

Genetic Divergence in Ridge Gourd [*Luffa acutangula* (L.) Roxb.] for Growth, Earliness, Yield, Quality and Seed Parameters

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Abstract In the present study 44 genotypes of ridge gourd collected from different places in the country were evaluated for growth, earliness, yield, quality and seed parameters and genetic diversity was measured among the genotypes through D^2 statistics. Seven clusters were formed. The cluster V was the largest, comprising of 18 genotypes. Intra-cluster distance revealed that cluster V with 18 genotypes showed maximum intra-cluster diversity ($D^2 = 992.649$) and indicated that genotypes included in this cluster are very diverse. Based on distance between clusters, i.e., inter-cluster distances, the maximum divergence was observed between clusters I and VI ($D^2 = 9848.6$). Cluster II had the least inter-cluster distance ($D^2 = 118.897$) with the cluster III. This indicated close relationship among the genotypes included in the clusters II and III. Fruit yield per plant was highest contributor of the diversity

(40.69%) and the highest cluster mean for this trait was observed in the cluster VI (1404.4 g) followed by cluster V (69142 g). Diversity was also maximum ($D^2 = 7518.292$) between these clusters. Hence the crosses between genotypes of these clusters may be tried for improvement of yield.

Keywords Ridge gourd, D^2 statistics, Genetic diversity.

Introduction

Ridge gourd (*Luffa acutangula* L.) is popularly known as kalitori and also called as angled gourd, angled loofah, chinese okra, silky gourd and ribbed gourd. It belongs to genus *Luffa* of *Cucurbitaceae* family and has a chromosome number $2n = 26$. The genus derives its name from product loofah which is used in bathing sponges, doormats, pillows and also cleaning utensils. The genus *Luffa* comprises seven species out of which only two are important and economically cultivated vegetables viz ridge or ribbed gourd [*Luffa acutangula* (L.) Roxb.] and sponge gourd (*Luffa cylindrica* Roem). Both species contains gelatinous compound called luffein and has medicinal importance. It is emetic and traditionally used for the treatment of stomach ailments and fever [1].

Ridge gourd is a climber with long tap root system and leaves green, simple and ovate with five to

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Table 1. Cluster classification and source of collection of 44 genotypes based on D^2 analysis.

Clusters	Number of genotypes	Genotypes included in the cluster
I	15	IC-92637, IC-92638, IC-92645, IC-105579, IC-344652, IC-385911, IC-385912, IC-385915, IC-397606, IC-398591 (NBPGR, New Delhi), DMRG-1 and DMRG-15 (UAS, Dharwad), Kadahatti Local and ERG-1 (KRCCH, Arabhavi) and NS-474 (Namdhari Seed)
II	2	Dalasanur Local and Green Long (KRCCH, Arabhavi)
III	2	ERG-2 (KRCCH, Arabhavi) and Malada (Mritunjaya Seeds)
IV	2	NS-3 (Namdhari Seed) and Chintamani Local (KRCCH, Arabhavi)
V	18	DMRG-3, DWD-2, DMRG-44 and DMRG-14 (UAS, Dharwad,) KRCCH-1 Srinivasapur Local, Ghataprabha Local, Ponoor Local, Mudigere Local, ERG-3, ERG-4, IC-92637 and Vijaywada Local (KRCCH, Arabhavi), Jaipur Long-1 (Mritunjaya Seeds), Jaipur Long-2 (Classic Seeds), Jaipur Long-3 (Annadhata), Jaipur Long-4 (Dhisha crop tech) and Rekha (Ankur Seeds)
VI	2	Arka Sujat and Arka Summet (IIHR, Bangalore)
VII	3	Kolar Local (KRCCH, Arabhavi), DMRG-1 and DWD Local (UAS, Dharwad)

seven lobes. Though cultivated species are monoecious in nature different sex forms viz., androecious, gynoecious, gynomonoecious, and romonoecious and hermaphrodite plants are also reported Choudhary and Thakur [2].

Improvement in yield and quality is normally achieved by selecting genotypes with desirable character combinations existing in the nature or by hybridization. Selection of parents identified on the basis of divergence analysis would be more promising for a hybridization program. The D^2 statistics developed by Mahalanobis [3] used to measure of magnitude of divergence between two genotypes under comparison. Grouping of genotypes based on D^2 analysis will be useful in choosing suitable parental lines for heterosis breeding which intern can help farmers by making available the elite varieties. The present investigation was conducted by keeping an objective to study the nature and extent of divergence in ridge gourd for growth, earliness, yield, quality and seed parameters.

Materials and Methods

The experiment was conducted in the field of vegetable science unit of Kittur Rani Channamma Col-

lege of Horticulture, Arabhavi, Belagavi District (Karnataka) during the year 2013-14. Forty four genotypes of ridge gourd were grown in randomized complete block design with two replications. The seeds of all genotypes were sown at the spacing of 1.2 × 0.9 m. In each plot, there were 10 plants (in a row) with net plot area 10.8 square meters. All the other recommended cultivation practices were followed as per the Package of practices of UHS, Bagalkot [4]. Five randomly chosen plants in each replication of each entry were labeled and used for recording the observations for the growth parameters viz., vine length (cm) at 45 and 90 days after sowing (DAS), number of branches at 45 and 90 DAS and number of leaves at 45 and 90 DAS. Earliness parameters viz., days to first male and female flowering, node up to first male and female flowering, days to 50% flowering, days to first and last harvest and sex ratio. Yield parameters viz., fruit length (cm), fruit diameter (mm), per cent fruit set, number of fruits per plant, average fruit weight (g), fruit yield per plant (g), fruit yield per plot (kg) and fruit yield per hectare (t/ha). Fruit quality and seed parameters viz., rind thickness (mm), flesh thickness (cm), number of ridges per fruit, seed yield per fruit (g), hundred seed weight (g) and number of seeds per fruit were recorded.

Table 2. Average intra and inter-cluster D^2 values along with their D values (in parenthesis) for 28 characters formed by 44 genotypes of ridge gourd. Diagonal values indicate intra-cluster distances.

Clusters	I	II	III	IV	V	VI	VII
I	724.273 (26.912)	662.919 (25.747)	484.926 (22.021)	703.861 (26.530)	1038.92 (32.232)	9848.6 (99.240)	1125.429 (33.547)
II		72.103 (8.491)	118.897 (10.904)	157.01 (12.530)	755.755 (27.491)	8982.527 (94.776)	416.128 (20.399)
III			76.679 (8.757)	166.21 (12.892)	704.529 (26.543)	9240.632 (96.128)	493.644 (22.218)
IV				80.711 (8.984)	720.995 (26.851)	8059.989 (89.777)	263.891 (16.245)
V					992.649 (31.506)	7518.292 (86.708)	927.288 (30.451)
VI						94.087 (9.700)	7125.01 (84.410)
VII							429.452 (20.723)

Mahalanobis [5] D^2 statistic was used for assessing the genetic divergence between different populations. All the $n(n-1)/2D^2$ values were clustered using Tocher's method [6]. The intra and inter-cluster distances were calculated by the methods of Singh and Choudary [7]. The analysis was done using the program GENRES.

Results and Discussion

Forty four genotypes were grouped into seven clusters [8]. Cluster classification and source of collection of 44 genotypes based on D^2 analysis is given in Table 1. Of the seven clusters studied the cluster V was the largest, comprising of 18 genotypes followed by cluster I with 15 genotypes. The clusters II, III, IV and VI comprised two genotypes in each and the cluster VII comprised with three genotypes.

The average D^2 values of intra and inter cluster distance are given in Table 2. Intra-cluster distance revealed that cluster V with 18 genotypes showed maximum intra-cluster diversity ($D^2 = 992.649$) followed by cluster I ($D^2 = 724.273$), cluster VII ($D^2 = 429.452$) and cluster VI ($D^2 = 94.087$). Cluster II showed minimum ($D^2 = 72.103$) intra-cluster diversity. Maximum intra-cluster diversity indicating existence of wide genetic divergence among the constituent genotypes in it as compared to other cluster. High degree of divergence among the genotypes within a cluster would produce more segregating

breeding material and selection within such cluster might be executed based on maximum mean values [8—10].

Based on distance between clusters i.e., inter-cluster distances, the maximum divergence was observed between clusters I and VI ($D^2 = 9848.6$) followed by clusters III and VI ($D^2 = 9240.632$), cluster II and VI ($D^2 = 8982.527$), cluster IV and VI ($D^2 = 8059.989$), cluster V and VI ($D^2 = 7518.292$), cluster VI and VII ($D^2 = 7125.01$), cluster I and VII ($D^2 = 1125.429$) and cluster I and V ($D^2 = 1038.92$). Cluster II had the least inter-cluster distance ($D^2 = 118.897$) with the cluster III. This indicated close relationship among the genotypes included in the clusters II and III. Maximum inter-cluster D^2 value was observed between the clusters I and VI indicating that the genotypes in these clusters can be used as parents in hybridization program to get higher heterotic hybrids and segregating population contribution of characters [8, 11].

These clusters have been formed based on the contribution of different characters to the divergence. Mean value of 28 characters for seven clusters along with relative per cent contribution of different characters to divergence is given in Table 3. Fruit yield per plant (40.69 %) contributed maximum towards expression of genetic divergence followed by fruit yield per plot (27.48%), seed yield per fruit (7.92%) and highest cluster mean for this traits were

Table 3. The mean values and percent contribution of 28 characters for seven clusters in ridge gourd. # : Contribution of individual character towards total genetic divergence (%) 1. Vine length at 45 DAS 2. Vine length at 90 DAS 3. Number of branches at 45 DAS 4. Number of branches at 90 DAS 5. Number of leaves at 45 DAS 6. Number of leaves at 90 DAS 7. Days to first male flowering 8. Days to first female flowering 9. Node up to first male flowering 10. Node up to first female flowering 11. Days to 50% flowering 12. Days to first harvest 13. Days to last harvest 14. Sex ratio 15. Fruit length (cm) 16. Fruit diameter (cm) 17. Per cent fruit set 18. Number of fruits per plant 19. Average fruit weight (g) 20. Fruit yield per plant (g) 21. Fruit yield per plot (kg) 22. Fruit yield per hectare (t/ha) 23. Rind thickness (mm) 24. Flesh thickness (cm) 25. Number of ridge per fruit 26. Seed yield per fruit (g) 27. 100 seed weight (g) 28. Number of seeds per fruit.

Char- acters	I	II	III	IV	Clusters V	VI	VII	#
1	126.64	172.15	152.55	165.65	148.5	175.95	173.23	0.1057
2	237.76	281.5	265.5	296.5	269.77	384.75	310.83	0
3	2.02	2.1	1.9	2.2	2.1	2.2	2.13	0
4	4.26	4.7	4.75	4.9	4.66	6.5	5.1	0
5	21.3	21.85	23.25	23.35	23.25	29.8	26.1	0
6	68.92	84.2	78.25	89.65	79.58	141.35	103.03	3.5941
7	34.5	36.25	37.1	35.9	35.78	39.4	35.43	0
8	40.75	41.95	40	41.12	41.38	45.1	41.03	0
9	3.18	3.15	3.4	3.05	3.36	3.6	3.36	2.1142
10	8.25	10.1	9.7	9.55	9.5	13	9.9	0.1057
11	40.3	40.6	41.15	41.05	40.7	41.7	40.53	0
12	52.57	52.5	52.4	54.45	52.26	55.35	51.93	0.7400
13	82.47	81.6	81.85	82.85	81.88	88.2	81.7	0.1057
14	6.884	6.672	6.085	6.372	8.532	21.785	7.365	0
15	14.82	17.77	18.9	19.45	18.55	21.75	20.1	0.2114
16	38.578	41.362	39.22	41.205	41.941	46.415	41.565	0.2114
17	65.521	63.302	66.315	63.112	65.42	77.05	62.888	2.1142
18	5.32	5.95	6	5.85	6.01	7.5	5.76	0.8457
19	83.8	80.7	79.7	78.35	97	174.5	82.46	2.6427
20	484.16	497.65	504.85	487.55	691.42	1404.4	597.96	40.6977
21	4.846	4.975	5.048	4.47	6.91	14.038	6.14	27.4841
22	4.483	4.6	4.668	4.503	6.394	12.99	5.525	2.6427
23	3.85	4.086	3.912	3.831	3.828	3.613	3.777	3.1712
24	3.059	3.105	3.055	3.04	3.029	3.035	3.057	3.3827
25	10.02	10.05	10	10	10.02	10	10	0.3171
26	7.989	6.183	7.336	8.434	8.234	15.031	8.695	7.9281
27	11.635	11.916	10.707	12.363	11.952	13.648	12.255	1.2685
28	65.21	65.05	76.5	78.2	70.4	105.05	75.46	0.3171

observed in the cluster VI (1404.4 g, 14.03 kg and 15.031 g respectively) followed by cluster V (691.42 g, 6.91 kg and 8.23 g respectively) and cluster VII (597.96 g, 6.14 kg and 8.69 g respectively). The inter-cluster distance between cluster V and cluster VI ($D^2 = 7518.292$) and cluster VI and cluster VII ($D^2 = 7125.01$) were comparatively high. therefore, it would be logical to attempt cross among these genotypes belonging to these clusters so as to evolve progenies with high fruit yield per plant, fruit yield per plot and seed yield per fruit [12].

The characters like number of leaves at 90 DAS (3.59%) [13], flesh thickness (3.38%) and rind thick-

ness (3.17%) were contributed slightly towards expression of total genetic diversity. While, number of branches at 45 DAS, number of leaves at 45 DAS, vine length at 90 DAS, number of branches at 90 DAS, days to first male and female flowering, days to 50% flowering and sex ratio had no contribution for diversity.

The study also indicated that the characters such as number of leaves at 90 DAS and flesh thickness should also be considered while selecting parents for hybridization as they are important contributors of genetic divergence. For number of leaves at 90 DAS highest cluster mean was observed in the clus-

ter VI followed by cluster VII. For flesh thickness highest cluster mean for this character was observed in the cluster II followed by cluster I.

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