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Short communication

Breeding potential of Indian ridge gourd germplasm for important horticultural traits

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ABSTRACT

Using Mahalanobis D^2 statistics method, 51 genotypes of ridge gourd were grouped into 15 divergent clusters. Cluster X was the largest comprising 14 genotypes, followed by cluster VI with 6 genotypes and cluster I with 5 genotypes. Rest of the clusters had either two or three genotypes. The pattern of distribution of genotypes from different regions into different clusters was random indicating that; there is no association between geographical distance and genetic divergence. Intra cluster distance was highest in cluster VI and lowest in cluster II. Maximum inter cluster distance (10.79) was observed between clusters XII and XIV followed by between cluster III and XIV (10.22) and between cluster IV and XIV (10.18). Cluster XIII with two genotypes ranked first for most of the yield contributing characters and appeared to be containing the most potential genotypes for hybridization programmes aimed at increasing ridge gourd yields. The important characters responsible for maximum divergence were fruit yield/ha, fruit yield/vine, number of fruits/vine and number of branches /vine. Hence during selection, considerable emphasis should be given on these characters to increase fruit yield in ridge gourd.

Key words: *Luffa acutangula*, Genetic diversity, D^2 statistics.

Ridge gourd [*Luffa acutangula* (Roxb.) L.] is one of the most important vegetables grown throughout the year in all the tropical regions of the country and in the Asian and African countries. It is rich in vitamin A, C and iron (Fe). The genetic diversity present in the breeding material is an important pre-requisite for starting any systematic breeding programme. It is an established fact that genetically diverse parents are likely to contribute desirable segregates and/or to produce high heterotic crosses. More diverse the parents; greater are the chances of obtaining high heterotic F_1s and broad spectrum of variability in segregating generations (Murthy and Arunachalam, 5). The parents identified on the basis of divergence analysis would be more promising for hybridization. In both cross and self-pollinated crops, genetic diversity is one of the most important tools to quantify genetic variability (Varalakshmi *et al.,* 9). Genetic diversity is also important to know the source of gene for a particular trait within the available germplasm. Mahalanobis's D^2 statistic has been proved to be a powerful tool in quantifying the genetic divergence in genotypes and has been successfully utilized in various crops. Since very little information on genetic divergence in ridge gourd is available, the present study was carried out to ascertain nature and magnitude of genetic diversity among 51 genotypes of ridge gourd using the D^2 statistic. The information on such aspects can be of great help in planning appropriate breeding programmes aimed at the development of superior varieties/hybrids.

The experiments were carried out at the Vegetable Farm, ICAR-Indian Institute of Horticultural Research, Bangalore during Rabi-summer seasons of 2011-12, 2012-13 and 2013-14. The experiments were laid out in Randomized Block Design with 51 genotypes in two replications in all the three years. Ten plants per replication were raised. Two weeks old seedlings were planted at 150 x 50 cm spacing and the plants were trained on single trellis. The recommended agronomical practices were adopted to raise the crop. Observations were recorded on five randomly selected plants from each replication on 11 quantitative traits such as node number for first female flower appearance, days taken for first female flower appearance, vine length (m), number of branches/plant, peduncle length (cm), fruit length (cm), fruit girth (cm), fruit number/plant, fruit weight (g), fruit yield/plant (kg) and fruit yield/ha (t). Genetic diversity was estimated following Mahalanobis's (4) generalized distance (D^2) extended by Rao (7). Tochers method (Rao, 7) was followed for determining the group constellations. GENRES Statistical Software Package (GENRES, 2) was employed for analysis of variance and estimation of D^2 values and Cluster formation.

The analysis of variance revealed significant variations among the ridge gourd genotypes for all

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*Corresponding author's Email: varalaxmi.b@icar.gov.in the eleven characters studied. The D^2 values ranged from 2.84 to 116.00, showing high divergence among the genotypes. On the basis of relative magnitude of D^2 values, the 51 genotypes of ridge gourd were grouped into 15 clusters with the assumption that those within the cluster have smaller differences in D^2 values among themselves than those belonging to different clusters. Cluster X was the largest comprising 14 genotypes, followed by cluster VI with 6 genotypes and cluster I with 5 genotypes. Rest of the clusters had either two or three genotypes.

In general, the pattern of distribution of genotypes from different regions into different clusters was random indicating that; there is no association between geographical distance and genetic divergence. Similar observations were also reported in ridge gourd [Varalakshmi *et al.*, 9; Choudhary et al., 1; Rabbani et al., 8].

One of the possible reasons may be the fact that it is very difficult to establish the actual location of origin of genotypes. The free and frequent exchange of genetic material among farmers and breeders in the country makes it very difficult to maintain the real identity of the genotypes. 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. Therefore, selection of genotypes for hybridization should be based on genetic diversity rather than geographic divergence. (Murthy and Arunachalam, 5; Varalakshmi *et al.,* 9).

Intra cluster distances ranged from 1.68 in cluster II to 6.39 in cluster VI. Maximum inter cluster distance (10.79) was observed between clusters XII and XIV followed by between cluster III and XIV (10.22) and between cluster IV and XIV (10.18). It is desirable to select accessions from clusters having high inter-cluster distance and with high fruit yield as parents in the recombination breeding programmes to get more variability. The genotypes, IC-110893, IC-308561 and IC-395846 from cluster XII and IIHR-4 and IIHR-58 from cluster XIV are the best choice for hybridization. On the other hand, minimum inter-cluster distance (2.27) occurred between cluster IV and cluster VII indicating the close relationship of the genotypes included in these clusters (Table 1).

Differences in cluster means existed for almost all the characters (Table 2). The highest mean value for fruit yield (t/ha), fruit yield/vine (kg) and peduncle length (cm) was observed in cluster XIII indicating that the genotypes included in this cluster are potential sources for exploiting these yield related traits in ridge gourd. Similarly cluster XII ranked first for fruit girth (cm) and number of fruits/vine, cluster XIV for fruit length (cm) and fruit weight (g), cluster XV for number of branches/vine in, cluster IX for vine length (m) in, cluster VII for node number for first female flower appearance (in desirable direction) and cluster VIII for days taken for first female flower appearance (in desirable direction). Though the cluster XIV ranked first in fruit weight, it ranked lowest for fruit yield/ha which might be due to less

Table 1. Mean intra - (bold) and inter-cluster distances (D^2 values) in ridge gourd.

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV	XV
I	**4.52**	4.47	6.96	6.31	5.60	6.08	6.08	6.21	6.91	6.50	4.92	8.26	4.83	6.96	7.55
II		**1.68**	4.96	4.11	3.55	4.91	4.16	4.21	6.45	4.81	4.46	6.29	5.32	7.02	6.57
III			**1.72**	3.19	2.87	6.75	2.66	2.98	8.28	4.60	7.50	3.97	8.30	10.22	7.22
IV				**1.72**	3.07	6.74	2.27	3.31	8.79	4.22	7.17	5.12	7.03	10.18	8.07
V					**1.81**	5.78	2.41	3.03	7.41	4.06	5.67	4.68	7.01	8.63	5.95
VI						**6.39**	6.47	6.53	6.06	6.79	5.59	7.75	7.21	6.99	7.24
VII							**2.05**	2.65	8.36	4.11	6.83	4.93	7.31	9.77	7.17
VIII								2.38	8.46	4.68	6.86	4.82	7.70	9.86	6.63
IX									**5.01**	8.33	5.81	9.10	7.94	5.46	7.86
X										**5.44**	6.80	6.02	7.47	9.45	7.65
XI											**3.64**	8.27	6.09	5.11	6.08
XII												**6.01**	9.59	10.79	7.92
XIII													4.27	7.74	9.68
XIV														**4.49**	8.49
XV															5.38

Table 2. Cluster means for eleven characters in ridge gourd.

Cluster	Node number of first female flower appearance	Days taken for first female flower appearance	Vine length (m)	Number of branches / vine	Peduncle length (cm)	Fruit length (cm)	Fruit girth (cm)	Number of fruits / vine	Fruit weight (g)	Fruit yield / vine (kg)	Fruit yield (t/ha)
I	9.88	45.39	4.90	8.46	10.42	30.76	10.82	13.68	235.21	2.48	32.18
II	10.48	49.48	3.20	7.13	8.22	26.74	10.50	11.27	173.07	1.76	24.20
III	8.90	46.08	3.18	4.45	7.42	12.78	12.35	20.01	109.49	1.71	22.54
IV	7.42	43.85	3.10	4.05	6.39	17.35	10.67	14.78	132.01	1.79	22.85
V	7.77	48.78	3.57	6.20	7.33	17.23	13.65	16.68	132.98	1.77	23.64
VI	12.11	52.00	4.23	8.53	8.32	24.93	9.95	9.39	199.91	1.59	21.63
VII	6.73	44.52	3.57	5.08	7.67	16.62	10.70	16.13	133.80	1.66	23.43
VIII	8.22	41.66	3.48	5.88	6.99	16.63	10.78	20.33	125.28	1.82	27.63
IX	15.83	57.42	5.42	9.69	9.74	27.79	10.43	6.39	232.16	1.37	17.92
X	7.94	45.62	3.39	5.31	7.50	19.11	12.00	14.55	141.97	1.65	21.47
XI	10.86	45.25	4.25	9.60	8.81	29.08	14.28	8.57	209.43	1.65	21.98
XII	9.37	46.03	2.71	4.23	5.77	11.62	14.42	21.42	103.97	1.53	20.09
XIII	11.43	46.38	5.18	6.38	11.63	38.65	12.07	10.70	237.82	2.68	34.37
XIV	13.99	57.91	5.01	10.94	11.13	39.18	13.00	5.19	280.79	1.36	17.93
XV	9.12	47.41	3.98	12.03	6.90	14.55	13.80	16.31	109.59	1.69	23.53

number of fruits/vine and lowest fruit yield/vine of the genotypes included in this cluster viz., IIHR-4 and IIHR-58. It is observed from the Table 2 that crossing between genotypes of cluster XIII with genotypes of cluster IX, cluster XII and cluster XIV is likely to be exploited for high heterosis for fruit yield/vine intern fruit yield/ha in ridge gourd. Varalakshmi *et al.* (9), Quamruzzaman *et al*. (6), Choudhary *et al*. (1) and Rabbani *et al*. (8) also reported similar findings with respect to fruit related traits in ridge gourd.

The percentage contribution of different characters towards total divergence is given in Table 3. The important characters responsible for maximum divergence were fruit yield/ha, fruit yield/vine, number of fruits/vine and number of branches /vine. Hence considerable emphasis should be given on these characters to increase fruit yield in ridge gourd. Similar observations were reported in cucumber by Hanchinamani and Patil (3).

Thus this information, generated on genetic divergence should be utilized for the development of gene pools, which serve as the reservoirs of genes. The genetic diversity can also be utilized for the exploitation of hybrid vigour. Morphological approach to explore variation and divergence is more of a conventional method with several limitations and influenced by environmental factors. So, to get more accurate results, molecular approach using RAPD, RFLP, SSR markers is suggested for identification of individual accessions to avoid duplication in conservation of the genotypes for future use as well as to study genetic divergence in ridge gourd (*L. acutangula*).

Table 3. Relative contribution of eleven characters to the total divergence in ridge gourd.

Sl. No.	Character	% Contribution
1	Node number of first female flower appearance	8.63
2	Days taken for first female flower appearance	0.63
3	Vine length (m)	2.27
4	Number of branches / vine	13.57
5	Peduncle length (cm)	0.71
6	Fruit length (cm)	9.65
7	Fruit girth (cm)	0.39
8	Number of fruits per vine	17.88
9	Fruit weight (g)	3.92
10	Fruit yield per vine (kg)	19.06
11	Fruit yield (t/ha)	23.29
	Total	100.00

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