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Genetic Divergence Studies of Bottle Gourd (*Lagenaria siceraria* (MOL.) STANDL.) in Garo Hills Region of Meghalaya

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ABSTRACT

The present investigation was carried out at Horticultural Research Farm, Department of Horticulture, North Eastern Hill University, Tura Campus, Chasingre, Meghalaya, India during 2019 in a Randomized Block Design with three replications. Genetic divergence was assessed among thirty indegenous genotypes of bottle gourd for thirty-three quantitative characters using Mahalanobis' D^2 statistics. The genotypes were grouped into seven clusters. Maximum number of genotypes including seven genotypes was grouped in cluster IV (GHA-30, GHA-8, GHA-21, GHA-20, GHA-23, GHA-29 and GHA-25). Maximum inter-cluster distance was found between cluster I and cluster III (10.940) and minimum inter-cluster distance was recorded between cluster VII and cluster VI (7.425). Cluster IV showed highest cluster mean for maximum characters namely, number of primary branches (30.83), number of marketable fruit harvest (4.60), fruit width (15.24), fruit weight (3005.65), number of fruits per plant (17.92), total carbohydrate % (2.73), calcium mg/100g (11.95), yield of marketable fruits kg/plant (54.20) and yield t/ha (135.50). Cluster VII exhibited highest mean for five characters namely, vine length (461.93), days to last fruit harvest (158.77), number of leaves (217.13), seed length-breadth ratio (2.41) and ascorbic acid (9.55). Cluster I and Cluster II exhibited highest mean for five characters, sex ratio (0.74), number of seeds per fruit (449.65), 100 seed weight (13.43), total soluble protein % (0.95) and total phenols % (44.04). In the present study it was found that Cluster I (GHA-4, GHA-2, GHA-5 and GHA-1) was highly divergent from all other genotypes.

Keywords Bottle gourd, Genetic divergence, D^2 statistic, Genotypes, Yield.

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INTRODUCTION

Bottle gourd (*Lagenaria siceraria* (Mol.) Standl.) is one of the most important vegetable crops belongs to Cucurbitaceous family having chromosomes number 2n=22, originated in Africa. Bottle gourd is the largest produced vegetable among other cucurbitaceous vegetables in the world. The area under bottle gourd cultivation in India is 193 thousand hectare and

production is 3171 thousand metric tones (NHB, 2020-21). It contains considerable amount of moisture (95.54%), Vitamin C (10.01g), Vitamin A (16 IU), thiamine (0.029g), riboflavin (0.022g), carbohydrates (3.39g), fats (0.02g) and potassium (150 mg/100g) (USDA 2018). Yamane *et al.* (2009), stated in their studies that broad based plant genetic resources are imperative for sound and fruitful crop improvement program and the range of cultivated plant species depends upon mutation and hybridization, range of dispersal and processes of cultivation and domestication. There are number of local cultivars with wide range of variability in fruit size, fruit shape and fruit color available in Garo Hills of Meghalaya but a very limited attempt has been made for genetic improvement of this crop in Garo Hills Region of Meghalaya. Assessment of genetic diversity in germplasm collections imposes the categorization of accessions and useful in assigning genotypes to specific heterotic groups to create segregating progenies with maximum genetic variability for further breeding purposes. Genetic divergence is one of the useful tools for selection and efficient use of parents for hybridization to develop high yielding potential cultivars. Keeping the above considerations in view D^2 analysis was conducted in thirty locally available genotypes for divergence study.

MATERIALS AND METHODS

The study was carried out during (2018 and 2019) at Horticulture Research farm, North Eastern Hill University, Tura Campus, Chasingre, Meghalaya. Tura is situated at 25°31' N latitude and 90° 13'E longitude having an altitude of 527 m above the mean sea level. The experiment comprised of thirty genotypes of bottle gourd collected from different districts of Garo Hills Region of Meghalaya. The experiment was laid out in a Randomized Block Design with three replications at 2 × 2m row to row and plant to plant spacing. The crop was grown under rainfed condition. The data of qualitative and quantitative characters were recorded as per minimal descriptors developed for bottle gourd by NBPGR. The investigated data recorded for 33 quantitative characters were used for cluster analysis and to select the parents for hybridization using Mahalanobis (1936) D^2 statistics. The collected genotypes were grouped into different clusters by Tocher's method (Rao 1952). The population of genotypes was arranged in order of their relative distances from each other. For including a particular population in the clusters, a level of D^2 was fixed by taking the maximum D^2 values between any two populations in the first row of the table and the D^2 values were arranged in increasing order of magnitude.

RESULTS AND DISCUSSION

The analysis of variance revealed significant differences among bottle gourd genotypes for all characters under study which suggests considerable genetic variability in the population.

On the basis of D^2 analysis, thirty bottle gourd germplasm lines were grouped into seven clusters as shown in the Table 1. Maximum number of genotypes including seven genotypes were grouped in cluster IV (GHA-30, GHA-8, GHA-21, GHA-20, GHA-23, GHA-29 and GHA-25) followed by cluster II which included five genotypes (GHA-15, GHA-6, GHA-12, GHA-3 and GHA-22) and cluster VII which also included five genotypes (GHA-26, GHA-16, GHA-28, GHA-17 and GHA-24). Cluster I included four genotypes viz; GHA-4, GHA-2, GHA-5 and GHA-1 whereas, cluster III included three genotypes viz; GHA-7, GHA-11 and GHA-18. Cluster V included three genotypes (GHA-10, GHA-9 and GHA-13) and cluster VI also included three genotypes (GHA-19, GHA-27 and GHA-14).

Table 1. Composition of clusters for yield and its components.

Cluster number	Number of genotypes included	Name of genotypes
I	4	GHA-4, GHA-2, GHA-5, GHA1
II	5	GHA-15, GHA-6, GHA-12, GHA-3, GHA-22
III	3	GHA-7, GHA-11, GHA-18
IV	7	GHA-30, GHA-8, GHA-21, GHA-20, GHA-23, GHA-29, GHA-25
V	3	GHA-10, GHA-9, GHA-13
VI	3	GHA-19, GHA-27, GHA-14
VII	5	GHA-26, GHA-16, GHA-28, GHA-17, GHA-24

Table 2. Inter cluster distance values in bottle gourd germplasm.

Cluster number	I	II	III	IV	V	VI	VII
I	**6.476**	9.974	10.940	9.438	10.431	8.649	7.716
II	9.974	**6.211**	7.871	7.732	7.973	7.532	7.963
III	10.940	7.871	**6.798**	8.557	7.700	7.609	8.834
IV	9.438	7.732	8.557	**7.316**	8.335	7.651	8.571
V	10.431	7.973	7.700	8.335	**6.335**	8.158	8.119
VI	8.649	7.532	7.609	7.651	8.158	**6.005**	7.425
VII	7.716	7.963	8.834	8.571	8.119	7.425	**6.283**

GHA- Garo Hills Accession.

From the Table 2 it can be observed that maximum inter-cluster distance was found between cluster I and cluster III (10.940) followed by cluster I and cluster V (10.431), cluster I and cluster II (9.974), cluster IV and cluster I (9.438), cluster VII and cluster III (8.834), cluster VI and cluster I (8.649), cluster VII and cluster IV (8.571), cluster IV and cluster III (8.557), cluster V and cluster IV (8.335), cluster VI and cluster V (8.158), cluster VII and cluster V (8.119), cluster V and cluster II (7.973), cluster VII and cluster II (7.963), cluster III and cluster II (7.871), cluster II and cluster IV (7.732), cluster VII and cluster I (7.716), cluster v and cluster III (7.700), cluster VI and cluster IV (7.651), cluster VI and cluster III (7.609), cluster VI and cluster II (7.532) and cluster VII and cluster VI (7.425).

Among the seven clusters, minimum inter-cluster distance was recorded between cluster VII and cluster VI (7.425). The higher distance indicates that there was greater genetic divergence between the genotypes of that cluster, while lower inter-cluster distance values between the clusters suggested that the genotypes of the cluster were not much genetically diverse from each other.

The critical pursual of the result obtained from the present study also revealed interesting feature that expression of cluster distance was not according to the geographical location. For instance, GHA-19, GHA-27 and GHA-14 were collected from different locations but grouped into same cluster (VI) whereas, GHA-27 and GHA-28 collected from nearby locations but they shared diverse cluster name cluster VI and cluster VII, respectively.

From the Table 3 it can be observed that the mean performance for different clusters of genotypes for yield and its components. The data of cluster means for all the characters showed considerable differences. The cluster mean for various traits showed that different cluster respond differently for various traits. Cluster IV showed highest cluster mean for maximum characters namely, number of primary branches (30.83), number of marketable fruit harvest (4.60), fruit width (15.24), fruit weight (3005.65), number of fruits per plant (17.92), total carbohydrate% (2.73), calcium mg/100g (11.95), yield of marketable fruits kg/plant (54.20) and yield t/ha (135.50). Cluster VII exhibited highest mean for five characters namely, vine length (461.93), days to last fruit harvest (158.77), number of leaves (217.13), seed length-breadth ratio (2.41) and ascorbic acid (9.55). Cluster I also showed highest mean for five characters viz; internode length (7.51), petiole length (10.96), days to 50% flowering (38.83), fruit length (51.19) and dry matter % (9.63). Cluster II also showed highest mean for five characters, sex ratio (0.74), number of seeds per fruit (449.65), 100 seed weight (13.43), total soluble protein% (0.95) and total phenols % (44.04) whereas, cluster VI exhibited least mean value for most of the traits. The better genotypes can be selected for most of the characters on the basis of mean performance in the cluster.

The higher inter-cluster distances in present investigation showed wider diversity among the breeding lines of the distant group. Hence, it is suggested that intercrossing of genotypes from different clusters showing high mean performance will be useful in obtaining better recombinants with high genetic variability.

Genetic divergence is one of the useful tools for

Table 3. Mean performance of genotypes in individual cluster for yield and its components in bottle gourd.

Characters/clusters	I	II	III	IV	V	VI	VII
Vine length	444.58	438.69	471.27	485.25	414.42	421.92	461.93
Internode length	7.51	6.92	7.19	7.40	7.23	7.42	6.36
Petiole length	10.96	8.65	8.87	9.56	9.42	9.90	9.35
No. of primary branches	26.89	26.64	25.89	30.83	26.68	26.37	28.32
Node no. at which 1st female flower appears	24.40	25.84	24.76	25.60	24.10	27.18	27.00
Days to 50% flowering	38.83	37.39	34.39	36.93	37.30	34.96	36.74
Sex ratio	0.47	0.74	0.41	0.43	0.63	0.41	0.45
Days to 1st fruit harvest	87.73	90.27	82.86	82.32	84.26	91.83	81.89
No. of marketable fruit harvest	3.41	2.78	3.35	4.60	3.45	3.23	4.08
Days to last fruit harvest	150.28	155.95	156.53	157.79	147.35	148.89	158.77
No. of leaves	159.05	187.26	195.83	210.35	175.61	197.56	217.13
Fruit length	51.19	25.59	15.52	18.85	15.68	19.08	19.36
Peduncle length	11.05	9.84	11.54	9.45	9.25	9.74	9.49
Fruit width	12.74	13.39	12.56	15.24	10.91	11.49	12.42
Fruit weight	2161.14	1920.99	1862.08	3005.65	2573.46	1922.49	2168.37
No. of fruits/plant	12.62	12.63	11.26	17.92	12.10	10.12	13.94
No. of seeds/fruit	352.02	449.65	402.77	437.43	274.33	318.26	340.37
100 seed wt	11.33	13.43	12.04	12.30	10.33	10.75	11.03
Seed L-B ratio	2.02	2.17	2.02	2.14	2.39	2.37	2.41
TSS (˚Brix)	3.11	3.26	3.79	3.36	3.12	3.31	3.23
Total sugar (%)	2.01	1.88	2.79	2.47	2.26	1.57	2.07
Reducing sugar (%)	1.60	1.43	2.48	2.08	1.69	1.08	1.70
Ascorbic acid (mg/100g)	8.57	8.62	8.36	9.30	9.08	7.87	9.55
Total soluble protein (%)	0.85	0.95	0.87	0.86	0.91	0.82	0.79
Total carbohydrate (%)	2.19	2.25	2.06	2.73	2.38	1.78	2.13
Moisture (%)	90.37	91.73	91.76	90.86	92.20	90.49	91.57
Dry matter (%)	9.63	8.27	8.24	9.14	7.80	9.51	8.43
Total ash (%)	0.75	0.59	0.86	1.31	1.06	1.41	1.02
Total phenols (%)	34.65	44.04	38.50	41.24	38.91	41.20	43.42
Calcium (mg/100g)	9.55	11.76	10.96	11.95	11.34	10.52	10.15
Crude fiber (%)	0.68	0.62	0.67	0.65	0.70	0.69	0.63
Yield of marketable fruits (kg)/ plant	26.68	24.43	22.07	54.20	31.08	19.55	29.95
Y (T/ha)	66.70	61.08	55.17	135.50	77.70	48.88	74.88

selection and efficient use of parents for hybridization to develop high yielding potential cultivars. Addition of more diverse parents in hybridization is assumed to increase the probability of obtaining stronger heterosis and gives wide-ranging of variability in segregating generations. Hence, this implies that there was no parallelism between genetic divergence and environmental divergence.

In the present study as per D^2 analysis it was found that cluster I (GHA-4, GHA-2, GHA-5 and GHA-1) were highly divergent from all other genotypes and may be used as parents in breeding programs or they can be directly used as a pure line for traits fruit yield and its components in bottle gourd for Garo Hills, Meghalaya. Thakur *et al.* (2020) reported in their divergence studies among 73 genotypes of bottle gourd that cluster analysis grouped all 73 genotypes into 6 major clusters based on D^2 values and maximum number of genotypes were grouped into cluster III which included 22 genotypes and the maximum inter cluster distance was found between cluster I and VI (9.347). Thakur *et al.* (2020) also reported maximum intra cluster distance was observed in cluster VI (2.865) followed by cluster IV (2.436), cluster I showed highest mean value for number of fruits per plant, yield (q/ha) and lowest mean performance for node number at which 1st male flower appears. Rambabu *et al.* (2020) reported their genetic divergence studies in bottle gourd that the 21

genotypes were grouped into six clusters and reported fruit yield per plant (53.81%) contributed maximum towards divergence. Rambabu *et al.* (2020) also reported highest inter cluster distance between cluster V and VI and highest cluster mean values observed for most of the traits with genotypes present in cluster I. Chetaria and Vaddoria (2017) reported similar findings in their genetic divergence analysis of 50 genotypes of bottle gourd that the genetic diversity revealed the formation of 13 clusters suggesting the presence of wide genetic diversity. Visen *et al.* (2015) reported in their genetic divergence studies in 31 genotypes of bottle gourd that the cluster analysis grouped all 31 bottle gourd genotypes into 5 major clusters and the also reported maximum number of genotypes were grouped into cluster V and least were grouped in cluster IV and III and fruit length, fruit girth and average fruit weight contributed maximum towards genetic divergence.

CONCLUSION

In the present study as per D^2 analysis it was found that cluster I (GHA-4, GHA-2, GHA-5 and GHA-1) were highly divergent from all other genotypes and may be used as parents in breeding programs or they can be directly used as a pure line for traits fruit yield and its components in bottle gourd for Garo Hills, Meghalaya.

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