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# Genetic divergence in bottle gourd

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## ABSTRACT

Genetic divergence among twenty eight bottle gourd (*Lagenaria siceraria*) genotypes was estimated using D2 and Canonical analysis. The genotypes were grouped into five clusters. The maximum intercluster distance was between cluster III and cluster I, and the minimum was between cluster IV and II. .The crosses between the genotypes LS001, LS002, LS007, LS010, LS013, LS016, LS017, LS028 of cluster II and LS018, LS023 in cluster V would exhibit maximum heterosis and produce new recombinants with desired traits in bottle gourd.

Key words: *Lagenaria siceraria*, genetic divergence, cluster and canonical analysis

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## INTRODUCTION

Bottle gourd (*Lagenaria siceraria* L.) belongs to the family Cucurbitaceae. The cultivated species is commonly known as bottle gourd, birdhouse gourd, trumpet gourd, calabash gourd and white flowered gourd. Bottle gourd originated in Africa and from there it spread all over the world (Whitkar and Davis, 1962). Now a days it is grown in many countries including Bangladesh, India, Malaysia, Indonesia, Japan, China, the Philippines, Taiwan, Thailand, South Africa and Sudan ( Yonernori and Fujeda, 1985). Bottle gourd fruits are used as cooked as vegetables. Its leaves and tender stems are used as delicious and nutritious vegetables. It is reported as an easily digestible vegetable which keeps the body cool and prevents constipation (Haque, 1985). Each 100g bottle gourd contain protein 1.1g, carbohydrate 15.1g, fat 0.1g, minerals 0.6g and some Vitamins (Seshadri and Parthasarathy, 2002). The average yield is only 8.6 t/ha (BBS, 2007). The poor productivity and production is because of the poor genetic make-up of open pollinated mixed seed or local strains. It may be mentioned that up to-date there is no release variety of bottle gourd with a high yield potential and better quality. Geographic and phenotypic diversity serve as inferential criteria and it is not practical to quantify or genetically discriminates among population. Precise information on the nature and degree of genetic divergence would help the breeder in choosing the right type of parents for purposeful hybridization or heterosis breeding programmes. The importance and extent of genetic divergence have been investigated in many crops (Kumar et al., 1998; Singh et al., 1999; Ram 2001; Asfaw et al., 2001; Hazra et al., 2002). Sharma et al. (1993) worked on heterosis and Samadia and Khandelwal (2002) worked on the combining ability in bottle gourd, but the information on the genetic diversity of the bottle gourd is scant. Thus the present investigation has been carried out with 28 bottle gourd genotypes to ascertain the nature and magnitude of genetic diversity present in the material.

## MATERIALS AND METHODS

The experimental material comprised 28 genotypes of bottle gourd collected from different parts of Bangladesh (13 from Plant Genetic Resources center, Bangladesh Agricultural Research Center, 6 from Comilla, 4 from Mymensingh and 5 from Noakhali). The experiment was conducted in the research field of Horticulture Research Center, Bangladesh Agricultural Research Institute, Joydebpur, Gazipur during the period from September 2007 to March 2008. The seedlings were raised in ploythene bags. Two- week-old healthy seedlings were transplanted in the previously prepared pit. Plant to plant distance was 2m. Three seedlings were transplanted in each pit. The recommended cultural practices were followed to produce a better crop. The experiment was laid out in a Randomized Complete Block Design with three replications. Data were recorded on ten plants from each genotype. The observations recorded were leaf length, breadth, petiole length, lobe number, days to first male and female flower, nodal position of first female flower, days to edible maturity, sex ratio, fruits/plant, fruit weight (kg), fruit length and diameter (cm), yield/plant (kg), number of seeds/fruit, 1000-seed weight (g), days to seed maturity, seed length, breadth and thickness (mm).

## RESULTS AND DISCUSSION

The analysis of variance showed significant differences among the characters. On the basis of D2 values, twenty eight genotypes were grouped into five different clusters (Table 1). This indicated the existence of genetic diversity among the genotypes. Maximum genotypes were in cluster I involving 10 genotypes, followed by cluster II with 9 genotypes. Cluster III, cluster IV and cluster V had 4, 3 and 2 genotypes, respectively. The genotypes from different origins (districts) assembled into a cluster with plants of close affinity. The genotype LS004, LS005, LS006, LS011 collected from PGRC, BARI, LS014 from Commila, LS021 from Mymensingh and LS024, LS025, LS026 from Noakhali formed cluster I. This suggests that the genotypes within a cluster might have some degree of ancestral relationship. On the other hand, 8 genotypes collected from PGRC, BARI, 3 genotypes collected from Mymensingh, 5 genotypes collected from Comilla and 2 genotypes collected from Noakhali were distributed in different clusters. These results showed that geographic diversity may not necessarily be related with genetic diversity. Therefore, the selection of genotypes for hybridization should be based.

Table 1
Distribution of 28 genotypes of bottle gourd in different clusters

| Cluster | Number of genotypes | Genotypes and their origin |
|---|---|---|
| I | 10 | LS004 (PGRC, BARI), LS005 (PGRC, BARI), LS006 (PGRC, BARI), LS008 (PGRC, BARI), LS011 (PGRC, BARI), LS014 (Comilla), LS021 (Mymensingh), LS024 (Noakhali), LS025 (Noakhali), LS026 (Noakhali). |
| II | 9 | LS001 (PGRC, BARI), LS002 (PGRC, BARI), LS007 (PGRC, BARI), LS010 (PGRC, BARI), LS013 (PGRC, BARI), LS016 (Comilla), LS017 (Comilla), LS020 (Mymensingh), LS028 (Noakhali). |
| III | 4 | LS003 (PGRC, BARI), LS012 (PGRC, BARI), LS015 (Comilla), LS022 (Mymensingh). |
| IV | 3 | LS009 (PGRC, BARI), LS019 (Comilla), LS027 (Noakhali). |
| V | 2 | LS018 (Comilla), LS023 (Mymensingh). |

on genetic diversity rather than on geographic diversity. On the basis of present findings it can be suggested that though geographic diversity may not necessarily be an index of genetic diversity, sufficient genetic diversity can be accumulated in the genotypes. The tendency of genotypes to occur in clusters cutting across geographic boundaries demonstrates that geographical isolation is not the only factor causing genetic diversity. This may be due to wide soil and climatic differences in the

region. These results conformed with the findings of Bhadra and Akhtar (1991) in mungbean, Lee et al. (1996) in onion, Prasad and Singh (1997) in pointed gourd, Masud et al. (2002) in sponge gourd, Prasad et al. (2002) in watermelon and Islam et al. (2002) in muskmelon. On the contrary, Joshi and Dhawan (1966) and Narayan and Macefield (1976) found close relationships between geographic and genotypic diversity. Murty and Arunachalam (1996) and Singh et al. (1989) have suggested that genetic drift and natural selection forces under diverse environmental conditions within a country could cause more considerable diversity than geographic isolation.

Table 2
Average inter cluster distance ($D^2$) and intra cluster distance (bold) for 28 genotypes and 14 characters in bottle gourd

| | I | II | III | IV | V |
|---|---|---|---|---|---|
| I | 1.179 | | | | |
| II | 26.97 | 1.301 | | | |
| III | 31.10 | 9.34 | 1.182 | | |
| IV | 25.74 | 6.51 | 14.76 | 1.234 | |
| V | 11.81 | 15.63 | 20.43 | 14.79 | 1.289 |

Average intra and inter cluster distance are presented in Table 2. The average intra cluster distance ranged from 1.179 (cluster I) to 1.301 (cluster II) suggesting that the genotypes in cluster II were relatively more diverse than the genotypes in other clusters. The maximum inter cluster distance was between cluster III and cluster I (31.10) followed by that between cluster II and cluster I (26.97), suggesting a large difference between these groups. On the other hand, the minimum distance between cluster IV and cluster II (6.51) indicates a close relationship and the genotypes of these clusters had the maximum of common gene complexes. The magnitude of heterosis largely depends on the degree of genetic diversity in the parental lines. The greater the distance between two clusters, the wider the genetic difference between their genotypes. Several researchers have suggested that selection of parents for hybridization should be done from two clusters with wider intercluster distances in order to get more variability among the segregates. However, while considering genetic diversity among the parents to be included in hybridization programme, their yield potential should not be ignored.

Cluster I showed longest leaf, maximum yield, highest no. of seeds/fruit, maximum seed breadth and thickness with earlier female flowering (Table 3). Whereas the cluster mean for different characteristics indicated that the number of leaf lobe, leaf breadth, days to seed maturity, single fruit weight were highest in cluster II (Table 3). Cluster IV was the latest in days to first male and female flowering. Cluster IV showed the maximum no. of fruits/plants, maximum fruit length and width, maximum days for the fruits to become edible and highest sex ratio. Masud et al. (1995) found the maximum fruit length and highest no. of fruits/plant in cluster I, highest fruit weight in cluster II and highest fruit diameter and yield/plant in cluster IV in pumpkin. The relative contributions of different characteristics towards genetic divergence were studied using the coefficient of variation (Table 3). Characteristics like yield (t/ha) (0.97%), no. of fruits per plant (7.91%), fruit weight (5.75%) and fruit length (0.69%) were important contributors towards genetic divergence among the genotypes. Rasheed et al. (2002) reported that fruit weight and yield/plant were the maximum contributors in pumpkin whereas Islam et al. (2002) found that fruit length, weight, number of fruits and yield/plant were the most important contributors to the total divergence in muskmelon.

Table 3
Cluster mean and coefficient of variation of different characters of bottle gourd

| characters | Cluster I | Cluster II | Cluster III | Cluster IV | Cluster V | CV (%) |
|---|---|---|---|---|---|---|
| Days to 1st male flower opening | 52.05 | 66.14** | 58.78 | 59.41 | 50.48* | 0.53 |
| Days to 1st female flower opening | 57.71* | 68.18** | 61.73 | 67.89 | 58.1 | 0.95 |
| Days to 1st harvest | 76.75* | 84.74 | 86.39* | 86.04 | 78.1 | 0.47 |
| No. of fruit/plant | 23.33 | 24.11 | 23.52 | 24.61** | 22.01* | 1.80 |
| Single fruit weight (kg) | 6.67 | 6.32* | 7.668** | 6.66 | 6.85 | 5.75 |
| Fruit length (cm) | 2.97 | 2.71 | 3 | 3.08** | 2.73* | 0.69 |
| Fruit width (cm) | 34.57 | 35.98 | 33.34 | 38.25** | 33.17* | 0.96 |
| Yield (t/ha) | 14.86** | 12.85 | 14.26 | 12.62* | 13.5 | 0.97 |
| Days to edible maturity | 43.05 | 36.74 | 40.77 | 46.68** | 38.64* | 3.02 |
| Leaf length (cm) | 21.57** | 21.75 | 20.44 | 19.76* | 20.68 | 0.67 |
| Leaf breadth (cm) | 28.12 | 28.59** | 27.78 | 24.8* | 26.24 | 0.60 |
| Leaf petiole length (cm) | 16.83 | 13.23 | 20.21** | 11.15 | 16.86* | 2.02 |
| Leaf lobe no. | 6.78 | 7.14** | 7.08 | 6.19 | 6* | 2.32 |
| No. of seed/fruit | 958.29** | 222.83 | 114.83* | 344.08 | 664.28 | 7.91 |
| 1000 seed weight (gm) | 200.61** | 198.69 | 193.8 | 210.53 | 189.03* | 0.60 |
| Days to seed maturity | 175.75 | 126.82* | 188.61** | 109.79 | 158.39 | 0.39 |
| Seed length (mm) | 17.51 | 17.33 | 17.06* | 17.41 | 17.54** | 1.26 |
| Seed breadth (mm) | 10.14** | 9.56 | 9.42 | 9.35* | 9.67 | 1.78 |
| Seed thickness (mm) | 3.49** | 3.35 | 3.43 | 3.28* | 3.38 | 4.43 |
| Sex ratio (M:F) | 2.31* | 2.98 | 2.78 | 4.59** | 3.39 | 7.74 |

In rows, where * and ** indicates minimum and maximum values, respectively

The cluster constellation obtained by D2 analysis was also confirmed by canonical analysis. Canonical analysis was carried out by calculating the first two vectors, which accounted for 58.88% of the total diversity and the first three canonical vectors, which accounted for 75.31% of the total genetic divergence (Islam, 2004). In order to get a clear dimensional representation, the contribution by three canonical roots should be more than 95%. Therefore, a slight deviation is expected in such analysis. More or less observation was reported by Chowhdury et al. (1996) in field pea. The mean values of the first two vectors for the 28 genotypes were plotted on a two-dimensional graph and the D2 value superimposed over it (Figure 1). The scatter diagram of bottle gourd showed a distribution of genotypes in clusters similar to that of Table 1. The genotypes were more heterogeneous in cluster IV and genotypes were comparatively closed to each other in cluster I (Figure 1).

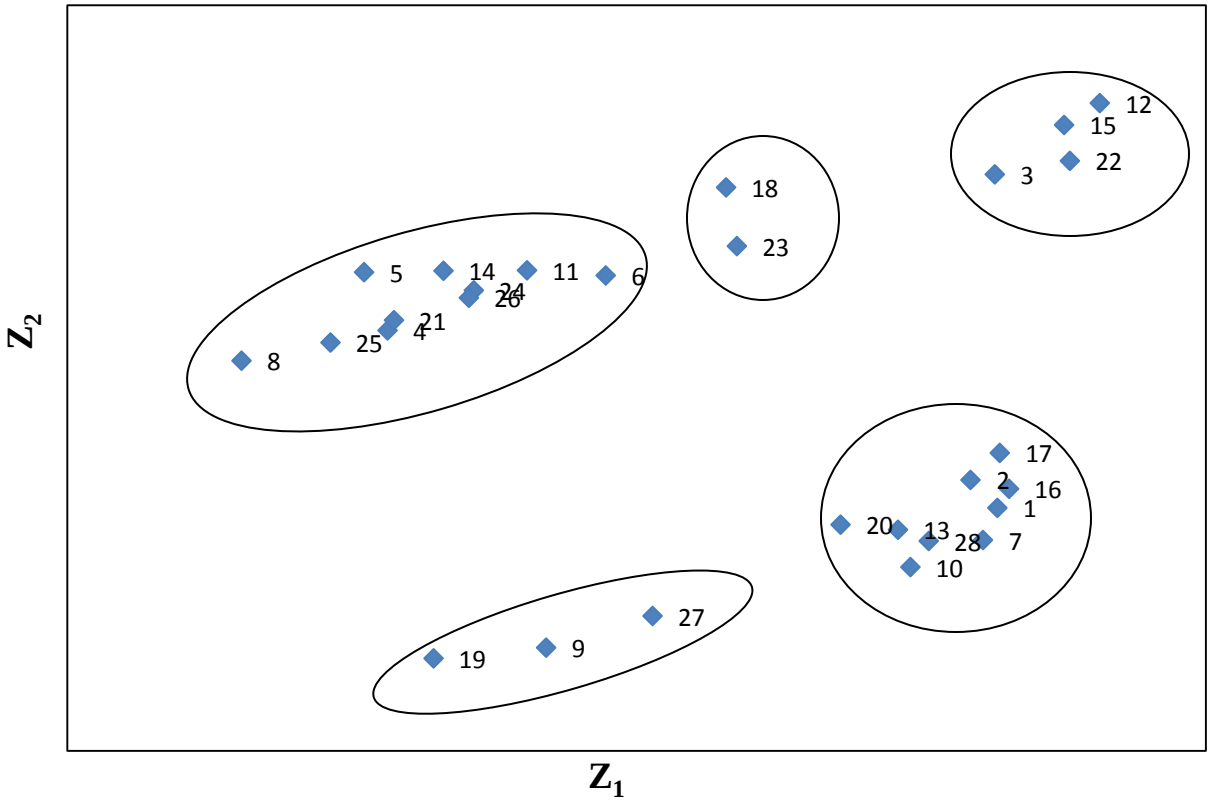


Figure 1
Canonical diagram of the first two canonical vectors showing relative position of twenty eight bottle gourd genotypes.

The crosses involving parents from the most divergent clusters are expected to manifest maximum heterosis and generate wide variability of genetic architecture. Thus the crosses between the genotypes LS001, LS002, LS007, LS010, LS013, LS016, LS017, LS028 of cluster II and LS018, LS023 in cluster V would exhibit maximum heterosis and produce new recombinants with desired traits in bottle gourd.

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