SAARC J. Agri., 10(2): 01-10 (2012)

VARIABILITY, CHARACTER ASSOCIATION AND DIVERSITY ANALYSIS OF RIDGE GOURD (*luffa acutangula* Roxb.) GENOTYPES OF BANGLADESH

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ABSTRACT

Sixty genotypes of ridge gourd (*Luffa acutangula* Roxb.) were collected from different locations of Bangladesh and were used to study their variability, character association and genetic diversity. Seventeen traits studied, of these, eight showed high heritability (over 80%). Correlation coefficient study indicated that yield per plant had highly significant positive relationship with the number of fruits per plant (r = 0.874**), average fruit weight (r = 0.707**), vine length at harvest (r = 0.359**) and length of fruit (r = 0.334**). On the other hand, the sex ratio and circumference of fruit exhibited negative association with yield. Path co-efficient analysis showed that number of fruits per plant exhibited the highest positive direct effect (0.7192) on yield followed by average fruit weight (0.4656). Based on Mahalanobis' D^2 statistics, the sixty genotypes were grouped into four different clusters. Clustering pattern revealed that genotypes collected from the same location were grouped into different clusters. The average intercluster distances were always higher than the average intracluster distances suggesting wider genetic diversity among the genotypes within the cluster. Custer-III had the highest intracluster distance (97.9).

Keywords**:** Variability, character association, ridge gourd, diversity analysis.

INTRODUCTION

Ridge gourd (*Luffa acutangula*) is one of the most important vegetables available during summer season of Bangladesh when there is a scarcity of vegetables. It is rich in vitamin A, C and iron (Fe) (Yawalkar, 1985). It has great medicinal value. A glycoprotein was isolated from seeds of *L. acutangula*, which was found to be immunologically distinct from abortifacient proteins isolated from other members

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Received: 08.02.2012

of the Cucurbitaceae family (Yeung *et al.*, 1991). The luffaculin, a protein isolated from its seed, exhibited abortifacient, antitumor, ribosome inactivating and immunomodulatory activities (Ng *et al.*, 1992). Another ribosome inactivating peptide isolated from seeds of ridge gourd designated luffangulin inhibited cell-free translation (Wang and Ng, 2002). *L. acutangula* Linn contains trypsin inhibitors (Haldar *et al.*, 1996). Recently, this crop has been tested for its antioxidant (free radical scavenging-FRS) activity confirming the great interest of the nutraceutical sciences (Ansari *et al.*, 2005). Effectiveness of its extract as larvicide (Prabakar and Jebanesan, 2004) and its seed oils as grain protectant against certain insects are not very far discoveries (Mishra *et al.*, 2007). So far, 106 local landraces of *L. acutangula* have been reported in Bangladesh (Rabbani, 2007). The average yield of the crop in Bangladesh is about 1.83 mt per acre in 2007-2008 (BBS, 2008) indicating low yield performances of the cultivars. Several factors are responsible for such a low yield. Varietal uniformity is one of the main requirements for the improved cultivars. Variability, on the other hand, is highly desired in germplasm collection and conservation purposes as genetic variation may exist or created, is the first step to any crop improvement programme (Singh, 2000). Knowledge of genetic diversity among existing cultivars of any crop is essential for long-term success in breeding program and to maximize the exploitation of the germplasm resources (Belaj *et al.*, 2002). Growing interest to this vegetable crop was achieved through studies on its constituents, but no systematic research has so far been done to evaluate the potentialities of the available germplasm with a view to releasing modern varieties to meet increasing demands to come. Under such circumstances, this study was conducted to assess the variability among the 60 genotypes of ridge gourd collected from different parts of Bangladesh for yield and yield contributing characters, their interrelationship and genetic diversity through biometrical procedures.

MATERIALS AND METHODS

A total of 60 ridge gourd landraces were used in this study. The materials were collected from 16 locations which represent four major divisions of Bangladesh (Figure.1). The experiment was laid out in the Randomized Complete Block Design (RCBD) with three replications. One accession represented one treatment and three plants in an accession represented one replication. Data on seventeen characters covering stem, leaf, flower, fruit and seeds were recorded from the studied plants. Computation of the data was carried out using MSTAT-C program. Genotypic and phenotypic coefficient of variation was calculated as described by Burton (1952). Heritability was estimated according to Lush (1943). Simple correlation co-efficient was worked out according to Singh and Chaudhury (1985). Path coefficient analysis was carried out following the procedure employed by Dewey and Lu (1959) using simple correlation values. Analysis of genetic divergence was done according to Mahalanobis' D^2 (1936) statistics.

RESULTS AND DISCUSSION

Different variability parameters estimated in seventeen traits are presented in table1. Range of all traits revealed that there was a wide variation in the collected genotypes. Genotypic co-efficient of variation (GCV) was always smaller than phenotypic coefficient of variation (PCV) indicating the effect of environment to some extent in the expression of the characters. However, dry weight of flesh, the GCV (25.89%) and the PCV (26.71%) differed with very narrow margin showing little environmental effect. That is why the character was highly heritable (97.89%). On the contrary, the trait peduncle length was severely affected by the surrounding environment as revealed by the wide difference in GCV (21.25%) and PCV (29.52%) values. As a result, the character showed very low heritability (51.85%). The yield ranged from 307.5 g to 2467.5 g with the average of 952.77 g per plant. Low difference between the GCV (58.0%) and the PCV (59.67%) and the high heritability (94.16%) indicated a little contribution of environment to the phenotype. Out of seventeen characters, eight were found highly heritable (above 80%) and the rest had medium heritability (50-80%).

Table1. Range, mean and heritability of seventeen characters of 60 ridge gourd genotypes

Characters	Range	Mean ± SE	GCV (%)	PCV (%)	Heritability in broad sense (%)
Vine length at harvest (cm)	235.4 – 955.5	548.58 ± 70.69	29.61	33.55	77.70
Leaf length (cm)	6.95 – 16.0	12.26 ± 0.97	18.23	20.64	78.04
Leaf breadth (cm)	12.00 – 27.40	18.90 ± 2.16	16.59	21.72	58.38
Petiole length (cm)	3.35 – 13.80	7.87 ± 1.67	26.38	32.04	67.82
Internode length (cm)	24.00 – 46.70	32.91 ± 2.22	14.75	16.90	77.61
Primary branch at harvest	15.67 – 42.67	29.94 ± 2.74	22.24	24.90	79.78
Male: Female flower	14.74 – 41.62	24.89 ± 2.20	31.14	32.69	90.71
Length of fruit (cm)	8.00 – 34.67	19.16 ± 2.74	26.54	31.81	69.63
Fruit circumference (cm)	8.95 – 20.67	11.66 ± 1.47	20.23	25.43	63.27
Peduncle length (cm)	2.67 – 11.17	7.69 ± 1.29	21.25	29.52	51.85
Dry weight of flesh (g)	3.50 – 11.12	5.58 ± 0.17	25.89	26.71	97.89
Seed length (cm)	0.93 – 1.29	1.11 ± 0.02	7.52	8.04	87.50
Seed breadth (cm)	0.58 – 0.80	0.68 ± 0.02	12.29	13.13	87.50
100-seed weight (g)	5.75 – 16.46	11.67 ± 0.63	18.62	19.76	88.66
No. of fruit per plant	4.67 – 19.00	9.96 ± 0.76	39.28	40.36	94.69
Average fruit weight (g)	39.73 – 173.69	93.31 ± 7.98	31.56	33.25	90.07
Fruit yield per plant (g)	307.5 – 2467.5	952.77 ± 112.33	58.00	59.77	94.16

SE= Standard error, GCV= Genotypic coefficient of variation, PCV= Phenotypic coefficient of variation

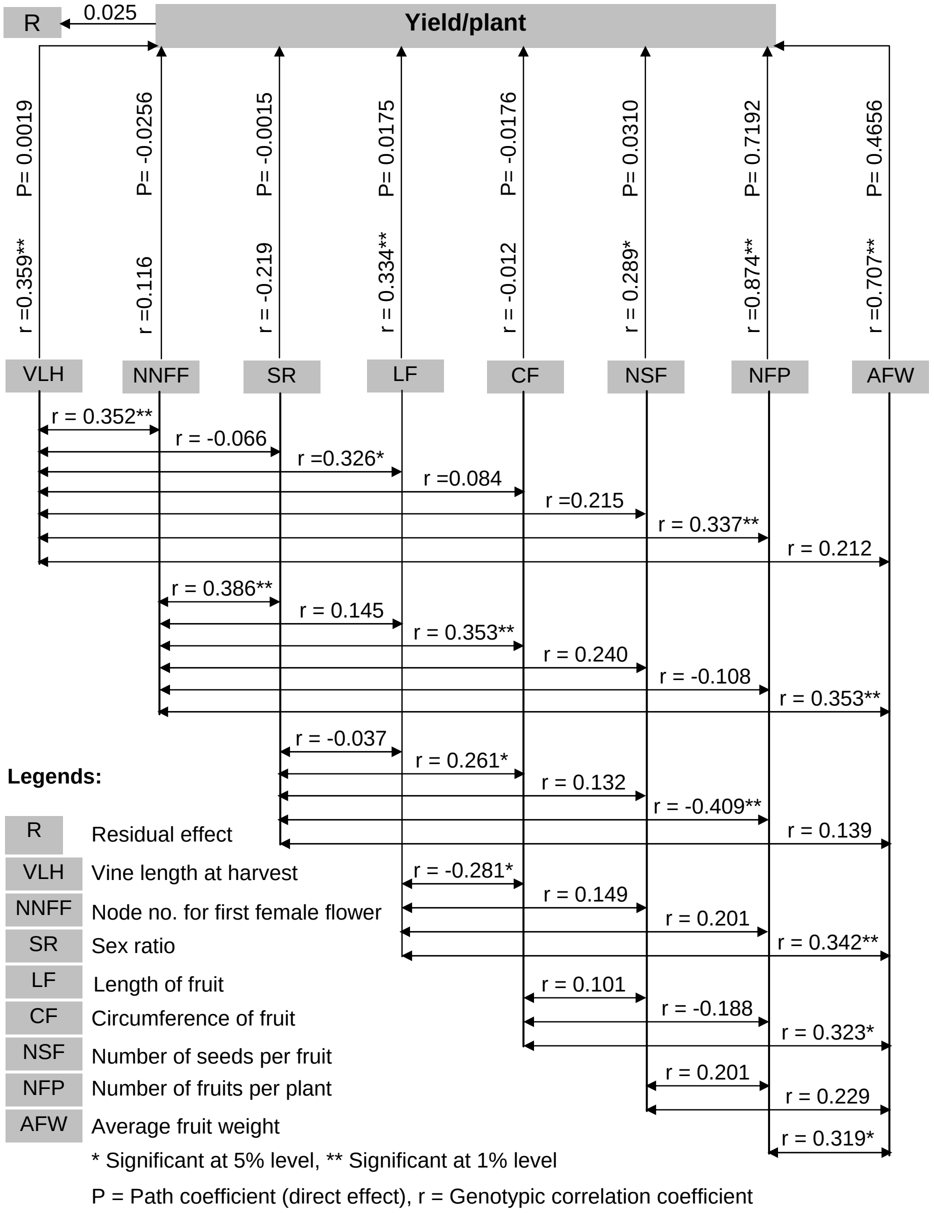

Figure.2. Path diagram constructed using correlation coefficients among yield and eight of its component traits in ridge gourd

Genotypic correlation coefficients (r) and path coefficients (P) of yield versus eight important yield contributing traits were calculated. Detailed relationship among the characters is presented in Figure 2. Yield per plant had highly significant positive relationship with number of fruits per plant (r = 0.874**) (Figure.3a), average fruit weight (r = 0.707**) (Figure.3b), vine length at harvest (r = 0.359**) (Figure.3c) and length of fruit (r = 0.334**) (Figure.3d). On the other hand, sex ratio and circumference of fruit exhibited negative relationship with yield per plant. The diagram also shows the genotypic direct effects of eight component characters on yield per plant as obtained through path analysis. Number of fruit per plant showed the highest positive direct effect (0.7192) on yield followed by average fruit weight (0.4656). Moreover, vine length at harvest (0.0019); length of fruit (0.0175) and number of seeds per fruit (0.0310) had also positive direct effect on the yield per plant. On the contrary, node number for first female flower (-0.0256); male: female flower ratio (-0.0015) and circumference of fruit (-0.0176) showed negative direct effect on the yield.

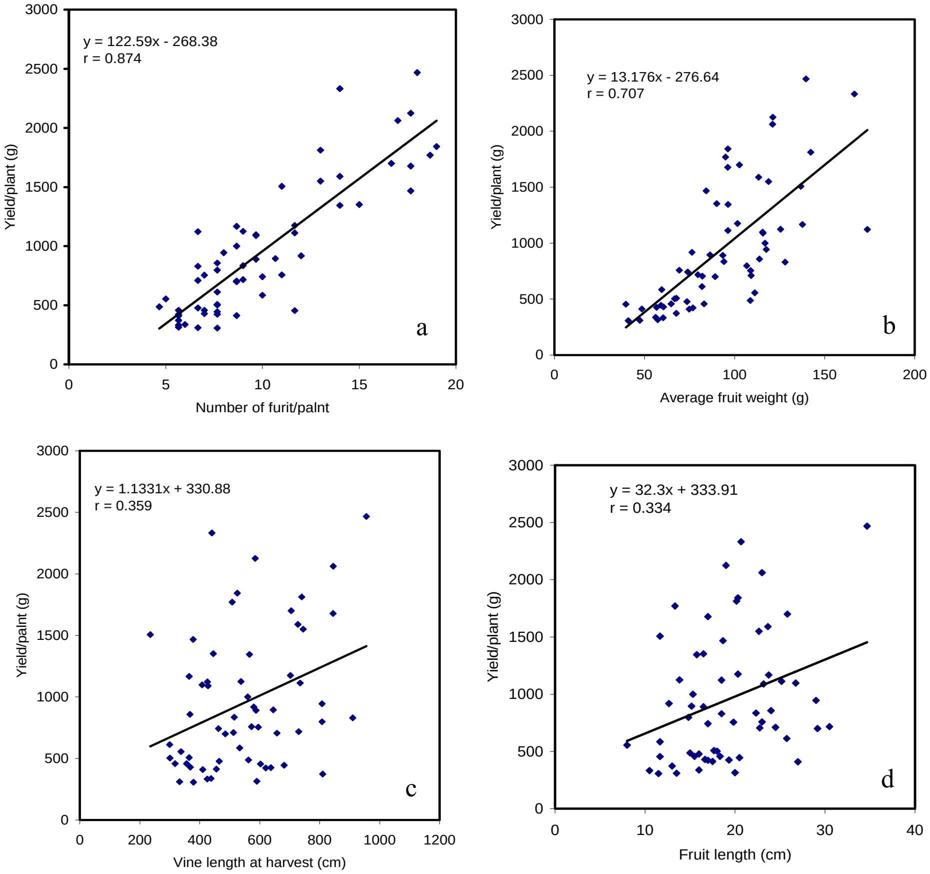

Figure 3a-d. Graphical representation of relationship of yield with different traits in ridge gourd

The multivariate analysis using Mahalanobis' D^2 statistics was carried out to study genetic diversity among 60 genotypes of ridge gourd. The genotypes grouped together are less divergent than the one which fall into different cluster. By application of non-hierarchical clustering using covariance matrix, 60 genotypes were grouped into four clusters. Cluster-I was the largest comprising of 31 genotypes followed by cluster-II with 19, cluster-III with 9 and cluster-IV with single accession. It is interesting to note that 51.67% of the genotypes fell under cluster-I, 31.67% under cluster-II, 15.0% under cluster-III and 1.67% under cluster-IV (Table 2). Clustering pattern of the genotypes revealed that the accession collected from the same region did not fall in a single cluster. As for example, 6 genotypes collected from Mymensingh region were grouped into all the four clusters (Table 2).

Table 2. Distribution of 60 genotypes of ridge gourd in different clusters

Cluster No.	No. of acc in cluster	Contribution to diversity (%)	No. of locations the genotypes collected from (of the total of 16 locations)
I	31	51.67	12
II	19	31.67	7
III	9	15	8
IV	1	1.67	1

It was observed that the average inter cluster distances were always higher than the average intra cluster distances suggesting wider genetic diversity among the genotypes of the groups. Custer-III had the highest intra cluster distance (97.9) whereas cluster-IV had zero. The maximum inter cluster distance (301.73) was recorded between them. The later (cluster-IV) also maintained the minimum distance (122.21) with cluster-II (Figure. 4). Mean performance of different clusters for seven characters are shown in the table 3. Although cluster-I had the maximum number of genotypes (31), no remarkable feature was found in this cluster for different traits. Cluster II scored second position in all seven traits but fruit length. The highest mean value for sex ratio and circumference of fruit were showed by the genotypes under cluster III. Cluster IV ranked first in terms of yield per plant. Next position was held by cluster II followed by cluster III and cluster I.

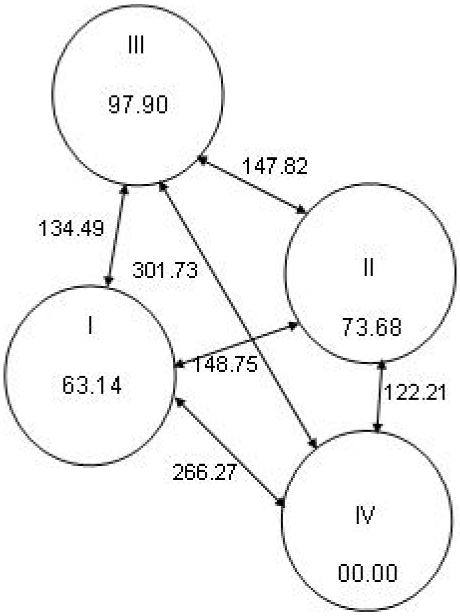

Fig.4. Cluster diagram showing the average intra- and intercluster distances ($D = \sqrt{D^2}$) of ridge gourd genotypes. The values along the lines indicate inter-cluster distances and the values within the circle indicate intracluster distances.

Table 3. Mean for seven characters in sixty ridge gourd genotypes

Characters	**Cluster mean**			
	I	**II**	**III**	**IV**
Vine length at harvest (cm)	530.76	553.49	471.74	955.50
Sex ratio	22.35	24.81	34.37	19.98
Length of fruit (cm)	18.11	19.76	19.78	34.67
Circumference of fruit (cm)	11.14	12.04	12.78	10.37
Number fruits per pant	8.32	13.67	6.89	18.00
Average fruit weight (g)	74.84	112.63	110.96	139.69
Fruit yield per plant (g)	620.29	1508.39	756.67	2467.50

There are three ways to estimate variability in a given population: 1) using simple measures- range, arithmetic mean, standard deviation, standard error, coefficient of variation (CV) etc; 2) by estimating the various component of variation; and 3) by studying the genetic diversity (Singh, 2000). The first and the third approach were tried in the present study among 60 *L. acutangula* genotypes. Simple statistical measurement of mean, range standard error, genotypic as well as phenotypic coefficients of variations were done, which proved wider variation in the population (Table1). GCV for all seventeen characters was lower than PCV as was found by Chowdhury and Sharma (2002) in 12 *L. acutangula* cultivars. It was an indication of environmental interference in the expression of genetic make up for the characters studied. The amount of interference was also calculated in terms of heritability- the proportion of total phenotypic variance that was due to genotype. The efficiency of selection largely depends on the extent of genetic variability present in a population, and the heritability of the concerned character. Selection is generally more effective for traits with high heritability than those having low heritability. So it can be claimed that selection for eight characters (Male: female flower, dry weight of flesh, seed length, seed breadth, 100-seed weight, number of fruit per plant, average fruit weight and fruit yield per plant) should be fairly easy in the present study as all the above mentioned characters showed heritability over 80% (Singh, 2000). High values of heritability were also recorded for vine length, yield per hectare and fruit weight by Chowdhury and Sharma (2002); for number of nodes for appearance of first male and female flower, fruit per plant, fruit set, fruit length, fruit weight and yield per plant by Singh *et al.,*(2002a). Heritability was high for most characters examined by Sahni *et al.,* (1987) in 21 *Luffa acutangula* genotypes.

Higher yield is the main breeding objective in all the crops. Yield is regarded as a complex character which is influenced by many components or contributing traits both in positive and negative directions. Generally, direct selection for yield is not sufficiently effective due to its low heritability, and it is desirable to select indirectly for improved yield. Some biometrical techniques provide information about the relative contributions of the various component traits to yield. Therefore, these techniques aid in the isolation of superior yielding genotypes from genetically variable population by providing information on indirect selection for yield. Correlation coefficient and path coefficient are two of those techniques among others (Singh, 2000). Correlation coefficient analysis measures the mutual relationship between various plant characters and determines the component characters on which selection can be based for improvement in yield. The results of the present study revealed that selection for yield of ridge gourd should be based on the trait like number of fruits per plant; average fruit weight; vine length at harvest and length of fruit as the traits showed significant positive relationship with fruit yield (Figure. 2a-d). Shah and Kale (2002) conducted an experiment on correlation co-efficient analysis of yield components of 55 genotypes of ridge gourd. The fruit weight per vine was positively and significantly correlated with number of fruits per vine, average fruit weight, number of female flower per vine and vine length, indicating the close association and dependency of yield on these characters. Yield per plant, in an assessment of genetic variability and correlation for yield and its attributes in pointed gourd (*Trichosanthes dioica*), was reported to have significant positive correlation with number of fruits per plant (Dora *et al.,* 2003).

Path analysis, another important aid to selection, splits the correlation coefficient into the measures of direct and indirect effects of a set of independent variables on the dependent variable (in this case yield). The characters number of fruits per plant and average fruit weight exerted relatively high positive direct effect (0.7192 and 0.04656, respectively) on yield. A greater yield response is obtained when the character for which indirect selection is practiced has a high heritability and high correlation with yield. It is noted that both the traits had highly significant positive relationship with yield as well as heritability value of over 0.94. Rao *et al.,* (2000) conducted an experiment on the segregating population of ridge gourd to estimate correlation and path coefficient analysis. Path analysis revealed that yield improvement could be achieved by direct selection for days to 50% flowering, girth of fruit, fruits per plant or vine, fruit per branch and length of the vine of ridge gourd. Path coefficient analysis among some important yield related traits in cucumber also indicated that fruit weight had the highest direct effect on fruit yield (Singh *et al.*, 2002b).

Sixty genotypes in this study were grouped into four clusters (Table 2). Though, in another study for the genetic divergence among thirty genotypes of ridge gourd landraces, six clusters were reported using D^2 and principal component analysis (Quamaruzzaman *et al.*, 2008). Clustering pattern of the genotypes revealed that the accession collected from the same region did not fall in a single cluster. This result indicated that factors other than geographical separation are also responsible for divergence, and the genotypes that have originated from the same place might have different genetic architecture or vice-versa. The genetic diversity should be utilized for the development of gene pools, which serve as the reservoirs of genes. Information on genetic diversity can also be utilized for the exploitation of hybrid vigor. Morphological approach to explore variation and divergence is more conventional method with several limitations and influenced by environmental factors. So, to get more accurate results, molecular approach using RAPD, RFLP, SSR are suggested for identification of individual accession to avoid duplication in conservation of the germplasm for future use as well as to study genetic study in ridge gourd (*L. acutangula*).

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