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Estimation of genetic divergence in Bottle gourd [*Lagenaria siceraria* (Mol.) Standl.] for yield and it's attributing traits

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Abstract
The present investigations was carried out in two years with aims to Estimation of genetic divergence (D2) involving 10 lines (NDBG-504, NDBG-509, NDBG-517, NDBG-522, NDBG-601, NDBG-603, NDBG-749-2, NDBG-11, NDBG-10, Narendra Rashmi), 4 testers (Pusa Naveen, NDBG-624, NDBG-S-5, NDBG-104) of bottle gourd and their 40 F1 hybrids produced in L × T fashion at Horticulture Research Farm, Department of Applied Plant Science (Horticulture), Babasaheb Bhimrao Ambedkar University, Lucknow (U.P.) India during Zaid 2017-18 and 2018-19. Genetic divergence was assessed among 4 testers and their 40 F1 hybrids of bottle gourd for eighteen quantitative characters using Mahalanobis' D2 statistics. The genotypes were grouped into eight clusters. Clustering pattern of the genotypes of heterogeneous origin, indicating no parallelism between genetic and geographical diversity. All the parents and F1's were grouped into eight clusters with different genotypes in both the seasons which suggested that there were ample diversity within the experimental material. Reducing sugars in Y1 and total soluble solids in Y2 contributed maximum contribution towards total divergence while, minimum contribution was reflected by days to first pistillate flower anthesis and total sugars in both the years the lines/crosses between the genotypes of clusters with high inter cluster distance with that of distant clusters may give rise desirable segregants.

Keywords: Bottle gourd, Genetic divergence, D^2 statistic, cluster

Introduction
Bottle gourd [*Lagenaria siceraria* (Mol.) Standl.] is one of the most popular vegetable of the family Cucurbitaceae, with a diploid chromosome number, 2n=22. It is a fast growing climbing annual, native to Africa. It is grown in both rainy and summer season and its fruits are available in the market throughout the year. Bottle gourd is a rich source of minerals and vitamins. In Chhattisgarh, no comprehensive systematic research has been done in this crop. A large number of local lines are cultivated in this region but there is no recommended cultivar. In crop improvement programme, genetic diversity has been considered as an important factor which is also essential pre-requisite for hybridization programme for obtained progenies with important desirable characters like disease resistance, earliness, quality or even performance of a particular character for the yield improvement and future utilization of local germplasm. Such study also selects the genetically divergent parents to obtain desirable combinations in the segregating generations. Information on nature and degree of genetic divergence would help the plant breeder in choosing the right parents for the breeding programme.
Genetic diversity analysis among elite germplasm is prerequisite for choosing promising genetic diverse lines for desirable traits and to reveal genetic distinctness among genotypes. 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 experiment was conducted at Horticulture Research Farm, Department of Applied Plant Science (Horticulture), Babasaheb Bhimrao Ambedkar University, Lucknow (U.P.) India during Zaid 2017-18 and 2018-19 with involving 10 lines (NDBG- 504, NDBG-509, NDBG-517, NDBG-522, NDBG-601, NDBG-603, NDBG-749-2, NDBG-11, NDBG-10, Narendra Rashmi), 4 testers (Pusa Naveen, NDBG-624, NDBG-S- 5, NDBG-104) of bottle gourd and their 40 F1 hybrids produced in L × T fashion.

The experiments were laid out in RBD with three replications having each experimental unit of single row with spacing of 3.0 m × 0.5 m.

The data obtained on above 18 characters was used for cluster analysis and investigated to select the parents for hybridization using Mahalanobis (1936) [4] D^2 statistics. The genotypes were grouped into different clusters by Tocher's method (Rao, 1952) [6] calculating intra and inter cluster distances (Singh and Chaudhury, 1985) [7] were studied.

Statistical analyses were carried out using Genstat 5 software. The population was arranged in order of their relative distances from each other. For including a particular population in the clusters, a level of D2 was fixed by taking the maximum D2 values between any two populations in the first row of the table where D2 values were arranged in increasing order of magnitude.

Results and Discussion

Based on the degree of divergence 54 (10 lines, 4 testers and 40 F1's) genotypes of bottle gourd were grouped into 8 different non over lapping clusters (Table-1). Cluster III had highest number of genotypes (29) followed by cluster I (19) and Cluster II, IV, V, VI, VII, VIII having monogenotypic cluster [Table-1]. The estimates of intra and inter-cluster distance represented by D2 values had given in table-2. The intra- cluster D2 value ranged from 0.00 to 573.59 while the inter-cluster value ranged from 297.08 to 3833.71 indicated that the selected breeding lines were highly divergent (Table-2). The highest intra-cluster distance was shown by cluster III (573.59) while it was zero for monogenotypic clusters II, IV, V, VI, VII, VIII. The maximum inter-cluster distance was observed between cluster VII and cluster VIII (3833.71), followed by cluster VI and cluster VIII (3702.30), cluster IV and cluster VIII (3321.49).

The comparison of clusters means revealed considerable differences among the clusters of different quantitative and quality characters (Table-3). Cluster VI showed high mean value for maximum 8 characters *viz*., days to first staminate flower anthesis (53.87 days), days to first pistillate flower anthesis (53.27 days), node number to first staminate flower (10.08), node number to first pistillate flower (11.47), days to first fruit harvest (65.53 days), vine length at last picking stage (6.67 m), fruit length (43.93 cm) and ascorbic acid (10.52 mg). Cluster VIII showed high mean value for number of primary branches per plant (19.10), reducing sugar (2.30%) and total sugars (2.82%) and cluster VII showed high mean value for fruit circumference (29.00 cm), fruit yield per plant (10.05 kg) and non-reducing sugar (0.99%) whereas, cluster I, II, IV and V each showed high mean value for single character which were fruit weight (1.43 kg), dry matter content in fruit (4.77%), total soluble solids (3.58%), number of fruits per plant (7.27), respectively.

Highest per cent contribution towards total genetic divergence (Table-4) was exhibited by reducing sugar (34.94%) followed by dry matter content in fruit (19.15%), total soluble solids (18.80) and ascorbic acid (16.91). Rest of the characters exhibited low contribution towards total genetic divergence.

In Y2, fifty four genotypes were grouped into 8 different non over lapping clusters (Table-1). Cluster I had highest number of genotypes (23) followed by cluster VI (12) and Clusters II, IV, V, VII having monogenotype [Table-1]. The estimates of intra and inter-cluster distance represented by D2 values were given in table-2. The intra-cluster D2 value ranged from 0.00 to 1088.31 while, the inter-cluster value ranged from 142.37 to 2849.61 indicated that the selected breeding lines were highly divergent (Table-2). The highest intra-cluster distance was shown by cluster VIII (573.59) whereas the minimum one was zero for monogenotype clusters II, IV, V, VII. The maximum inter-cluster distance was observed between cluster IV and cluster VIII (2849.61), followed by cluster V and cluster VIII (2838.87) and cluster VI and cluster VIII (2727.10).

The comparison of cluster means revealed considerable differences among the clusters of different quantitative and quality characters (Table-3). Cluster III showed high mean value for maximum six characters *viz*., vine length at last picking stage (6.04 m), number of primary branches per plant (18.12), fruit circumference (29.40 cm), fruit weight (1.42 kg), reducing sugar (2.08%), total sugars (2.73%) followed by cluster V for four characters *viz*., days to first fruit harvest (62.57 days), fruit weight (1.42 kg), number of fruits per plant (6.10), fruit yield per plant (8.66 kg) and cluster II which showed high mean value for two characters *viz*., node number to first staminate flower (11.10) and non-reducing sugar (0.88%). Cluster IV, VII and VIII showed high mean value for two characters. Cluster IV showed high mean value for fruit length (47.87 cm) and ascorbic acid (9.95 mg). Cluster VII showed high mean value for node number to first pistillate flower (11.17) and dry matter content in fruit (3.62%) while cluster VIII showed high mean value for days to first pistillate flower anthesis (50.49 days) and total soluble solids (3.46° B). Cluster VI showed high mean value for days to first staminate flower anthesis (49.68 days). Highest per cent contribution towards total genetic divergence (Table-4) was exhibited by total soluble solids (48.43%) followed by fruit length (13.28%), reducing sugar (13.00%), days to first fruit harvest (11.60%) and dry matter content in fruit (8.39%). Rest of the characters exhibited low contribution towards total genetic divergence.

Varalakshmi *et al*. (1994) [9] and Mathew *et al.* (2001) [5] also reported similar findings. As heterosis can be best exploited and chances of getting transgressive segregants are maximum when generating diverse lines are crossed (Karuppaiah *et al.*, 2005; Singh *et al.*, 2007 and Islam *et al.*, 2010) [3, 8, 2]. High inter-cluster value indicated that the selected breeding lines were highly divergent in both the years.

Table 1: Clustering pattern of fifty four genotypes of bottle gourd on the basis of Mahalnobis 'D^2' statistics

Cluster number	Years	No. of genotypes	Genotypes
I	Y1	19	BG-517 × BG-624, BG-603 × BG-624, BG-517, BG-509 × BG-624, BG-603, BG-517 × BG-S-5, BG-522 × BG-S-5, BG-504, BG-11, BG-504 × BG-104, BG-11 × BG-104, BG-S-5, BG-504 × Pusa Naveen, BG-10, BG-10 × BG-104, BG-11 × BG-624, BG-603 × BG-104, BG-504 × BG-S-5, BG-601 × BG-104
	Y2	23	BG-504 × BG-104, BG-10 × BG-104, BG-11, BG-10, BG-504 × Pusa Naveen, BG-603, BG-749-2 × BG-104, BG-S-5, BG-517 × BG-104, BG-11 ×BG-104, BG-522 × BG-S-5, BG-603 × BG-624, BG-517, BG-522, BG-522 × BG-624, BG-517 × BG-624, BG-509 × BG-624, BG-509 × BG-S-5, BG-603 × BG-104, BG-509 ×BG-104, BG-10 × BG-624, BG-504, BG-517 × Pusa Naveen

II	Y1	1	BG-104
	Y2	1	BG-504 × BG-S-5
III	Y1	29	BG-509 × BG-104, BG-749-2 × BG-104, BG-601 × Pusa Naveen, BG-10 × Pusa Naveen, BG-522 × BG-624, BG-509 × BG-S-5, Narendra Rashmi × BG-S-5, BG-10 × BG-624, BG-504 × BG-624, BG-601 × BG-624, Pusa Naveen, BG-522, BG-749-2 × Pusa Naveen, BG-522 × Pusa Naveen, BG-603 × BG-S-5, BG-522 × BG-104, BG-601, Narendra Rashmi × BG-104, BG-11 × Pusa Naveen, BG-749-2 × BG-624, Narendra Rashmi × Pusa Naveen, BG-11 × BG-S-5, Narendra Rashmi × BG-624, BG-509 × Pusa Naveen, BG-601 × BG-S-5, BG-624, BG-749-2, BG-509, BG-603 × Pusa Naveen
	Y2	10	Narendra Rashmi × BG-624, Narendra Rashmi × BG-S-5, Pusa Naveen, Narendra Rashmi, BG-601 × BG-S-5 BG-603 × Pusa Naveen, BG-11 × BG-S-5, BG-517 × BG-S-5, BG-624, BG-749-2 × BG-624
IV	Y1	1	BG-10 × BG-S-5
	Y2	1	BG-522 × Pusa Naveen
V	Y1	1	BG-517 × Pusa Naveen
	Y2	1	BG-10 × Pusa Naveen
VI	Y1	1	BG-517 × BG-104
	Y2	12	BG-603 × BG-S-5, BG-104, BG-601 × BG-624, BG-504 × BG-624, BG-522 × BG-104 BG-601 × Naveen, BG-11 × Pusa Naveen, BG-749-2 × BG-S-5, BG-601 × BG-104, BG-749-2 × Pusa Naveen, BG-509 × Pusa Naveen, BG-11 × BG-624
VII	Y1	1	BG-749-2 × BG-S-5
	Y2	1	BG-601
VIII	Y1	1	Narendra Rashmi
	Y2	5	Narendra Rashmi × Pusa Naveen, Narendra Rashmi × BG-104, BG-10 × BG-S-5, BG-509, BG-749-2

Y1=2017-18 and Y2=2018-19

Table 2: Intra-inter clusters D2 values for eight clusters in bottle gourd (Y1=2017-18 and Y2=2018-19)

	Years	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VII
Cluster I	Y1	288.65	509.10	689.16	425.23	409.41	463.91	594.02	2266.20
	Y2	521.62	730.18	981.17	1008.54	1123.95	1118.35	979.55	1394.74
Cluster II	Y1		0.00	1032.55	865.67	548.16	619.66	830.89	2656.57
	Y2		0.00	1470.76	142.37	395.80	654.13	1947.47	2477.33
Cluster III	Y1			573.59	1198.60	1044.52	1292.10	1426.14	1237.77
	Y2			715.36	1626.59	1499.91	1630.95	1155.62	1378.58
Cluster IV	Y1				0.00	297.08	469.43	483.24	3321.49
	Y2				0.00	209.44	685.54	2241.86	2849.61
Cluster V	Y1					0.00	619.03	398.24	2927.30
	Y2					0.00	680.45	2188.02	2838.87
Cluster VI	Y1						0.00	610.34	3702.30
	Y2						613.87	1908.49	2727.10
Cluster VII	Y1							0.00	3833.71
	Y2							0.00	1163.97
Cluster VIII	Y1								0.00
	Y2								1088.31

Y1=2017-18 and Y2=2018-19

Table 3: Intra-cluster group mean for 18 clusters in bottle gourd (Y1=2017-18 and Y2=2018-19)

Cluster number	Years	Days to first staminate flower anthesis	Days to first pistillate flower anthesis	Node number to first staminate flower	Node number to first pistillate flower	Days to first fruit harvest	Vine length at last picking stage (m)	Number of primary branches per plant	Fruit length (cm)	Fruit circumference (cm)
I	Y1	49.44	49.55	8.96	10.07	60.93	5.76	16.54	42.89	25.51
	Y2	49.61	49.69	8.81	9.96	60.71	5.70	15.68	42.73	25.67
II	Y1	51.93	50.47	7.50	8.30	61.90	5.54	15.70	42.10	25.50
	Y2	49.40	47.80	11.10	10.87	58.80	4.86	16.63	47.73	25.03
III	Y1	49.09	49.76	8.63	10.21	62.04	5.18	14.94	41.53	25.97
	Y2	48.15	49.04	8.44	10.22	62.39	6.04	18.12	38.86	29.40
IV	Y1	44.33	47.53	8.97	9.40	59.83	6.09	18.63	43.90	26.03
	Y2	44.30	46.73	9.33	10.20	58.63	4.78	14.43	47.87	24.67
V	Y1	50.13	49.53	7.57	10.80	60.03	4.06	11.63	40.90	27.13
	Y2	47.80	48.87	7.63	8.60	62.57	3.85	11.93	45.87	27.87
VI	Y1	54.87	53.27	10.80	11.47	65.53	6.67	16.57	43.93	22.40
	Y2	49.68	49.57	8.44	9.59	61.91	5.19	14.41	42.55	25.82
VII	Y1	48.83	49.67	7.97	10.53	61.90	5.08	17.90	43.80	29.00
	Y2	49.23	46.07	10.50	11.17	59.37	5.09	10.13	33.93	21.80
VIII	Y1	48.13	48.03	7.40	11.17	61.00	5.83	19.10	35.33	25.53
	Y2	47.89	50.49	9.45	10.76	62.15	5.32	15.28	39.23	25.41

Y1=2017-18 and Y2=2018-19

Contd….

Cluster number	Years	Fruit weight (kg)	Number of fruits per plant	Fruit yield per plant (kg)	Total soluble solids (°B)	Ascorbic acid (mg/100 g fresh fruit)	Reducing sugars (%)	Non-reducing sugars (%)	Total sugars (%)	Dry matter content in fruit (%)
I	Y1	1.43	3.86	5.42	2.91	9.57	1.67	0.88	2.56	3.04
	Y2	1.34	4.20	5.54	2.94	9.54	1.72	0.85	2.57	3.19
II	Y1	1.31	3.27	4.25	2.18	9.71	1.54	0.95	2.49	4.77
	Y2	1.33	5.17	6.87	2.46	9.30	1.70	0.88	2.58	2.94
III	Y1	1.38	4.23	5.67	2.83	8.96	1.95	0.72	2.67	3.22
	Y2	1.42	4.79	6.41	3.07	8.50	2.08	0.65	2.73	2.88
IV	Y1	1.39	5.12	7.10	3.58	10.12	1.51	0.95	2.46	3.01
	Y2	1.17	4.45	6.36	2.31	9.95	1.86	0.82	2.69	3.23
V	Y1	1.26	7.27	9.10	3.08	9.71	1.51	0.96	2.47	3.60
	Y2	1.42	6.10	8.66	2.31	9.13	1.93	0.73	2.66	3.33
VI	Y1	1.02	3.02	3.07	2.95	10.52	1.43	0.85	2.28	2.81
	Y2	1.29	4.38	5.57	2.42	9.27	1.76	0.83	2.59	3.35
VII	Y1	1.40	7.19	10.05	2.45	10.13	1.50	0.99	2.49	2.57
	Y2	0.99	3.66	3.60	3.10	8.95	1.65	0.80	2.45	3.62
VIII	Y1	0.96	6.08	5.77	2.95	7.24	2.30	0.50	2.82	4.47
	Y2	1.36	4.70	6.13	3.46	9.07	1.91	0.75	2.66	3.32

Y1=2017-18 and Y2=2018-19

Table 4: Per cent contribution of 18 characters towards total genetic divergence in bottle gourd (Y1=2017-18 and Y2=2018-19)

S. No.	Characters	Contribution (%)	
		Y1	Y2
1.	Days to first staminate flower anthesis	0.07	0.14
2.	Days to first pistillate flower anthesis	0.00	0.00
3.	Node number to first staminate flower	0.70	0.00
4.	Node number to first pistillate flower	0.35	0.00
5.	Days to first fruit harvest	0.07	11.60
6.	Vine length at last picking stage (m)	0.98	0.00
7.	Number of primary branches per plant	1.12	2.17
8.	Fruit length (cm)	2.87	13.28
9.	Fruit circumference (cm)	0.49	1.68
10.	Fruit weight (kg)	0.00	0.07
11.	Number of fruits per plant	1.89	0.07
12.	Fruit yield per plant (kg)	0.49	0.49
13.	Total soluble solids (°B)	18.80	48.43
14.	Ascorbic acid (mg/100 g fresh fruit)	16.91	0.07
15.	Reducing sugar (%)	34.94	13.00
16.	Non-reducing sugar (%)	1.19	0.63
17.	Total sugars (%)	0.00	0.00
18.	Dry matter content in fruit (%)	19.15	8.39

Y1=2017-18 and Y2=2018-19

The present findings of diverse crosses (clusters V, VI, VII in Y1 and clusters IV and V in Y2) involving parents with different clusters not only revalidates the findings of previous workers but also reflects the chances of getting tansgrassive segregates either by making the three way crosses between clusters IV, VI and VII in Y1 and IV, V and VI in Y2 with cluster VIII in Y1 and Y2 or double crosses between cluster III in Y1 and II, IV, V and VI in Y2 with IV, V, VI and VII in Y1 and VIII in Y2.

A perusal of Table-3 showed that cluster means for different traits indicated considerable differences between the clusters. Cluster VI, VII and VIII in Y1 and cluster V, II and III in Y2 had in general medium mean performance for most of the characters. Maximum cluster means for fruit yield per plant was observed in cluster VII followed by cluster V in Y1, while in Y2 cluster V recorded maximum cluster means for fruit yield followed by cluster II. In Y1, reducing sugars contributed maximum contribution towards total divergence while minimum contribution was reflected by days to first pistillate flower anthesis, fruit weight and total sugars and in the year Y2, total soluble solids contributed maximum contribution towards total divergence, while minimum contribution was reflected by days to first pistillate flower anthesis, node number to first staminate flower, node number to first pistillate flower, vine length at last picking stage and total sugars. Therefore, necessary attention is required to be focused on these characters. Similar results had also been reported by earlier workers (Badade *et al.*, 2001 and Mathew *et al.*, 2001) [1, 5].

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