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GENETIC DIVERSITY STUDIES IN RIDGE GOURD [*LUFFA ACUTANGULA* (L.) ROXB.] GENOTYPES

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ABSTRACT

The present investigation was carried out on 38 genotypes collected from different locations and evaluated for 13 quantitative traits. The studied genotypes were grouped into fourteen clusters based on the relative magnitudes of their D^2 values. Among these clusters, the most extensive was cluster I, consisting of 18 genotypes, followed by clusters II and III, each comprising 5 and 4 genotypes. In contrast, clusters IV, V, VI, VII, VIII, IX, X, XI, XII, XIII and XIV consisted of only 1 genotype each, rendering them monogenotypic clusters. The greatest inter-cluster distance was observed between clusters II and XI (32.69), followed by clusters XI and XIV (30.40). Conversely, the smallest inter-cluster distance was between clusters V and VI (10.27). Among the traits examined, fruit diameter contributed the most to the observed divergence, accounting for 27.17%, providing basic material for future improvement breeding programmes of ridge gourd.

Keywords: Ridge gourd, diversity, cluster, fruit, vine

Introduction

Ridge gourd [*Luffa acutangula* (L.) Roxb.] is a significant cucurbitaceous vegetable with a chromosome number of 2n=26, widely cultivated in India's tropical and subtropical regions. It is known by various names such as kalitori and angled gourd, its juice serves as a natural remedy for jaundice, promoting liver purification and detoxification, especially after alcohol consumption. The fibre extracted from the mature dry fruit finds application in industries for manufacturing different types of filters, reliable pot holders, durable table mats, bathroom mats, as well as slipper and shoe soles (Narasannavar *et al*., 2014). Moreover, this fibre has proven to be an effective insulator for various purposes. Additionally, the dry fruits that exhibit good storability are sometimes utilized for ornamental purposes too (Chakravarthy, 1959).

Ridge gourd as a high-volume crop, present a significant opportunity for enhancement through the development of high yielding varieties and hybrids to address the disparity between supply and demand. The common method of selecting parents on their performance on an individual basis does not always result in successful outcomes. The complete genetic information of potential parents and their regarded prepotency must be considered when selecting the best parents for hybridization. The presence of genetic diversity is crucial for the success of a plant breeding programme. It serves as a valuable and necessary resource for selecting suitable parents for hybridization, enabling the development of cultivars with high yield potential that exhibit a greater heterotic effect and also more variability could be expected in the segregating generations (Gaur *et al*., 1978) . Genetic diversity between populations/genotypes indicates the differences in gene frequencies, D^2 statistic proposed by Mahalanobis (1928) has been generally used as an efficient tool in the quantitative estimation of genetic diversity for a rational choice of potential parent in a breeding programme. Through the segregation and recombination of genes at heterozygous polygenic blocks, this selection process can generate a wide spectrum of variability. Ultimately, this genetic divergence analysis plays a fundamental role in enhancing crop productivity (Khan *et al*., 2016).

Materials and Methods

The experiments were carried out at the field of Vegetable Farm, College of Horticulture, Bagalkot, during the rabi-summer season of the year 2023-24. The experiment was laid out in Randomized Block Design, with 38 genotypes in two replications. Ten plants per replication were raised. Two-week-old seedlings were planted at 2m x 1m spacing. Recommended agronomic practices were applied to the crop. Observations were recorded on five randomly-selected plants in each replication on 13 quantitative traits (vine length at final harvest (cm), number of primary branches per plant at final harvest, days to appearance of first male flower, days to appearance of first female flower, node to first male flower, node to first female flower, days taken to first harvest, sex ratio, number of fruits per vine, average fruit weight (g), fruit length (cm), fruit diameter (cm) and fruit yield per vine (kg/ vine).

Statistical analysis: Mahalanobis (1928) generalized distance, D^2 statistics, were employed for calculating genetic divergence. Using Tocher's method, as explained by Rao (1952) , the genotypes were clustered.

Results and Discussion

Genetic diversity in ridge gourd is crucial for improving the crops yield, disease resistance and adaptability. It plays a vital role in identifying genetically diverse parents and supporting effective hybridization programmes, leading to potential transgressive segregants and novel gene pool combinations. An assessment of genetic diversity was conducted by analyzing data from 13 growth and yield traits across 38 genotypes using Mahalanobis D^2 analysis.

Trocher's method of grouping was the chosen procedure for clustering and all 38 genotypes were classified into fourteen clusters (Table 1) (Fig. 1) based on the relative magnitudes of their D^2 values. Among these clusters, the most extensive was cluster I, consisting of 18 genotypes, followed by clusters II and III, each comprising 5 and 4 genotypes. In contrast, clusters IV, V, VI, VII, VIII, IX, X, XI, XII, XIII and XIV consisted of only 1 genotype each, rendering them monogenotypic clusters.

In selection of the parents for hybridization programme using D^2 it is important to keep two points under consideration *i.e*., the relative contribution of different traits to diversity under study and average inter cluster distance. The formation of these clusters was based on the contribution from various characters to the genetic divergence. The character, fruit diameter had shown the highest contribution towards divergence by ranking first with a contribution of 27.17 % followed by average fruit weight at 16.93% and fruit length at 13.66%. Additionally, the characters sex ratio, vine length at final harvest, fruit yield per vine, node at first male flower, number of fruits per vine, days to appearance of first female flower, node at first female flower and days to appearance of first male flower contributed 12.09%, 10.81%, 9.10%, 4.27%, 2.28%, 1.99%, 1.00% and 0.71% respectively. However, number of primary branches at final harvest and days to first harvest made no contribution to the overall diversity (Table 2). Gugulothu (2022) , Nithinkumar (2021) in bitter gourd and Hasan *et al.* (2015) in cucumber for the traits fruit diameter, average fruit weight and fruit length. Apart from the divergence, the performance of genotypes and the character with maximum contribution towards divergence should also be given due to consideration which appears desirable for improvement of ridge gourd.

Table 1 : Distribution of ridge gourd genotypes into different clusters

Cluster No.	No. of genotypes	Name of genotype
Cluster 1	18	G-16, G-24, G-30, G-33, G-17, G-2, G-11, G-5, G-4, G-39, G-20, G-29,G-32, G-10, G-31, G-15, G-34, G-9
Cluster 2	5	G-1, G-23, G-12, G-3, G-14
Cluster 3	4	G-37, G-38, G-36, G-28
Cluster 4	1	G-26
Cluster 5	1	G-6
Cluster 6	1	G-27
Cluster 7	1	G-21
Cluster 8	1	G-19
Cluster 9	1	G-8
Cluster 10	1	G-25
Cluster 11	1	G-35
Cluster 12	1	G-22
Cluster 13	1	G-18
Cluster 14	1	G-7

Table 2 : Contribution of characters towards divergence in ridge gourd

SL. No	Characters	Number of times ranked first	Per cent contribution
1	Vine length at final harvest (cm)	76	10.81
2	Number of primary branches per vine at final harvest	0	0.00
3	Days to appearance of first male flower	5	0.71
4	Days to appearance of first female flower	14	1.99
5	Node at first male flower	30	4.27
6	Node at first female flower	7	1.00
7	Days taken to first harvest	0	0.00
8	Sex ratio (M: F)	85	12.09
9	Number of fruits per vine	16	2.28
10	Average fruit weight (g)	119	16.93
11	Fruit length (cm)	96	13.66
12	Fruit diameter (cm)	191	27.17
13	Fruit yield per vine (kg)	64	9.10
	Total	**703**	**100.00**

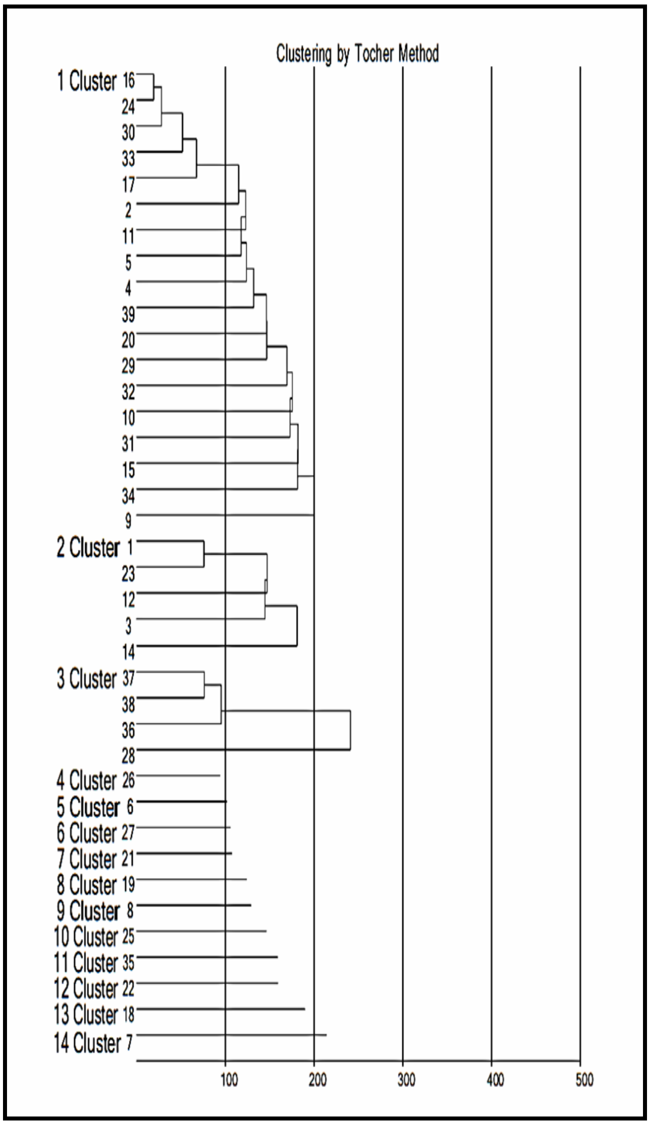

Fig. 1: Dendrogram showing clustering pattern for divergence in ridge gourd genotypes

Studies on intra cluster distance revealed that cluster III with 4 genotypes showed maximum intra-cluster distance (14.87) followed by cluster II (14.14) with 5 genotypes and cluster I (12.98) with 18 genotypes. The cluster IV, V, VI, VII, VIII, IX, X, XI, XII, XIII and XIV had zero intra cluster distance as they possessed single genotype in each (Table 3). These results are in accordance with Manoj *et al.* (2018) reported 8 clusters, Varalakshmi *et al.* (2019) reported 15 clusters, Rabbani *et al.* (2012) , Kumar *et al.* (2021) in bottle gourd reported 11 clusters and Shabharish (2017) in cucumber reported 10 clusters, as the number of genotypes assessed and sources of genotypes used in these studies are different from present studies.

For vine length at final harvest the higher means recorded in cluster XI (501.24) followedby XII, IV and XIV. The inter cluster distance between cluster XI and XII (25.47), XI and IV (26.00) and cluster XI and XIV (30.40) were comparatively high. Hence, hybridization between the genotypes of these respective clusters could be attempted to get heterotic hybrids as it simultaneously increases the branches, flowers, fruits and hence yield. Number of primary branches at final harvest, the higher means recorded in cluster XI (4.07) followed by VII, V and III (Table 4). The inter cluster distance between cluster XI and VII (22.29) and cluster XI and V (28.12) were comparatively high. Hence, hybridization between the genotypes of these respective clusters could be attempted to get high heterosis. For days to appearance of first male flower and days to appearance of first female flower the least cluster mean was obtained in cluster XI (38.60) followed by VIII, III and XIV. The inter cluster distance between cluster XI and VIII (24.96), XI and III (18.58), cluster XI and XIV (30.40) were comparatively high (Table 4). Hence, hybridization between the genotypes of these respective clusters could be attempted to exploit the earliness. For node at first male flower the least cluster mean was obtained in cluster XI (4.59) followed by X, XII and IX. The inter cluster distance between cluster XI and X (23.37), cluster XI and XII (25.47), cluster XI and IX (23.21) were comparatively high. Hence, hybridization between the genotypes of these respective clusters could be attempted to exploit the earliness. Node at first female flower recorded least cluster mean in cluster XI (7.16) followed by IV, XII and XIII. The inter cluster distance between cluster XI and IV (26.00), cluster XI and XII (25.47), cluster XI and XIII (27.60), were relatively high and for trait sex ratio least cluster mean was obtained in cluster XI (18.83) followed by X, VI and V. The inter cluster distance between cluster XI and X (23.37), cluster XI and VI (24.12), cluster XI and V (28.12) (Table 4). Therefore, it is suggested to consider hybridization among the genotypes of these respective clusters to harness earliness and yield. Concerning the average fruit weight, the cluster with the highest mean was reported in the cluster XI (261.79) followed by III, XIII and VIII. The inter cluster distance between cluster XI and III (18.58), cluster XI and XIII (27.60), cluster XI and VIII (24.96) were relatively high. Hence, hybridization among the genotypes of these respective clusters leads to potentially enhance fruit size. For fruit diameter the

Table 3 : Average inter and intra – cluster (diagonal) distance D^2 values in ridge gourd diagonal values indicate intra clusterdistance

	I	**II**	**III**	**IV**	**V**	**VI**	**VII**	**VIII**	**IX**	**X**	**XI**	**XII**	**XIII**	**XIV**
I	12.98	18.16	21.30	16.16	16.87	16.10	16.79	15.99	16.37	16.19	21.12	16.88	20.18	22.38
II		14.14	29.12	19.01	19.28	20.68	21.94	21.06	18.75	20.86	32.69	18.23	23.04	25.04
III			14.87	25.91	25.72	20.41	19.06	23.51	22.03	23.82	18.58	25.77	20.23	28.02
IV				0.00	22.95	24.73	25.58	21.87	19.52	18.27	26.00	12.63	26.68	25.60
V					0.00	10.27	18.79	18.11	23.95	18.33	28.12	22.25	18.66	14.63
VI						0.00	15.84	16.51	22.34	17.56	24.12	23.53	15.68	17.91
VII							0.00	14.76	15.01	21.64	22.29	24.70	14.38	26.57
VIII								0.00	21.91	20.79	24.96	26.73	20.26	26.72
IX									0.00	22.79	23.21	15.16	19.00	27.54
X										0.00	23.37	20.02	25.78	27.77
XI											0.00	25.47	27.60	30.40
XII												0.00	25.20	22.35
XIII													0.00	21.99
XIV														0.00

Table 4 : Cluster means for growth, earliness and yield parameters in ridge gourd

SL. No	**Characters**	**I**	**II**	**III**	**IV**	**V**	**VI**	**VII**	**VIII**	**IX**	**X**	**XI**	**XII**	**XIII**	**XIV**
1	**VL**	407.85	347.89	421.08	429.00	344.00	371.50	346.86	362.50	417.54	351.83	501.24	450.67	340.46	424.83
2	**NPB**	3.04	2.59	3.38	2.50	3.50	2.84	3.67	3.00	3.16	3.17	4.07	2.50	2.50	2.67
3	**DMF**	42.45	45.90	41.45	43.26	42.75	42.26	42.60	40.83	43.35	43.00	38.60	44.00	42.52	42.00
4	**DFF**	49.39	53.34	48.78	50.31	49.69	49.10	49.22	48.17	52.10	49.33	46.60	51.96	49.69	48.17
5	**NMF**	5.37	5.70	5.33	6.00	5.32	5.16	5.23	6.22	5.06	4.67	4.59	5.05	5.59	5.67
6	**NFF**	8.21	9.38	7.98	7.16	8.00	9.50	7.66	8.67	7.66	8.33	7.16	7.50	7.50	8.00
7	**DFH**	58.45	62.85	58.18	59.67	58.35	59.00	58.62	58.24	60.88	58.00	55.17	60.29	57.82	59.44
8	**SR**	25.00	30.75	21.88	27.07	21.18	19.86	26.97	26.53	31.63	19.67	18.83	26.05	28.47	21.56
9	**NFV**	16.73	14.38	20.48	14.16	13.28	12.84	20.83	14.00	20.83	13.33	24.73	20.50	13.33	15.97
10	**AFW**	165.25	119.27	235.66	131.23	80.73	176.18	182.43	194.19	178.24	185.07	261.79	106.37	202.54	48.42
11	**FL**	20.76	17.64	41.46	24.33	15.30	20.90	25.75	20.60	24.50	25.54	27.05	20.67	29.67	12.91
12	**FD**	5.09	5.07	4.88	5.65	4.39	4.42	4.59	4.63	4.97	6.55	5.40	5.38	3.58	3.18
13	**FYV**	2.74	1.97	3.29	1.70	1.48	2.63	3.80	2.92	3.72	2.47	3.86	2.26	1.71	0.59

VL-Vine length at final harvest(cm)
NPB-Number of primary branches per vine at final harvest
DMF-Days to appearance of first male flower
DFF-Days to appearance of first female flower
NMF-Node at first male flower
NFF- Node at first female flower
DFH- Days taken to first harvest
SR- Sex ratio (M: F)
NFV- Number of fruits per vine
AFW- Average fruit weight (g)
FL- Fruit length (cm)
FD- Fruit diameter (cm)
FYV- Fruit yield per vine (kg)

higher means recorded in cluster X (6.55) followed by IV, XI and XII. The inter cluster distance between cluster X and IV (18.27), cluster X and XI (23.37), cluster X and XII (20.02) were comparatively high and for fruit length cluster with the highest mean was reported in the cluster III followed by XIII, XI and VII. The inter cluster distance between cluster III and XIII (20.23), cluster III and XI (18.58), cluster III and VII (19.06) were high (Table 4). Therefore, hybridization among the genotypes from these respective clusters can be explored to improve yield attributes. Regarding fruit yield per vine, the cluster with the maximum mean was cluster XI (3.86) followed by VII, IX and III. The inter cluster distance between cluster XI and VII (22.29), cluster XI and IX (23.21), cluster XI and III (18.58) were high (Table 4). Thus, hybridization among the genotypes within these clusters may lead to the development of superior varieties with a higher yield potential.

Based on the inter cluster distance data, crossing between the genotypes of cluster XI with genotypes of cluster II (32.69) and cluster XI with cluster XIV (30.40) is likely to be exploited for high heterosis for fruit yield per vine intern fruit yield per hectare in ridge gourd as they have high inter- cluster distance indicating high degree of diversity. Similar findings reported by Varalakshmi *et al.* (1994) , Quamruzzaman *et al.* (2008) , Choudhary *et al.* (2011) and Rabbani *et al.* (2012) also reported similar findings with respect to fruit related traits in ridge gourd.

Conclusion

In this study, genetic diversity was evaluated using Mahalanobis D^2 statistics, resulting in the formation of fourteen distinct clusters of ridge gourd genotypes. The greatest inter-cluster distance was observed between clusters II and XI (32.69), followed by clusters XI and XIV (30.40). Conversely, the smallest inter-cluster distance was between clusters V and VI (10.27). This suggests that crossing genotypes from these diverse clusters could enhance heterosis for fruit yield per vine and per hectare. Among the traits examined, fruit diameter contributed the most to the observed divergence, accounting for 27.17%, followed by average fruit weight at 15.10% and fruit length at 13.66%. This research offers valuable insights into the genetic diversity of ridge gourd hybrids, laying a strong foundation for future crop improvement efforts.

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