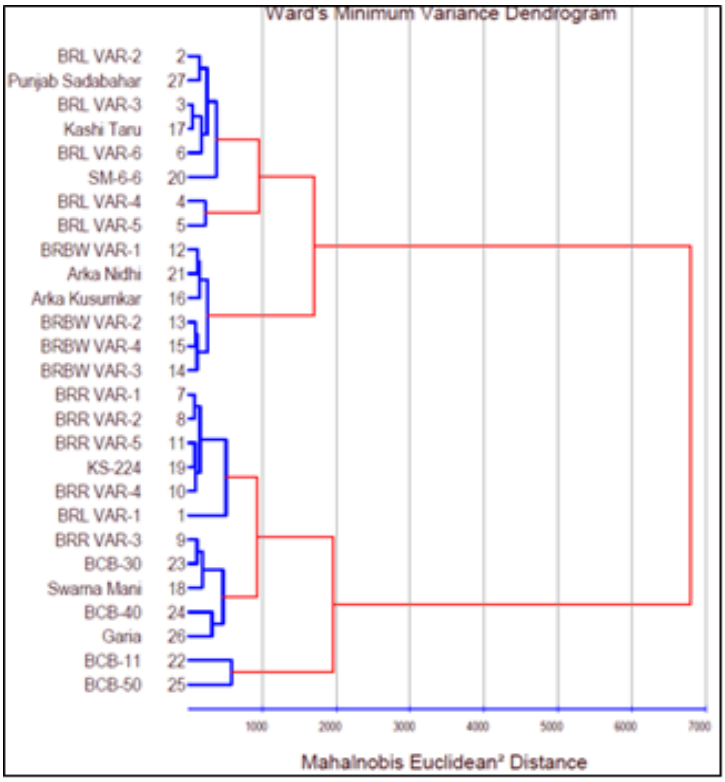

Fig 1: Dendrogram of genotypes of brinjal following ward's method. Genotypes are in left most column

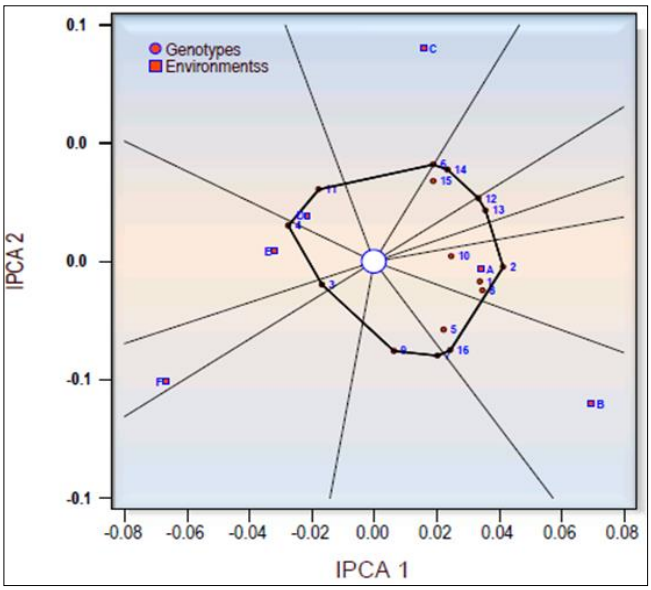

Fig 2: Biplot of regression factor scores for the first and second components as determined by principal component analysis. Points in diagram closest to the intersection of 0 on the X- and Y-axes indicate similarity. Outliers on the X-axis, that is, 1 and 4, indicate diversity. Numbers correspond to the name of the genotype, see Figure 1.

Conclusion

Based on determination of divergence, 27 genotypes could be grouped into 6 clusters emphasizing the relative contribution of various quantitative characters to total variability. The clusters do not represent place of origin indicating genotypes in a cluster were geographically diverse; genotypes obtained from the same region were genetically different. Six geneotypes BCB-50, BCB-11, BCB-30, BCB-40, Garia, and Punjab Sadabahar possessed optimum combinations of all variables and were identified as potential donors in FSB resistant breeding programme.

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