

Genetic Divergence in Bottle Gourd Genotypes Under Mid Hill Conditions of Uttarakhand

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ABSTRACT

The genetic divergence among 18 genotypes of bottle gourd (*Lagenaria siceraria*) was evaluated using D^2 and Cluster analysis. The genotypes were divided into five groups. This suggested that the genotypes had a lot of variability. Cluster I had the most genotypes overall (seven), followed by Cluster II (six) and Cluster IV (three), while the remaining two clusters only contained single genotype. Cluster IV and cluster V had the greatest intercluster distance, whereas cluster I and cluster III had the smallest. Greater genetic divergence between the genotypes among these clusters was indicated by a larger inter-cluster distance, whereas a smaller inter-cluster value between clusters revealed that the genotypes of the clusters were not very genetically different from one another. The greatest mean values for the days to first female flowering, number of node displaying the first female flower, vine length (m), and number of nodes per vine were displayed in Cluster VI. While cluster I displayed the highest mean values for certain other parameters, including fruit yield per plant. The genotype LC-1 of cluster V and Arka Bahar, LC- 3, and LC- 5 in cluster IV would yield new recombinants with desirable characteristics in bottle gourds when crossed.

Key words: *Lagenaria siceraria*, genetic divergence, D^2 analysis and Cluster analysis

INTRODUCTION

Bottle gourd, also known as lauki [*Lagenaria siceraria* (Mol.) Standl. ($2n = 2x = 22$)], is a significant vegetable crop in the Cucurbitaceae family. Since it is monoecious and andromonoecious, this crop is heavily cross pollinated (Swiander et al. 1994). The human race receives edible and nourishing fruits from the cucurbitaceous family, which is commercially the most significant family. The tender fruits are prepared into pickles, sweet dishes, and rayta as well as utilised as a vegetable. The genus *Lagenaria* has been recognised as consisting of a total of six different species. *L. siceraria* is one of the domesticated monoecious species, whereas the other five are wild perennial dioecious forms (Bisognin 2002). It is an abundant source of several necessary minerals, iron, protein, and fibre, all of which aid in digestion. Fruit juice is highly beneficial for coughs and is advised for diabetics and those with heart disease. It is effective in preventing constipation and night blindness and serves as an antidote to several toxins. For treating jaundice, a leaf decoction is consumed. In dropsy, seeds are used. Oil found in seeds is beneficial for body hydration and brain growth. As a result, it is

utilised in Ayurvedic formulations (Robinson and Decker-Walter 1999).

Prior to starting a breeding programme for any crop, it is essential to assess the level of genetic diversity and genetic divergence in the breeding material. The probability of selecting superior genotypes would improve with more variability in the germplasm (Simmonds 1962). Researchers have found that parents with differing genetic profiles may always produce high frequencies of favourable segregants and large amounts of heterotic effects in offspring. When Mahalanobis created the D^2 statistic in 1936, he established the guidelines for the study of population variability. By specifying the degrees of exploitable variability and forecasting the outcomes of a breeding programme, this inexorably bolstered the notion of breeding for superior genotypes. Before actually executing a cross to model the cultivars in a specific genetic architecture, D^2 analysis enables accurate comparison across all feasible pairs of populations. To achieve the expected improvement in yield components and other bottle gourd traits, the present study has attempted to identify genetically dissimilar promising lines and their F_1 offspring. This has been done either by crossing two different parents to produce a heterotic

F₁ generation or by making single crosses, three-way crosses, double crosses, and selfing of crosses (F₁) achieved by the differing parental genotypes of bottle gourd.

MATERIALS AND METHODS

The experimental material included 18 bottle gourd genotypes that were gathered from various sources. The experiment was carried out at the Vegetable Production and Demonstration Block of the College of Horticulture at the V.C.S.G. Uttarakhand University Horticulture and Forestry, Bharsar, Pauri Garhwal, (Uttarakhand). The seeds were sown in polythene bags. Healthy seedlings of one month old were transplanted into the previously made ridges. In a plot of 6 x 1 m², there were 6 seedlings of each genotype in each replication. Plants were spaced apart by 1m. To generate a superior harvest, the suggested cultural practices were adopted. Three replications of the experiment were set up using a randomized complete block design. The observations were recorded on days to first female flowering, node number bearing first female flower, days to first fruit maturity from transplanting, fruit length (cm), fruit diameter (cm), fruit weight (Kg), flesh thickness (cm), number of marketable fruits per plant, total number of pickings, harvest duration, marketable yield per plant (Kg), marketable yield per plot (Kg), total yield per plot (Kg), vine length (m), number of branches per vine, number of nodes per, TSS (⁰B) and 100 seed weight (g).

Using Mahanalobis' D² statistics, the population was divided into clusters according to Toucher's approach, and the genetic divergence was determined (Mahanalobis, 1953, Rao 1952). The Singh and Choudhary (1979) formula was used to compute the intra- and inter-cluster distances.

RESULTS AND DISCUSSION

The results of the analysis of variance revealed notable variations among the characters. 18 genotypes were divided into five separate groups based on D² values (Table 1). This demonstrated that the genotypes' genetic makeup varied. Cluster I has the most genotypes, with seven, followed by Cluster II having six, and Cluster IV with three. Mono

genotypes are seen in clusters III and V. Several genotypes from various sources came together to form a cluster of plants with a high degree of affinity.

Table 2 displays the average intra and inter-cluster distance. The genotypes in cluster II were substantially more varied than the genotypes in the other clusters, according to the average intra cluster distance, which extended from 54.09 (cluster I) to 111.82 (cluster II). Cluster V and cluster IV had the greatest intercluster distance (371.91), which was followed by cluster IV and cluster II (266.97), indicating a significant divergence between these groupings. Contrarily, the shortest distance (102.37) between clusters IV and I suggests a strong link, and the genotypes from these groups had the greatest number of related gene complexes. These findings broadly concur with those of Visen et al. (2015) and Rambabu et al. (2020). The level of genetic variation in the parental lines has a significant impact on how extensive a heterosis is. The genetic variation between the genotypes of two clusters increases with distance. In order to increase the variety among the segregates, it has been recommended by a number of studies that the parents chosen for hybridization should come from two clusters with greater intercluster distances. However, their yield potential shouldn't be underestimated when taking into account the genetic variety among the parents that will be used in the hybridization procedure.

Table 3 displays the mean performance of different genotype clusters for yield and related components. The highest mean value for yield, fruit weight, flesh thickness, and TSS was shown in Cluster I. With earlier female blooming, Cluster III had the highest mean value for the number of marketable fruits, number of pickings, length of the fruit, and duration of the harvest. In terms of initial female blooming, Cluster IV was the last to occur. Cluster IV displayed the maximum vine length, the seed index, and the maximum number of days from transplantation until the first fruit reaches maturity. These findings generally agree with that of Masud et al. (1995), who observed that cluster I of pumpkin had the longest fruit length and the highest number of fruits per plant, cluster II had the highest fruit weight, and cluster IV had the highest fruit diameter and yield per plant.

Table 1. Cluster Information

Clusters	No. of genotypes	Genotypes
I	7	Vidhan, Gutkha G2 Improved, Pusa Naveen, LC- 6, Sarita, Chandra Long Special, RK Cross 3
II	6	PBC Launki, G2 Chandra, Aditi, LC- 2, KGP Bottle Gourd, LC- 4
III	1	LC-7
IV	3	ArkaBahar, LC- 3, LC- 5
V	1	LC- 1

Table 2. Inter- and intra-cluster distances

Clusters	I	II	III	IV	V
I	54.09	152.05	107.20	102.37	243.73
II		111.82	201.84	266.97	236.40
III			0.000	128.69	241.19
IV				0.000	371.91
V					0.000

Table.3 Cluster means for different characters among eighteen genotypes of bottle gourd

S.No.	Traits	Clusters				
		I	II	III	IV	V
1	Days to first female flowering	52.96	52.53	52.33	61.86	56.07
2	Node number. bearing first female flower	11.84	11.30	11.33	13.04	11.67
3	Days to first fruit edible maturity from transplanting	70.09	68.89	74.91	84.16	76.24
4	Fruit Length (cm)	44.99	45.12	46.30	33.37	19.63
5	Fruit Diameter (cm)	7.48	6.64	6.91	6.39	13.12
6	Fruit weight (Kg)	1.48	1.27	1.13	0.83	1.20
7	Flesh thickness (cm)	7.07	6.39	6.49	6.17	12.73
8	No. of marketable fruits per plant	6.37	6.32	7.93	4.20	4.83
9	Total number of pickings	4.45	4.56	6.13	3.24	2.60
10	Harvest duration	40.57	47.44	55.67	38.56	37.33
11	Marketable yield per plant (Kg)	9.09	7.28	8.61	3.24	4.73
12	Marketable yield per plot (Kg)	53.91	42.22	49.57	20.09	34.46
13	Total yield per plot (Kg)	57.69	48.35	56.08	22.04	34.79
14	Vine length (m)	5.11	5.19	4.92	6.56	4.95
15	Number of branches per vine	20.17	20.94	22.78	16.06	17.58
16	Number of nodes per plant/vine	97.51	110.44	100.91	101.11	97.74
17	TSS (p B)	2.65	2.59	2.63	2.53	1.97
18	Seed Index (g)	14.24	14.13	9.47	17.55	17.37

CONCLUSION

For the purposes of the current study, it can be said that the bottle gourd genotypes chosen had sufficient genetic variation in terms of growth, yield, and

quality traits both within and across clusters, and these genotypes could be employed in hybridization schemes for future crop improvement. Therefore, in addition to choosing genotypes for hybridization from clusters with a large inter-cluster distance, one

can consider choosing parents based on the degree of genetic divergence with regard to a particular feature of interest. This means that if a breeder wants to increase fruit production, he can choose parents that are very different from one another in terms of these traits.

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