



Evaluation of Genetic Diversity in Bottle Gourd Germplasm Based on Phenotypic Characters for Yield and Yield Associated Traits

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Authors' contributions

This work was carried out in collaboration among all authors. Author MA conducted the study, performed the statistical analysis, wrote the protocol, and wrote the first draft of the manuscript. Author BS, Author KA and Author SP managed the analyses of the study. Author AG and Author M managed the literature searches. All authors read and approved the final manuscript.

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ABSTRACT

The experiment was conducted during Kharif season 2018 at Horticulture Research Centre, Sardar Vallabhbhai Patel University of Agriculture & Technology; Modipuram, Meerut (U.P.) assess the genetic diversity among fifteen genotypes of bottle gourd [*Lagenaria siceraria* (Mol.) Standl.]. The genetic diversity analysis according to that the formation of five clusters suggesting the presence of wide genetic diversity. The clustering pattern showed that geographical diversity wasn't related to genetic diversity. The analysis of % contribution of assorted characters toward the expression of total genetic divergence showed that the Days to 50% flowering (14.48%) followed Days of fruit set (12.95%), Vine length (m) (11.67%), Number of fruits per plant (10.93%), Number of the primary branches (10.37%), Days to first fruit harvest (10.16%), Average fruit weight (g) (9.44%), Fruit diameter (cm) (6.63%) contributed maximum towards total genetic divergence. Based on the maximum genetic distance. It is advisable to attempt a crossing of the genotype from cluster II (GP-7) with the genotype of cluster I (GP-5), cluster IV (GP-2) and cluster III (GP-1), which may cause to the generation of a broad spectrum of favorable genetic variability for yield improvement in bottle gourd.

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1. INTRODUCTION

Bottle gourd [*Lagenaria siceraria* (Mol.) Standl.] belong to the family Cucurbitaceae, sub family cucurbitoidae and tribe benincaseae [1]. It has a diploid somatic chromosomes number ($2n=2x=22$). Its primary Centre of origin is Africa [2]. This family is composed of 118 genera and 825 species, which are widely distributed in the warmer regions of the world. The names "*lagenaria*" and "*siceraria*" are derived from Latin words "lagena" for bottle and "sicera" for drinking utensil. It is also known as Calabash, Doodhi and Lauki in different parts of India [3]. India is the wealth of bottle gourd germplasm and also presented both types of germplasm like wild and cultivated. It is grown in both rainy and summer season crops. Bottle gourd fruits are available in market throughout the year.

India occupies a prime position and is the second-largest producer of vegetables next to China in the world. It is grown in an area of 10.38 million hectares with a production of 179.69 million tones which contributes 14% of the total world production of vegetables. Bottle gourd has covered an area of 15.6 lakh hectares with the production of 26.08 metric tons in India [4].

Genetic variability present in any population is the primary source for any selection programme in plant breeding. More number of variabilities in any crop plants provides a good opportunity for a breeder for selecting desirable traits. The D^2 statistic measures divergence at two levels, namely, intercluster and intracluster levels, and thus helps in the selection of genetically divergent parents for exploitation in the hybridization programme [5]. Genetic diversity plays an important role in plant breeding because hybrids between lines of diverse origin generally display greater heterosis than those between closely related strains [6]. These are the following way to assess the genetic diversity and genotype identification within species.

2. MATERIALS AND METHODS

The experiment was conducted during Kharif season 2018 at Horticulture Research Centre, Sardar Vallabhbhai Patel University of Agriculture & Technology, Modipuram, Meerut (U.P.). To assess the genetic diversity among fifteen genotypes of bottle gourd was collected from different parts of India. Each genotype was

accommodated in a single row of 10 m length with a spacing of 3.0 m between row and 1.0 m between plant to plant within the row. Recommended agronomic practices were followed to raise a good crop. The observation was recorded from five randomly selected plants from each genotype on ten different characters viz., Days to 50% flowering, Days of fruit set, Days to first fruit harvest, vine length (m), number of primary branches per plant, fruit weight (g), fruit length (cm), fruit girth (cm), number of fruits per plant and fruit yield per plant (kg). Therefore, whereas up fruit yield, choice of parents having wide divergence for a variety of characters is of prime importance, which is assessed by D^2 statistics developed by Mahalanobis [5]. Grouping of the genotypes into different clusters was carried out by following Tocher's method [7].

3. RESULTS AND DISCUSSION

The analysis of variance showed a significant difference among the genotypes for the characters studied. On the basis of D^2 values, 15 genotypes were grouped into 4 clusters (Table 1). This indicated the existence of genetic diversity among the genotypes. The maximum genotypes were in cluster II (GP-7) with the genotype of cluster I (GP-5), cluster IV (GP-2), and cluster III (GP-1), which 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 to genetic diversity. Therefore, the choice of genotypes for hybridization should be based on genetic diversity rather than on geographical diversity. On the basis of the 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 the 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 with the findings of Badade et al. [8] Mathew et al. [9], Singh et al. [10], Ara et al. [11], Visen et al. [12] and Kumar et al. [13] in bottle gourd; Masud et al. [14] in sponge gourd; Prasad et al. [15] in watermelon and Islam et al. [16] in musk melon. Murty and Arunachalam [6] and

Table 1. Clustering pattern of 15 genotypes of bottle gourd on the basis of Mahalanobis D² statistics

Parameters	No of genotypes	Genotypes
I	5	Mahima hybrid, IC-092467, VRBG-408, VRBG-100, VRBG- 107
II	7	NDBG-S-101, NDBG-S-102, NDBG-S-103, NDBG-S-104, NDBG-S-105, Kanak, Sonali
III	1	IC-144389
IV	2	BOG-VAR-1, BOG-VAR-2

Table 2. Average intra and inter cluster (D² value) distance in thirty genotypes of bottle gourd

Parameters	I	II	III	IV
I	2.416			
II	3.032	2.532		
III	3.877	4.154	1.856	
IV	3.685	3.725	4.680	1.804

Table 3. Cluster mean of different genotype of bottle gourd

Parameters		Days to 50% flowering	Days of fruit set	Days to first fruit harvest	Fruit length (cm)	Fruit diameter (cm)	Average fruit weight(g)	Number of fruits per plant	Number of primary branches	Vine length(m)	Fruit yield q/h	contribution %
I	Mean	32.61	36.59	55.19	34.52	27.89	880.41	9.07	6.87	5.56	250.59	14.48
	±SE	1.33	0.43	4.93	8.10	10.85	136.05	1.27	0.96	0.48	42.35	12.95
II	Mean	35.59	38.23	57.00	31.81	11.23	784.17	11.55	7.10	5.60	311.79	10.16
	±SE	1.67	1.73	2.55	4.39	6.29	144.15	1.00	1.73	0.46	80.03	6.42
III	Mean	33.20	40.33	48.50	49.80	22.07	768.60	9.00	7.53	5.70	318.93	6.63
	±SE	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	9.44
IV	Mean	31.80	38.07	50.33	32.23	8.87	830.45	10.63	3.40	4.57	266.07	10.93
	±SE	3.96	1.79	0.38	1.46	1.70	90.82	1.27	0.00	0.42	52.51	10.37
												11.67
												6.94

Singh et al. [17] 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 fifteen genotypes and ten characters are present in the Table 2. The average intra cluster distance ranged from 1.80 to 4.68, which was an indicator of considerable diversity available in the material evaluated. Cluster II have maximum inter-cluster distance with cluster III (4.154) followed by cluster IV (3.725). The minimum inter-cluster distance (1.804) in cluster IV and maximum was found cluster II (2.532) followed by cluster I (2.416) and cluster III (1.856). Cluster I show the maximum inter-cluster with cluster III (3.877) followed by cluster IV (3.685), and with minimum cluster II (3.032). Cluster II have maximum inter-cluster distance with cluster III (4.154) followed by cluster IV (3.725), was found between clusters III and IV indicates a close relationship and genotypes of these clusters have the maximum of common gene complexes.

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 of 50% flowering exerts highest mean for cluster II (35.59) followed by the cluster III (33.20), cluster I (32.61) cluster IV (31.80). Days of fruit set shows highest mean with cluster III (40.33) followed by cluster II (38.23), cluster IV (38.07) and cluster I (36.59). Days to fruit harvest shows highest mean with cluster II (57.00) followed by cluster I (55.19), cluster IV (50.33) and cluster III (48.50). Fruit length shows highest mean with cluster III (49.80) followed by cluster I (34.52), cluster IV (32.23), and cluster II (31.81). Fruit diameter shows highest mean with cluster I (27.89) followed by cluster III (22.07) and cluster II (11.23). Average fruit weight shows highest mean with cluster I (880.41) followed by cluster IV (830.45), cluster II (784.17) and cluster III (768.60).

4. CONCLUSION

The final conclusion that can be reached from results and discussion on genetic divergence is

that Days to 50% flowering, Days of fruit set, Days to first fruit harvest, vine length (m), number of primary branches per plant, fruit weight (g), fruit length (cm), fruit girth (cm), number of fruits per plant and fruit yield per plant (kg), are the most important component characters. Therefore, these traits ought to be thought of as choice criteria for yield improvement in the gourd. Further, it is advisable to attempt a crossing of the genotypes from genotype from cluster II (GP-7) with the genotype of cluster I (GP-5), cluster IV (GP-2), and cluster III (GP-1), which may lead to the generation of a broad spectrum of favorable genetic variability for yield improvement in bottle gourd.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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