



Genetic divergence studies in bottle gourd [*Lagenaria siceraria* (Molina) Standl.] genotypes

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Abstract

The present study was carried out at the Department of Horticulture, Faculty of Agriculture, Annamalai University, Chidambaram during Jan-Mar 2020. The field was laid out in randomized block design (RBD) with three replications. Cluster analysis grouped thirty five genotypes of bottle gourd into five clusters. Cluster III had highest number of genotypes (19) followed by cluster I (10), cluster IV (3), cluster II (2) and cluster V (1). The inter cluster distance highest was recorded between cluster IV and V (14.407) followed by cluster I and II (9.044). Yield per vine, Number of fruits per vine, Fruit length and Fruit width contributed highest towards total genetic divergence.

Keywords: clusters, divergence, selection, genotypes, d^2 statistics, cluster distance

Introduction

Bottle gourd (*Lagenaria siceraria* (Molina) Standl) also called white flowered gourd belongs to the family Cucurbitaceae having chromosome number $2n=22$. It is one of the most important cucurbits cultivated in India. It is rich in nutritive and medicinal properties of bottle gourd. The fruit is rich in moisture (96.1 g), protein (0.2 g), carbohydrate (2.5 g) and traces of minerals like calcium (20 mg), phosphorus (10 mg) and iron (0.7 mg) in 100 gm of fruit (Thamburaj and Singh, 2000) [8]. Its tender fruits are used as cooked vegetable and also for making sweets in India. The dried fruits are used as containers, utensils, fishing floats and some musical instruments. Comprehensive information of the nature of genetic divergence of the genotypes is the prerequisite of a variety development programme. The quantification of genetic diversity through biometrical procedures has made it possible to choose genetically diverge parents for a successful hybridization programme.

Materials and Methods

The study was carried out at vegetable unit, Department of Horticulture, Faculty of Agriculture, Annamalai University, Chidambaram during Jan-Mar 2020. Experiment field is situated at 11.24°N latitude and 79.41°E longitude at an altitude of 4m above mean sea level. The material for the present study consisted of thirty five diverse genotypes. The investigation was laid out in the randomized block design with three replications. The net area of the experimental plot is fifty cents. Row to row spacing was 1.8 m and 0.9 m was maintained between plants from within a row. Five plants were randomly selected in each genotype from each replication and labeled for recording observations on quantitative characters like Vine length, Primary branches, Node at first male flower appears, Node at first female flower appears, Days to first male flower anthesis, Days to first female flower anthesis, Sex ratio, Days to first harvest, Fruit length, Fruit width, Fruit flesh thickness, Fruit weight,

Number of fruits per vine and Yield per vine. All suggest cultural and management practices were followed to maintain the crop healthy. Genetic diversity (Mahalanobis, 1936) [5], generalized distance (D2) and clustering (Rao, 1952) [6], calculating intra and inter cluster distances (Singh and Chaudhury, 1985) [7] were studied. Statistical analyses were carried out using "GENSTAT" software.

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^2 statistics. The genotypes segregated into five clusters as presented in Table 1. In clustering pattern maximum number of nineteen genotypes are shown in cluster III followed by cluster I with 10 genotypes; cluster IV had 3 genotypes, cluster II 2 genotypes and cluster V with one genotype. The average intra and inter cluster distance were computed for five clusters and values are presented in Table 2. The intra cluster distance ranged from 0.000 to 10.139. Cluster II showed minimum intra cluster distance (0.000). Highest intra cluster distance was exhibited by cluster III (10.139) followed by cluster IV (9.690). The inter cluster distances were larger than the intra cluster distances. The inter cluster distance was highest between clusters IV and V (14.407). This was followed by clusters III and IV (13.718), clusters I and IV (12.236), cluster II and III (10.833), cluster I and III (10.502), cluster III and V (10.434) in order. lowest inter cluster distance was observed between clusters I and II (9.044). This is in conformity with the findings of Banik (2003) [2], Islam (2004) [4], Khatun and Rehman (2010) [4] and Ara *et al.*, (2014) [1].

The cluster mean values for 14 characters are presented in Table 3. The maximum mean value for Vine length was control by cluster IV (383.13) and lowest mean value by cluster V (245.10). The cluster mean performance for more Number of primary branches was recorded in cluster IV (10.62) and less Primary branches was recorded in cluster V

(7.75). Highest node at first male flower appears in cluster V (13.03) and minimum node at first male flower appears was recorded cluster II (7.76). Maximum node at first female flower appears cluster III (13.47) and minimum node at first female flower appears cluster IV (9.17). The genotypes of cluster V took maximum days to first male flower anthesis (51.29). Minimum days to first female flower anthesis was recorded cluster IV (43.84). Sex ratio was the maximum in cluster II (0.52) and minimum sex ratio was recorded in cluster I (0.42). Highest mean value of days to first harvest was recorded in cluster V (62.91) and lowest first harvest was recorded in cluster I (60.25). Maximum fruit length was recorded cluster V (40.58) and minimum fruit length was observed cluster III (37.46). The genotypes of cluster I took maximum fruit width (23.58) and minimum fruit width was observed in cluster II (22.42). The cluster mean performance for more fruit flesh thickness was observed in cluster V (2.06) and less fruit thickness was observed in cluster I (1.49). Maximum fruit weight was recorded in cluster II (2.09) and minimum fruit weight was recorded in cluster V (1.51). More number of fruits per vine

was observed in cluster I (2.87) and less number of fruits per vine was observed in cluster II (2.22). Highest fruit yield per vine was recorded in cluster I (18.72) and lowest fruit yield per vine was observed in cluster III (15.85).

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. Parents could be selected from various groups with desirable values for specific traits. 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.

Table 1: Distribution of thirty five bottle gourd genotypes in clusters

Cluster No	Number of genotypes	Genotypes
Cluster I	10	CO1, Ambrit, Punjab Komal, Arka Bahar, Ajmer local, Subam, Uttam, Angad, AVT – 1 2018-BOG VAR-6 and Velore local
Cluster II	2	Paraivai local and Karaikal local
Cluster III	19	Peralam local, Karnal local, AVT – 1 2018-BOG VAR-1, AVT – 1 2018-BOG VAR-2, AVT – 1 2018-BOG VAR-3, AVT – 1 2018-BOG VAR-4, AVT – 1 2018-BOG VAR-5, AVT – 1 2018-BOG VAR-7, Mannadipet local, Kumbakonam local, Vedaraniyam local, Pusa Naveen, C.B.H.1, Ramapuram local, Vari surai, Sati surai, Neetu surai, Kuduvai surai and vathu surai
Cluster IV	3	Waman, Pachai surai and Thiruvurur local
Cluster V	1	Kumbu surai

Table 2: Average Inter and intra cluster distances in bottle gourd genotypes

Cluster	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V
Cluster I	9.097	9.044	10.502	12.236	9.462
Cluster II		4.493	10.833	9.191	10.029
Cluster III			10.139	13.718	10.434
Cluster IV				9.690	14.407
Cluster V					0.000

Table 3: Cluster means for 14 characters in bottle gourd genotypes

Characters/ clusters	I	II	III	IV	V
Vine length (cm)	299.47	330.30	295.49	383.13	245.10
Primary branches	7.81	8.10	7.76	10.62	7.75
Node at first male flower appears	8.29	7.76	8.49	9.05	13.03
Node at first female flower appears	12.95	12.57	13.47	9.17	12.27
Days to first male flower anthesis	43.86	42.30	42.75	41.27	49.18
Days to first female flower anthesis	48.89	48.81	48.75	43.84	51.29
Sex ratio	0.42	0.52	0.51	0.45	0.44
Days to first harvest	60.25	61.62	60.76	61.66	62.91
Fruit length	39.23	39.87	37.46	38.13	40.58
Fruit width	23.58	22.42	23.32	22.88	23.01
Fruit cavity	7.87	6.84	7.81	7.69	7.54
Fruit flesh thickness	1.49	1.58	1.68	1.68	1.54
Fruit weight	1.76	2.09	1.73	2.06	1.51
Number fruits per vine	2.87	2.22	2.44	2.25	2.30
Yield per vine	18.72	16.99	15.85	17.93	18.49

Table 4: Relative per cent Contribution of each character to divergence in bottle gourd

Characters	Number of ranking pattern	Per cent contribution
Vine length (cm)	49	8.23
Primary branches	0	0.00

Node at first male flower appears	1	0.16
Node at first female flower appears	4	0.67
Days to first male flower anthesis	4	0.67
Days to first female flower anthesis	4	0.67
Sex ratio	23	3.86
Days to first harvest	0	0.00
Fruit length	77	12.94
Fruit width	65	10.92
Fruit cavity	122	20.50
Fruit flesh thickness	18	3.02
Fruit weight	17	2.85
Number of fruits per vine	87	14.62
Yield per vine	124	20.84
Total	595	100

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