

Original Research Article

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## Genetic Divergence Studies in Bottle Gourd [*Lagenaria siceraria* (Molina) Standl.]

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### ABSTRACT

#### Keywords

Clusters, Divergence, Selection, Genotypes, D<sup>2</sup> Statistics, Cluster distance

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The present investigation was carried out at the Experimental Field, Division of Vegetable Science, SKUAST-K, Shalimar during Kharief 2018. The experiment was laid out in randomized complete block design (RCBD) with three replications. Cluster analysis grouped thirty genotypes of bottle gourd into three clusters. Cluster I had maximum number of genotypes (25) followed by cluster II (4) and cluster III (1). Maximum inter cluster distance was observed between cluster I and III (311.28) followed by cluster I and II (189.07). Fruit length, fruit yield plant<sup>-1</sup> and fruit diameter contributed maximum towards total genetic divergence.

### Introduction

Bottle gourd [*Lagenaria siceraria* (Molina) Standl.] (2n=2x=22) belongs to family Cucurbitaceae and is one of the most ancient crop cultivated during summer throughout the world. The genus *Lagenaria* is derived from the word lagena, meaning the bottle. It is also known as Calabash, Doodhi and Lauki in different parts of India (Deore *et al.*, 2009). Its primary centre of origin is Africa (Singh, 1990). The fossil records indicate its culture

in India even before 2000 B.C. It has been found wild in India, the Moluccas and Ethiopia. It has spread to western countries from India and Africa. The genus *Lagenaria* includes six species that are distributed in Africa, Madagascar, Indo-Malaysia and the neotropics. There is only one cultivated species, *Lagenaria siceraria*, which is annual and monoecious. The five other species are wild, perennial and dioecious, occurring in East Africa and Madagascar. In India the total area under its cultivation is 185 thousand

hectares with an annual production of 3072 thousand MT (NHB, 2018). However in Jammu and Kashmir it is grown over an area of 1.60 thousand hectares with a production of 36.17 thousand MT (Anonymous, 2018). It is a highly cross pollinated crop due to its monoecious and andromonoecious nature (Swiander *et al.*, 1994) and shows large amount of variation for various economic traits of which the most interesting variation is found for size, shape and colour of fruits. On the basis of fruit shape, the cultivars of bottle gourd are broadly classified into two groups viz., long fruited and round fruited.

### Materials and Methods

The present investigation was carried out at Vegetable Experimental Farm, Division of Vegetable Science, SKUAST-Kashmir, Shalimar, Srinagar during *Kharif* 2018. The altitude of the location is 1685 meter above mean sea level and situated 34° N of latitude and 74.89° E of longitude. The climate is temperate characterized by mild summers. The mean minimum and maximum temperatures are recorded in months of January and June (respectively). The maximum rain fall is received during March to April. Thirty genotypes of bottle gourd were evaluated for various yield and yield attributing traits. A single factor experiment was laid out in randomized complete block design (RCBD) with three replications of each accession per plot. Plants from each genotype were transplanted at random to each block at spacing of 1 m between rows and 0.60 m between plants. Recommended package of practices were adopted to raise a healthy crop. The observations were recorded on node number at which first male flower appeared, node number at which first female flower appeared, days to anthesis of first male flower, days to anthesis of first female flower, days to first fruit harvest, days to last fruit harvest, fruit length, fruit diameter, number of

fruits plant<sup>-1</sup>, fruit yield plant<sup>-1</sup>, fruit yield hectare<sup>-1</sup>, dry matter content, total chlorophyll and total sugars. The data recorded on 14 traits was subjected to cluster analysis using Mahalanobis D<sup>2</sup> statistics. The genotypes were grouped into different clusters by Tocher's method (Rao, 1952).

### Results and Discussion

In the present study, thirty genotypes of bottle gourd were evaluated to estimate the genetic divergence for identification of potential parents using Mahalanobis D<sup>2</sup> statistics. The genotypes were grouped into three clusters. Cluster I had maximum number of genotypes (25) followed by cluster II (4) and cluster III (1) (Table 1 and Fig. 1). Intracluster distance (D<sup>2</sup>) was maximum in cluster II (70.46) followed by the cluster I (51.96). The intercluster distance (D<sup>2</sup>) was maximum between the cluster I and III (311.28) followed by cluster I and II (189.07) and cluster II and III (142.31) (Table 2 and Fig. 2). The maximum intracluster distance (D<sup>2</sup>) (cluster II) indicated high heterogeneity in genetic constitution of genotypes in that cluster while minimum intracluster distance (D<sup>2</sup>) (cluster I) indicated homogeneity in genetic constitution of genotypes in that cluster. As well as the highest value of intercluster distance (cluster I and III) indicated also more heterogeneous genetic constitution of genotypes included in both clusters. In contrast, minimum intercluster distance (cluster II and III) indicated closer relationship among the genotypes included. This was in conformity with the findings of Banik (2003), Islam (2004), Khatun and Rehman (2010) and Ara *et al.*, (2014).

The per cent contribution (Table-3) of traits towards the total genetic divergence revealed that the fruit length was the main factor contributing to divergence in the present study, accounting for about 32.41 %, followed

by fruit yield plant<sup>-1</sup> (16.13%), fruit diameter (14.71%), days to first fruit harvest (8.97%), days to anthesis of first male flower (7.19%), days to last fruit harvest (6.44%), dry matter content (6.44%), days to anthesis of first female flower (2.7%), total sugars (1.84%),

node number at which first male flower appeared (1.8%), number of fruits plant<sup>-1</sup> (0.46%), fruit yield plant<sup>-1</sup> (0.46%), total chlorophyll (0.46%), node number at which first female flower appeared (0.23%) and fruit yield hectare<sup>-1</sup>(0.23%).

**Table.1** Distribution of bottle gourd genotypes in different clusters

Cluster number	No. of genotypes	Genotypes
<b>I</b>	25	SH-BG-3, SH-BG-7, SH-BG-64, SH-BG-83, SH-BG-43, SH-BG-23, SH-BG-88, SH-BG-14, SH-BG-48, SH-BG-53, IC-337078, SH-BG-91, IC-331088, SH-BG-10, SH-BG-95, SH-BG-27, SH-BG-34, IC-339187, SH-BG-86, SH-BG-72, SH-BG-1, Shalimar Improved, IC-383252, IC-331025, SH-BG-17
<b>II</b>	4	VRBG-1, VRBG-7, VRBG-59, VRBG-18
<b>III</b>	1	VRBG-5

**Table.2** Average intra cluster (Diagonal) and inter cluster (Above Diagonal) distance values in bottle gourd [*Lagenaria siceraria* (Molina) Standl.]

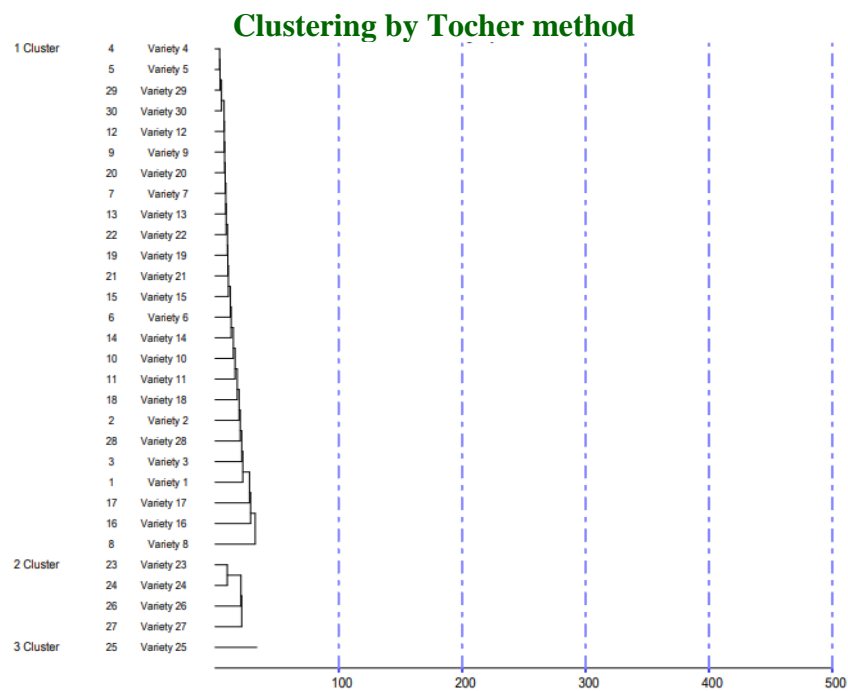
S. No.	Cluster	I	II	III
<b>1</b>	I	<b>51.96</b>	189.07	311.28
<b>2</b>	II		<b>70.46</b>	142.31
<b>3</b>	III			<b>0.00</b>

**Table.3** Per cent contribution of fourteen characters towards total genetic divergence in bottle gourd [*Lagenaria siceraria* (Molina) Standl.]

S. No.	Characters	Per cent contribution
<b>1.</b>	Node no. at which first male flower appeared	1.8%
<b>2.</b>	Node no. at which first female flower appeared	0.23%
<b>3.</b>	Days to anthesis of first male flower	7.19%
<b>4.</b>	Days to anthesis of first female flower	2.7 %
<b>5.</b>	Days to first fruit harvest	8.97%
<b>6.</b>	Days to last fruit harvest	6.44%
<b>7.</b>	Fruit length (cm)	32.41%
<b>8.</b>	Fruit diameter (cm)	14.71%
<b>9.</b>	Number of fruit plant <sup>-1</sup>	0.46%
<b>10.</b>	Fruit yield plant <sup>-1</sup> (kg)	16.13%
<b>11.</b>	Total sugars (%)	1.84%
<b>12.</b>	Total chlorophyll (mg100g <sup>-1</sup> )	0.46%
<b>13.</b>	Dry matter content (%)	6.44%
<b>14.</b>	Fruit yield per hectare (qha <sup>-1</sup> )	0.23%
	<b>Total</b>	<b>100.00</b>

**Table.4** Clusters means for various characters in bottle gourd [*Lagenaria siceraria* (Molina) Standl.] genotypes

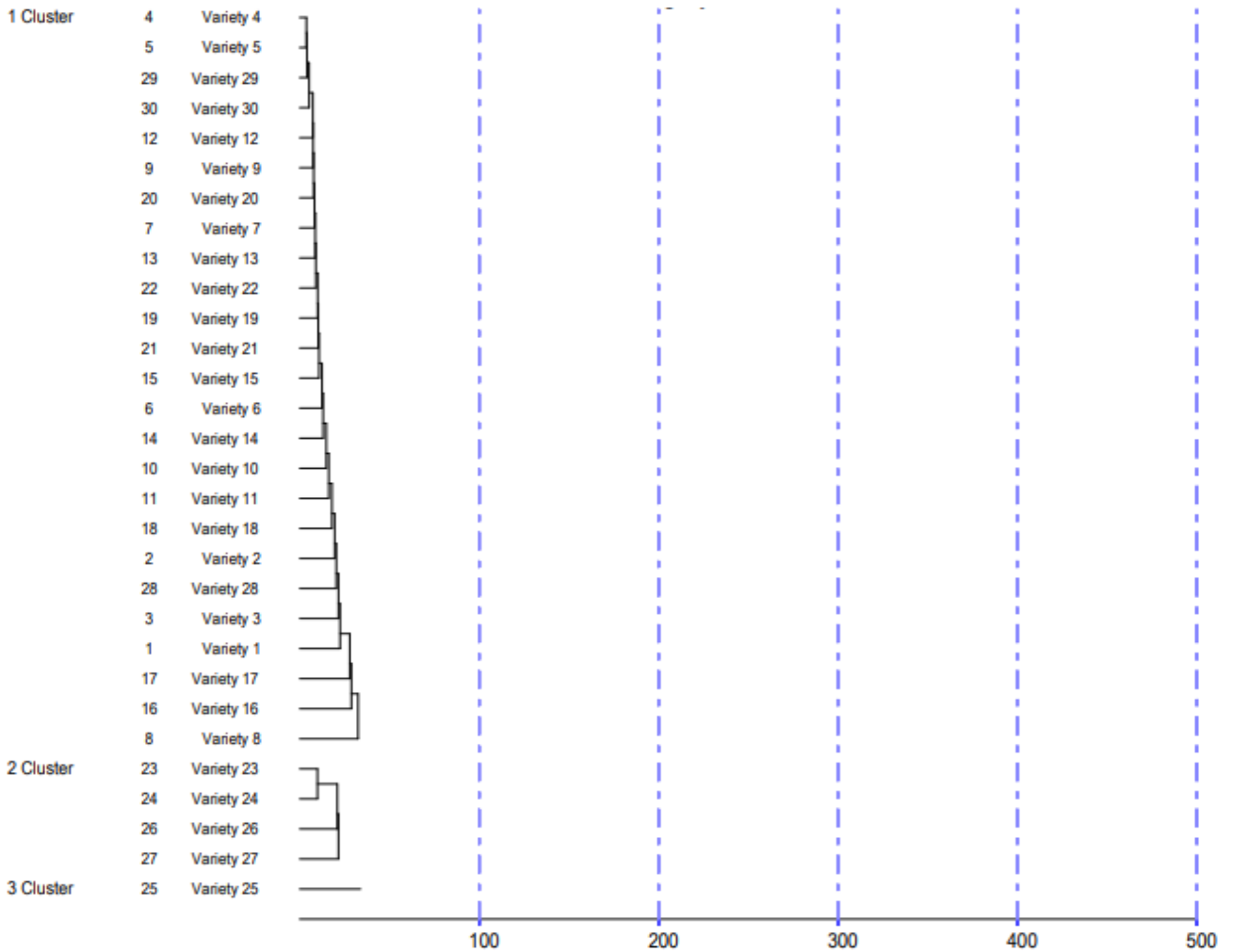
Clusters	Node no. at which first male flower appeared	Node no. at which first female flower appeared	Days to anthesis of first male flower	Days to anthesis of first female flower	Days to first fruit harvest	Days to last fruit harvest	Fruit length (cm)	Fruit diameter (cm)	No. of fruits plant <sup>-1</sup>	Fruit yield plant <sup>-1</sup> (kg)	Total sugars (%)	Total Chlorophyll (mg100g <sup>-1</sup> )	Dry matter content (%)	Fruit yield (qha <sup>-1</sup> )
<b>I</b>	7.56	10.77	45.04	50.78	68.80	146.29	63.50	4.47	5.31	6.23	1.61	43.21	5.77	1038.80
<b>II</b>	6.78	9.22	43.42	50.85	68.02	147.80	40.23	8.99	4.52	6.97	1.56	50.84	6.88	1162.00
<b>III</b>	7.27	10.80	46.40	53.07	67.20	142.27	14.47	5.74	4.47	4.63	1.60	42.28	7.17	771.80



**Fig.1** Clustering by Tocher method (Dendrogram)

1= Shalimar improved, 2= SH-BG-86, 3= SH-BG-1, 4= SH-BG-3, 5= SH-BG-7, 6= SH-BG-10, 7= SH-BG-14, 8= SH-BG-17, 9= SH-BG-23, 10= SH-BG-27, 11= SH-BG-34, 12= SH-BG-43, 13= SH-BG-48, 14= SH-BG-95, 15= IC-331088, 16= IC-331025, 17= IC-383252, 18= IC-339187, 19= IC-337078, 20= SH-BG-88, 21= SH-BG-91, 22= SH-BG-53, 23= VRBG-1, 24= VRBG-7, 25= VRBG-5, 26= VRBG-59, 27= VRBG-18, 28= SH-BG-72, 29= SH-BG-64, 30= SH-BG-83

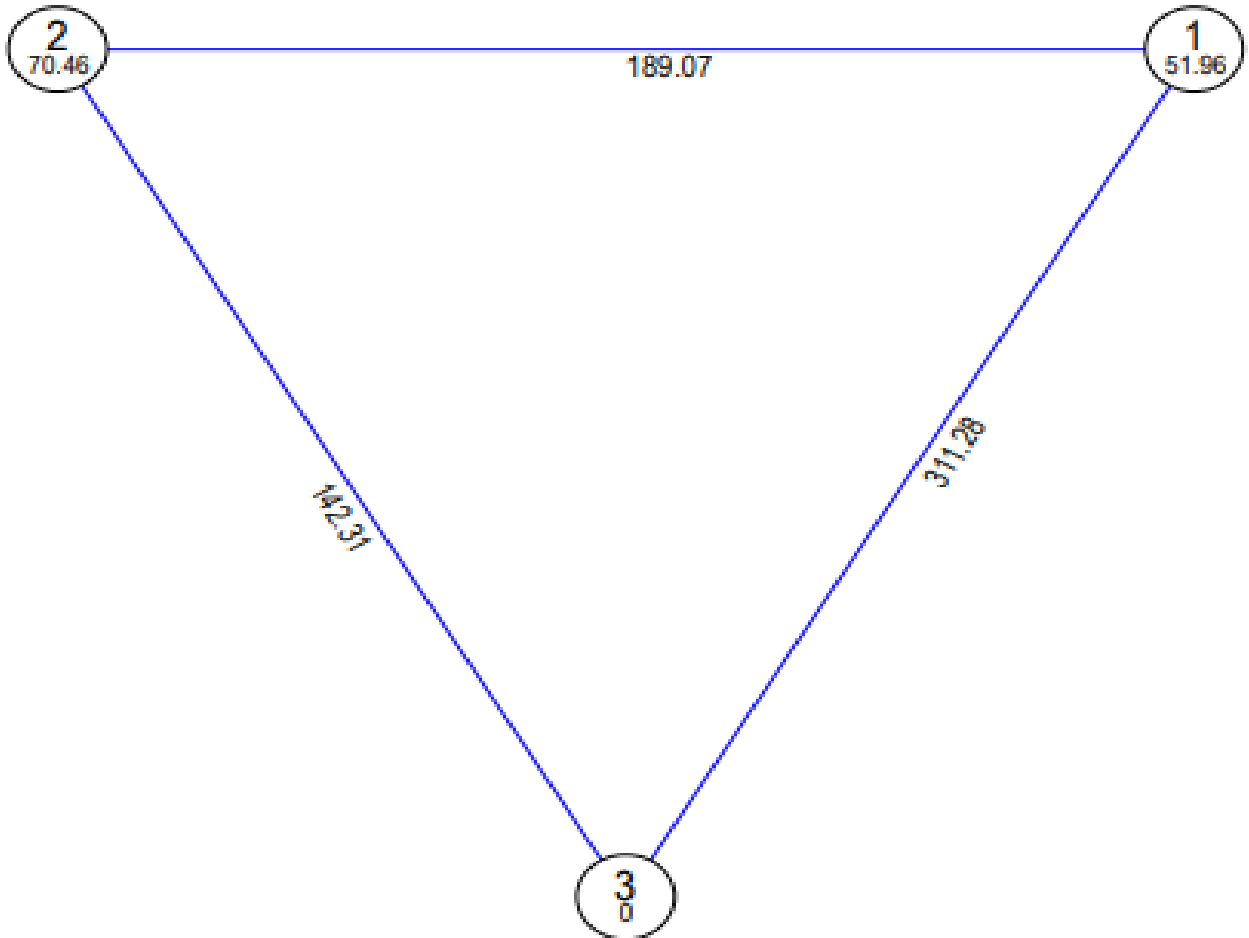
**Clustering by Tocher method**



**Fig.1** Clustering by Tocher method (Dendrogram)

1= Shalimar improved, 2= SH-BG-86, 3= SH-BG-1, 4= SH-BG-3, 5= SH-BG-7, 6= SH-BG-10, 7= SH-BG-14, 8= SH-BG-17, 9= SH-BG-23, 10= SH-BG-27, 11= SH-BG-34, 12= SH-BG-43, 13= SH-BG-48, 14= SH-BG-95, 15= IC-331088, 16= IC-331025, 17= IC-383252, 18= IC-339187, 19= IC-337078, 20= SH-BG-88, 21= SH-BG-91, 22= SH-BG-53, 23= VRBG-1, 24= VRBG-7, 25= VRBG-5, 26= VRBG-59, 27= VRBG-18, 28= SH-BG-72, 29= SH-BG-64, 30= SH-BG-83

**Mahalanobis Euclidean distance**



**Fig.2** Mahalanobis Euclidean distance (not to the scale)

The traits contributing maximum towards the divergence should be given great emphasis for deciding the clusters to be chosen for hybridization and the subsequent selection of the parents from the clusters be based on their *per se* performance. In bottle gourd, maximum contribution from traits towards divergence has been reported to be different for different sets of materials used in experimentation depending upon the genotypes under study. which is in conformity to the findings of Mathew *et al.*, (2001), Badade *et al.*, (2001), Banik, (2003), Bharati *et al.*, (2005) and Visen *et al.*, (2015)<sup>[9,3,4,5,14]</sup>.

Persual of the results representing cluster means (Table 4) for different growth characters revealed that minimum cluster mean for node number at which first male flower appeared (6.78), node number at which first female flower appeared (9.22) and days to anthesis of first male flower (43.42) were recorded in cluster II, for days to anthesis of first female flower (50.78) in cluster I and for days to first fruit harvest (67.20) in cluster III. Maximum cluster mean for fruit length (63.50), number of fruits plant<sup>-1</sup> (5.31), total sugars (1.61) and fruit yield hectare<sup>-1</sup> (1038.80) were recorded in cluster I, for days to last fruit harvest (147.80), fruit diameter (8.99), fruit yield plant<sup>-1</sup>(6.97) and total chlorophyll (50.84) in cluster II and for total sugars (1.60) and dry matter content (7.17) in cluster III. Thus the traits showing high contribution towards genetic divergence can be improved upon by selecting the genotypes from those clusters having maximum/minimum cluster means for the respective traits, which in turn depends upon the objective of the breeding programme.

In conclusion, it is clear from the above discussion that tremendous potential exists for converging the elite allelic resources present in these bottle gourd genotypes through a systematic breeding and selection approach so

as to recover high yielding recombinants, with good quality characteristics. Selection of the parents for hybridization should be done from different clusters having wide inter-cluster distance and those selected parents should have high *per se* performance for the traits contributing maximum towards divergence. Clusters consisting of only one genotype with specific traits could be used in hybridization programme for the exploitation of heterosis mainly as testers for expression of maximum heterosis.

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