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STUDIES ON GENETIC DIVERSITY IN BOTTLE GOURD (*LAGENARIA SICERARIA* (MOL.) STANDL.)

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Abstract

An experiment was carried out to analyze genetic diversity for yield and its contributing characters in 20 bottle gourd genotypes by adopting Randomized Block Design (RBD) with three replication to assess the nature and magnitude of association among yield and its contributing traits in bottle gourd and genetic diversity. Based on D^2 analysis, twenty genotypes of bottle gourd were grouped into six clusters. Maximum number of genotypes was in cluster IV includes six genotypes, whereas cluster II included five genotypes. The cluster I had four genotypes, which is followed by cluster III and cluster V had only two genotypes in each cluster. Genotypes collected from different districts were scattered in different clusters revealed that geographic diversity need not be a supporting factor for genetic divergence.

Key words : Bottle gourd, genetic divergence, clusters, genotypes and yield.

Introduction

Bottle gourd (*Lagenaria siceraria* (Mol) Standl) is one of the most important cucurbitaceous vegetable crop in India grown in both rainy and summer seasons. It belongs to the family cucurbitaceae having chromosome number 2n = 22. It is highly cross pollinated crop due to its monoecious and andromonoecious nature (Swiander *et al.,* 1999). It has been found in wild form in India and Southern Africa. Bottle gourd is a white flowered, monoecious, diploid self compatible, annual climbing or prostrate species in the cucurbitaceae. It is widely cultivated in tropics and subtropical region in India. The fruits are used as a vegetable, container, bowl, decoration, musical instrument or fishing floats. Seeds, tendrils, leaves and immature fruits of the bottle gourds are also utilized for different purposes especially for some medicinal treatments. Bottle gourd are known to lower cholesterol, triglyceride, low density lipoproteins, pain and inflammation (Ghule *et al.,* 2006).

In Tamilnadu maximum diversity is found for its fruit shape and colour. There are different types of fruit shape in bottle gourd viz., elongate, oblong, globular, elliptical, and cylindrical and bottle shape etc. Productivity of bottle gourd is still low in India. Inspite of extensive cultivation and consumption, bottle gourd has not been taken for systematic research work in order to understand the genetic architecture and endeavour in an improvement programme.

Materials and Methods

The basic material for the study included 20 accessions of bottle gourd of diverse origin were evaluated during 2017-18 in Vegetable Unit, Department of Horticulture, Faculty of Agriculture, Annamalai University. The trial was laid out in Randomised Block Design with three replications. The crop management practices were adopted according to the package of practices recommended by Tamilnadu Agricultural University. Observation were recorded on five randomly selected plants of each genotype in each replication for twelve characters *viz.,* vine length (cm), days to first male flowering, days to first female flowering, node number of first male flower, node number of first female flower, days to first fruit harvest, fruit length (cm), fruit girth (cm), average fruit weight (kg), number of fruits per vine, 100 seed weight (g) and yield per vine (kg). Genetic diversity was estimated using Mahalanobis (1936) D^2 statistics. Tochers method (Rao, 1952) was followed for determining the group constellations.

Results and Discussion

The analysis of variance revealed significant among the genotypes of bottle gourd for all the characters studied. After computing D^2 value for all the possible traits, twenty genotypes were grouped into six clusters, which indicated a large genetic diversity table 1. The cluster IV was the largest comprising six genotypes followed by cluster II with five and cluster I with four genotypes. The cluster III and V had two genotypes and genotypes from different geographical regions were grouped in the same cluster indicating that there is no association between geographical distances of genetic divergence. One of the possible reasons may be the fact that it is very difficult to establish the actual location of origin of genotype. Frequent exchange of genetic materials among farmers and breeders in the country makes it very difficult to maintain the real identity of the genotypes. The present results supports the findings of. The absence of relationship between genetic diversity and geographical distance indicates that forces other than geographical origin such as genetic drift, exchange of genetic stock, spontaneous variation, natural or artificial selection are responsible for genetic diversity. The present results supports the findings of Singh *et al*., (2007), Visen *et al*., (2015) and Alli Rani *et al*., (2017). Intra cluster distances ranged from 644.61 to 687.00. Maximum intercluster distance was observed between clusters I and cluster VI followed by cluster I and cluster III and cluster IV and cluster VI. Genotypes belonging to the cluster I and cluster VI may be used for hybridization programme for evincing good hybrids (or) segregants. On the other hand, minimum inter cluster distance occur between cluster II and cluster V indicating the close relationship of the genotypes included in these clusters table 2.

Table 1: Grouping of 20 bottle gourd genotypes into different clusters.

S. No.	Cluster	No. of Genotypes	Genotypes
1.	I	4	LS1, LS2, LS5, LS17
2.	II	5	LS3, LS4, LS6, LS13, LS19
3.	III	2	LS15, LS16
4.	IV	6	LS7, LS8, LS9, LS10, LS11, LS14
5.	V	2	LS18, LS20
6.	VI	1	LS12

The comparison of cluster mean of the various characters indicated considerable differences between clusters for all the traits table 3. The higher mean value for vine length, number of fruits per vine, yield per vine and earliness was observed in cluster VI, for fruit length, fruit girth, average fruit weight in cluster III. Cluster V had genotypes with lowest yield.

The percentage contribution of different characters towards genetic divergence is given in table 4. Vine length had highest contribution followed by average fruit weight, fruit length and yield per vine indicating as the major characters contributing to genetic divergence. Similar results were reported by Singh *et al*., (2007), Visen *et al*., (2015) and Alli Rani *et al*., (2017). Hence selection of divergent parents based on the characters will be useful for heterosis breeding of bottle gourd.

Computing the cluster mean values, it was found that, the cluster VI showed high values for the few characters *viz.,* vine length, days to first male flowering, days to first female flowering, node number of first male flower, node number of first female flower, days to first fruit harvest, number of fruits per vine and fruit yield per vine. Interestingly, it is noticed that these three characters like vine length, days to first fruit harvest and yield per vine were contributed only by a single genotype LS12. Hence, this genotype may serve as an ideal plant for hybridization programme for improving the yield per plant and its important component traits, since this genotype had more number of traits in a single cluster than other genotype. Based on cluster mean values, the genotypes for hybridization programme can be selected on the character basis *viz.,* the genotype LS12 can be selected for longest vine, earliest fruit harvest and maximum yield which falls under cluster VI. The genotypes LS3 had lower values for days to first female flowering, node number of first male flower and node number of first female flower in the cluster II. Similarly the genotype LS15 which

Table 2: Average Intra and Inter cluster distances (D^2 values) in bottle gourd.

Cluster	I	II	III	IV	V	VI
I	482.55 (21.97)	870.39 (29.50)	1737.77(41.69)	717.67 (26.79)	563.34 (23.74)	2322.80 (48.20)
II		618.06 (24.86)	678.56 (26.05)	566.32 (23.80)	410.65 (20.26)	951.24 (30.84)
III			44.61 (6.681)	900.25 (30.00)	652.05 (25.54)	563.87 (23.75)
IV				687.00 (26.21)	411.81 (20.29)	1270.97 (35.65)
V					314.05 (17.72)	1147.02 (33.81)
VI						0.000(0.00)

Values in parenthesis indicate D value, Bold value indicate intra cluster distance.

Table 3: Cluster mean of 12 characters in bottle gourd.

Characters	Clusters					
	I	II	III	IV	V	VI
Vine length (cm)	546.43	624.94	699.06	604.09	604.77	720.82
Days to first male flowering	52.10	54.30	58.36	52.10	56.07	49.79
Days to first female flowering	58.55	61.99	69.00	60.38	61.87	55.38
Node number of first male flower	13.86	14.92	19.00	13.97	17.82	13.43
Node number of first female flower	21.90	21.85	29.88	22.14	28.05	19.96
Days to first fruit harvest	73.17	76.19	90.29	76.31	77.16	66.50
Fruit length (cm)	29.24	31.39	32.20	27.68	23.32	26.82
Fruit girth (cm)	34.42	37.95	59.56	39.19	37.42	34.20
Average fruit weight (kg)	1.03	1.29	2.11	1.25	0.78	1.12
Number of fruits per vine	13.32	13.12	7.67	12.27	16.37	16.67
100 seed weight (g)	15.43	15.80	21.01	17.61	16.10	13.36
Yield per vine (kg)	14.22	13.73	16.11	13.56	12.66	18.80

Table 4: Relative contribution of 12 characters towards genetic divergence of bottle gourd.

S. No.	Characters	Contribution %
1.	Vine length (cm)	31.05
2.	Days to first male flowering	2.11
3.	Days to first female flowering	0.53
4.	Node number of first male flower	0.00
5.	Node number of first female flower	0.53
6.	Days to first fruit harvest	3.68
7.	Fruit length (cm)	16.84
8.	Fruit girth (cm)	4.74
9.	Average fruit weight (kg)	17.37
10.	Number of fruits per vine	8.95
11.	100 seed weight (g)	2.63
12.	Yield per vine (kg)	11.58

Table 5: Parents selected for hybridization programme for bottle gourd based on cluster mean values.

Cluster	Character	Genotypes
VI	Vine length, Days to first fruit harvest and Yield per vine	LS12
II	Days to first female flowering, Node number of first male flower and Node number of first female flower	LS3
II	Fruit length and Average fruit weight	LS4
III	Fruit girth, 100 seed weight	LS15
V	Number of fruits per vine	LS18

contributed maximum fruit girth and 100 seed weight which fall under cluster III.

The genotype LS4 which showed high values for fruit length, average fruit weight respectively, which falls in cluster II may be selected as the parent for hybridization programme. The genotype LS18 registered higher mean values for number of fruits per vine, which falls in cluster V may be selected as one of the parent table 4.

Among the five parents selected for hybridization programme, they fell into different divergent clusters table 5. LS12, LS15 and LS18 belongs to cluster VI, III and V respectively, while LS3 and LS4 belongs to the cluster II. Thus from the present study, the genotypes LS12, LS3, LS4, LS18 and LS15 were identified as suitable parents for hybridization programme to develop superior varieties in bottle gourd.

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