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## Genetic divergence studies in bottle gourd (*Lagenaria siceraria* (Molina.) Standl.) Genotypes

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### Abstract

Thirty four genotypes of bottle gourd collected from different indigenous sources were planted in randomized complete block design with two replications to study the genetic diversity among them. The genotypes were grouped into four clusters using Tocher's method. Among four clusters, the cluster I was the largest, comprising of 31 genotypes. While Cluster II, Cluster III cluster IV had one genotype each. Genotypes usually did not clustered according to geographical distributions. There was no direct relationship between geographical distribution and genetic distance. Based on distances between clusters, the maximum divergence was observed between cluster II and cluster IV followed by cluster III and IV. The clusters have been formed based on the contribution of different characters to the divergence. Therefore, the hybridization between the genotypes of these cluster can be made for getting superior hybrids or recombinants in segregating populations. Number of seeds per fruit contributed maximum (61.68%) to the genetic diversity among the characters followed by 100 seeds weight (9.63%).

**Keywords:** *Lagenaria siceraria* (Molina.) Standl, bottle gourd, genotype, divergence

### Introduction

Bottle gourd is an unique plant species that was known to the man in both the new and old world from very early pre-historic times. It is also called as doodhi or lauki belongs to the family Cucurbitaceae, with a chromosome number  $2n=22$ . In India it is grown throughout the country for its tender fruits. Though it is originated in Tropical Africa, India is considered as secondary centre of origin because of availability of diverse germplasm in the country. Information on genetic divergence among the available germplasm is vital to a plant breeder for an efficient choice of parents for hybridization. It is an established fact that genetically diverse parents are likely to contribute desirable segregants. It was also observed that the more diverse the parents, greater are the chances of obtaining high heterotic  $F_1$ s and broad spectrum of variability in the segregating generation (Arunachalam, 1985) [2]. Of the several methods available, Mahalanobis generalized distance estimated by  $D^2$  statistic (Rao, 1952) [8] is a unique method for disseminating populations considering a set of parameters together rather than inferring from indices based upon morphological similarities, eco-geographical diversity and phylogenetic relationships.

### Materials and methods

The present research study was carried out at Department of Vegetable science, Kittur Rani Channamma College of Horticulture, Arabhavi during 2020-21. The material used for research work consisted thirty four cultivars of bottle gourd which were procured from different sources (Table 1). The experiment was laid out in accordance with Randomized Complete Block Design (RCBD) comprising of thirty four treatments and two replications. All the cultural practices were same for all the cultivars used. Observations on growth, flowering and yield parameters were recorded and subjected to statistical analysis.

### Results and Discussion

The material for present study includes 34 genotypes and grouped into four clusters using Tocher's method. Of the four clusters studied, the cluster I was the largest, comprising of 31 genotypes. While Cluster II, Cluster III cluster IV had one genotype each genotypes usually did not clustered according to geographical distributions (Table 2) There was no direct relationship between geographical distribution and genetic distance. This was in agreement with results of Ara *et al.* (2014) [1] and Visen *et al.* (2015) [9].

Based on distances between clusters, inter cluster distances, the maximum divergence was observed between cluster II and cluster IV followed by cluster III and IV, cluster I and IV, cluster I and III and cluster II and III. The least distance was found between cluster I and II as presented in table 3. Maximum inter cluster  $D^2$  values between the clusters II and IV indicated that the genotypes included in these clusters can be used as a parent in hybridization programme to get higher heterotic hybrids from the segregating population. These clusters have been formed based on the contribution of different characters to the divergence. Number of seeds per fruit contributed maximum (61.68%) to the genetic diversity

among the characters followed by 100 seeds weight (9.63%), cavity diameter (6.24%), days to first harvest (4.63%), fruit yield per vine (4.46%), fruit length (3.92%), rind thickness (3.03%) and pericarp thickness (2.14%). However, there was no substantial contribution from number of fruits per vine (1.96%), vine length at final harvest (1.25%) and fruit girth (0.23%). There was no contribution for genetic divergence from number of primary branches per vine, number of secondary branches per vine, inter nodal length, days to first male flower opening, days to first female flower opening, sex ratio, and average fruit weight (Table 4).

**Table 1:** List of genotypes used in the study

Sl. No.	Genotype	Sl. No.	Genotype
1.	Kashi Ganga	18.	HUB-3
2.	Arka Bahar	19.	HUB-4
3.	Pusa Santhushti	20.	HUB-5
4.	Pusa summer prolific long	21.	HUB-6
5.	Pusa Sandesh	22.	HUB-7
6.	Punjab Bahar	23.	IC392392A
7.	Pant Lauki -3	24.	IC339199
8.	Samrat	25.	IC392392
9.	G-7	26.	IC2878953
10.	G-7-1	27.	NBB212
11.	G-4-1	28.	IC4211962
12.	G-6	29.	IC342078
13.	G-6-1	30.	IC342079
14.	L-1	31.	IC308564A
15.	G-2	32.	Warnad
16.	HUB-1	33.	Anand
17.	HUB-2	34.	Andra-1

**Table 2:** Classification of bottle gourd genotypes into different clusters based on  $D^2$  value

Clusters	Number of genotypes	Genotypes included in the cluster
I.	31	Kashi Ganga, Pusa Summer Prolific Long, Arka Bahar, Anand, Pusa Sandesh, Andra-1, Pant Lauki-3, Warnad, Samrat, Pusa Santhushti, HUB-1 HUB-2, HUB-3, HUB-5, HUB-6, HUB-7, IC392392A, IC339199, IC392392, IC2878953, NBB212, IC4211962, IC342078, IC342079, IC308564A, G-2, G-4-1, G-6, G-6-1, G-7, G-7-1,
II.	1	Punjab Bahar
III.	1	HUB-4
IV.	1	L-1

**Table 3:** Average intra and inter cluster  $D^2$  values for 18 characters formed by 34 genotypes of bottle gourd

	Cluster 1	Cluster 2	Cluster 3	Cluster 4
Cluster 1	28.98	41.05	43.94	47.59
Cluster 2		0.00	43.07	68.46
Cluster 3			0.00	54.60
Cluster 4				0.00

**Note:** Diagonal values indicate intra cluster distances

**Table 4:** Relative per cent contribution of different characters to divergence in bottle gourd

Sl. No	Characters	Times ranked first	Per cent contribution
1.	No. of primary branches	0	0.00
2.	No. of secondary branches	0	0.00
3.	Inter nodal length (cm)	0	0.00
4.	Days to first male flower opening	0	0.00
5.	Days to first female flower opening	0	0.00
6.	Sex ratio	0	0.00
7.	Days to first fruit harvest	26	4.63
8.	Length of the fruit (cm)	22	3.92
9.	Girth of the fruit (cm)	6	1.07
10.	Average fruit weight (g)	0	0.00
11.	No. of fruits per vine	11	1.96

12.	Vine length at final harvest (m)	7	1.25
13.	Fruit yield per vine (kg)	25	4.46
14.	Cavity diameter	35	6.24
15.	Rind thickness (mm)	17	3.03
16.	Pericarp thickness(mm)	12	2.14
17.	No. of seeds per fruit	346	61.68
18.	100 seeds weight (g)	54	9.63

**Table 5:** Mean value of 18 characters for 4 clusters in bottle gourd

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18
Cluster 1	11.43	7.55	14.75	50.12	59.13	0.48	70.15	28.23	7.88	671.94	7.02	5.12	4.72	3.68	1.49	13.97	439.09	16.96
Cluster 2	9.13	6.61	14.45	54.26	62.46	0.45	73.46	17.50	13.95	575.00	7.63	6.03	4.39	6.66	1.28	11.90	541.61	14.93
Cluster 3	15.50	9.83	18.42	58.90	57.02	0.57	63.07	23.50	17.15	1075.00	9.75	7.13	10.48	6.36	1.61	15.05	488.14	17.19
Cluster 4	15.75	9.97	18.98	44.25	52.05	0.56	75.00	25.20	7.00	900.00	10.00	6.45	9.00	2.70	1.43	17.00	497.05	17.25

1. Number of primary branches per vine

2. Number of secondary branches per vine

3. Intermodal length (cm)

4. Days to first male flower opening

5. Days to first female flower opening

6. Sex ratio

7. Days to first harvest

8. Length of the fruit (cm)

9. Girth of the fruit (cm)

10. Fruit weight (g)

11. Number of fruits vine

12. Vine length (m)

13. Fruit yield per vine (kg)

14. Cavity diameter (cm)

15. Rind thickness (mm)

16. Pericarp thickness (mm)

17. Number of seeds per vine

18. 100 seeds weight (g)

Cluster mean for all the characters have been studied (Table 5). Number of seeds per fruit contributed maximum (61.68%) to the genetic divergence and lowest cluster mean for this trait was observed in cluster I (439.09) followed by cluster III (488.14) and cluster IV (497.05). The highest inter cluster distance was observed between cluster I and IV (47.59) followed by cluster I and III (43.94). Hence, the crosses between these genotypes may be tried to increase the consumer preference of having less number of seeds per fruit. The findings are in line with the results obtained by Ara *et al.* (2014)<sup>[1]</sup> and Khan *et al.* (2016)<sup>[5]</sup>. Hundred seed weight was the second highest contributor for genetic diversity (9.63%) and highest cluster mean for this trait was observed in cluster IV (17.25 g) followed by cluster III (17.19 g) and cluster I (16.96 g). The highest inter cluster distance was observed between cluster III and IV (54.60) followed by cluster I and III (43.19). Hence hybridization between the genotypes of these respective clusters could be attempted to get heterotic hybrids. The similar findings were reported by Visen *et al.* (2015)<sup>[9]</sup>.

Cavity diameter had significant contribution towards the diversity (6.24%). The lowest cluster mean for this character was observed in cluster IV (2.70 mm) followed by cluster I (3.68 mm) and cluster III (6.36 mm). The highest inter cluster distance was observed between cluster III and IV (54.60) followed by cluster I and III (47.59). Hence, crosses between these clusters may help to reduce the cavity diameter. Days to first fruit harvest also showed significant contribution towards divergence (4.63%). The lowest cluster mean for this character was observed in cluster III (63.07) followed by cluster I (70.15) and cluster II (73.46). The highest inter cluster distance was observed between cluster I and III (43.94) followed by cluster I and II (41.05). Hence, crosses between genotypes belonging to these respective clusters may be tried to improve earliness. The findings are in line with the results obtained by Ara *et al.* (2014)<sup>[1]</sup> and Gulshan *et al.* (2014)<sup>[4]</sup>.

Fruit yield per vine contributed 4.46 per cent to total diversity. The highest cluster mean for this character was observed in cluster III (10.48 kg) followed by cluster IV (9.00 kg) and cluster I (4.72 kg). The highest inter cluster distance was observed between cluster III and IV (54.60) followed by cluster I and III (47.59). Hence, crosses between these respective clusters may be tried to improve this trait which

ultimately contribute towards total yield. The similar finding was reported by Chetariya and Vaddoria in 2017<sup>[3]</sup>.

Fruit length meagrely contributed towards the total diversity (3.92%). The highest cluster mean for this character was observed in cluster I (28.23 cm) followed by cluster IV (25.20 cm) and cluster III (23.50). The highest inter cluster distance was observed between cluster III and IV (54.60) followed by cluster I and III (47.59). Therefore crosses between genotypes belonging to these respective clusters may be tried to improve this character. The findings are in line with the results obtained by Manoj *et al.*, 2018<sup>[6]</sup>.

Rind thickness has meagrely contributed (3.03%) to the genetic divergence and lowest cluster mean for this trait was observed in cluster II (1.28 mm) followed by cluster IV (1.43 mm) and cluster I (1.49 mm). The highest inter cluster distance was observed between cluster II and cluster IV (68.46) followed by cluster I and IV (47.59). Hence, the crosses between these genotypes may be tried to increase the consumer preference. The findings are in line with the results obtained by Ara *et al.* (2014)<sup>[1]</sup> and Visen *et al.* (2015)<sup>[9]</sup>.

Pericarp thickness meagrely contributed towards the total diversity (2.14%). The highest cluster mean for this character was observed in cluster IV (17.00 mm) followed by cluster III (15.05 mm) and cluster I (13.97 mm). The highest inter Cluster distance was observed between cluster III and IV (54.60) followed by cluster I and III (47.59). Hence, crosses between these clusters may improve pericarp thickness. The similar findings were reported by Rambabu *et al.* (2020)<sup>[27]</sup>.

Fruit weight has contributed 1.96 per cent towards the total diversity. The highest cluster mean for this character was observed in cluster III (1075 g) followed by cluster IV (900 g) and cluster I (671.94 g). The highest inter cluster distance was observed between cluster III and IV (54.60) followed by cluster I and III (47.59). Hence, crosses between genotypes belonging to these respective clusters may be tried to improve the fruit weight. The findings are in line with the results obtained by Manoj *et al.*, 2018<sup>[6]</sup>.

No substantial contribution was found from vine length towards the total diversity (1.25%). Highest cluster mean for this character was observed in the cluster III (7.13 m) followed by cluster IV (6.45 m) and cluster II (6.03 m). The highest inter cluster distance was observed between cluster II and IV (68.46) followed by cluster III and IV (54.60). Hence hybridization between the genotypes of these respective

clusters could be attempted to get heterotic hybrids. The similar findings were reported by Manoj *et al.*, 2018<sup>[6]</sup> and Rambabu *et al.* (2020)<sup>[27]</sup>.

Fruit girth contributed very little to the total diversity (0.23%). Highest cluster mean for this character was observed in the cluster III (17.15 cm) followed by cluster II (13.95 cm) and cluster I (7.88 cm). The highest inter cluster distance was observed between cluster I and III (43.94) followed by cluster II and III (43.07).

Improvement in yield and quality is normally achieved by selecting genotypes with desirable character combinations existing in the nature or by hybridization. Genetic diversity study helps a plant breeder for an efficient selection of parents for hybridization as genetically diverse parents are likely to contribute desirable segregants. The present work identified promising genotypes of bottle gourd for hybridization programme on the basis of divergence analysis. Hence these genotypes can be selected to get high heterotic combinations.

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