Journal of Applied and Natural Science 9 (4): 1949 -1953 (2017)

JANS

Genetic divergence analysis in bottle gourd [*Lagenaria siceraria* (Mol.) Standl.]

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Received: December 21, 2016; Revised received: March 27, 2017; Accepted: September 11, 2017

Abstract: The study was conducted during *summer* 2014-15 at the Instructional Farm, College of Agriculture, Junagadh Agricultural University, Junagadh to assess the genetic diversity among 50 genotypes of bottle gourd (*Ligenaria siceraria* L.*)*. The genetic diversity analysis revealed the formation of 13 clusters suggesting the presence of wide genetic diversity. The clustering pattern indicated that geographic diversity was not associated with genetic diversity. The analysis of per cent contribution of various characters towards the expression of total genetic divergence indicated that number of fruits per vine (22.45%) followed by number of primary branches per vine (13.80%), average fruit weight (11.51%), vine length (11.18%), fruit yield per vine (10.61%), number of male flowers (7.84%), fruit length (6.45%), ratio of male to female flowers (4.82%), days to first picking (4.49%) and days to opening of first male flower (3.84%) contributed maximum towards total genetic divergence. Based on the maximum genetic distance.It is advisable to attempt crossing of the genotypes from cluster XII(GP-14) with the genotypes of cluster IV (GP-25) and XI (GP-53), which may lead to the generation of broad spectrum of favourable genetic variability for yield improvement in bottle gourd.

Keywords: Genetic divergence, D^2 statistic, *Lagenaria siceraria* L.

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 (Singh, 1990), although it is considered as a poor man's crop due to the socioeconomic restrictions governing its production and use. It has a pan-tropical distribution with regional economic importance and is used as a vegetable, container, musical instrument or float while its seeds are used for oil and protein. A lot of information is known on the medicinal aspects of bottle gourd (Milind and Satbir, 2011). However, its potential as a possible food security crop has been lowly documented. In nature, bottle gourd exhibits great morphological and genetic variability. This alone could indicate its wide environmental adaptation (Koffi *et al.*, 2009).

According to Decker-Walters *et al.* (2001), the dispersal of bottle gourd fruit from Africa to Asia and the Americas occurred during pre-Columbian times followed by independent domestication on all three continents.Today, India is the second largest producer of vegetables in the world with a production of over 90 million tonnes. Cucurbits belonging to family cucurbitaceae (gourd family) represented by about 34 genera, 108 species and 38 endemic species in India account for nearly 20% of vegetable production in the country. In India, area under other vegetables during 2013-14 was 1.5 lakh hectares with production of 19.11 million metric tonnes and productivity of 12.74 tonnes per hectare which also include bottle gourd. In Gujarat, area under other vegetables was 1.9 lakh hectares with production of 2.69 million metric tonnes and productivity of 14.17 tonnes per hectare which include bottle gourd (Anonymous, 2014). According to an estimate, India will need to produce 230 mt vegetables by 2030 to provide food and nutritional security at individual level and being the largest group of vegetable; cucurbits provide better scope to enhance overall productivity and production (Anonymous, 2011).

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. 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 (Kumar *et al*., 1994). D^2 statistic is a useful tool to measure genetic divergence among genotypes in any crop as developed by Ma-

ISSN : 0974-9411 (Print), 2231-5209 (Online)

halanobis (1936). Hence, in the present study, an attempt has been made to obtain such information in 50 germplasm lines of bottle gourd(*Lagenaria siceraria* (Mol.) Standl.)

MATERIALS AND METHODS

The study was conducted during *summer* 2014-15 at the Instructional Farm, College of Agriculture, Junagadh Agricultural University, Junagadh to assess the genetic diversity among 50 genotypes of bottle gourd (*L. siceraria* (Mol.) Standl.) collected from different parts of India and maintained by Vegetable Research Station, J. A. U., Junagadh. Each genotype was accommodated in a single row of 10 m length with a spacing of 2.5 m between row and 1.0 m between plants within the row. Recommended agronomic practices were followed to raise a good crop. Observations were recorded from five randomly selected plants from each genotype on 15 different characters *viz*., days to opening of first female flower, days to opening of first male flower, number of node bearing first female flower, internodal length (cm), number of male flowers, number of female flowers, ratio of male to female flowers, days to first picking, vine length (cm), number of primary branches per vine, number of fruits per vine, average fruit weight, fruit length (cm), fruit girth (cm) and fruit yield per vine (kg). The data were analysed as per the multivariate analysis of genetic divergence using Mahalanobis (1936) D^2 statistic. The genotypes were grouped into different thirteen (I to XIII) clusters following the Tocher's method (Rao, 1952).

RESULTS AND DISCUSSION

The analysis of variance showed significant difference among the genotypes for the characters studied. On the basis of D^2 values, 50 genotypes were grouped into 13 clusters (Table 1). This indicated the existence of genetic diversity among the genotypes. The maximum genotypes were in cluster I having 30 genotypes, followed by cluster II with eight genotypes, cluster III had two genotypes, while remaining clusters (IV to XIII) had one genotype. This suggests that the genotypes within a cluster might have some degree of ancestral relationship. These results showed that geographical diversity may not necessarily be related with genetic diversity. Therefore, the selection of genotypes for hybridization should be based on genetic diversity rather than on geographical diversity. On the basis of present finding, it can be suggested that though geographical diversity may not necessarily be an index of genetic diversity, sufficient genetic diversity can be accumulated in the genotypes. The tendency of genotypes to occur in clusters cutting across geographical boundaries demonstrated that geographical isolation is not only factor causing genetic diversity. This may be due to wide soil and climatic differences in the region. The results obtained in the present study are in accordance to the findings of Badade *et al.* (2001), Mathew *et al*. (2001), Singh *et al*. (2013), Ara *et al*. (2014), Visen *et al.* (2015) and Kumar *et al.* (2015) in bottle gourd; Masud *et al.* (2002) in sponge gourd; Prasad *et al*. (2002) in water melon and Islam *et al*. (2002) in musk melon. Murty and Arunachalam (1996) and Singh *et al*. (1989) have suggested that genetic drift and natural selection forces under diverse environmental conditions within a country could cause more considerable diversity than geographical isolation.

Average intra and inter cluster distance for 50 genotypes and 15 characters are present in the Table 2. The average intra cluster distance ranged from 07.49 to 19.09, which was an indicator of considerable diversity available in the material evaluated. The maximum inter-cluster distance (D=19.09) was found between clusters IV and XII carrying one genotype followed by that between clusters XI and XII (D=18.28), III and IV (D=18.00), III and XIII (D=17.86), III and XI (D=17.64), III and IX (D=17.60) suggesting a large difference between these groups. On the other hand, the minimum inter-cluster distance (D=7.97) was found between clusters IX and IV indicates a close relationship and genotypes of these clusters have the maximum of common gene complexes. The Intra cluster distance ranged from 8.25 (cluster I) to 9.17 (cluster II). The clusters III, IV, V, VI, VII, VIII, IX, X, XI, XII, and XIII each contained single genotype and therefore, their intra cluster distance was zero. The genotypes belonging to different clusters separated by high statistical distance could be used in hybridization programme for obtaining a wide spectrum of variation among the segregates. In this context, the genotypes from cluster IV (GP-25) and XI (GP-53) can be crossed with XII (GP-14) in hybridization programme for obtaining a wide range of variation among the segregants.The present findings are in conformity with those reported earlier in bottle gourd by Badade *et al.* (2001), Singh *et al*. (2013), Ara *et al*. (2014) and Kumar *et al*. (2015).

The clustering pattern could be utilized in selecting the parents and deciding the cross combinations which may generate the highest possible variability for various traits. The genotypes with high values of any cluster can be used in hybridization programme for further selection and improvement. The mean performance and the contribution of each character to divergence are presented in Table 3. The results showed that the days to opening of female flower had the maximum cluster mean in cluster VI followed by X and XIII. The days to opening of first male flower had the maximum cluster mean in cluster IV followed by VI, X and XII. The number of node bearing first female flower had the maximum cluster mean in cluster VIII followed by VI and V. The internodal length had the maximum cluster mean in cluster XI followed by VII and II. The number of male flowers has maximum cluster mean in

Table 1. Grouping of 50 genotypes of bottle gourd in various clusters on the basis of D^2 statistic.

Cluster	No. of genotypes	Name of the genotypes	Source
	30	GP-20, GP-24, GP-9, GP-26, GP-21, GP-62,GP-31, GP-3, GP-19, GP-5, GP-4, GP-8, GP-29, GP-2	JAU, Junagadh
		GP-58, GP-13, GP-46, Pusa Naveen, Pusa Samrudhi	IARI, New Delhi
		GP-18, GP-63(B), GP-48	Faizabad
		GP-51, GP-50	Pantnagar
		GP-22	Lucknow
		GP-59	IIVR, Varansi
		GP-36(B)	Punjab
		GP-35	PAU, Ludhiana
		GP-42(B)	AAU, Anand
		GP-43	IIHR, Bangalore
	8	GP-63(A), GP-15, GP-47	Faizabad
		GP-42(A)	AAU, Anand
		GP-57	IIHR, Bangalore
		GP-67	IIVR, Varansi
		GP-56	JAU, Junagadh
		GP-39	Punjab
	2	GP-27	JAU, Junagadh,
		GP-61	Hissar
	1	GP-25	JAU, Junagadh
	1	GP-36(A)	JAU, Junagadh
	1	NDBG-104	Faizabad
	1	GP-38	Faizabad
	1	GP-30	JAU, Junagadh
	1	GP-60	IIHR, Bangalore
	1	GP-6	JAU, Junagadh
	1	GP-53	JAU, Junagadh
	1	GP-14	Faizabad
	1	GP-28	JAU, Junagadh

Table 2. Average inter and intra-cluster distance (D) $= \sqrt{D^2}$ values for 50 genotypes of bottle gourd.

	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII
I	08.25	10.03	14.02	09.70	09.46	09.56	09.92	09.42	09.57	09.70	11.23	14.74	13.05
II		09.17	16.30	12.81	11.42	11.52	10.64	11.84	10.96	12.97	12.51	14.44	13.09
III			08.69	18.00	11.56	16.22	15.00	16.51	17.60	12.57	17.64	11.81	17.86
IV				00.00	13.69	08.22	14.12	10.11	07.97	09.27	12.18	19.09	15.60
V					00.00	11.75	07.49	11.08	13.76	09.80	11.75	11.72	11.40
VI						00.00	12.63	10.52	09.39	08.93	09.76	17.29	13.88
VII							00.00	11.91	11.51	13.15	10.22	13.58	10.60
VIII								00.00	11.73	11.06	12.31	17.36	13.58
IX									00.00	11.67	11.05	17.63	15.00
X										00.00	13.83	12.92	15.18
XI											00.00	18.28	12.00
XII												00.00	15.44
XIII													00.00

cluster XI followed by IX and IV. The number of female flowers had the maximum cluster mean in cluster III followed by VIII and I. The ratio of male to female flowers had the maximum cluster mean in cluster XIII followed by XI and X. The days to picking had the maximum cluster mean in cluster X followed by V and VI. The vine length had the maximum cluster mean in cluster XI followed by II and V. The number of primary branches per vine had maximum cluster mean in cluster XI followed by VI and IV. The number of fruits per vine had the maximum cluster mean in cluster XII followed by XI and IX. The average fruit weight had the maximum cluster mean in cluster II followed by XI, VI and VIII. The fruit length had the maximum cluster mean in cluster II followed by XI and XIII. The fruit girth had the maximum cluster mean in cluster X followed by XI and VIII. The fruit yield per vine had the maximum cluster mean in cluster XI and XIII followed by II. The better genotypes can be selected for most of the characters on the basis of mean performance in cluster and inter-crossing of genotypes involved in these clusters would be useful for inducing

Table 3. Cluster mean and contribution of characters towards divergence for 15 different characters in 50 genotypes of bottle gourd.

Clusters	DFF	DMF	NNF	IL	NMF	NFF	M/F	DFP	VL	PB/V	F/V	AFW	FL	FG	FY/V
	52.93	51.95	01.01	06.83	71.53	09.42	07.74	67.78	230.28	02.72	01.46	00.57	27.28	11.97	00.71
	54.48	53.39	01.01	07.88	73.00	09.41	07.92	69.22	308.18	03.19	01.31	00.73	33.31	12.44	00.90
	49.80	47.87	01.00	06.90	71.47	09.72	07.37	65.20	220.43	01.73	01.00	00.57	22.17	12.12	00.53
	54.93	56.80	01.00	07.83	78.63	08.50	10.27	69.27	246.80	03.80	01.67	00.42	27.54	12.69	00.68
	53.80	51.80	01.07	07.57	78.43	08.45	09.27	71.87	265.27	01.53	01.00	00.49	28.19	09.33	00.59
	56.27	54.33	01.13	06.18	76.43	08.51	10.07	70.87	165.73	03.87	01.07	00.66	28.20	11.92	00.76
	52.87	50.87	01.00	08.53	65.83	09.18	07.20	68.27	236.77	02.47	01.20	00.44	19.18	10.87	00.89
	50.20	48.13	01.27	06.45	63.60	09.55	06.67	70.00	183.27	02.40	01.00	00.66	29.47	12.85	00.65
	49.20	47.20	01.00	07.20	83.10	09.34	09.03	67.47	255.87	02.67	02.00	00.37	24.68	12.13	00.63
	56.00	54.00	01.00	06.11	73.40	08.18	10.47	84.67	173.67	01.70	01.00	00.62	25.20	13.00	00.69
	51.80	49.80	01.00	09.19	87.47	07.68	12.27	69.93	324.27	04.87	03.13	00.71	30.88	12.91	00.93
	53.91	54.00	01.00	05.64	76.10	08.59	08.88	67.80	206.70	02.83	03.35	00.47	26.58	11.47	00.61
	55.87	53.87	01.00	07.44	76.50	06.63	15.00	65.80	247.53	01.87	01.27	00.63	29.97	12.52	00.93
Mean	53.24	52.16	01.01	07.05	72.74	09.21	08.21	68.53	242.14	02.79	01.50	0.58	28.06	12.03	00.74
S.Em. ±	01.72	00.78	00.03	00.63	01.85	00.39	00.45	01.36	13.81	00.22	00.11	00.03	01.25	00.51	00.03
C.V.%	05.59	02.62	06.57	15.70	04.42	07.49	09.55	03.44	09.88	13.94	12.80	10.04	07.73	07.37	08.32
contribution of characters towards divergence															
Number of times appearing first	00	47	11	09	96	06	59	55	137	169	275	141	79	11	130
% contribution	0.00	03.84	00.90	00.73	07.84	00.49	04.82	04.49	11.18	13.80	22.45	11.51	06.45	00.90	10.61

Where, DFF = Days to open first female flower, DMF = Days to open first male flower, NNF = Number of node bearing first female flower, IL = Internodal length(cm), NMF= Number of male flowers, NFF = Number of female flowers, M/F = Ratio of male to female flowers, DFP=Days to first picking, VL = Vine length(cm), PB/V= Number of primary branches per vine, F/V = Number of fruits per vine, AFW = Average fruit weight(kg), FL = Fruit length(cm), FG = Fruit girth(cm) and FY/V = Fruit yield per vine(kg).

variability in respective characters and their rational improvement for increasing the fruit yield in bottle gourd. High cluster means for various characters were also reported by Visen *et al.* (2015) and Kumar *et al.* (2015) for bottle gourd.

The analysis of per cent contribution of various characters (Table 3) towards the expression of total genetic divergence indicated that number of fruits per vine (22.45%) followed by number of primary branches per vine (13.80%), average fruit weight (11.51%), vine length (11.18%), fruit yield per vine (10.61%), number of male flowers (7.84%), fruit length (6.45%), ratio of male to female flowers (4.82%), days to first picking (4.49%) and days to opening of first male flower (3.84%) contributed maximum towards total genetic divergence in present study. While, days to open first female flower (0.0%), node bearing first female flower (0.90%), internodal length (0.73%), number of female flowers (0.49%) and fruit girth (0.90%) accounted minimum tow ards total divergence in the material studied. The present finding of bottle gourd are supported with earlier reports of Badade *et al*. (2001), Mathew *et al*. (2001), Singh *et al.* (2013), Visen *et al.* (2015) and Kumar *et al.* (2015).

In all, 13 clusters were formed from 50 genotypes. The composition of cluster is given in Table 1. The maximum number of accessions were grouped in cluster-I (30 accessions) followed by cluster-II (eight accessions) and cluster-III (two accessions), while cluster-IV to XII were found to be mono genotypic (solitary clusters). In general, intra-cluster distance values were lower than the inter-cluster distances. Thus, the genotypes included within a cluster tended to diverse less from each other.

Conclusion

The final conclusion that can be reached from results and discussion on genetic divergence is that number of fruits per vine, fruit yield per vine, average fruit weight, number of primary branches per vine, vine length, ratio of male to female flowers, fruit length and number of female flowers are the most important component characters. Hence, these traits should be considered as selection criteria for yield improvement in bottle gourd.

Further, it is advisable to attempt crossing of the genotypes from cluster XII (GP-14) with the genotypes of cluster IV (GP-25) and XI (GP-53), which may lead to the generation of broad spectrum of favourable genetic variability for yield improvement in bottle gourd.

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