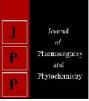


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Lal Vijay Singh

Department of Horticulture, Udai Pratap Autonomous College Varanasi, Uttar Pardesh, India

Diwaker Singh

Department of Horticulture, Udai Pratap Autonomous College Varanasi, Uttar Pardesh, India

Amit Kumar Singh

Department of Horticulture, Udai Pratap Autonomous College Varanasi, Uttar Pardesh, India

Dharmender Singh

Department of Horticulture, Udai Pratap Autonomous College Varanasi, Uttar Pardesh, India

NK Tiwari

Faculty of Agricultural Sciences SGT University, Gurgaon, Haryana, India

Correspondence NK Tiwari Faculty of Agricultural Sciences SGT University, Gurgaon, Haryana, India

Genetic diversity in promising lines and their F₁ progeny of bottle gourd [*Lagenaria siceraria* (Mol.) Standl.]

Lal Vijay Singh, Diwaker Singh, Amit Kumar Singh, Dharmender Singh, and NK Tiwari

Abstract

The experiment was conducted in Randomized Block Design with three replications. In present investigation 54 genotypes (10 lines + 4 testers + 40 F₁'s) of bottle gourd were grouped into 8 distinct non over lapping clusters. This indicated presence of considerable diversity in the genotypes. The clusters contained genotypes of heterogenous origin. The genotypes of same geographic region were also found to be grouped together in the same clusters. Thus, there was no consistent relationship between genetic divergence and geographical distribution. Cluster III had maximum number of genotypes (29) followed by cluster I with nineteen genotypes, while rest of the six clusters contains mono genotypes. The intra cluster D² values ranged from 0.00 (cluster II, IV, V, VI, VII and VIII) to 573.59 (cluster III), while the inter cluster D² values ranged from 297.08 (cluster IV and V) to 3833.71 (cluster VII and VIII). The inter cluster distances between cluster VI to cluster VIII (3702.30) and cluster IV to cluster VIII (3321.49) were also very high. The higher inter cluster distance indicated greater genetic divergences between the genotypes of those clusters, while lower inter cluster values between the clusters suggested that the genotypes of the cluster were not much genetically diverse from each other. Cluster VI showed the maximum means values for 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, fruit length and ascorbic acid whereas, cluster VII showed maximum mean values for fruit yield per plant and some other traits too. The results suggested that crosses between selected lines/F1 from widely separated clusters are most likely to give desirable recombinants/hybrids.

Keywords: Bottle gourd, genetic divergence, d² analysis, cluster analysis

Introduction

Among the cultivated vegetables, cucurbits are associated with the origin of agriculture and dawn of civilization. Among food crops, cucurbits are largest producer of biological water, easily digestible and recommended even to sick and frail patients. Bottle gourd [*Lagenaria siceraria* (Mol.) Standl.] is also known as white-flowered gourd and most important vegetables of ancient China. Because of hard mature rind of mature fruits, it is known as gourd. It is also commonly grown in Ethiopia, Africa, Central America and other warmer regions of the world. It is one of the important cucurbits in India, both as rainy and summer season vegetable.

Out of the all cultivated cucurbits, bottle gourd with its high yield potential and adaptability to diverse climatic conditions holds a great promise to cope up with the per capita per day requirement of vegetables in the balanced diet (Singh, 1998) ^[11] of the fast growing population pressure and greater dietary awareness, particularly among the literate masses of a country like India. Bottle gourd was one of the first plant species to be domesticated for human use, providing food, medicine and a wide variety of utensils and musical instruments made from the large hard shelled mature fruits. A total of six species have been recognized belonging to the genus *Lagenaria*. Out of six species of *Lagenaria* only *Lagenaria siceraria* is domesticated annual and monoecious in nature while the other five are wild congeners, perennial and dioecious (Bisognin, 2002) ^[2].

The tender fruits of bottle gourd can be used as a vegetable or for making sweets (*e.g., Halva, kheer, petha* and *burfi*), kofta and pickles. The fruit is rich in pectin also, which showed good prospects for jelly preparation. A decoction made from the leaf is a very good medicine for jaundice. The fruit has cooling effect, it is a cardiotonic and diuretic, good for people suffering from biliousness, indigestion and convalescences *i.e.*, regain health after illness. The pulp is good for overcoming constipation, cough, night blindness and as an antidote against certain

poisons. The plant extract is used as a cathartic and seeds are used in dropsy. In addition, the seeds and seed oil are edible. The fruits contain 96.3 per cent moisture, 2.9 per cent carbohydrate, 0.2 per cent protein, 0.1 per cent fat, 0.5 per cent mineral matter and 11 mg of vitamin C (Ascorbic acid) per 100 g fresh weight (Thamburaj and Singh, 2005) ^[14].

To develop a new variety there is need of high magnitude of genetic variability in the base material and the vast of variability for desired characters. A good knowledge on genetic diversity or genetic similarity could be helpful in long term selection gain in plants (Kumar *et al.*, 2012)^[6]. Hence, genetic variability and diversity is of prime interest to the plant breeder as it plays a key role in framing a successful breeding programme. The genetically diverse parents are always able to produce high heterotic effects and great frequency of desirable segregants in further generations as already reported by Kumar et al. (1994)^[5]. D² statistic is a useful tool to measure genetic divergence among genotypes in any crop as developed by Mahalanobis (1936) ^[7]. However, in the present study, an attempt has been made to identify genetically divergent promising lines and their F₁ progenies, so as to select the potential parents for breeding programme to attain the anticipated improvement in fruit yield per plant of bottle gourd either by crossing two dissimilar parents to get heterotic F₁ or by making single cross, three way cross, double cross and selfing of crosses (F₁) obtained by the divergent parents of bottle gourd.

Materials and Methods

The experimental materials consisted of 14 promising parental lines of bottle gourd and their F_1 progenies. Out of these advanced breeding parental lines 10 parents were choosen as lines and four as testers and crossed as per $L \times T$ design to get 40 F₁ at U P AC Varanasi, (U.P.). These experimental materials were grown under Randomized Block Design (RBD) with three replications at the Main Experiment Station (MES) of the Department of Horticulture, Udai Pratap Autonomous College Varanasi (U.P.) India. The treatments were sown in rows spaced 3.0 meters apart with a plant to plant spacing of 0.5 meter. The experiment was sown on 12th March, 2016. All the recommended agronomic package of practices and protection measures were followed to raise a good crop. Fertilizers and manures were applied as per recommended dose. Observations were recorded on all the six plants maintained carefully in each plot for eighteen quantitative characters viz., 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), 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 sugar (%), non-reducing sugar (%), total sugars (%) and dry matter content in fruit (%). Analysis of variance was carried out as suggested by Panse and Sukhatme (1967)^[9]. Genetic divergence was estimated by using D² statistics of Mahalanobis (1936) [7] and clustering of genotypes was done according to Tocher's method as described by Rao (1952)^[10]. The per cent contribution of characters towards genetic divergence was calculated according to Singh and Chaudhary (1985) [12].

Results and Discussion

The analysis of variance revealed that the significant differences were present for all the characters studied and the

experimental materials were genetically divergent from each other (Table-1). This indicates that there is ample scope for selection of promising lines and their F₁ progenies from the present gene pool aimed at enhancing genetic yield potential of bottle gourd. All the fifty four genotypes were grouped into 8 different non over lapping clusters following Mahalanobis's methods (Table-2). Cluster III had highest number of genotypes (29) followed by cluster I (19) and cluster II, IV, V, VI, VII, VIII were found as monogenotypic clusters. The estimates of intra and inter-cluster distances represented by D² values are given in table-3. The intra-cluster D² value ranged from 0.00 (cluster II, IV, V, VI, VII and VIII) to 573.59 (cluster III) while the inter-cluster values ranged from 297.08 (cluster IV and cluster V) to 3833.71 (cluster VII and cluster VIII) indicated that the selected breeding lines as well as F₁'s were highly divergent (Table-3). The highest intra-cluster distance was shown by cluster III (573.59), whereas minimum was zero for monogenotypic clusters (clusters II, IV, V, VI, VII, and 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) suggesting that the genotypes/ F_1 's belonging to these clusters may be used as parents for hybridization programme to develop desirable type because crosses between genetically divergent lines/ F_1 will generate heterotic segregants (Varalakshmi et al., 1994 and Mathew et al., 2001)^[15, 8]. As heterosis can be best exploited and chances of getting transgressive segregants are maximum when genetically diverse lines are crossed (Karuppaiah et al., 2005; Singh et al., 2007 and Islam et al., 2010) [4, 13, 3]. The present findings of diverse crosses (cluster V, VI, VII) 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 with cluster VIII or double crosses between cluster III with IV, V, VI and VII.

The comparison of clusters means revealed considerable differences among the clusters of different quantitative and quality characters (Table-4). 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 are 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%) therefore necessary attention is required to be focused on these characters (Badade *et al.*, 2001)^[1].

Intra and inter-cluster distance diagram for different quantitative characters in bottle gourd is given in fig.-1. Clustering by Tocher method shows that the lines/ F_1 's fall into same cluster having lowest degree of divergence from each other (Fig.-2) and crosses among the lines/ F_1 of the same

cluster will be unable to produce any transgressive segregants. While, the lines/ F_1 's belonging to different clusters having maximum divergence can be successfully utilize in

hybridization programmes to get desirable heterotic $F_1\sp{s}\sp\sp{s}\sp{s}\sp{s}\sp{s}\sp{s}\sp{s}\sp{s}\sp{s}\sp{s}$

Table 1: Analysis of variance	(mean square) for randomized bloc	k design for 18 characters in bottle gourd

S. No.	Characters	Treatments (df=53)	CV (%)
1.	Days to first staminate flower anthesis	14.363**	1.47
2.	Days to first pistillate flower anthesis	9.246**	1.26
3.	Node number to first staminate flower	4.502**	3.18
4.	Node number to first pistillate flower	4.473**	2.96
5.	Days to first fruit harvest	12.000**	1.41
6.	Vine length at last picking stage (m)	3.699**	4.77
7.	Number of primary branches per plant	31.001**	3.65
8.	Fruit length (cm)	86.697**	2.45
9.	Fruit circumference (cm)	13.699**	2.34
10.	Fruit weight (kg)	0.217**	8.58
11.	Number of fruits per plant	4.395**	9.57
12.	Fruit yield per plant (kg)	6.938**	7.70
13.	Total soluble solids (°B)	0.467**	1.31
14.	Ascorbic acid (mg/100 g fresh fruit)	1.302**	0.56
15.	Reducing sugar (%)	0.144**	0.87
16.	Non-reducing sugar (%)	0.046**	1.95
17.	Total sugars (%)	0.035**	0.95
18.	Dry matter content in fruit (%)	1.646**	2.57

Cluster number	No. of genotypes	Genotypes
I	19	$\label{eq:ndbg-517} \begin{array}{l} \text{NDBG-624, NDBG-603} \times \text{NDBG-624, NDBG-517, NDBG-509} \times \text{NDBG-624, NDBG-603,} \\ \text{NDBG-517} \times \text{NDBG-S-5, NDBG-522} \times \text{NDBG-S-5, NDBG-504, NDBG-11, NDBG-504} \times \text{NDBG-104,} \\ \text{NDBG-11} \times \text{NDBG-104, NDBG-S-5, NDBG-504} \times \text{Pusa Naveen, NDBG-10, NDBG-10} \times \text{NDBG-104,} \\ \text{NDBG-11} \times \text{NDBG-624, NDBG-603} \times \text{NDBG-104, NDBG-504} \times \text{NDBG-S-5, NDBG-601} \times \text{NDBG-104} \\ \end{array}$
II	1	NDBG-104
ш	29	NDBG-509 × NDBG-104, NDBG-749-2 × NDBG-104, NDBG-601 × Pusa Naveen, NDBG-10 × Pusa Naveen, NDBG-522 × NDBG-624, NDBG-509 × NDBG-S-5, Narendra Rashmi × NDBG-S-5, NDBG-10 × NDBG-624, NDBG-504 × NDBG-624, NDBG-601 × NDBG-624, Pusa Naveen, NDBG-522, NDBG-749-2 × Pusa Naveen, NDBG-522 × Pusa Naveen, NDBG-603 × NDBG-S-5, NDBG-522 × NDBG-104, NDBG- 601, Narendra Rashmi × NDBG-104, NDBG-11 × Pusa Naveen, NDBG-749-2 × NDBG-624, Narendra Rashmi × Pusa Naveen, NDBG-11 × NDBG-S-5, Narendra Rashmi × NDBG-624, NDBG-509 × Pusa Naveen, NDBG-601 × NDBG-S-5, NDBG-624, NDBG-749-2, NDBG-603 × Pusa Naveen
IV	1	NDBG-10 \times NDBG-S-5
V	1	NDBG-517 × Pusa Naveen
VI	1	NDBG-517 \times NDBG-104
VII	1	NDBG-749-2 \times NDBG-S-5
VIII	1	Narendra Rashmi

Table 3: Intra and inter clusters D^2 values for eight clusters in bottle gourd

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VII
Cluster I	288.65	509.10	689.16	425.23	409.41	463.91	594.02	2266.20
Cluster II		0.00	1032.55	865.67	548.16	619.66	830.89	2656.57
Cluster III			573.59	1198.60	1044.52	1292.10	1426.14	1237.77
Cluster IV				0.00	297.08	469.43	483.24	3321.49
Cluster V					0.00	619.03	398.24	2927.30
Cluster VI						0.00	610.34	3702.30
Cluster VII							0.00	3833.71
Cluster VIII								0.00

Table 4: Clusters mean values and	per cent contribution of eighteen	characters in bottle gourd
Table 4: Clusters mean values and	per cent contribution of eighteen	characters in bottle gould

S. No.	Characters	Cluster I	Cluster	Contribution						
5. NO.	Characters		II	III	IV	V	VI	VII	VIII	(%)
1.	Days to first staminate flower anthesis	49.44	51.93	49.09	44.33*	50.13	54.87**	48.83	48.13	0.07
2.	Days to first pistillate flower anthesis	49.55	50.47	49.76	47.53*	49.53	53.27**	49.67	48.03	0.00
3.	Node number to first staminate flower	8.96	7.50	8.63	8.97	7.57	10.80**	7.97	7.40*	0.70
4.	Node number to first pistillate flower	10.07	8.30*	10.21	9.40	10.80	11.47**	10.53	11.17	0.35
5.	Days to first fruit harvest	60.93	61.90	62.04	59.83*	60.03	65.53**	61.90	61.00	0.07
6.	Vine length at last picking stage (m)	5.76	5.54	5.18	6.09	4.06*	6.67**	5.08	5.83	0.98
7.	Number of primary branches per plant	16.54	15.70	14.94	18.63	11.63*	16.57	17.90	19.10**	1.12
8.	Fruit length (cm)	42.89	42.10	41.53	43.90	40.90	43.93**	43.80	35.33*	2.87
9.	Fruit circumference (cm)	25.51	25.50	25.97	26.03	27.13	22.40*	29.00**	25.53	0.49
10.	Fruit weight (kg)	1.43**	1.31	1.38	1.39	1.26	1.02	1.40	0.96*	0.00
11.	Number of fruits per plant	3.86	3.27	4.23	5.12	7.27**	3.02*	7.19	6.08	1.89
12.	Fruit yield per plant (kg)	5.42	4.25	5.67	7.10	9.10	3.07*	10.05**	5.77	0.49
13.	Total soluble solids (°B)	2.91	2.18*	2.83	3.58**	3.08	2.95	2.45	2.95	18.80
14.	Ascorbic acid (mg/100 g fresh fruit)	9.57	9.71	8.96	10.12	9.71	10.52**	10.13	7.24*	16.91
15.	Reducing sugar (%)	1.67	1.54	1.95	1.51	1.51	1.43*	1.50	2.30**	34.94
16.	Non-reducing sugar (%)	0.88	0.95	0.72	0.95	0.96	0.85	0.99**	0.50*	1.19
17.	Total sugars (%)	2.56	2.49	2.67	2.46	2.47	2.28*	2.49	2.82**	0.00
18.	18. Dry matter content in fruit (%)		4.77	3.22	3.01	3.60	2.81	2.57*	4.47	19.15

*Lowest mean value among different clusters, ** Highest mean value among different clusters

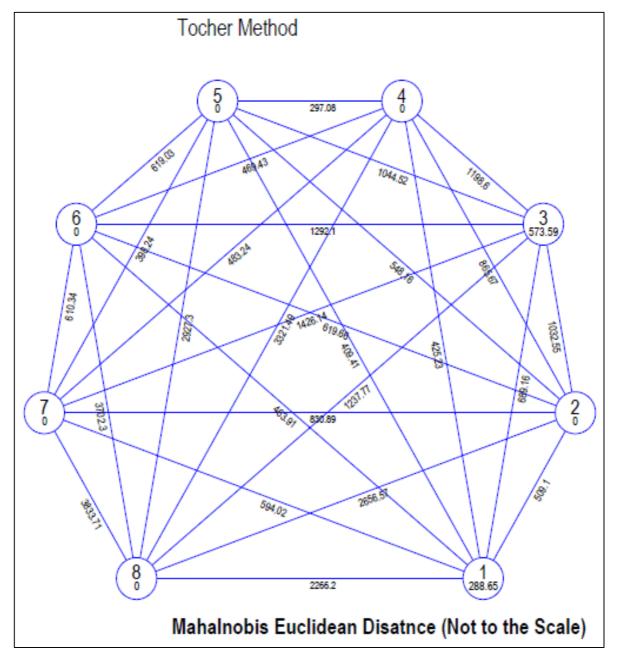


Fig 1: Intra and inter cluster distance diagram for different quantitative characters in bottle gourd

			Clustering by Tocher Method
1 Cluster	10	BG-517*BG-624	
	22	BG-603"BG-624	<u> </u>
	43	BG-517	
	6	BG-509*BG-624	
	45	BG-603	
	11	BG-517*BG-8-5	I I I I I I
	15	BO-522"BO-8-5	
	41	BG-504	
	48	BG-11	
	4	BG-504"BG-104	
	32	BG-11*BG-104	
	53	80-8-5	
	1	BG-504"Pusa Navee	
	49 36	BG-10	
		BG-10*BG-104	
	30 24	BG-11*BG-624 BG-603*BG-104	
	3	BG-504"BG-8-5	
	20	80-601"80-104	
2 Cluster	54	BG-104	_
3 Cluster	8	BG-509*BG-104	
	28	BO-749-2"BO-104	-
	17	BG-601"Pusa Navee	
	33	BG-10"Pusa Navee	-1 ! !
	14	BG-522"BO-624	-1
	7	BG-509"BG-8-5	
	39	N. Rashmi*BG-8-5	
	34	BG-10*BG-624	
	2	BG-504"BG-624	
	18	BG-601"BG-624	
	51	Pusa Naveen	
	25	BG-749-2"Pusa Navee	
	13	BG-522"Puse Nevee	
	23	BG-603*BG-8-5	
	16	BG-522"BG-104	
	45	BG-601	
	40	N. Rashmi*BG-104	
	29	BG-11"Pusa Navee	
	26	BG-749-2"BG-024	
	37	N. Rashmi"Pusa Navee	
	31	80-11"80-8-5	
	38	N. Rashmi*BG-624	
	5	BG-509"Puse Navee	
	19 52	BG-601*BG-8-5 BG-624	
	47		
	42	BG-749-2 BG-509	
	21	BG-603"Puse Navee	
4 Cluster	35	BG-10"BG-8-5	_
5 Cluster	9	BG-517"Pusa Navee	
6 Cluster	12	BG-517*BG-104	—
7 Cluster	27	BG-749-2"BG-8-5	
8 Cluster	50	N. Rashmi	
			500 1000 1500

Fig 2: Clustering by Tocher method in bottle gourd

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