

Genetic divergence in hermaphrodite ridge gourd (*Luffa acutangula*)

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Abstract The present investigations were carried out on 35 genotypes collected from different locations of India and evaluated for 8 quantitative traits. A wide range of variability in shape (long, round, oblong) and colour (green, light green, dark green) of hermaphrodite ridge gourd [*Luffa acutangula* (Roxb.) L.] fruits exist in India. The studied genotypes were grouped in to four clusters irrespective of geographic divergence, indicating no parallelism between geographic and genetic diversity. Cluster IV was very large containing 16 genotypes, while cluster III was represented by three genotypes. The maximum inter-cluster distance was recorded between cluster II and IV, while minimum distance was between cluster I and II. Cluster IV showed superiority for fruit yield per plant which indicates the potentiality of these genotypes, providing basic material for future improvement breeding programmes of hermaphrodite ridge gourd.

Introduction

The genus *Luffa* has essentially old world origin in subtropical Asia region particularly India (Kalloo, 1993). Plants are monoecious, andromonoecious, hermaphrodite and having gynoeceous sex form (Richharia, 1948; Choudhury and Thakur, 1965). Hermaphrodite ridge gourd is an important under-utilized cucurbitaceous crops grown for tender fruits and consumed as vegetable (Chandra, 1995). Fruits of *Luffa* spp are very nutritious and good source of vitamin A, calcium, phosphorus, ascorbic acid and iron (Aykroyd, 1963). Medicinally used as toothache, disinfectant, anti-helminthic, anti-diarrhea, anti-syphilitic, purgative, cordio tonic, laxative and also potentially cure to diabetes and hypertension.

Plants bear hermaphrodite flowers in cluster. It is being commercially cultivated in Bihar and Uttar Pradesh in both summer and rainy seasons (Choudhary *et al.*, 2007). India particularly Northern-Eastern parts, endowed with a wide range of diversity in fruit shape and size in this crop (Choudhary *et al.*, 2009). Despite its economic importance and presence of considerable variability, no systematic information is available on the genetic amelioration of hermaphrodite ridge gourd. The explorations of northern eastern part of India have been taken and variable samples have been collected from the local growers. The collected materials have been selfed up to 3 consequent generations for purification. Identification of superior genotypes among the existing germplasm becomes imperative for promoting improvement in yield and yield related traits. Multivariate analysis is a potent tool for measuring divergence among a set of populations based on multiple characters. D² statistic proposed by Mahalanobis (1936) 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. Considering these points, the present investigation was undertaken to assess the multivariate components of genetic divergence in a set of 35 genotypes of hermaphrodite ridge gourd.

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Materials and Methods

The experimental material comprised of 35 diverse genotypes of hermaphrodite ridge gourd selected from purified materials, which were maintained at IIVR Seed Production Centre, Sargatia, Kushinagar (Uttar Pradesh), India. The selection of lines was based on genetic as well as eco-geographical diversity. The experiment was laid out in a Randomized Block Design (RBD) with three replications at IIVR Seed Production Centre, Sargatia, Kushinagar (UP) during rainy season of 2008 and 2009. Sowing was done at hill keeping spacing of 2.5m between rows and 0.5cm within rows. The recommended NPK fertilizer doses and cultural practices along with plant protection measures were followed to raise an ideal crop (De *et al.*, 2003). The observations were recorded on 8 quantitative traits *i.e.*, node at which

1st hermaphrodite flower appeared, days to 1st hermaphrodite flower, days to first fruit harvest, number of fruits per cluster, fruit length (cm), fruit weight (g), number of fruits per plant and yield per plant (kg) from five randomly selected plants in each line and replication. The fruits were harvested at marketable stage and size. Data were averaged and statistically analyzed for genetic divergence according to D² analysis of Mahalanobis (1936). Based on the D² values the genotypes were grouped in to various clusters according to Tocher's method (Rao, 1952). The unweighted pair group method with arithmetic averages (UPGMA) based dendrogram was constructed using the SAHN module of the software. The MXCOMP module of NTSYSpc was used to compare the Jaccard's (1908) average taxonomic distance values derived from 8 quantitative characters.

Table 1: Mean performance of 35 genotypes

Genotypes	Node at which 1 st hermaphrodite flower appeared	Days to 1 st hermaphrodite flower	Days to first fruit harvest	number of fruits/ cluster	Fruit length (cm)	Fruit weight (g)	Number of fruits/ plant	Yield/ plant (kg)
VRS-1	6.40	41.13	45.07	5.93	16.42	31.78	147.53	4.69
VRS-2	7.33	50.87	51.40	5.00	12.42	28.81	134.13	3.87
VRS-3	8.47	51.07	56.67	4.07	10.28	31.99	122.93	3.92
VRS-4	6.60	49.60	53.13	4.33	12.40	30.64	126.67	3.88
VRS-5	8.20	52.13	57.27	4.13	14.48	31.18	133.33	4.16
VRS-6	7.27	48.47	54.73	4.40	11.65	26.82	138.27	3.71
VRS-7	6.47	43.00	48.33	5.27	15.60	33.64	129.80	4.36
VRS-8	7.20	47.07	52.47	4.07	11.73	26.13	140.13	3.66
VRS-9	7.40	50.33	55.87	4.00	12.66	27.87	136.87	3.81
VRS-10	7.53	51.27	55.20	4.13	13.34	29.34	137.67	4.04
VRS-11	7.20	44.33	50.60	5.20	14.69	38.64	122.94	4.67
VRS-12	7.27	47.93	53.13	3.93	13.35	29.92	126.13	3.77
VRS-13	6.40	49.87	53.93	4.20	12.89	25.33	136.67	3.46
VRS-14	7.47	48.73	53.27	4.40	14.28	24.53	141.53	3.47
VRS-15	8.53	50.33	61.03	4.27	13.98	26.55	142.40	3.78
VRS-16	9.33	48.60	53.47	5.07	12.27	23.68	138.27	3.27
VRS-17	8.27	52.67	57.67	4.53	14.50	20.95	141.87	2.96
VRS-18	9.20	50.87	54.33	5.00	12.25	26.01	143.47	3.73
VRS-19	7.10	48.13	53.40	4.20	12.27	25.86	145.27	3.76
VRS-20	13.53	50.87	54.27	4.93	14.16	27.82	135.53	3.77
VRS-21	6.47	46.60	51.40	4.27	11.50	28.48	142.67	4.06
VRS-22	6.90	46.33	51.27	4.60	11.22	23.92	140.80	3.37
VRS-23	8.67	51.13	56.87	4.53	13.81	25.49	141.27	3.60
VRS-24	7.53	50.00	54.13	4.40	3.90	18.95	145.20	2.75
VRS-25	8.20	51.07	55.20	4.13	4.84	19.29	143.53	2.77
VRS-26	6.47	48.87	52.13	4.20	4.88	18.42	128.67	2.37
VRS-27	7.33	47.27	51.67	4.00	4.81	20.15	146.93	2.96
VRS-28	8.40	50.20	54.33	5.07	13.77	29.22	145.73	4.25
VRS-29	6.47	46.53	51.40	4.33	12.24	27.30	138.93	3.79
VRS-30	6.53	46.07	51.60	4.60	12.47	28.69	143.80	4.12
VRS-31	8.33	49.33	53.13	4.40	12.40	25.82	144.67	3.73
VRS-32	8.27	45.93	50.47	4.47	13.60	29.53	139.87	4.12
VRS-33	9.40	50.13	55.60	3.87	12.72	28.59	142.27	4.07
VRS-34	8.60	51.07	56.13	4.53	11.80	27.35	143.20	3.92
VRS-35	7.47	49.20	53.60	4.87	13.47	29.12	139.33	4.06
CD (<i>P</i> =0.05)	1.45	5.31	3.67	0.95	1.26	5.52	17.07	0.83

Table 2: Clustering pattern of hermaphrodite ridge gourd genotypes

Cluster No.	Genotypes in the clusters	Genotypes and their source
I	12	VRS-2 (Deoria, UP), VRS-4 (Gorakhpur, UP), VRS-6 (Varanasi, UP), VRS-8 (Gopalganj, Bihar), VRS-12 (Kushinagar, UP), VRS-13 (West Champaran, Bihar), VRS-14 (Deoria, UP), VRS-21 (Basti, UP), VRS-22 (Kushinagar, UP), VRS-29 (Deoria, UP), VRS-30 (Balai, UP), VRS-32 (Kushinagar, UP).
II	4	VRS-24 (Deoria, UP), VRS-25 (Kushinagar, UP), VRS-26 (Varanasi, UP), VRS-27 (West Champaran, Bihar).
III	3	VRS-1 (Kushinagar, UP), VRS-7 (Deoria, UP), VRS-11 (Gorakhpur, UP).
IV	16	VRS-3 (Basti, UP), VRS-5 (Gopalganj, UP), VRS-9 (Varanasi, UP), VRS-10 (Mau, UP), VRS-15 (Gorakhpur, UP), VRS-16 (West Champaran, Bihar), VRS-17 (Deoria, UP), VRS-18 (Kushinagar, UP), VRS-19 (East Champaran, Bihar), VRS-20 (West Champaran, Bihar), VRS-23 (Kushinagar, UP), VRS-28 (Gorakhpur, UP), VRS-31 (Deoria, UP), VRS-33 (Gopalganj, UP), VRS-34 (Varanasi, UP), VRS-35 (Kushinagar, UP).

Results and Discussion

The data on mean performance of the genotypes with respect to flowering, yield and yield associated traits were presented in table 1. Hermaphrodite flower on earliest node was observed on 6.40 node in the genotype VRS-1 and VRS-13. In addition to early node flowering, VRS-1 was very early in appearance of female flower (41.13 days after seed sowing), whereas, VRS-17 was recorded to be late in flowering (60 days after seed sowing). The first harvesting was started after 45 days of seed sowing. The genotype VRS-1 exhibited maximum number of fruits per cluster (5.93) as well as per plant (147.53). The genotype VRS-1 also had maximum fruit length and yield. While genotype VRS-11 exhibited maximum fruit weight. The analysis of variance for 8 quantitative traits showed significant differences among 35 genotypes indicating the existence of genetic diversity. The fruit shape was found to be long, round and oblong, whereas fruit color was recorded as green, light green and dark green.

Table 3: Average inter and intra-cluster distances (D^2)

Clusters	Cluster I	Cluster II	Cluster III	Cluster IV
Cluster I	1.458	2.086	3.972	6.182
Cluster II		0.892	4.861	7.867
Cluster III			1.714	3.860
Cluster IV				1.814

Table 4: Cluster mean for different traits

Cluster No.	Node at which 1 st hermaphrodite flower appeared	Days to 1 st hermaphrodite flower	Days to first fruit harvest	No. of fruits/cluster	Fruit length (cm)	Fruit weight (g)	No. of fruits/plant	Yield/plant (kg)
I	6.99	47.83	52.35	4.38	12.48	27.51	137.47	3.74
II	7.38	49.30	53.28	4.18	4.61	19.20	141.08	2.71
III	6.69	42.82	48.00	5.47	15.57	34.82	133.42	4.57
IV	8.67	50.46	55.55	4.48	13.01	27.30	139.63	3.80
Overall Mean	7.43	47.60	52.29	4.63	11.42	27.50	137.90	3.70

Thirty-five genotypes were grouped in to four clusters when analyzed with Tocher's method of D^2 analysis (Table 2). It was apparent that 12 genotypes grouped in cluster I, 4 in cluster II, 3 in cluster III and 16 in cluster IV. The D^2 values between each pair of genotypes were estimated after confirming that the genotypic differences were highly significant for all the quantitative traits under study (Table 3). Among four clusters the intra-cluster distance varied from 0.892 to 1.814. The maximum inter-cluster distance exhibited between the cluster II and cluster IV. The inter-cluster distance was lowest between clusters I and II.

The differences in cluster means existed for all the characters (Table 4). Cluster III showed desirable values for days to first fruit harvest (48 days after seed sowing), days to 1 hermaphrodite flower (42.82 days after seed sowing), fruit weight (34.82g), fruit length (15.57cm) and node at which 1 hermaphrodite flower appeared (6.69). Fruit yield per plant, the most important economic trait was also maximum for cluster III (4.57kg) followed by cluster IV (3.80kg). Number of fruit per plant was found to be maximum in cluster II (141.08) followed by cluster IV (139.63).

The taxonomic distance matrix of 8 quantitative traits for the 35 genotypes was employed for cluster analysis and a dendrogram was constructed (Figure 1); all the genotypes grouped into four major clusters. In the dendrogram, the longest branch separates genotype VRS-1 and VRS-7 from all the genotypes at a taxonomic

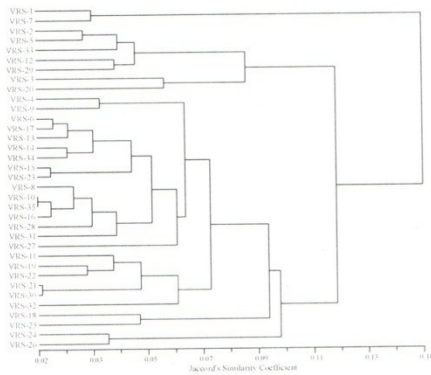


Fig. 1: Genetic relationship among the 35 genotypes hermaphrodite ridge gourd on the basis of 8 quantitative traits using UPGMA cluster analysis of the distance matrix

distance of 0.14 and these genotypes were the only member of the cluster I. At the taxonomic distance of 0.12, the next node resolved rest of the 7 genotypes as cluster II. The cluster III was major cluster, which can be further divided into 4 sub clusters. The sub cluster IIIA had 2 genotypes, *viz.*, VRS-4 and VRS-9. The sub cluster IIIB included 14 genotypes. The sub cluster IIIC and IIID has 6 and 2 genotypes, respectively. While the genotype, VRS-24 and VRS-26 comes under cluster IV.

Germplasm characterization is an important component of breeding programme for an effective and efficient management / utilization of plant genetic resources. Morphological characterization has been used for assessment of relationships and estimating genetic diversity among *Luffa hermaphrodita* genotypes (Choudhary *et al.*, 2007 & 2009). The germplasm used in the present study showed a wide variation in morphological traits *viz.*, fruit shape (long, oblong and round), color (green, light green and dark green) and fruit size. As expected, the number of fruits per plant was more in the genotypes with more number of fruits per cluster. Genotype, VRS-1 and VRS-11 showed maximum potential for yield per plant due to their fruit length and number of fruits per cluster; owing to its superior yield, the accession, VRS-1 has recently been identified for pre-released for commercial cultivation and multi-location testing (Choudhary *et al.*, 2010). The genotype VRS-1 could be utilized in future breeding programme for development of high yielding cultivars. Yield per plant showed maximum deviation from their mean and some of the traits like fruit weight, fruit length and number of fruits per plant showed significant

variation within the genotype indicating the role of environment in expression of these traits. In case of hermaphrodite ridge gourd, cluster bearing is important traits and most of the genotypes are very small fruited. Genotype VRS-1 has cluster bearing character coupled with more length of fruits makes it more attractive to consumers (Choudhary *et al.*, 2010).

Genotypes were grouped into 4 clusters mainly considering the wide variation in length of fruits. Genotype VRS-1 and VRS-11 has been grouped into the same cluster as both the genotypes have maximum number of fruits per plant and number of fruits per cluster. The minimum fruit length was recorded in VRS-25, VRS-26 and VRS-27, grouped in same cluster. Among four clusters the intra-cluster distance varied from 0.892 to 1.814. The relatively low values of intra-cluster distance depicted the presence of genetic diversity within a cluster. The lines grouped in to cluster IV were relatively most diverse than clusters II, as intra cluster distance was very high. Therefore, selection of parents for hybridization should be done from cluster IV having wide inter-cluster distance indicating more variability. The inter-cluster distance was lowest between clusters I and II, thus these should not be used for recombinant breeding.

The differences in cluster means existed for all the characters (Table 4). The mean value in cluster III was found to be maximum for fruit weight, fruit length and fruit yield per plant. Genotypes of cluster III also have desirable mean values for days to first fruit harvest, days to first hermaphrodite flower and node at which first hermaphrodite flower appeared. So, it may be concluded that there is a vast scope to develop new varieties with more yield potential and other attributes of economic importance by using germplasm collection grouped under cluster III. To develop early varieties with more yields, selection from cluster III will be more effective as it showed higher yield coupled with early maturity. The genotypes included in the diverse clusters namely II and IV could be effectively utilized in hybridization for generating highly diverse recombinant materials to improve yield and horticultural traits in hermaphrodite ridge gourd. The genotypes of the highly divergent clusters may also be utilized in different crossing fashion for effective exploitation of heterosis (Rao *et al.*, 2003).

In the dendrogram based on the quantitative traits, the genotypes VRS-1 and VRS-7 separated from VRS-24 and VRS-26 as they fall either side of the dendrogram, indicating high genetic diversity among these 4 genotypes. Similarly, the genotypes VRS-1 and VRS-7 were grouped in the cluster III and VRS-24 and VRS-

26 in the cluster II. It's indicated that the clustering of genotypes is almost similar as in case of D² or UPGMA cluster analysis. This vegetable is grown only in eastern parts of India, hence during grouping or clustering, genotypes were not separated on the basis of collection place. The wide range dissimilarity values suggested that the germplasm collection represent genetically diverse population (Pandey *et al.*, 2008).

In general, the pattern of distribution of genotypes from different regions into different clusters was random. This absence of relationship between genetic diversity and geographical distance indicates that factors other than geographical origin, such as exchange of genetic stocks, genetic drift, spontaneous variation, natural and artificial selection are responsible for genetic diversity. Therefore, selection of genotypes for hybridization should be based on genetic diversity rather than geographic divergence. Similar observations were also reported in ridge gourd (Varalakshmi *et al.*, 1994), bitter gourd (Wahab and Gopalakrishnan, 1993, Pandey *et al.*, 2008 and Dey *et al.*, 2007) and cucumber (Rao *et al.*, 2003).

The morphological traits are controlled by a number of genes and are highly influenced by the environment, whereas molecular markers are not confounded by the environmental effects. For more efficient determination of genetic diversity in hermaphrodite ridge gourd germplasm with the morphological traits, molecular system could be utilized. Nevertheless, the information about the genetic diversity in the 35 genotypes of hermaphrodite ridge gourd could be successfully utilized in further breeding programmes.

सारांश

भारत के विभिन्न क्षेत्रों से एकत्रित किये गये 35 प्रभेदों में आठ संख्यात्मक गुणों का अध्ययन किया गया। भारत में उभयलिगी तरौई के फलों के आकार (ल. गोलाई, उर्ध्वाकार) एवं रंग (हरा, हल्का हरा, गहरा हरा) में विस्तृत विभिन्नता दिखाई दिये भौगोलिक विभिन्नता के आधार पर अध्ययन किये गये प्रभेदों को 4 समूहों में बांटा गया है। जो कि प्रदर्शित करता है कि भौगोलिक एवं जनीनिक विभिन्नता में कोई समानता नहीं है। समूह 4 में सबसे ज्यादा 16 प्रभेद पाये गये जबकि समूह-3 में 3 प्रभेद प्रदर्शित हुए। सबसे ज्यादा अन्तर-समूह विस्तार समूह 2 एवं समूह 4 में पाया गया जबकि समूह 1 एवं 2 में सबसे कम, समूह 4 फल उपज प्रति पौध के आधार पर प्रदर्शित करता है कि इसके प्रभेद सबसे ज्यादा उत्पादक है। यह समूह भविष्य में प्रजनन सुधार कार्यक्रम के लिए उभयलिगी तरौई के मूल पदार्थ प्रदान कर सकता है।

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