Original Research Article

STUDIES ON GENETIC DIVERGENCE OF PARENTAL LINES AND THEIR F_1 PROGENY IN BOTTLE GOURD [*Lagenaria siceraria* (Mol.) Standl.]

ABSTRACT

The experiment was conducted in Randomized Complete Block Design with three replications. In present investigation forty-three genotypes (10 lines + 3 testers + 30 F_1's) of bottle gourd were grouped into seven distinct non over lapping clusters. This indicated presence of considerable diversity in the genotypes. The genotypes of same geographic region were also found to be grouped together in the same clusters. Thus, there was no consistent relationship between genetic divergence and geographical distribution. Number of genotypes per cluster ranged from fifteen to one. The cluster II was the largest with fifteen genotypes followed by cluster III and cluster I, cluster VII, cluster VI while, clusters IV had one genotype. The maximum intra cluster distance was recorded in cluster VII followed by cluster V and cluster III. Maximum inter-cluster distance was observed between cluster I and V followed by that between cluster V and VI and cluster III and VI. The higher inter cluster distance indicated greater genetic divergences between the genotypes of those clusters. The inter-cluster distance was least between cluster IV and VI indicated, that the genotypes of these clusters were genetically least diverse and almost of the same genetic architecture. Percent character contribution towards genetic divergence among the bottle gourd genotypes were maximum for fruit length followed by days to first harvest, fruit circumference, node number to first pistillate flower appearance and number of primary branches plant^{-1}. Therefore, these traits must be included while studying genetic divergence in bottle gourd. The results suggested that crosses between selected lines/F_1's from widely separated clusters are most likely to give desirable recombinants/hybrids.

KEW WORDS: Genetic divergence, Bottle gourd, Cluster analysis, Genotypes, D^2 analysis

1. INTRODUCTION

Bottle gourd [*Lagenaria siceraria* (Mol.) Standl.] is one of the most popular vegetable of the family Cucurbitaceae, with a diploid 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. It is also commonly grown in Ethiopia, Africa, Central America and other warmer regions of the world. It is one of the important cucurbits in India, both as rainy and summer season vegetable. Out of the all cultivated cucurbits, bottle gourd with its high yield potential and adaptability to diverse climatic conditions holds a great promise to cope up with the per capita per day requirement of vegetables in the balanced diet [14] of the fast growing population pressure and greater dietary awareness, particularly among the literate masses of a country like

India. A total of six species have been recognized belonging to the genus *Lagenaria*. Out of six species of *Lagenaria* only *Lagenaria siceraria* is the domesticated annual and monoecious in nature while the other five are wild congeners, perennial and dioecious [4]. The fruits contain 96.3 per cent moisture, 2.9 per cent carbohydrate, 0.2 per cent protein, 0.1 per cent fat, 0.5 per cent mineral matter and 11 mg of vitamin C (Ascorbic acid) per 100 g fresh weight [16]. High levels of genetic variability in the base material and a wide range of variability for desired traits are essential for developing a new variety. Long-term selection gains in plants may benefit from knowledge of genetic diversity or genetic similarity [9]. Hence, genetic variability and diversity is of prime interest to the plant breeder as it plays a key role in framing and successful breeding programme. As earlier shown by [8], the genetically varied parents are always capable of producing strong heterotic effects and a great frequency of desirable segregants in subsequent generations. D^2 statistic is a useful tool to measure genetic divergence among genotypes in any crop as developed by [10]. To achieve the anticipated increase in fruit yield per plant of bottle gourd, either by crossing two dissimilar parents to produce heterotic F_1 or by making single crosses, three-way crosses, double crosses, and selfing of crosses obtained by the divergent parents of bottle gourd, an effort has been made to identify genetically divergent promising lines and their F_1 progeny in the current study.

2. MATERIALS AND METHODS

The experimental materials consisted of thirteen promising parental lines of bottle gourd and their F_1 progenies. Out of these advanced breeding parental lines, 10 parents were chosen as lines and 3 as testers and crossed as per L × T design to get 30 F_1's at Main Experiment Station, Department of Vegetable Science, College of Horticulture and Forestry, ANDUA&T, Kumarganj, Ayodhya (U.P.). These experimental materials were grown under Randomized Block Design (RBD) with three replications. The treatments were sown in rows spaced 3.0 meters apart with a plant to plant spacing of 0.5 meter. All the recommended agronomic package of practices and protection measures were followed to raise a good crop. Observations were recorded on all the six plants maintained carefully in each plot for eighteen quantitative characters *viz*., days to first staminate flower anthesis, days to first pistillate flower anthesis, node number to first staminate flower appearance, node number to first pistillate flower appearance, days to first fruit harvest, vine length (m), number of primary branches plant^{-1}, fruit length (cm), fruit circumference (cm), average fruit weight (kg), number of fruits plant^{-1}, total soluble solids (%), ascorbic acid (mg/100 g fresh fruit), reducing sugars (%), non-reducing sugar (%), total sugars (%), dry matter content in fruit (%) and fruit yield plant^{-1}. Genetic divergence was estimated by using D^2 statistics of [10] and clustering of genotypes was done according to Tocher's method as described by [13]. The per cent contribution of characters towards genetic divergence was calculated according to [15].

3. RESULTS AND DISCUSSION

Genetic Divergence Analysis

After compiling D^2 values for all the possible pairs, the 43 genotypes were grouped into seven clusters (Table 1). Number of genotypes per cluster ranged from fifteen to one. The cluster II was the largest with fifteen genotypes followed by cluster III (eight genotypes) and cluster I (four genotypes), cluster VII (three genotypes), cluster VI (two genotypes) while, clusters IV had one genotype. The genotypes got distributed randomly among the different clusters irrespective of their geographical origin. The separation of germplasm lines into so many distinct clusters suggested that the material under consideration contained sustainable variety, which is in agreement with earlier findings of [17], [5], [6].

The intra and inter-cluster D represent the index of genetic diversity among clusters as given in (Table 2). The maximum intra cluster distance was recorded in cluster VII (86.54) followed by cluster V (52.10), cluster III (39.65), cluster II (38.21), cluster I (29.18) and cluster VI (18.66). Maximum inter-cluster distance was observed between cluster I and V (268.18) followed by that between cluster V and VI (245.07), cluster III and VI (212.21), cluster I and IV (191.28), cluster IV and V (187.95), cluster II and V (181.76), cluster I and VI (169.13), cluster V and VII (168.71), cluster III and IV (165.13), cluster IV and VII (139.88) and between cluster VI and VII (137.20). As a result, genotypes belonging to clusters I and V followed by that between cluster V and VI, cluster III and VI are more divergent than the rest of the clusters, implying that crossing between superior genetic divergences of the above-mentioned clusters could result in acceptable recombinants for the development of high bulb output onion genotypes. The inter-cluster distance was least between cluster IV and VI (31.58), indicated that the genotypes of these clusters were genetically least diverse and almost of the same genetic architecture [7]. Similar results were also reported by [11] and [3].

Comparison of cluster means for different characters indicated considerable differences between clusters for all the characters (Table 3). The genotypes of cluster V ($\bar{X}$ = 45.26) showed early days to first staminate flower anthesis and those of cluster I ($\bar{X}$ = 50.71) showed maximum days to first staminate flower anthesis. Days to first pistillate flower anthesis was early in genotypes of cluster V ($\bar{X}$ = 47.75) and first pistillate flower anthesis was late in genotypes of cluster I ($\bar{X}$ = 53.73). Lowest mean value of node number to first staminate flower appearance was found in cluster IV ($\bar{X}$ = 9.42) and highest mean value of node number to first staminate flower appearance was found in cluster I ($\bar{X}$ = 15.14). Lowest mean value of node number to first pistillate flower appearance was found in cluster IV ($\bar{X}$ = 12.10) and highest mean value was found in cluster I ($\bar{X}$ = 18.94). Early first fruit harvest was observed in genotypes of cluster V ($\bar{X}$ = 57.05) whereas, first fruit harvesting was late in genotypes of cluster I ($\bar{X}$ = 63.71). Cluster V ($\bar{X}$ = 6.82) showed highest cluster means for vine length followed by cluster VI ($\bar{X}$ = 6.55). However, the lowest value was recorded in cluster I ($\bar{X}$ = 5.15). The genotypes of cluster V ($\bar{X}$ = 19.08) possessed maximum number of primary branches plant^{-1}. The genotypes with least number of primary branches plant^{-1} was concentrated in cluster I ($\bar{X}$ = 14.58). The genotypes of cluster V ($\bar{X}$ = 37.25) possessed maximum fruit length. The genotypes with minimum fruit length was observed in cluster VI ($\bar{X}$ = 23.69). Fruit circumference was maximum in genotypes of

cluster IV ($\bar{X}$ = 28.33) and minimum fruit circumference means value was recorded for genotypes in cluster I ($\bar{X}$ = 22.85). Genotypes of cluster IV ($\bar{X}$ = 0.96) exhibited maximum average fruit weight. However, genotypes in cluster I ($\bar{X}$ = 0.80) exhibited minimum average fruit weight. Number of fruits plant-1 were maximum in genotypes of cluster V ($\bar{X}$ = 7.32) and minimum fruits plant-1 were in recorded in genotypes of cluster VI ($\bar{X}$ = 5.96). Cluster V ($\bar{X}$ = 4.14) and Cluster III ($\bar{X}$ = 4.14) comprised of entries observed with highest mean for total soluble solids. The lower value was recorded for cluster I ($\bar{X}$ = 3.49). Genotypes in cluster VII ($\bar{X}$ = 8.86) exhibited high ascorbic acid content and those of cluster VI ($\bar{X}$ = 7.16) exhibited low ascorbic acid content. Rest of the clusters showed moderate mean value for this character. Reducing sugars content were high in genotypes of cluster IV ($\bar{X}$ = 3.62). However, reducing sugars were low in genotypes of cluster VII ($\bar{X}$ = 2.01). Non-reducing sugars content were high in genotypes of cluster V ($\bar{X}$ = 0.78). However, Non-Reducing sugars were low in genotypes of cluster IV ($\bar{X}$ = 0.61). Rest of the clusters showed moderate mean value for this character. Genotypes of cluster IV ($\bar{X}$ = 4.23) exhibited high total sugars. However, genotypes in cluster VII ($\bar{X}$ = 2.67) exhibited low total sugar content. Dry matter content was high in genotypes of cluster IV ($\bar{X}$ = 4.84) and those of genotypes in cluster VI ($\bar{X}$ = 2.70) exhibited low dry matter content. The highest cluster means for fruit yield plant^{-1} was observed in case of cluster V ($\bar{X}$ = 6.76). The genotypes with low fruit yield plant^{-1} were grouped in cluster I ($\bar{X}$ = 5.04). Cluster mean indicates performance of all genotypes included in a particular cluster for a particular character. High cluster mean for a particular character denotes higher vigor is possessed by the genotypes included in a cluster for that particular character. Related observations and recommendations have been documented by [12] and [1].

Percent character contribution towards genetic divergence (Table 4) among the bottle gourd genotypes were maximum for fruit length (57.92%) followed by days to first harvest (11.96%), fruit circumference (7.09%), node number to first pistillate flower appearance (6.09%), number of primary branches plant^{-1} (5.32%), days to first pistillate flower anthesis (4.21%), node number to first staminate flower appearance (3.88%), days to first staminate flower anthesis (1.99%), ascorbic acid (0.66%), number of fruits plant^{-1} (0.44%), vine length (0.11%), reducing sugars (0.11%), total sugars (0.11%) and fruit yield plant^{-1} (0.11%). Therefore, these traits must be included while studying genetic divergence in bottle gourd. Related observations and recommendations have been reported by [2].

4. CONCLUSION

The D^2 cluster analysis grouped forty-three genotypes into seven distinct clusters, indicated existence of high degree of genetic diversity in the germplasm. Therefore, these germplasms may serve as valuable source for selection of diverse parent in the present study. The seven clusters in divergence analysis contained genotypes of heterogenous origin thereby indicating no parallelism between genetic and geography diversity. Therefore, crosses between the members of clusters separated by high inter cluster distance are likely to produce desirable segregants. In this context, cluster pairs exhibiting maximum inter-cluster distance were between cluster I and V

followed by that between cluster V and VI and cluster III and VI. The different clusters showed considerable differences in intra-cluster group means for all the eighteen characters. Therefore, crosses between members of cluster having high cluster mean for important characters coupled with high inter-cluster distances between them are likely to be more rewarding.

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Table 1: Clustering pattern of forty-three genotypes of bottle gourd on the basis of Mahalnobis D^2 statistics over season pooled (2021 & 2022)

Cluster number	Number of genotypes	Genotypes
I	4	Solan Selection × Narendra Kamna, Solan Selection × Kashi Ganga, Pusa Naveen, HAU-22
II	15	Pusa Santushti, Kalyanpur Long Green, Punjab Komal, Kashi Kirti, Punjab Komal × Pusa Naveen, Arka Bahar × Pusa Naveen, Kashi Kirti × Pusa Naveen, Pant Lauki-3, HAU-22 × Pusa Naveen, Pusa Santushti × Pusa Naveen, HAU-22 × Kashi Ganga, Punjab Komal × Kashi Ganga, Kashi Kirti × Kashi Ganga, Arka Bahar, Punjab Komal × Narendra Kamna
III	8	Solan Selection × Pusa Naveen, Kashi Ganga, Narendra Kamna, Arka Bahar × Kashi Ganga, Arka Bahar× Narendra Kamna, Pant Lauki-4, Pant Lauki-4 × Kashi Ganga, Rajendra Chamatkar × Kashi Ganga
IV	1	Kashi Kirti × Narendra kamna
V		Kalyanpur Long Green × Narendra Kamna, Kalyanpur Long Green × Kashi Ganga, Rajendra Chamatkar × Narendra Kamna, Pant Lauki-3 × Narendra Kamna, Pant Lauki-3 × Kashi Ganga, Pant Lauki-4 × Pusa Naveen, Pant Lauki-4 × Narendra Kamna, Rajendra Chamatkar × Pusa Naveen, Pant Lauki-3 × Pusa Naveen, Kalyanpur Long Green × Pusa Naveen
VI	2	Pusa Santushti × Narendra Kamna, Pusa Santushti × Kashi Ganga
VII	3	Rajendra Chamatkar, Solan Selection, HAU-22 × Narendra Kamna

Table 2: Intra and inter cluster D^2 values for eighteen characters in bottle gourd over season pooled (2021 & 2022)

Cluster number	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII
I	29.18	84.66	125.24	191.28	268.18	169.13	74.19
II		38.21	111.45	61.52	181.76	62.45	74.93
III			39.65	165.13	101.70	212.21	104.84
IV				0.00	187.95	31.58	139.88
V					52.10	245.07	168.71
VI						18.66	137.20
VII							86.54

Table 3: Cluster mean for different characters in bottle gourd over season pooled (2021 & 2022)

Cluster number	Days to first staminate flower anthesis	Days to first pistillate flower anthesis	Node number to first staminate flower appearance	Node number to first pistillate flower appearance	Days to first fruit harvest	Vine length	Number of primary branches plant^{-1}	Fruit length	Fruit circumference
I	50.71**	53.73**	15.14**	18.94**	63.71**	5.15*	14.58*	29.78	22.85*
II	48.75	51.71	12.47	16.14	61.55	6.06	16.89	28.51	27.26
III	48.64	51.81	11.10	15.31	61.88	6.15	16.88	36.58	24.43
IV	48.41	49.75	9.42*	12.10*	59.67	6.57	18.04	26.43	28.33**
V	45.26*	47.75*	11.29	14.69	57.05*	6.82**	19.08**	37.25**	25.30
VI	47.01	50.06	10.72	14.79	60.18	6.55	18.10	23.69*	27.68
VII	49.31	52.42	14.24	18.00	59.96	6.41	17.59	30.67	23.89

***Lowest value, **Highest value**

Table 3: Contd..

Cluster number	Average fruit weight	Number of fruits plant^{-1}	Total soluble solids	Ascorbic acid	Reducing sugars	Non-Reducing sugar	Total sugars	Dry matter	Fruit yield plant^{-1}
I	0.80*	6.31	3.49*	7.76	2.16	0.75	2.88	3.16	5.04*
II	0.89	6.22	3.69	8.18	2.65	0.73	3.38	3.59	5.49
III	0.86	6.48	4.14**	8.11	2.37	0.75	3.14	3.34	5.60
IV	0.96**	6.13	3.75	8.70	3.62**	0.61*	4.23**	4.84**	5.62
V	0.94	7.32**	4.14**	8.83	2.69	0.78**	3.46	3.48	6.76**
VI	0.91	5.96*	3.72	7.16*	3.02	0.75	3.77	2.70*	5.23
VII	0.92	6.57	3.81	8.86**	2.01*	0.67	2.67*	3.52	5.93

***Lowest value, **Highest value**

Table 4: Percent contribution of eighteen characters towards total genetic divergence in bottle gourd over season pooled (2021 & 2022)

S. No.	Characters	Contribution (%)
1.	Days to first staminate flower anthesis	1.99
2.	Days to first pistillate flower anthesis	4.21
3.	Node number to first staminate flower appearance	3.88
4.	Node number to first pistillate flower appearance	6.09
5.	Days to first fruit harvest	11.96
6.	Vine length	0.11
7.	Number of primary branches plant^{-1}	5.32
8.	Fruit length	57.92
9.	Fruit circumference	7.09
10.	Average fruit weight	0.00
11.	Number of fruits plant^{-1}	0.44
12.	Total soluble solids	0.00
13.	Ascorbic acid	0.66
14.	Reducing sugars	0.11
15.	Non-reducing sugar	0.00
16.	Total sugars	0.11
17.	Dry matter content in fruit	0.00
18.	Fruit yield plant^{-1}	0.11