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Genetic divergence studies in Bottle gourd [*Lagenaria siceraria* (Mol.) Standl.]

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Abstract
The present investigation was carried out at Horticultural Research Station, Mondouri, Bidhan Chandra Krishi Viswavidyalaya, Mohanpur, Nadia, West Bengal, India during spring summer seasons of 2015, 2016 and 2017 in a Randomized Block Design with three replications. Genetic divergence was assessed among twenty one genotypes of bottle gourd for sixteen quantitative characters using Mahalanobis' D^2 statistics. The genotypes were grouped into six clusters. Fruit yield per plant (53.81%) contributed maximum towards divergence followed ascorbic acid content of the pulp (28.10%), seed number per fruit (4.29%) and TSS of the pulp (4.29%). Highest inter cluster distance was observed between cluster I and VI followed by cluster V and VI. Highest cluster mean values were observed for most of the traits with the genotypes present in cluster I. Based on superior mean performance for fruit yield per plant, genetic distances and clustering pattern, six promising and diverse inbred lines or varieties of bottle gourd *viz.*, RJBGC-140, RJBGC-118, BOGVAR-2 and Pusa Samridhi (from cluster I) and Arka Bahar (from cluster VI) and Pusa Sandesh (from cluster V) selected as parents for the exploitation of hybrid vigour in bottle gourd.

Keywords: Bottle gourd, genetic divergence, D^2 statistic, genotypes and yield

Introduction
Bottle gourd (*Lagenaria siceraria* (Mol.) Standl.) is one of the most important crops in the cucurbitaceae family having somatic chromosomes number 2n=22. Tropical Africa is the primary gene centre of the bottle gourd, although it is considered as a poor man's crop due to the socioeconomic restrictions governing its production and use. Bottle gourd is the largest produced cucurbitaceous vegetables in the world preferred in both urban and rural population. Bottle gourd is a rich source of minerals and vitamins. In West Bengal, no comprehensive systematic research has been done in this crop. The yield potentiality of this crop needs to be improved through an effective breeding programme. Studies on the variations of yield and yield contributing characters are of great importance before planning a breeding program.
Genetic diversity analysis among elite germplasm is prerequisite for choosing promising genetic diverse lines for desirable traits and to reveal genetic distinctness among genotypes (Ali *et al*., 2008). Assessment of genetic diversity in germplasm collections imposes the categorization of accessions and useful in assigning genotypes to specific heterotic groups to create segregating progenies with maximum genetic variability for further breeding purposes. Looking to the above present study, we classify the genotypic set based on multivariate analysis for generating more heterotic cross combinations and finally superior useful hybrids.

Materials and Methods
The experimental material consisted of twenty one genotypes were laid out in a Randomized Block Design (RBD) with three replications at Horticultural Research Station, Mondouri, Bidhan Chandra Krishi Viswavidyalaya, Mohanpur, Nadia, West Bengal, India during spring summer seasons of 2015, 2016 and 2017. Each genotype was represented by a double row plot of 5 m length with 10 plants sown at a distance of 3 m between rows and 1 m between plants. Observations were recorded from five randomly selected plants for all the quantitative characters except days to first male flower appearance, days to first female flower appearance and 100 seed weight. Data on qualitative parameters was recorded on whole plot basis. The data on qualitative and quantitative characters were recorded as per minimal descriptors of

NBPGR developed for bottle gourd. TSS content of the pulp was determined by an ERMA Hand Refractometer. The sugar content of the pulp was estimated by following anthrone method as per Dubois *et al.* (1956) [3]. Ascorbic acid content of the pulp was determined by 2, 6-dichlorophenol indophenol titration method (Ranganna, 1986) [6].

The data obtained on above 16 characters was used for cluster analysis and investigated to select the parents for hybridization using Mahalanobis (1936) [5] D^2 statistics. The genotypes were grouped into different clusters by Tocher's method (Rao, 1952) [7]. The population was arranged in order of their relative distances from each other. For including a particular population in the clusters, a level of D^2 was fixed by taking the maximum D^2 values between any two populations in the first row of the table where D^2 values were arranged in increasing order of magnitude.

Results and Discussion

The analysis of variance revealed significant differences among bottle gourd genotypes for all characters suggesting considerable genetic variability in the population. Using the estimated D^2 values as squares of generalized distance, all genotypes were grouped into 6 clusters (table 1). Maximum number of genotypes were grouped into cluster II (RJBGC-118, RJBGC-140, Pusa Sandesh, BOGVAR-2, BOGVAR-4, Pusa Samridhi and Pusa Naveen) included seven genotypes, which was followed by cluster I (Mohon, Deb Jyoti, Lau Chameli, Tapan, Gutka Long and BOGVAR-1) and cluster IV (BOGVAR-3, Punjab Komal, Ganga Jamuna, Punjab Long and Arka Bahar) having six genotypes and five genotypes respectively. Rest of the clusters *viz*., cluster III (Punjab Barkat), cluster V (Pusa Santusti) and cluster VI (NDBG-104) had one genotype each. Grouping of the genotypes in less number of clusters as revealed in the present investigation amply suggested that mutual balancing and cancellation of characters was operative in bottle gourd genotypes which has reduced the biological distance among the genotypes based on such wide character constellation. Genotypes collected from same geographical location fall under different cluster showed that there is no geographical relationship among genotypes collected from same location.

The average inter and intra cluster distances among the six clusters are presented in table 2. The intra cluster D^2 value ranged from 0.00 (Cluster III, V, VI) to 339.518 (Cluster II). The cluster II had the maximum D^2 value (339.518) followed by Cluster IV (332.941) and Cluster I (181.764). No intra cluster distance was observed in clusters III, V and VI. Low intra-cluster distance amply suggested low divergence and high homogeneity in the group. Maximum inter cluster distance was observed between cluster I and VI (1675.185) followed by cluster V and VI (1384.497), cluster I and II (1330.830), cluster I and III (890.544), cluster II and V (753.449), cluster II and IV (710.462), cluster IV and VI (644.227), cluster IV and V (623.581), cluster I and V (604.227) and cluster I and IV (587.588). The higher inter-cluster distance indicated greater genetic divergence between the genotypes of those cluster. The genotypes belonging to the clusters with maximum inter cluster distance are genetically more divergent and these could be used in hybridization programme to obtain promising segregants. These results are in general agreement with the findings of Islam (2004) [4], Singh *et al*. (2007) [8] and Bhardwaj *et al*. (2013) [2].

The contribution of each character to divergence is presented in table 3. Fruit yield per plant (53.81%) contributed maximum to the total genetic diversity followed by ascorbic acid content of the pulp (28.10%), seed number per fruit (4.29%), TSS of the pulp (4.29%), total sugar content of the pulp (3.33%), 100 seed weight (2.86%), fruit width (1.43%), average fruit weight (0.95%), days to first male flower appearance (0.48%) and sex ratio (0.48%). This contribution is an important consideration for the purpose of further selection and choice of parents for hybridization. The results of the present study was close agreement with findings of Islam *et al*. (2004) [4] who reported that primary branches per plant, fruit length and weight, number of fruits and yield per plant contributed the most of the total genetic divergence; with findings of Thakur *et al*. (2013) [9] who reported that number of branches per plant and fruit yield contributed maximum to divergence.

The mean performance for different clusters of genotypes for yield and its components are presented in table 4. Cluster I emerged as unique because it had the high mean values for maximum number of yield contributing characters i.e. maximum vine length, maximum number of primary branches, more number of fruits per plant and fruit yield per plant. The better genotypes can be selected for most of characters on the basis of mean performance in the cluster. In this study, group constellation showed that cluster I (Mohon, Deb Jyoti, Lau Chameli, Tapan, Gutka Long, BOGVAR-1) included genotypes with most of the superior traits hence these genotypes could be directly selected and utilized on the basis of the observations recorded on a diverse group of bottle gourd genotypes, it may be concluded that Based on superior mean performance for fruit yield per plant, genetic distances and clustering pattern, six promising and diverse inbred lines or varieties of bottle gourd *viz.*, RJBGC-140, RJBGC-118, BOGVAR-2 and Pusa Samridhi (from cluster I) and Arka Bahar (from cluster VI) and Pusa Sandesh (from cluster V) selected as parents for the exploitation of hybrid vigour in bottle gourd may help in developing better genotype/varieties for fruit yield in bottle gourd for West Bengal plains.

Table 1: Clustering pattern of 21 genotypes of bottle gourd

Cluster	No. of genotypes	Genotypes
I	6	Mohon, Deb Jyoti, Lau Chameli, Tapan, Gutka Long, BOGVAR-1
II	7	RJBGC-118, RJBGC-140, Pusa Sandesh, BOGVAR-2, BOGVAR-4, Pusa Samridhi, Pusa Naveen
III	1	Punjab Barkat
IV	5	BOGVAR-3, Punjab Komal, Ganga Jamuna, Punjab Long, Arka Bahar
V	1	Pusa Santusti
VI	1	NDBG-104 (C)

Table 2: Intra (bold) and Inter cluster distance values in bottle gourd genotypes

Clusters	I	II	III	IV	V	VI
I	181.764	1330.830	890.544	587.588	604.227	1675.185
II		339.518	439.651	710.462	753.449	544.888
III			0.000	416.675	528.587	464.724
IV				332.941	623.581	644.227
V					0.000	1384.497
VI						0.000

Table 3: Contribution of character's towards divergence in bottle gourd genotypes

Character	Vine length (m)	No. of 1^0 branches	Days to first male flower	Days to first female flower	Days to first harvest	Number of fruits /plant	Average fruit weight (kg)	Fruit length (cm)	Fruit width (cm)	Fruit yield /plant (kg)	Sex ratio (M/F)	Seed number /fruit	100 seed weight (g)	TSS of the pulp (^{0}Brix)	Total sugar content (%)	Ascorbic acid content mg/100 g)
Number of times ranked first	0.01	0.01	0.48	0.01	0.01	0.01	0.95	0.01	1.43	53.81	0.48	4.29	2.86	4.29	3.33	28.10
Per cent contribution	0.00	0.00	0.48	0.00	0.00	0.00	0.95	0.0	1.43	53.81	0.48	4.29	2.86	4.29	3.33	28.10

Table 4: Mean performance of genotypes in individual cluster for yield and its components in bottle gourd genotypes

Cluster	Vine length (m)	No. of 1^0 branches	Days to first male flower	Days to first female flower	Days to first harvest	Number of fruits /plant	Average fruit weight (kg)	Fruit length (cm)	Fruit width (cm)	Fruit yield /plant (kg)	Sex ratio (M/F)	Seed number /fruit	100 seed weight (g)	TSS of the pulp (^{0}Brix)	Total sugar content (%)	Ascorbic acid content mg/100 g)
I	5.68	4.48	52.71	61.06	76.89	4.70	1.44	31.21	14.44	6.76	7.42	449.82	14.01	3.24	2.63	8.97
II	6.84	5.85	44.87	51.93	63.58	7.28	1.17	35.23	13.15	8.53	7.14	431.88	15.42	3.51	2.44	7.64
III	3.26	3.90	44.83	51.23	65.60	5.32	0.77	33.47	6.80	4.10	10.41	311.78	13.18	3.70	2.44	7.23
IV	5.66	5.61	48.14	55.37	70.83	5.44	1.01	31.33	12.54	5.63	8.98	492.76	14.23	3.03	2.79	9.26
V	4.93	5.14	43.10	51.77	65.67	5.22	1.20	32.40	15.21	6.27	6.57	580.96	19.73	3.90	2.91	7.18
VI	5.35	4.20	41.97	47.97	61.33	8.09	0.85	52.60	7.68	6.88	7.59	434.52	13.61	4.17	2.42	9.26

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