MORPHOLOGICAL CHARACTERIZATION AND GENTIC DIVERSITY IN OKRA (*Abelmoschus esculentus* L. Monech)

BY

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CERTIFICATE

*This is to certify that thesis entitled," **Morphological Characterization and Genetic Diversity in Okra" submitted to the Faculty of Agriculture, Sher-e-Bangla Agricultural University, Dhaka in partial fulfillment of the requirements for the degree of MASTER OF SCIENCE in GENETICS AND PLANT BREEDING, embodies the result of a piece of bonafide research work carried out by Md. Rezaul Karim Talukder, Registration No. 00911 under my supervision and guidance. No part of the thesis has been submitted for any other degree or diploma.*

I further certify that such help or sources of information, as has been availed of during the course of this investigation has duly acknowledged.

SHER-E-BANGLA AGRICULTURAL UNIVERSITY

Date: December 2008
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DEDICATED TO

MY BELOVED

PARENTS

&

MY SISTER TONNY

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The Author

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MORPHOLOGICAL CHARACTERIZATION AND GENETIC DIVERSITY IN OKRA (*Abelmoschus esculentus* L. Monech)

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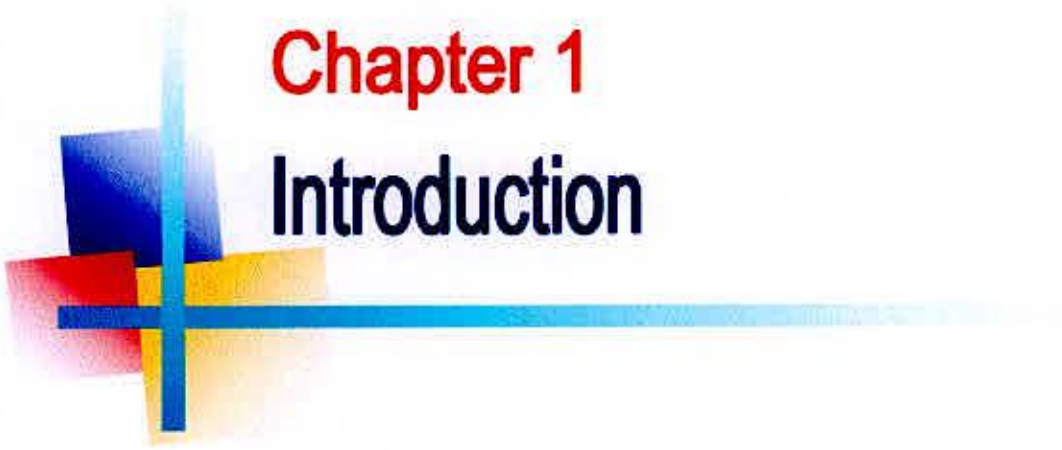
ABSTRACT

An experiment was conducted to study the morphological characterization and genetic diversity in okra genotypes at the experimental field of Genetics and Plant Breeding Department, Sher-e-Bangla Agricultural University from November 2007 to April 2008. The experiment was laid out in Randomized Complete Block Design (RCBD) with three replications. The present study was undertaken with a view to asses the performance of twenty okra genotypes in order to know the genetic parameter and variability of eleven quantitative characters and finally assessing the genetic diversity among these genotypes. Significant differences among the different genotypes for all characters were observed. The mean performance of the genotypes as the days to 50% flowering (67.18 days), days to edible maturity (81.70 days), plant height (69.16 cm), height to 1st node from the ground (14.02 cm), number of branches per plant (3.15), number of pods/plant (10.00), length of pod (10.10), diameter of pod (1.59 cm), individual pod weight (12.75 g), number of seeds/pod (54.80) and yield/plant (144.13 g) respectively were recorded. High heritability (>60%) was observed for days to flowering, days to edible maturity, plant height , height to 1st node from the ground, number of branches per plant, number of pods/plant, diameter of pod, individual pod weight, number of seeds/pod and yield/plant. For knowing the genetic diversity of okra genotypes, multivariate analysis was done by using Genstat. As per PCA, D^2 and cluster analysis, the genotypes were grouped into 5 clusters. Cluster I, II, III, IV and V composed of 4, 2, 5, 5 and 4 genotypes, respectively. PCA showed 97.55 % variation against first three eigen values. The highest intra-cluster distance (1.126) was found in cluster II and lowest (0.2628) in cluster I among the five clusters. Considering that the G_7, G_9 and G_{11} from cluster III, G_1 from cluster I, G_{10} from cluster II and G_5 and G_{13} from cluster IV were considered to be better parent for efficient hybridization. Therefore, considering group distance and the agronomic performance, the inter genotypic crosses between G_7 and G_1, G_7 and G_5, G_7 and G_{10}, G_7 and G_{13}, G_9 and G_1, G_9 and G_5, G_9 and G_{10}, G_9 and G_{13}, G_{11} and G_1, G_{11} and G_5, G_{11} and G_{10}, G_{11} and G_{13}, G_1 and G_5, G_1 and G_{10}, G_1 and G_{13}, G_5 and G_{10}, G_{10} and G_{13} might be considered for efficient hybridization programme.



Chapter 1

Introduction

CHAPTER 1
INTRODUCTION

Okra (*Abelmoschus esculentus* L. Monech) is a seed propagated and annual important vegetable crop belonging to the family Malvaceae. The okra is cultivated throughout Bangladesh for its immature fruits which are generally cooked as vegetable. The number of chromosome of okra varies from species to species, but the reason of variation is not known. The number of chromosome shows 66 to 144 (Rashid, 1999). Two wild species *Abelmoschus tuberculatus* (n=29) and *Abelmoschus ficulenneus* (n=36) are amphidiploid (Joshi and Hardas, 1976). It is known by many local names in different parts of the world, such as Lady's finger in England, Gumbu in USA, Gombu in France, Bhindi in India and Dherosh in Bangladesh.

Okra originated in tropical Africa (Purseglove, 1987), is grown as a popular vegetable throughout the tropical and sub-tropical regions of the world. Except okra the genus *Abelmoschus* also has two cultivated species and some wild species. The cultivated species one is *Abelmoschus manihot* another is *Abelmoschus moschatus.* Okra is very common vegetable in Bangladesh and popular among all classes of people. Though it is grown round the year but commercially cultivated mainly in summer season. About 17,300 metric tons of okra is produced from 5,400 hectares of land per year in Bangladesh and average yield is about 3.2 /ha (BBS, 1998) which is very low.

Okra is a multipurpose crop. Its tender pods are cooked as a vegetable, stewed with meat, cooked into soups and also canned and dried. When ripe the okra, the black or brown white eyed seeds are sometimes roasted and used as substitute for coffee in Turkey (Bokshi, 1993). Mature pods and stems containing crude fiber are used in the

paper industry. It has medicinal value too and used in genitor-urinary disorder, to control goiter and against constipation. The edible portion of the pods contain approximately 86.1 percent water, 2.2 percent protein, 0.2 percent fat, 9.7 percent carbohydrate, 1.0 percent fiber, 0.8 percent ash, calories and rich in vitamin A, B, C and iodine (Purseglove, 1987). It is easily digestible and less input consuming vegetable; it can be contribute much in solving the chronic nutritional problem of our people.

In Bangladesh, vegetable production and supply is not uniform round the year. Vegetables are abundant in winter, scanty in summer and there is an acute shortage during two slack seasons: mid March to April and from October to November due to transition from one season to another (Hossain, 1992). Less production and unequal supply of vegetable in market during various parts of the year resulted in the lowest per capita vegetable consumption (25 g/head/day) in Bangladesh (Hossain *et al.*, 1990). Okra is less sensitive to adverse environmental condition. It can be grown in 21-42^0 C temperature and can withstand drought to heavy monsoon during growing season.

Yield is complex character and various morphological and physiological characters contribute to yield. It is essential to have knowledge on variability of different characters for the yield improvement. The available variability in a population can be partitioned into heritable and non heritable parts with the aid of genetic parameters such as genetic coefficient variation, heritability and genetic advance (Miller *et al.*, 1958). The variability of a biological population is an outcome of genetic constitution of individuals making up that population in relation to prevailing environment. It

arises either due to geographical separation or due to genetic barriers to cross ability. A survey of genetic variability with the help of suitable parameters such as genotypic co-efficient of variation, heritability and genetic advance are absolutely necessary to start an efficient breeding programme (Mishra *et al.* 1995).

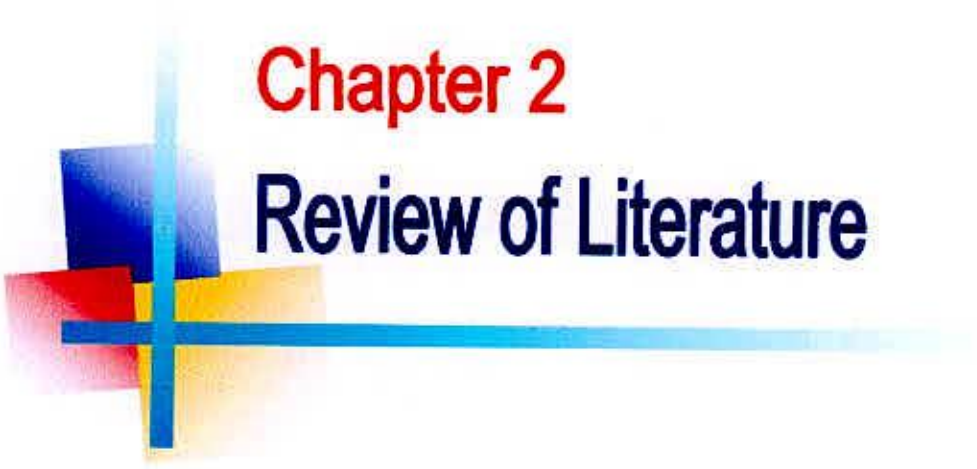
Genetic diversity plays an important role in plant breeding because hybrids between lines of diverse origin generally display a great heterosis than those between closely related stains which permits to select the genetically divergent parents to obtain the desirable recombination of the segregating generations (Singh, 1983). The variability among different genotypes of a species is known as genetic diversity. A plant breeding program can be divided into three stages, *viz.* building up a gene pool of variable germplasm, selection of individuals from the gene pool and utilization of selected individual to evolve a superior variety (Kempthorne, 1957). The availability of transgressive segregants in any breeding program depends upon the divergence of involving parents. A measure of genetic diversity would help to choose parents either to exploit heterosis or to select desirable segregants (Sarathe and Perraju, 1990). Genetic divergence is one of the criteria of parent selection. It is the function of heterosis. Genetic diversity is very important factor for any hybridization programme aiming at genetic improvement of yield, especially in self-pollinating crops (Joshi and Dhawan, 1966). The quantification of genetic diversity through biometrical procedures has made it possible to choose genetically diverse parents for a successful hybridization programme and evaluation of genetic diversity is important to know the source of gene for particular trait within the available germplasm (Anderson, 1957; Rao, 1952, and Tomooka, 1991). The genetic diversity is a must for a sound base selection (De *et al.* 1988). It is also essential to meet the diverse goals of plant

breeding such as producing cultivars with increased yield and wider adaptation, desirable quality, pest and diseases resistance (Joshi and Dawan, 1966, and Nevo *et al.*, 1982).

Multivariate analysis is a useful technique in quantifying the degree of divergence between biological populations at genotypic level and assessing the relative contribution of different components to the total divergence both at intra and inter-cluster levels (Murty and Arunachalam, 1966, and Naidu and Satanarayana, 1991). The D^2 statistic is one of the frequently used models of multivariate analysis.

The variety improvement of a population depends on the nature and relative magnitude of the variance of components. But the studies on the variety improvement of okra are limited. This may assist to design efficient breeding programme for the development of new varieties of okra in Bangladesh. Hence, present investigation was carried out with the following objectives:

1. To assess the mean performance of the twenty genotypes
2. To estimate variability and heritability for yield and yield contributing characters
3. To study genetic diversity among the genotypes in respect of different morphological characters
4. To find out the suitable genotypes for future breeding programme.



Chapter 2

Review of Literature

CHAPTER 2

REVIEW OF LITERATURE

The purpose of genetic studies on morphological characterization and genetic diversity in okra was to continue the genetic purity to improve the yield of okra. In Bangladesh and elsewhere in the world research effort seems to be limited in this regard. However, available relevant literatures on okra are reviewed under following paragraphs:

2.1 Genetic Variability

2.1.1 Genotypic, phenotypic variances and coefficient

Grewal *et al.* (1972 and 1973) studied the effect of four characters on the yield and quality of okra seeds cv. Pusa Swani. They recommended that seeds to be collected from 3-6 nodes for practical bulk seed production and from 3 and 4 nodes for breeding purpose.

Lal and Srivastava (1973) worked on hybrid vigour among 11 F_1 from 9 parental lines of *Abelmoschus esculentus* and observed wide range of variation in plant height, fruit length, fruit thickness, number of fruits per plant and fruit yield per plant.

Singh and Singh (1978) worked on the F_1 and F_2 populations of 25 female lines *Abelmoschus esculentus* with 5 testers and reported that the importance of non-additive gene action for days to flowering, plant height, first fruiting node, number of branches per plant, fruit length, number of fruits per plant and yield per plant.

Thaker *et al.* (1981) workd on the additive component was the chief determinant of genetic variance in fruit yield per plant, single fruit weight and fruit length. Non-additive components governed the number of fruits per plant.

Palaniswamy and Karivaratharaju (1984) reported that the varying plant populations of different germplasms were affected seed yield of okra significantly.

Sharman and Sharma (1984) observed variability for fruit numbers/plant, fruit length, shelf life and yield in okra.

Akorada (1986) considered 22 field plots differing with regard to genotype (12 cultivars), field site and cultivation regime for seed and fruit production. Plants randomly selected for the production of seed (mature pod harvested when 3-4 sutures split) or fresh fruits (immature fruits harvested every 3-4 days) had similar flowering pattern. The seed plants produced less fruits as there were fewer flowers and lower fruit setting. Of the number of floral buds visible on the day of first flowering, 70 % formed edible fruits in fruit plants but only 46 % in seed plants. Mature sun dried pods contained 57 % by weight of plantable seeds.

Ariyo (1987) worked on six *Hibiscus esculentus* genotypes from a pedigree breeding program and nine established varieties were evaluated for five agronomic characters over five environments (two sites and two or three planting dates). There was a significant genotype x environment interaction for number of days to flowering and number of branches per plants. Additive environment effects were significant for all characters. The cultivar U1313 was stable for pod yield per plant and edible pod weight. A genotype grouping technique showed that the breeding line U122-77 had below average coefficient of variation for pod yield per plant and above average yield.

Adetunji and Chheda (1989) study on ten newly developed lines and 5 established varieties of *Abelmoschus esculentus* were evaluated in 8 different environments (planting at different times for 3 consecutive years). They reported that there were

significant variations for seed yield among environments, even though all the trials were at the same site. A regression method of stability analysis indicated that the mean differences among environments, the varieties and their interactions were highly significant. The results suggested that, where limited resources prevent the use of several localities, different planting dates for 2 or more years could be used to evaluate varieties for seed yield.

Rao *et al.* (1989) conducted a test on four varieties of okra at three crop densities for pod yield and five yield components and found plant height and pod girth significantly higher in the cultivar Pusa Swani than the other materials but PS10, a mutant of Pusa Swani, was significantly better for number of branches per plant, pod number per plant and pod yield. Height and pod yield increased with the increased density, but branch number, pod length and pod number was greater at lower density.

Sardana *et al.* (1990) reported that in case of yield contributing characters like high variability for number of pods per plant of okra. Phenotypic coefficient of variability was higher than genotypic coefficient of variability for the characters like days to maturity, plant height and pod length

Veerargavathatham and Irulappan (1990) studied on the genetics of different characters of okra and suggested that dominance predominated for yield and individual fruit weight.

Patel and Dalal (1992) studied on the variability of okra for nine yield components in seven *Abelmoschus esculentus* genotypes and their F_1 hybrids. They reported significant variation among the genotypes for all the traits.

Khanobdee and Lertsilpmongkol (1993) worked on a trial at Lampang, Thailand, to study the seed production of two varieties of okra e.g. Early-five and better-five during November 1991 to April 1992. The result showed that average number of pods/plant was 8.5, seed weight/plant 20.7-24.1 g and number of ridges/pod was 5. Seeds of both the varieties reached their physiological maturity at 39 days after anthesis and the suitable harvesting period were 41 days after anthesis.

Kumbhani *et al.* (1993) worked on heterosis among 8 diverse parents and 28 different hybrids. They observed significant differences for plant height, internodal length, pod length, pod girth, number of pods per plant and yield/plant.

Das and Mishra (1995) worked on variation and character association of fruit yield and its component characters in 27 okra genotypes. They reported that all genotypes differed significantly for fruit yield/plant, fruit length, fruit girth, fruit weight, number of seeds/fruit and seed weight/fruit.

Wankhade *et al.* (1995) studied on the days to flowering and ridges on fruit, yield, fruits/plant, fruit diameter and girth of okra.

Gondane and Bhatia (1995) evaluated fifty genotypes of *Abelmoschus esculentus* for 11 yield-related traits in the rainy and summer seasons of 1987 at Pantnagar. They reported that all the genotypes responded differently to the environments. They also observed significant and marked variation in the yield components, particularly for yield/plant, plant height, pods/plant and nodes to first pod.

Hossain (1997) worked on the performance of okra for 9 characters in 4 genotypes ("IPSA Resistant", Parbhani Kranti, SL-44 and SL-46) and their 3 hybrids. He observed significant variation among the genotypes for fruit length, fruit diameter,

fruit weight, number of seed per fruit and 100-seed weight. From the results he concluded that there was considerable genetic variability in the materials.

Reddy and Kumar (1998) reported that among the yield contributing characters in okra phenotypic coefficient of variation for plant height, days to maturity, number of primary branches per plant and 1000 seed weight showed maximum contribution to total variability .

Kumar (1999) studied fifteen F_1s and eight parents of okra for genetic variability and reported higher level of genotypic variance and genotypic coefficient of variability for plant height, pod number, yield per plant and pod length.

2.1.2 Heritability and genetic advance

In Bangladesh, very limited information is available about the nature and extent of heritability in okra. The available information is reviewed here:

Govindaswami *et al.* (1978) reported high percentage of heritability for plant height and 1000- seed weight, while number of pods per plant and seed yield per pod had moderate heritability. They also observed high genetic advance in percent of mean for three characters like number of pods per plant, seed yield per pod and 1000- seed weight but the value was low for plant height.

Lal and Srivastava (1978) investigated eleven crosses of okra for hybrid vigor in respect of seven quantitative characters. They reported that one cross for plant height, two crosses for number of branches per plant, two crosses for fruit length, one cross for number of fruits per plant and two crosses for fruit yield per plant showed hybrid vigor.

Singh and Singh (1978) crossed 25 female lines of okra with 5 testers and studied the F_1 and F_2 populations. They observed heritability for number of days to flowering, plant height, fruit length, number of fruits per plant and yield per plant.

Swamy Rao (1978) reported that nine hybrids from a 6 x 6 diallel cross of *Abelmoschus esculentus* showed significant heritability for number of days to flowering, relative to the parent with higher values. Of these, four showed positive heterosis for fruit number.

Thaker *et al.* (1982) studied 21 crosses of seven varieties of *Abelmoschus esculentus* and reported per cent increase over the better parent in the F_1 which was the highest for fruit yield per plant, followed by number of fruits per plant and fruit length.

Balakrishna *et al.* (1983) evaluated 32 okra varieties and found high heritability estimates or plant height, number of pods per plant and number of seeds per pod. High genetic advance in percent of mean was obtained for number of pods per plant (39.5%) followed by plant height (31.29%) and number of seeds per pod (24.50%). The lowest genetic advance was obtained for pod length (7.20%).

Lal *et al.* (1983) observed okra varieties showing high heritability in plant height, pod length, number of seeds per pod, number of primary branches per plant and 1000-seed weight. Moderate genetic advance in percent of mean was observed for seed yield per pod (65.58%) and number of pods per plant (60.55%) where as it was minimum for pod length (8.60%).

Singh and Yunus (1985) reported the heritability value of okra ranged between 35.60% (harvest index) to 80.90% (plant height) and genetic advance from 5.98 (plant height) to 17.95% (biological yield).

De and Suriya (1986) reported the highest heritability for sterility percentage among the yield contributing characters of okra followed by number of pods per plant, yield per plant and 1000- seed weight. Sterility percentage, yield per plant and number of pods per plant showed higher genetic advance in percent of mean but 1000- seed weight exhibited high heritability with very low genetic advance in percent of mean.

Korla and Sharma (1988) studied six populations (P_1, P_2, F_1, F_2, BC_1, BC_2) of Abelmoschus *esculentus* for 3 seed characters. They reported that heritability was observed in none of the crosses for seeds/fruit, in one for seed weight/fruit and 1000-seed weight.

Gomathinayagam *et al.* (1991) reported moderate heritability (54.78%) for plant height but high heritability for days to maturity (98.88%). Genetic advance in percent of mean was high for pods per plant but low for days to maturity and plant height.

Loknath *et al.* (1991) worked on genetic variability and heritability of 8 yield components in 28 cultivars and found expected genetic advance as high as 68.4 % for plant height.

Sivagamasundhari *et al.* (1992) worked on heterosis among 30 hybrids in okra produced from a full diallel cross of 6 selected parents. They estimated heritability over the mid, better and best parents for yield and 7 related components. They found heterosis for all traits. They also reported that eight hybrid combinations exhibit positive and better than average heritability over the best parent for fruits/plant, fruit weight, fruit length and/or yield.

Wright (1992) reported that heritability in yield contributing characters of okra was high for days to maturity (94.88%) followed by 1000- seed weight (78.04%) and lowest for pods per plant (29.35%).

Kumbhani *et al.* (1993) studied on heterosis of okra on 28 hybrids derived from 8 x 8 diallel cross and observed significant differences between parents and hybrids for all characters studied. They reported high heterosis for yield/plant that seemed to have resulted from the combined effect of heterosis for yield component characters such as number of pods/plant, pod length, pod girth, plant height and internodal length.

Mandal and Dana (1993) studied on the F_1 and F_2 generations from a 6 x 6 diallel cross in *Abelmoschus esculentus,* without reciprocals and reported that only EMS 8 x Punjab Padmini shows significant heritability for earliness, while two crosses, Sel 10 x Punjab Padmini shows significant heritability for both plant height and fruits/plant.

Rajeswari and Nadarajan (1993) was observed high heritability coupled with moderate genetic advance in percent of mean for number of pods per plant and number of seeds per pod in okra. High heritability with low genetic advance in percent of mean was also reported for plant height, pod length and 1000- seed weight.

Singh and Mandal (1993) studied on the heritability of okra for yield and 8 component traits. They reported that heritability in broad sense, the highest for early yield (76 and 46 %) number of fruits/plant (69 and 58 %), number of branches/plant respectively.

Dayasagar (1994) studied on heterosis of 9 yield components in 6 cultivars and their 15 F_1 hybrids. He observed highest heritability for yield/plant in the cross Pusa Sawani x Parbhani Kranti.

Kumar (1994) estimated and noticed high heritability for plant height (64.65%) and low for pod length (19.58%) in okra.

Akanda *et al.* (1995) reported high values for heritability together with high genetic advance in percentage of mean (GA) for 1000- seed weight, plant height, seed yield per plant and pod length.

Chaubey and Singh (1995) evaluated 20 okra varieties and reported high heritability for total number of pods followed by seed yield per plant and 1000- seed weight. Genetics advances in percent of mean were higher for seed yield per plant followed by pod weight and total number of pods.

Poshiya and Vashi (1995) worked on heritability in okra and reported highest heritability of 27.32 % for fruit yield. The hybrids exhibiting significant heterosis for fruit yield and most of the other characters studied.

Choudhury and Das (1996) reported that eleven okra varieties were evaluated for yield and its attributing characters. High heritability with high genetic advance was found in seeds per pod followed by green pod yield per plant, and 100- seed weight.

Choudhury *et al.* (1996) found high heritability and high genetic advance for number of seeds per pod followed by seed yield per plant in okra. They also reported moderate value for number of pods per plant, number of primary branches and harvest index.

Shanthakumar *et al.* (1996) reported significant genotypic coefficient of variability together with heritability and genetic advance for plant height, number of pods per plant, seed yield per pod and harvest index.

Reddy *et al.* (1997) reported that thirty six genotypes of okra were evaluated in by and among the different characters and found high genetic advance along with moderate to high heritability and genetic coefficient of variation was observed for number of seeds per pod and 100- seed weight.

Kumar *et al.* (1998) studied 34 summer season growing okra genotypes and observed high genotypic advance with high heritability for plant height, number of pods per plant and 1000-seed weight in okra.

Mehetre *et al.* (1998) reported heritability estimation of eight okra varieties and found that estimates of heritability ranges from 89.60% (plant height) to 32.45% (stability). Expected genetic advance ranged from 7.10 % (pod length) to 49.60 % (green pod yield per plant).

Yousuf *et al.* (1998) reported in okra that broad sense heritability for grain yield per plant (69.56) and days to maturity (79.65) were high. Maximum genetic advance in percentage of mean was recorded for seed yield per plant (17.65) and 1000- seed weight (7.98). But pod length showed high heritability with moderate genetic advance in percentage of mean.

Paul and Sarmah (1999) reported that heritability estimates for yield contributing characters in okra like plant height, number of green pods per plant, 1000- seed weight and days to edible maturity were high except number of pod. Genetic advance in percentage of mean was high plant height and number of filled grains per pod and moderate for number of primary branch and harvest index.

Iffekhrauddaula *et al.* (2002) reported moderate value of heritability for number of pods per plant. They also observed that plant height; number of seeds per pod and 1000- seed weight had high heritability with moderate genetic advance in percentage of mean.

Sadhukhan and Chattapadhay (2003) studied 26 okra genotypes and reported that broad sense heritability was moderate to high for days to maturity, pod length, and number of seeds per pod along with high genetic advance in percentage of the population mean.

Hossain and Haque (2003) reported high heritability with high genetic advance in percentage of mean for the characters yield per plant, days to maturity and plant height but values were low for number of pods per plant, days to maturity and number of primary branches per plant.

2.2 Genetic Diversity

The wide diversity of genotypes showed by cluster analysis from the same geographical regions. To understand the usable variability, grouping or classification of genotypes based on suitable scale. Multivaiate analysis formulated by Mahalanobis (1963) is a powerful tool in quantifying the degree of divergence among biological population based on multiple characters. Studies on genetic diversity in okra carried out so far are presented as follows:

Nair and Mukharjee (1960) estimated degree of divergence between biological populations and relevant contribution of different components to the total divergence by D^2 statistic in teak.

Mahajan *et al.* (1980) worked on the genetic diversity (D^2 statistic) for 12 characters related to yield of okra developed from 14 crosses involving 22 parents. The genotypes were grouped into 5 clusters. Mostly the cultures in a cluster came from the same cross. The geographical diversity was associated with genetic diversity to some extent. Seven cultures were identified with genetic diversity, high yield component and multiple resistances to be utilized as parent's in future breeding program.

Kanwal *et al.* (1983) reported that genetic divergence studies on 100 strain using Mahalanobis's D^2 statistics and canonical variate analysis revealed that fruit weight, number of days to maturity, height and fruit size contributed most towards divergence. The strains were grouped into nine clusters, which were not correlated with geographical diversity.

Naskar *et al.* (1985) reported that when cluster analysis was applied to 9 characters in 22 diverse Indian genotypes in 1981 and 1982, all genotypes were grouped into 9 clusters in both years, although the clustering pattern was not consistent over the years. Genetically diverse (as estimated by Mahalanobis's D^2 statistic) use in crosses to give promising sergeants. High heterosis, it was suggested, could be achieved by crosses between members of distant clusters.

Pande and Ghorai (1986) also found that 52 improved varieties of cultivated okra genotypes from different eco-geographical areas were put to D^2 analysis. Grouping of genotypes in the same cluster confirmed that there is no parallelism between genetic diversity and geographical distribution. The differences between the characters were highly significant and the pattern of clustering was greatly influenced by environment. Genotypic variance was high for seeds per plant and pod length. Heading duration was affected by temperature in some varieties.

Reddy *et al.* (1987) worked on genetic divergence for pod yield/plant and 12 related characters by Mahalanobis's D^2 statistics, the greatest inter-cluster distance was observed between cluster I (with 10 to 11 varieties depending on years) and II (4 to 6 varieties) and between cluster I and IV.

Wu and Huang (1988) reported that on the basis of clustering analysis of quantitative characters, 35 slender grained, high quality rice varieties from southern China were grouped into 6 clusters Genetic distance was high between groups VI and I and between groups II and VI.

Digby *et al.* (1989) reported that the coordinates obtained from the Principal Component Analysis (PCA) to calculate distances among the points. PCA is used for the graphical representation of the points while PCO is used to calculate the minimum distance straight line between each pair of points.

Pyene et *al.* (1989) worked on the hierarchical nature of the grouping into various numbers of classes could impose undue constrains and the statistical properties of the resulting groups were not clear. Therefore, they have suggested non-hierarchical classification, as an alternative approach to optimize some suitability choosing criteria directly from the data matrix. They also reported that the squared distance between means were Mahalanobis's D^2 statistics when all the dimensions were used, could be computed using Principal Coordinate Analysis (PCO). They also commended the canonical vector analysis (CVA) for discriminatory purpose.

Sarathe and Perraju (1990) studied genetic diversity and heterosis in 62 okra varieties grouped into 18 clusters. Eight varieties were selected from these clusters on the basis of diversity estimates and popularity of variety. The 32 possible hybrids along with 8

parents fall into as many as 9 clusters. Direct relationship between genetic distance and heterobeltiosis did not occur but parental diversity seems to play an important role in expressing the positive heterobeltiosis. Most of the crosses did not show any relationship with divergence estimates.

Ibrahim *et al.* (1992) studied that the genetic divergence in okra population comprising nine morphologically different genotypes over the different environment (E) has been assessed through Mahalanobis's D^2-statistics. The analysis revealed considerable genetic divergence among genotypes. The genotypes under study fall into 3 constellations in E_1, E_2 and E_3 in D^2. Poongar, an indigenous short duration tall stature genotype, consistently occurred either in the same or closely related cluster in both stress (E_2 and E_3) and non-stress conditions (E_1).

Roy and Panwar (1993) studied divergence for yield/plant and 9 yield-related traits in 99 diverse genotypes using multivariate D^2 analysis. Genotypes were grouped into 16 clusters. Genetic divergence was controlled mainly by pods/plant, seed/pod, seed yield/plant, seeds/pod. The highest distance was between cluster XVI and cluster XIV.

Anandakumer and Subramaniam (1994) evaluated 28 cultures of okra genotypes to analysis genetic divergence. They found geographical diversity that need not necessarily be related to genetic divergence. Diverse plants of locally adopted may serve as better parent for upland rice environment.

Chauhan and Chauhan (1994) found 12 clusters through using D^2 statistics while studying genetic diversity. Thousand-grain weight contributed maximum to total

divergence. Other traits with appreciable contribution to total divergence were days to 50% flowering, pod weight and seeds/pod.

Mishra *et al.*, (1994) reported that the multivariance of divergence for 9 quantitative traits among 46 strains of okra grouped the genotypes into 5 clusters. The first cluster contained 36 genotypes, the second 5, while the third 3, fourth and fifth cluster each contained 1 genotype. Number of fertile seeds/plant, number of sterile seeds/plant and plant height were the highest contributors of Mahalanobis D^2 values.

Sawant *et al.*, (1995) analyzed data on 8 yield components of 75 genotypes and grouped into 10 clusters. The average inter-cluster distance was the highest between clusters IX and X (66.58), followed by cluster VI and XI (62.59) and cluster IV and X (56.52), suggesting that these groups of genotypes were highly divergent from each other.

Sarawgi and Shrivastava (1996) carried out D^2 analysis on data from 15 yield components measured in 16 parents and their 72 cross combinations under irrigated and rainfed conditions. On the basis of cluster distance, and performance within cluster, genotypes were grouped into 7 and 15 clusters, respectively, under irrigated and rainfed conditions.

Singh *et al.* (1996) noticed the nature and magnitude of genetic divergence in 40 genotypes of okra using Mahalanobis D^2-statistics for ten characters. The populations were grouped into six clusters. Yield contributed the most 39.56% of total divergence, and plant height contributed 15.65%. The genotypes belonging to cluster II and V having greater cluster distance are recommended for inclusion in a hybridization programme as they are expressed to produce good segregants.

Sardana *et al.* (1997) reported the nature of genetic divergence in the 82 local okra varieties of Tripura using D^2 statistics based on 15 agro-morphological characters. The cultivars were grouped into 18 clusters, of which cluster 1 with 15 genotypes was the largest. The genetic diversity was due to genetic drift, selection in peculiar topography and diverse agro-climatic condition of Tripura. Number of pods/plant, leaf area, seed weight/plant and seed yield/plant were the major components contributing to the genetic diversity.

Rao and Gomathinayagam (1998) assessed genetic divergence separately by using Mahalanobis D^2-statistics among 40 winter growing okra genotypes planted simultaneously under semi-dry condition at two different locations. Differential response of the genotypes to the environments has altered the clustering pattern between environments. Favorable environment yielded in lesser number of clusters by exploiting high genetic potential of different traits expressed by genotypes. Genotypes with stable genotype environment interaction in the expression of different traits were tending to group together in one cluster in both the environments.

Singh *et al.* (1998) reported the genetic divergence in okra that was carried out through multivariate analysis with 42 genotypes having 14 quantitative characters including grain yield. The genotypes were grouped into four clusters. No relationship between geographic origin and genetic diversity was observed. The four characters, viz. harvest index, total number of seeds/pod, number of fertile seeds/pod and stability accounted 92.65 % of the total divergence.

Kumari and Rangasamy (1999) estimated the genetic divergence using Mahalanobis D^2-statistics in 62 early okra genotypes. Based on eight important yield–contributing characters, these genotypes were grouped into six clusters. Cluster I was the largest,

containing 85% of genotypes. Cluster II, III, IV and V had two genotypes each. Cluster VI contained a single genotype. Character like seed yield per plant, pod length and plant height.

Soni *et al.* (1999) reported that genetic divergence of 132 okra genotypes (128 traditional cultivars and 4 standard genotypes) for 18 quality traits led to their grouping into 10 clusters. Grouping of genotypes in different clusters indicated the existence of significant amount of variability among the genotypes for the quality trials. Higher order of divergence was recorded between clusters VI and VII. Based on mean performance, genetic distance and clustering pattern, hybridization involving selected 10 genotypes are likely to give desirable segregants for seed quality.

Bansal *et al.* (2000) reported the genetic assessing of 36 okra stocks using Mahalanobis's D^2 statistics. Thirty four genotypes belonging to seven countries were divided into 15 clusters. The patterns of distribution of genotypes within various clusters were random and independent of geographical isolation. Based on the mean performance, genetic distance and clustering pattern, intercrossing of 15 selected genotypes may be useful in creating wider variability for early maturity, dwarf and high yielding segregants.

Hegde and Patil (2000) reported the genetic divergence in 40 genotypes of okra using Mahalanobis D^2-statistics. The cultivars fall into 7 clusters. Clusters I, II, III, and IV comprised 18, 14, 3 and 2 genotypes, respectively, while Cluster V, VI and VII were solitary clusters. The average inter-cluster D value was the highest (51.88) between the Clusters V and VII, indicating high genetic divergence between the cultivars of these 2 clusters. The highest contributing characters to D^2 values were pod number per plant, photosynthetic rate and 1000-seed weight.

Rather *et al.* (2001) studied the genetic divergence in 56 cultivars. Significant variations for days to 50% flowering, leaf length, leaf breadth, productive branches per plant, plant height, days to maturity, pod length, harvest index, seed yield, length breadth ratio of the seed and 100-seed weight were observed among cultivars. The highest mean value for harvest index and the lowest plant height were observed. Bases on the mean performance for plant height, maturity, seed yield and inter-cluster distance, cultivars from clusters II, and IV may be used for initiating hybridization.

Chapter 3

Materials and Methods

CHAPTER 3

MATERIALS AND METHODS

The investigation was carried out during the period from November 2007 to April 2008 to study on the morphological characterization and genetic diversity in okra. The details of the materials and methods employed have been presented below:

3.1 Experimental site

The experiment was conducted at the experimental field of the Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University (SAU), Sher-e-Bangla Nagar, Dhaka-1207. The location of the experimental site was at 23^0 74' N latitude and $90^0$35'E longitude with an elevation of 8.2 meter from the mean sea level. Field views of experimental plot are presented in Plate 1.

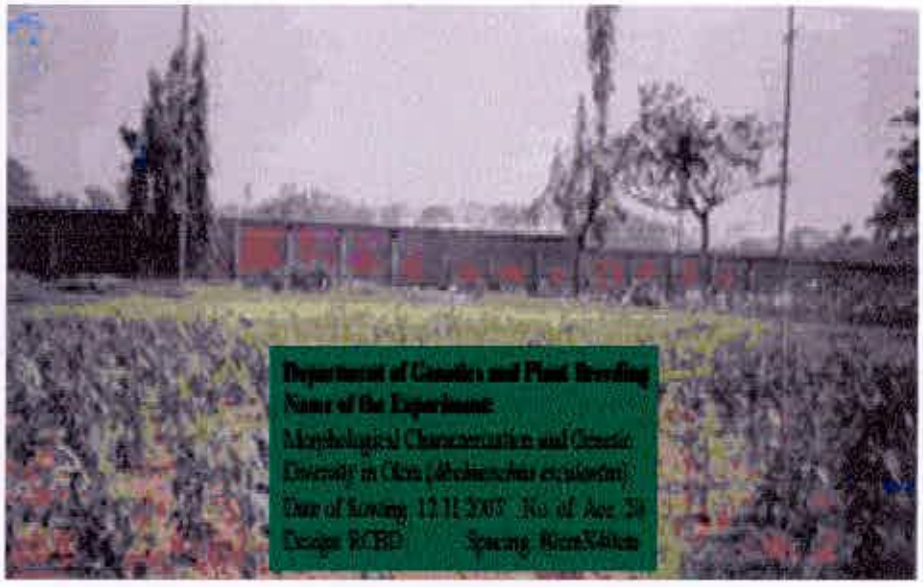
3.2 Characteristics of Soil

The soil of the experimental field was belonging to Madhupur Tract in Agro Ecological Zone (AEZ) 28. The soil of the experimental field was clay-loam in texture having a pH of around 6.2.

3.3 Climatic Condition of the Experimental Site

The experimental site is under the sub-tropical climatic zone. Details of the metrological data including maximum and minimum mean monthly temperature (^{O}C), relative humidity and sunshine (hours/day) for growing season was collected from the Bangladesh Metrological Department (Climate division), Agargaon, Dhaka-1207, presented in Appendix I.

a) Close field view



b) Field view

Plate 1. Field view of the experimental site

3.4 Planting Materials

Twenty genotypes of okra were used for the present research work. The all genotypes were produced in the 2006-2007 growing season of the crops. The purity and germination percentage were leveled as around 100 and above 92, respectively. The genetically pure and physically healthy seeds of these genotypes were collected from the Plant Genetic Resources Center (PGRC) and Horticulture Research Center (HRC) of Bangladesh Agricultural Research Institute (BARI), Gazipur. The name and origin of these genotypes are presented in Table 1.

Table 1. Name and origin of twenty okra gnotypes used in the present study

Sl. No.	Genotypes No.	BARI ACC Number	Origin
1	G_1	BD 9442	PGRC, BARI
2	G_2	BD 9444	PGRC, BARI
3	G_3	BD 9446	PGRC, BARI
4	G_4	BD 9454	PGRC, BARI
5	G_5	BD 9456	PGRC, BARI
6	G_6	BD 9457	PGRC, BARI
7	G_7	BD 9458	PGRC, BARI
8	G_8	BD 9460	PGRC, BARI
9	G_9	BD 9462	PGRC, BARI
10	G_{10}	BD 9463	PGRC, BARI
11	G_{11}	BD 9465	PGRC, BARI
12	G_{12}	BD 9470	PGRC, BARI
13	G_{13}	BD 9474	PGRC, BARI
14	G_{14}	BD 9475	PGRC, BARI
15	G_{15}	BD 9476	PGRC, BARI
16	G_{16}	BD 9477	PGRC, BARI
17	G_{17}	BD 9478	PGRC, BARI
18	G_{18}	BD 9480	PGRC, BARI
19	G_{19}	BD 9494	PGRC, BARI
20	G_{20}	BARI Okra-1	HRC, BARI

3.5 Land preparation

The experiment plot was prepared by several ploughing and cross ploughing followed by laddering and harrowing with tractor and power tiller to bring about good tilth in the first week of November 2007. Weeds and other stables were removed carefully from the experimental plot and leveled properly.

3.6 Design and layout

The experiment was laid out Randomized Complete Block Design (RCBD) with three replications. The individual plot was 4 m × 0.8 m in size. The twenty genotypes of the experiment were assigned at random into twenty plots of each replication. The distance maintained 80 cm × 40 cm spacing from row to row and plant to plant, respectively. The distance maintained between two blocks was 1m.

3.7 Fertilizers and manure application

The fertilizers N, P and K were applied in the form of Urea, TSP and MP respectively. The cowdung was used as manure. During the final land preparation, the whole amount of cowdung and TSP were applied as basal dose. Urea and MP were applied in three equal installments at 15 days after sowing (DAS), 35 days after sowing (DAS), and 50 days after sowing (DAS). The dose and method of application of fertilizers and manure are shown in Table 2.

3.8 Sowing of seeds

The seeds of okra were sown in lines in the experimental plots on November 12, 2007. The seeds were soaked for twenty four hours into water before sowing. The seeds were placed at about 1.5 cm depth in the soil. The seed rate was 4 kg/ha.

Table 2. Dose and method of application of fertilizers and manure in okra field

Sl. No.	Fertilizer/ Manure	Dose	Application procedure			
			Basal	1st Inst.*	2nd Inst.**	3rd Inst.***
01.	Cowdung	10 t/ha	10 t/ha	---	---	---
02.	Urea	150 kg/ha	---	50 kg/ha	50 kg/ha	50 kg/ha
03.	TSP	100 kg/ha	kg/ha	---	---	---
04.	MP	150 kg/ha	---	50 kg/ha	50 kg/ha	50 kg/ha

* = 15 days after sowing (DAS)
* * = 35 days after sowing (DAS)
* ** = 50 days after sowing (DAS)
Inst. = Installment.
(Source: Sobji Biggan by Dr. Mamunur Rashid, 1999)

3.9 Gap filling

Gap filling was done for maintaining a distance of 40 cm from plant to plant after 10 days after sowing (DAS).

3.10 Weeding

The weeding was done 15 days after sowing (DAS). The second weeding was done 35 days after sowing (DAS). Weeding was done to keep the plots free from weeds, easy aeration of soil and to conserve soil moisture, which ultimately ensured better growth and development.

3.11 Irrigation and after-care

The moisture was not sufficient in the soil so that a pre-sowing irrigation was given in the experimental field. The okra field was irrigated every fifth or sixth day whenever required in the crop season. Earthing up in the rows was done especially for there is no water logged condition.

3.12 Top dressing

Urea and MP were applied by three equal installments. The first, second and third one-third of the urea and MP were top dressed at 15 days after sowing (DAS), 35 days after sowing (DAS) and 50 days after sowing (DAS) at the time of flower initiation, respectively.

3.13 Pesticide application

Yellow vein mosaic virus was transmitted by an insect vector known as white fly. The crop was protected from the attack of white fly by spraying Ripcord @ 0.5 ml/liter of water and Marshal @ 0.5 ml/liter of water for 8 times at an interval of 12 days. Ridomyl Gold @ 0.2 % was sprayed 5 times at an interval of 10 days as a preventive measure against different fungal disease and foot rot. Both the insecticide and fungicide were applied in the evening.

3.14 Harvesting, threshing and cleaning

The edible green pods were harvested depending upon the maturity of each genotype. The okra pods were continuously harvested every second or third days. Harvesting was done manually. The matured pods were harvested for the seed and enough care was taken for harvesting, threshing and also cleaning of okra seed.

3.15 Data recording

Data were recorded on individual plant basis from 10 randomly selected plants in each line in every replication. The following characters were studied on the basis of plant phenology such as days to 50 % flowering, days to edible maturity, plant height, height to 1st node from the ground, no. of branches/plant, number pods/plant, length

of pod, diameter of pod, individual pod weight, number seeds/pod and yield/plant. The following data were collected from field and in the laboratory after harvest.

3.15.1 Days to 50 % flowering

Days to 50% flowering of each genotype was measured on the basis of 50% flowering of planted genotypes in field condition.

3.15.2 Days to edible maturity

Days to edible maturity of each genotype was measured on the basis of the number of days required from fruit setting to edible maturity.

3.15.3 Plant height (cm)

The plant height was taken from 10 randomly selected plants of each plot after harvest. Data was recorded in centimeter (cm). The height was measured from the ground level to the tip of the growing point of the main branch.

3.15.4 Height to 1st node from the ground (cm)

Recorded as the distance first node of the main branch from the ground level. The data was recorded in centimeter (cm) after harvest.

3.15.5 Number of branches per plant

The branches of the plant were counted after harvesting in manually.

3.15.6 Number pods per plant

Mean number of fruits (pods) from ten randomly selected plants of each genotype in each replication.

3.15.7 Length of pod (cm)

The length of pod excluding peduncle. Data was recorded in centimeter (cm) of mean length of ten randomly selected fruits

3.15.8 Diameter of pod (cm)

The diameter of pod at mid position. Data was recorded in centimeter (cm) of mean length of ten randomly selected fruits

3.15.9 Individual pod weight (g)

Mean weight of 10 randomly selected pod. The individual pod weight was recorded in gram (g) by measuring on electrical balance.

3.15.10 Number seeds per pod

Mean number of seeds from ten randomly selected pods.

3.15.11 Yield/plant (g)

Mean weight of pods from ten randomly selected plants. Data was recorded in gram (g) by measuring on electrical balance.

3.16 Statistical analysis

Mean data of the characters were subjected to both univariate and multivariate analysis. Univariate analysis of the individual character (Analysis of variance) was done for all characters under study using the mean values (Singh and Chaudhury, 1985) and was estimated using MSTAT-C computer program. Duncan's Multiple Range Test (DMRT) was performed for all the characters to test the differences between the means of the genotypes following Steal and Torrie (1960). Mean, range and co-efficient of variation (CV %) were also estimated using MSTAT-C. Multivariate analysis was done by computer using GENSTAT 5.13 and Microsoft Excel 2000 software through four techniques *viz.*, Principal Component Analysis (PCA), Principal Coordinate Analysis (PCO), Cluster Analysis (CA) and Canonical Variate Analysis (CVA).

3.16.1 Univariate Analysis

All recorded data obtained for each character were subjected to the analysis of variance following the RCBD design. Means (X), ranges and standard deviations (O_x) of characters studied in this experiment also were estimated.

3.16.1.1 Estimation of genotypic, phenotypic and error variances

Genotypic and phenotypic variances were estimated according to the formula given by Johnson *et al.* (1955)

$$\text{Genotypic variance } (\sigma^2_g) = \frac{GMS - EMS}{r}$$

Where,
GMS = Genotypic mean sum of squares
EMS = Error mean sum of square
r = number of replication

$$\text{Phenotypic variance } (\sigma^2_{ph}) = \sigma^2_g + \text{EMS}$$

Where,
σ^2_g = Genotypic variance
EMS = Error mean sum of square
$= \sigma^2_e$ (error variance)

3.16.1.2 Estimation of genotypic and phenotypic co-efficient of variation

Genotypic and phenotypic co-efficient of variation were calculated by the formula suggested by Burton (1952)

$$\text{Genotypic co-efficient of variation (GCV \%)} = \sqrt{\frac{\sigma^2_g}{\bar{x}}} \times 100$$

Where,
σ^2_g = Genotypic variance
σ_g = Genotypic standard deviation
$\bar{x}$ = Population mean

Similarly,

The phenotypic co-efficient of variation was calculated from the following formula.

$$\text{Phenotypic co-efficient variation (PCV)} = \sqrt{\frac{\sigma^2_{ph}}{\bar{x}}} \times 100$$

Where,

σ^2_{ph}= Phenotypic variance

σ_{ph} = Phenotypic standard deviation

$\bar{x}$ = Population mean

3.16.1.3 Estimation of heritability

Broad sense heritability was estimated (Lush, 1949) by the following formula, suggested by Hanson *et al.* (1956) and Johnson *et al.* (1955).

$$h^2_b\% = \frac{\sigma^2_g}{\sigma^2_{ph}} \times 100$$

Where,

h^2_b = Heritability in broad sense

σ^2_g = Genotypic variance

σ^2_{ph} = Phenotypic variance

3.16.1.4 Estimation of genetic advance

The expected genetic advance for different characters under selection was estimated using the formula suggested by Lush (1949) and Johnson *et al.* (1955).

$$\text{Genetic advance (GA)} = K.\, h^2.\, \sigma_{ph}$$

$$= K.\frac{\sigma^2_g}{\sigma^2_{ph}}.\sigma_{ph}$$

Where,

K = Selection intensity, the value which is 2.06 at 5% selection intensity

σ_{ph} = Phenotypic standard deviation

h^2_b = Heritability in broad sense

σ^2_g = Genotypic variance

σ^2_{ph} = Phenotypic variance

3.16.1.5 Estimation of genetic advance of mean

Genetic advance as percentage of mean was calculated from the following formula as proposed by Comstock and Robinson (1952):

$$\text{Genetic advance (\% of mean)} = \frac{Genetic\ advance\ (GA)}{Population\ \ mean\ (\bar{x})} \times 100$$

3.16.2 Multivariate analysis

The genetic diversity among the genotypes was assessed by Mahalanobis's (1936) general distance (D^2) statistic and its auxiliary analyses. The parent's selection in hybridization programme based on Mahalanobis's D^2 statistic is more reliable as requisite knowledge of parents in respect of a mass of characteristics is available prior to crossing. Rao (1952) suggested that the quantification of genetic diversity through biometrical procedures had made it possible to choose genetically diverse parents for a hybridization program. Multivariate analysis viz. Principal Component analysis, Principal Coordinate analysis, Cluster analysis and Canonical Variate analysis (CVA), which quantify the differences among several quantitative traits, are efficient method of evaluating genetic diversity. These are as follows:

3.16.2.1 Principal Component analysis (PCA)

Principal Component analysis, one of the multivariate techniques, is used to examine the inter-relationships among several characters and can be done from the sum of squares and products matrix for the characters. Thus, PCA finds linear combinations of a set variate that maximize the variation contained within them, thereby displaying most of the original variability in a smaller number of dimensions. Therefore, Principles components were computed from the correlation matrix and genotypes scores obtained for first components (which has the property of accounting for

maximum variance) and succeeding components with latent roots greater than unity (Jeger *et al.*, 1983). Contribution of the different morphological characters towards divergence is discussed from the latent vectors of the first two principal components.

3.16.2.2 Principal Coordinate analysis (PCO)

Principal Coordinate analysis is equivalent to PCA but it is used to calculate inter unit distances. Through the use of all dimension of p it gives the minimum distance between each pair of the n points using similarity matrix (Digby *et al.*, 1989).

3.16.2.3 Cluster analysis (CA)

Cluster analysis divides the genotypes of a data set into some number of mutually exclusive groups. Clustering was done using non-hierarchical classification. In Genstat, the algorithm is used to search for optimal values of chosen criterion proceeds as follows. Starting from some initial classification of the genotypes into required number of groups, the algorithm repeatedly transferred genotypes from one group to another so long as such transfer improved the value of the criterion. When no further transfer can be found to improve the criterion, the algorithm switches to a second stage which examines the effect of swooping two genotypes of different classes and so on.

3.16.2.4 Canonical Vector analysis (CVA)

Canonical Vector analysis (CVA) finds linear combination of original variabilities that maximize the ratio of between group to within group variation, thereby giving functions of the original variables that can be used to discriminate between the groups. Thus, in this analysis a series of orthogonal transformations sequentially maximizing of the ratio of the among groups to the within group variations. The

canonical variate are based upon the roots and vectors of WB, where W is the pooled within groups covariance matrix and B is the among groups covariance matrix.

3.16.2.5 Calculation of D^2 values

The Mahalanobis's distance (D^2) values were calculated from transformed uncorrelated means of characters according to Rao (1952), and Singh and Chaudhury (1979). The D^2 values were estimated for all possible combinations between genotypes. In simpler form D^2 statistic is defined by the formula:

$$D^2 = \sum_{i}^{x} d_i^2 = \sum_{i}^{x} (Y_i^j - Y_j^k) \qquad (j \neq k)$$

Where,

Y = Uncorrelated variable (character) which varies from i = 1 ----------to x
x = Number of characters.
Superscript j and k to Y = A pair of any two genotypes.

3.16.2.6 Computation of average intra-cluster distances

Average intra-cluster distances were calculated by the following formula as suggested by Singh and Chuadhury (1979).

$$\text{Average intra-cluster distance} = \frac{\sum D_i^2}{n}$$

Where,

D_i^2 = The sum of distances between all possible combinations (n) of genotypes included in a cluster.
n = Number of all possible combinations between the populations in cluster.

3.16.2.7 Computation of average inter-cluster distances

Average inter-cluster distances were calculated by the following formula as suggested by Singh and Chuadhury (1979).

$$\text{Average inter-cluster distance} = \frac{\sum D_{ij}^2}{n_i \times n_j}$$

Where,

$\sum D_{ij}^2$ = The sum of distances between all possible combinations of the populations in cluster i and j.

n_i = Number of populations in cluster i.

n_j = Number of populations in cluster j.

3.16.2.8 Cluster diagram

Using the values of intra and inter-cluster distances ($D = \sqrt{D^2}$), a cluster diagram was drawn as suggested by Singh and Chuadhury (1979). It gives a brief idea of the pattern of diversity among the genotypes included in a cluster.

3.16.2.9 Selection of varieties for future hybridization program

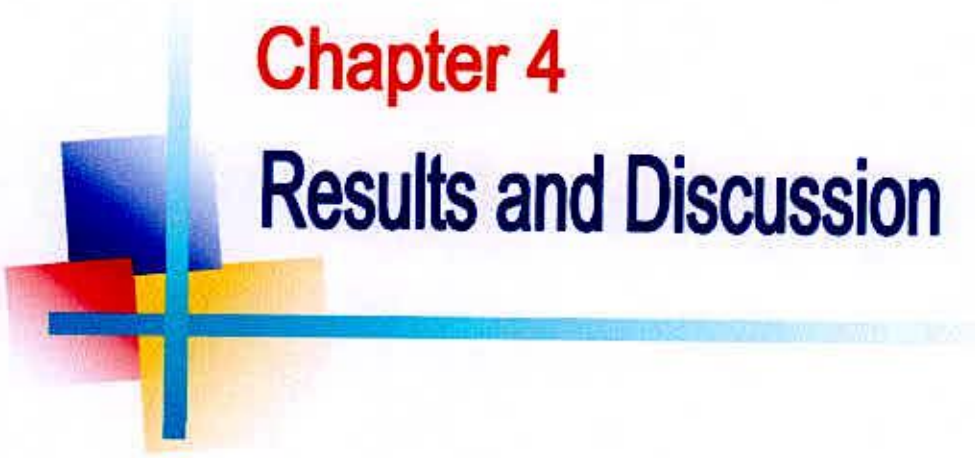
Divergence analysis is usually performed to identify the diverse genotypes for hybridization purposes. The genotypes grouped together are less divergent among themselves than those, which fall into different clusters. Clusters separated by largest statistical distance (D^2) express the maximum divergence among the genotypes included into these different clusters. Variety (s) or line(s) were selected for efficient hybridization program according to Singh and Chuadhury (1985). According to them the following points should be considered while selecting genotypes for hybridization program:

i. Choice of cluster from which genotypes are selected for use as parent (s)

ii. Selection of particular genotype(s) from the selected cluster(s)

iii. Relative contribution of the characters to the total divergence

iv. Other important characters of the genotypes (per se performance)



Chapter 4

Results and Discussion

CHAPTER 4

RESULTS AND DISCUSSION

The present study was carried out to determine the breeding values relating to mean performance and genotypic effects of the twenty different genotypes of okra. This part comprises the presentation and discussion of the findings obtained from the study. The analytical results (analysis of variance) are present in Table 3. The mean performance of twenty okra genotypes in respect of different quantitative characters such as days to 50 % flowering, days to edible maturity, plant height, height to 1st node from the ground, number of branches/plant, number pods/plant, length of pod, diameter of pod, individual pod weight, number seeds/pod and yield/plant were analyzed by Duncan's Multiple Range Test (DMRT) (Table 4). The range, mean, genotypic variance, phenotypic variance, environmental variance, genotypic co-efficient of variation, phenotypic co-efficient of variation, heritability, genetic advance and genetic advance in percent of mean are presented in Table 5. Plant breeding revolves around selection, which can be effectively practiced only in the presence of variability of desired traits. Hence, variability is the prerequisite for success of breeding. The data pertaining to 11 characters were computed and statistically analyzed and the results related to various genetic parameters of the genotypes studied are presented discussed following section-wise –

4.1 Mean performance of the twenty okra genotypes

4.2 Variability, heritability and Character association

4.3 Genetic diversity

4.4 Comparison of results based on different multivariate technique

4.5 Selection of the genotypes for future hybridization programme.

4.1 The Mean performance of the twenty okra genotypes

There were significant variations among the genotypes for all the characters showed by analysis of variance for the characters studied. As a result, there was genetic variation presented among the genotypes for the characters studied (Table 3).The mean performance of the twenty genotypes of okra for yield and yield related characters are given in Table 4. A comparative photograph of morphological view of different genotypes are presented in Plate 2.

4.1.1 Days to 50%flowering

The study of performance of different genotypes showed that the genotype BD 9458 took longest period for days to 50 % flowering (78.00 days) which was significantly different from the second highest genotype BD 9476 (74.30 days). The genotypes BD 9446 (63.3 days), BD 9460 (62.67 days), BD 9494 (62.33 days), BD 9478 (60.33 days) and BD 9470 (58.33 days) which were not significantly different from the one to another and were characterized as medium days to 50 % flowering type. The genotype BD 9463 was required minimum days to 50 % flowering (56.33 days).

The genotype required more days to flowering as they produced more fruits. The plant produced less fruits as there were fewer flowers and lower fruit setting. The number of floral buds visible on the day of first flowering, 70% formed edible fruits in fruit plants but only 46 % in seed plants (Akorada, 1986). There was a significant interaction for number of days to flowering and number of branches per plants (Ariyo, 1987).

Table 3: Analysis of variances for yield and yield related eleven characters of twenty okra genotypes

Source of variation (Characters)	Degrees of freedom (df)			Mean sum of squares		
	Replication	Genotypes	Error	Replication	Genotypes	Error
Day to 50% flowering	2	19	38	12.217	103.982**	14.603
Days to edible maturity	2	19	38	20.850	197.255**	20.306
Plant height (cm)	2	19	38	0.938	1329.034**	26.609
Height 1st node from the ground	2	19	38	1.927	14.613**	9.391
Number of branches/plant	2	19	38	0.447	3.463**	0.343
Number of pods/plant	2	19	38	1.477	20.755**	0.451
Length of pod (cm)	2	19	38	3.272	14.056**	4.990
Diameter of pod (cm)	2	19	38	0.014	0.071**	0.005
Individual pod weight (g)	2	19	38	0.889	28.795**	1.234
Number of seeds/pod	2	19	38	23.529	386.551**	14.026
Yield/plant (g)	2	19	38	0.365	3624.646**	25.733

**** Significant at 1% level of probability**

Table 4. Mean performance of twenty different okra genotypes in respect of eleven quantitative characters

Genotypes	BARI ACC Number	Days to 50 % flowering	Days to edible maturity	Plant height (cm)	Height to 1st node from the ground (cm)	Number of branches / plant	Number of pods / plant	Length of pod (cm)	Diameter of pod (cm)	Individual pod weight (g)	Number of seeds/ pod	Yield/ plant (g)
G_1	BD 9442	72.33 b-d	85.33 b-e	82.67 de	14.50 d-h	3.76 c-f	9.85 de	10.99 a-e	1.51 h-l	18.84 a	63.30 b-e	172.8 cd
G_2	BD 9444	67.00 c-h	80.33 d-g	66.27 gh	19.43 b-d	3.00 e-h	10.26 de	13.02 ab	1.70 b-e	15.33 bc	57.17 e-g	151.7 gh
G_3	BD 9446	63.30 f-j	76.00 f-i	57.57 h-j	20.20 b-d	2.69 f-j	8.55 f-h	8.68 b-e	1.61 d-i	11.38 f-h	49.35 h-j	124.8 k
G_4	BD 9454	68.67 c-g	81.00 d-f	92.33 c	16.37 d-f	3.61 d-f	10.45 d	10.65 a-e	1.73 b-d	16.97 b	61.47 c-f	168.7 de
G_5	BD 9456	69.33 b-g	82.00 c-f	58.30 h-j	22.50 a-c	2.73 f-j	9.06 e-g	8.96 b-e	1.90 a	15.67 bc	72.70 a	133.9 j
G_6	BD 9457	65.33 d-i	79.33 e-h	70.33 fg	17.73 c-e	3.10 e-g	10.37 d	9.90 b-e	1.71 b-e	12.93 d-f	58.00 d-g	158.6 fg
G_7	BD 9458	78.00 a	101.0 a	95.50 bc	5.36 l	4.69 a-c	17.04 a	9.17 b-e	1.63 c-h	11.67 f-h	52.53 g-i	190.6 a
G_8	BD 9460	62.67 g-j	74.33 f-i	50.57 jk	7.40 j-l	1.96 h-j	7.54 hi	8.18 de	1.49 i-l	10.67 g-i	45.07 jk	112.6 l
G_9	BD 9462	71.00 c-e	72.00 g-i	112.00 a	11.40 f-k	5.26 a	13.03 bc	12.69 a-c	1.59 e-j	14.3 c-e	67.80 a-c	182.6 ab
G_{10}	BD 9463	56.33 j	68.00 i	40.30 l	26.47 a	1.61 j	6.86 i	7.19 e	1.25 m	6.99 k	32.90 m	80.9 n
G_{11}	BD 9465	74.00 b-c	88.33 b-d	102.6 b	7.60 i-l	2.99 e-h	13.47 b	7.66 e	1.79 ab	14.60c-e	64.17 b-d	185.6 ab
G_{12}	BD 9470	58.33 ij	71.33 hi	52.67 i-k	13.37 e-i	3.23 e-g	6.99 i	12.98 ab	1.43 kl	8.96 ij	60.83 c-f	97.5 m
G_{13}	BD 9474	67.33 c-h	82.00 c-f	60.27 hi	11.27 f-k	4.92 ab	9.68 d-f	14.26 a	1.69 b-f	12.3 f-h	53.93 gh	148.3 hi
G_{14}	BD 9475	73.00 b-e	91.33 b	88.20 cd	15.37 d-g	3.96 b-e	12.23 c	12.17 a-d	1.53 g-l	12.68 e-g	68.67 ab	178.5 bc
G_{15}	BD 9476	74.30 b	92.00 b	44.20 kl	8.36 i-l	2.35 g-j	6.983 i	7.39 e	1.41 l	7.56 jk	36.17 lm	88.4 n
G_{16}	BD 9477	63.67 e-i	75.33 f-i	76.40 ef	10.27 g-l	2.82 f-i	9.18 d-f	9.36 b-e	1.66 b-g	11.93 f-h	55.10 f-h	142.8 i
G_{17}	BD 9478	60.33 h-j	89.67 bc	46.77 kl	24.43 ab	2.43 g-j	7.91 g-i	8.38 c-e	1.50 h-l	10.97 f-h	46.70 i-k	119.6 kl
G_{18}	BD 9480	70.33 b-f	85.33 b-e	80.53 de	12.63 e-j	4.36 a-d	12.61 bc	12.39 a-d	1.56 f-k	14.90 cd	66.77 a-c	180.6 bc
G_{19}	BD 9494	62.33 g-j	77.33 e-h	47.40 kl	9.33 h-l	1.83 ij	7.51 hi	7.99 de	1.46 j-l	10.33 hi	42.80 jk	102.6 m
G_{20}	BARI Okra-1	64.33 e-i	82.00 c-f	58.40 h-j	6.46 kl	1.72 ij	10.39 d	10.16 a-e	1.76 bc	15.90 bc	40.67 kl	161.6 ef
Mean		**67.18**	**81.70**	**69.16**	**14.02**	**3.15**	**10.00**	**10.10**	**1.59**	**12.75**	**54.80**	**144.13**
CV %		**5.69**	**5.52**	**7.46**	**21.85**	**18.57**	**6.72**	**21.10**	**4.47**	**8.71**	**6.83**	**3.52**

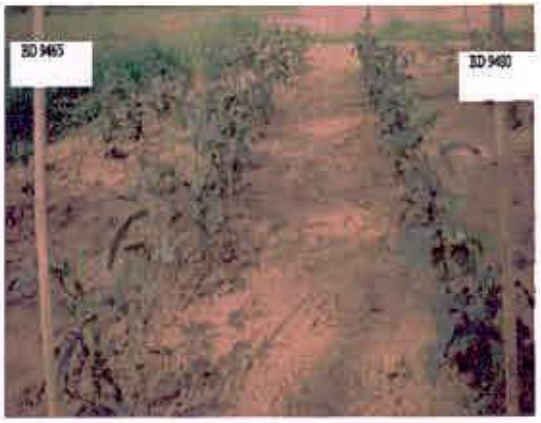
(A). Photograph showing morphology of BD 9442 and BD 9456

(B). Photograph showing morphology of BD 9454

(C). Photograph showing morphology of BD 9458 and BD 9463

(D). Photograph showing morphology of BD 9476 and BD 9457

(E). Photograph showing morphology of BD 9460 and BD 9475



(F).Photograph showing morphology of BD 9465 and BD 9480

Plate 2. A comparative field view of different genotypes of Okra

Plate 2. (Cont'd)

(G). Photograph showing morphology of BD 9444 and BARI Okra-1

(H). Photograph showing morphology of BD 9446 and BD 9474

(I). Photograph showing morphology of BD 9494, BD 9477 and BD 9462

(J). Photograph showing morphology of BD 9470 and BD 9478

4.1.2 Days to edible Maturity

Among the twenty different okra genotypes, the BD 9463 was the early maturity type (56.33 days) variety. On the other hand the genotype BD 9458 (78.00 days) was the mostly late maturity type which was significantly different from the other genotype. A significant variation was recorded among the genotypes in consideration of days to maturity (Table 4). Khanobdee and Lertsilpmongkol (1993) reported that average days to edible maturity among the genotypes reached at 14 days after flowering and the suitable harvesting period were 15 days after flowering.

4.1.3 Plant height (cm)

The genotype BD 9463 was the short type variety (40.30 cm) which was significantly different from the BD 9460 (50.57 cm), BD 9446 (57.57 cm). The BD 9462 (112.0 cm) was the tallest and significantly different from the BD 9465 (102.6 cm) genotype. Plant height significantly different among the genotypes for number of branches per plant, pod number per plant and pod yield (Reo *et al.*, 1989). The all genotypes respond differently and significant variation in the plant height (Gondane and Bhatia, 1995).

4.1.4 Height to 1st node from the ground (cm)

The height of the 1st node from the ground level BD 9463 showed (26.47 cm) highest height to 1st node from the ground and lowest BD 9458 showed lowest (5.36 cm) which were significantly different from the BD 9444 (19.43 cm) and BD 9474 (11.27 cm), respectively.

The height to 1st node from the ground was significantly different among the genotypes (Patel and Dalal, 1992). The less height to 1st node from the ground after

that the changes of more branches per plant were high. Gondane and Bhatia (1995) reported that significant and mark variation in the yield components and nodes to first pod.

4.1.5 Number of branches per plant

The highest number of branches per plant was produced by BD 9462 (5.26) followed by BD 9474 (4.92) and they were statistically similar (Table 4). The lowest number of branches per plant was produced by BD 9463 (1.61) which was not significantly different from BD 9470 (1.72), BD 9494 (1.83), BD 9460(1.97), BD 9476 (2.53), BD 9478 (2.43), BD 9446 (2.69) and BD 9456 (2.73).

The number of branches per plant was increased the number of pods per plant. Rao *et al.*, (1989) reported the number of branches was greater at the lower density.

4.1.6 Number of Pods per plant

The genotype BD 9458 (17.04) was produced highest number of pods per plant and highly significant followed by BD 9465 (13.47). The lowest number of pods per plant was produced by BD 9463 (6.86) which was not significantly different from BD 9476 (6.98), BD 9470 (6.99), BD 9494 (7.51), BD 9460 (7.54) and BD 9478 (7.91).

The number of pod was significantly different among the genotypes. Singh and Singh (1978) reported that highly significant of the number the pods per plant among the genotypes. The BD 9458 (17.04) was significantly better for pod number per plant and pod yield (Rao *et al.*, 1989). Das and Mishra (1995) reported that all genotypes differed significantly for pod yield per plant.

4.1.7 Length of pods (cm)

The highest length of pods was produced by BD 9474 (14.26 cm) which was not significantly different from BD 9444 (13.02 cm), BD 9470 (12.98 cm), BD 9480 (12.69 cm), BD 9480 (12.39 cm), BD 9475 (12.17 cm), BD 9442 (10.99 cm), BD 9454 (10.65 cm) and BARI Okra-1 (10.16 cm). The lowest length of pods was produced by BD 9463 (7.19 cm) which was not significantly different from BD 9476 (7.39 cm), BD 9465 (7.66 cm), BD 9494 (7.99 cm), BD 9460 (8.18 cm), BD 9478 (8.38 cm), BD 9446 (8.68 cm) and BD 9456 (8.96 cm).

The length of pod was related to the number of branches, plant density and the length of pod was greater at lower density (Rao *et al.*, 1989). Kumbhani *et al.* (1993) was observed significant different for pod length. Das and Mishra (1995) reported that all genotypes differed significantly for fruit length.

4.1.8 Diameter of pod (cm)

A significant variation was recorded among the genotypes in consideration of diameter of pod (cm) (Table 4). Maximum identical diameters of pod (1.90 cm and 1.79 cm) were recorded among the genotypes BD 9456 and BD 9465, respectively followed by BARI Okra-1 (1.76 cm). Minimum diameter of pod (1.25 cm) were obtained from the genotype BD 9463 followed by BD 9476 (1.41 cm).

The significant difference for diameter of pod among the genotypes (Kumbhani *et al.*, 1993). The all genotypes differed significantly for pod diameter (fruit girth) (Das and Mishra, 1995). Hossain, (1997) that the significant variation among the genotypes for pod diameter and from the results showed that there was considerable genetic variability in the genetic materials

4.1.9 Individual pod weight (g)

The highest individual pod weight was produced by BD 9442 (18.84 g) which was significantly different from BD 9454 (16.97 g). The lowest individual pod weight was produced by BD 9463 (6.99 g) followed by BD 9476 (7.57 g).

The significant variation among the genotypes for individual pod weight was observed and concluded that there was considerable genetic variability in the materials (Hossain, 1997). Das and Mishra (1995) reported that all genotypes differed significantly for individual pod weight.

4.1.10 Number of seeds per pod

The highest number of seeds per pod was produced by BD 9456 (72.70) which was not significantly different from BD 9475 (68.67), BD 9462 (67.80), BD 9480 (66.77). The lowest number of seeds per pod was produced by BD 9463 (32.90) and BD 9476 (36.17) followed by BARI Okra-1 (40.67).

The significant difference for number of seeds per pod among the genotypes. The all genotypes differed significantly for number of seeds per pod (Das and Mishra, 1995). The significant variation among the genotypes for number of seeds per pod and from the results showed that there was considerable genetic variability in the genetic materials (Hossain, 1997). Reddy and Kumar, (1998) reported that the yield contributing characters in okra 1000 seed weight showed maximum contribution to total variability.

4.1.11 Yield per plant (g)

The highest yield per plant produced by genotype BD 9458 (190.6 g) which was not significantly different from BD 9465 (185.6 g) and BD 9462 (182.6 g). The lowest

yield per plant produced by genotype BD 9463 (80.90 g) and BD 9476 (88.40 g) followed by BD 9470 (97.50 g) and BD 9494 (102.6 g).

It is noticeable from the results that differences among the genotypes are low in respect of yield per plant which might be due to local genotypes. All the genotypes responded differently to the environments (Gondane and Bhatia, 1995). The all genotypes differed significantly for yield per plant (Das and Mishra, 1995). Hossain, (1997) reported that the significant variation among the genotypes for fruit yield as well as yield per plant and from the results showed that there was considerable genetic variability in the genetic materials.

4.2 Studies on variability, heritability and Character association

4.2.1 Variability, Heritability and Genetic Advance

The genotypes differed significantly for all the characters (Table 5). Estimate of mean, range, genotypic variance (σ^2g), phenotypic variance (σ^2p) and environmental variance (σ^2e), genotypic coefficient of variation (GCV), phenotypic coefficients of variation (PCV), heritability (h^2b), genetic advance (GA) and Genetic Advance in percentage of mean are presented in Table 5. Variability of twenty okra genotypes is described below for each character.

4.2.2 The different genetic parameter in respect of different characters are discussed below:

4. 2.2.1 Days to 50%flowering

Analysis of variance for days to 50% flowering showed highly significant variation among the genotypes for this trait (Table 3). The mean value for this trait was 67.18 and ranged from 56.33 (G_{10}) – 78.00 days (G_7) (Table 5). The genotypic and phenotypic variances were 29.79 and 44.396 respectively. The difference between

Table 5: Genetic component of variation for eleven yield & yield contributing characters of twenty okra genotypes

Characters	Range		Mean	Genotypic mean sum of square	σ^2_g	σ^2_e	σ^2_p	h^2b	GA (5%)	GA (5%) of mean	GCV (%)	PCV (%)	ECV (%)
	Min.	Max.											
Day to 50% flowering	56.33	78.00	67.18	103.982**	29.79	14.603	44.396	67.107	9.211	13.710	8.125	9.917	5.688
Days to edible maturity	68.00	101.00	81.70	197.255**	58.97	20.306	79.279	74.386	13.644	16.700	9.399	10.898	5.516
Plant height (cm)	40.30	112.00	69.16	1329.034**	434.14	26.609	460.750	94.229	41.664	60.240	30.126	31.035	7.458
Height 1st node from the ground (cm)	5.367	26.47	14.02	14.613**	35.07	9.391	44.465	78.880	10.835	77.268	42.230	47.551	21.853
Number of branches/plant	1.613	5.26	3.15	3.463**	1.04	0.343	1.383	75.199	1.822	57.760	32.333	37.286	18.569
Number of pods/plant	6.867	17.04	10.00	20.755**	6.77	0.451	7.219	93.753	5.189	51.890	26.015	26.868	6.716
Length of pod (cm)	7.190	14.26	10.10	14.056**	3.02	4.990	8.012	37.718	2.199	21.756	17.196	28.00	22.097
Diameter of pod (cm)	1.250	1.90	1.59	0.071**	0.02	0.005	0.027	81.481	0.276	17.281	9.293	10.295	4.430
Individual pod weight (g)	6.990	18.84	12.75	28.795**	9.19	1.234	10.421	88.159	5.863	45.977	23.770	25.316	8.712
Number of seeds/pod	32.90	72.70	54.80	386.551**	124.18	14.026	138.201	89.851	21.759	39.703	20.333	21.451	6.834
Yield/plant (g)	80.90	190.6	144.13	3624.646**	1199.64	25.733	1225.371	97.899	70.596	48.980	24.030	24.287	3.519

these values was mark-able which indicated large of effect of environment on this trait. The values of genotypic coefficient of variation (8.125 %) and phenotypic coefficient of variation (9.917 %) were least difference. Moderate heritability (67.107 %) and low genetic advance (9.211%) was observed for the character of growth duration. It indicates non-additive genetic control of this character that though the character is influenced by environmental effects but moderate heritability with GA selection would be effective.

4.2.2.2 Days to edible Maturity

Analysis of variance for days to edible maturity showed highly significant variation among the genotypes for this trait (Table 3). The mean value for this trait was 81.70 and ranged from 68 days (G_{10}) -101.0 days (G_7). The genotypic and phenotypic variances were 58.97 and 79.279, respectively (Table 5). The difference between these values was high which indicated large type of effect of environment on this feature. The values of genotypic coefficient of variation (9.399%) and phenotypic coefficient of variation (10.898%) were moderately low. Rather *et al.* (2001) also reported similar significant variations for days to edible maturity among 20 cultivars. Heritability (74.386%) and moderate low genetic advance (13.644%) was observed for the character of growth duration

4.2.2.3 Plant height (cm)

Analysis of variance for plant height showed significant variation among the genotypes (Table 3). The mean values for this trait was 69.16 cm and ranged from 40.30 cm (G_{10}) to 112.0 cm (G_9). The phenotypic and genotypic variances for this

trait were 460.75% and 434.14%, respectively. The lower value of environmental variance suggested slight influence of environment on the expression of this trait. The difference between phenotypic coefficient of variation (31.035%) and genotypic coefficient of variation (30.126%) was negligible (Table 5). Heritability estimates for this trait was high (94.229%) with extreme genetic advance (41.664%) indicating effective selection based on this trait. This result conformed the finding of Sardeana *et. al.* (1990) & Kumbhani *et. al.* (1993). Plant height showed very high heritability 94.229% along with moderate genetic advance 41.664%. The results suggest that importance of additive and non-additive gene effect on the control of plant height Kumar *et al.* (1999) found high heritability coupled with genetic advanced for plant height.

4.2.2.4 Height to 1st node from the ground (cm)

Height to 1st node from the ground showed a highly significant mean sum of squares due to genotypes, which indicated considerable range of variation among the genotypes for this character (Table 5). The mean value was 14.02 that ranged from 5.367 (G_7) to 26.47 (G_{10}). The phenotypic variance (44.465%) was a little bit higher than genotypic variance (35.07%). Such result indicated moderately influence of environment on the expression of the trait and genetic factor had significant role in controlling this trait. The phenotypic coefficient of variation (47.551%) and genotypic coefficient of variation (42.230%) indicating moderate influence of environment. Estimation of heritability (78.88%) for this trait was high. However, the genetic advance was high (77.268%). So selection based on this character would be effective due to its additive gene action. Kumar (1999) also reported similar results in fifteen F_1s and eight parents involving okra.

4.2.2.5 Number of branch per plant

Number of branches per plant showed a significant mean sum of squares due to genotypes, which indicated considerable range of variation among the genotypes for this character (Table 5). The mean value was 3.15 that ranged from 1.61 (G_{10}) to 5.26 (G_9). The phenotypic variance (1.38%) was a little bit higher than genotypic variance (1.04%). Such result indicated minimum influence of environment on the expression of the trait and genetic factor had significant role in controlling this trait. The phenotypic coefficient of variation (37.28%) was close to genotypic coefficient of variation (32.33%) indicating little influence of environment. Estimation of heritability (75.199%) for this trait was high. However, the genetic advance was (57.76%). So selection based on this character would be effective due to its additive gene action. Reddy and Kumar (1998), Hossain and Haque (2003) and Patel and Dalal (1992) also reported similar results among the genotype.

4.2.2.6 Number of pods per plant

Significant mean sum of squares due to genotypes for this trait indicated considerable difference among the genotypes studied (Table 3). The mean of panicle length ranged from 17.38 cm (G6) to 24.00 cm (G_{14}) (Table 5). The genotypic variance (6.77 %) was closer to phenotypic variance (7.219 %). The character showed medium estimates of phenotypic (26.868 %) and genotypic (26.015 %) coefficient of variations. The character showed high heritability (93.753 %) and low genetic advance (5.189). Such results indicated that this trait had maximum genetic effect and high heritability but low genetic advance hence, selection would be ineffective. Govindaswami *et al.* (1978), Lal and Srivastava (1978) and Singh and Singh (1978) were reported related results on okra genotypes in their study.

4.2.2.7 Length of pods (cm)

Genotypic and phenotypic co-efficient of variation were moderate for length of pods. There was a little difference between phenotypic (28.00 %) and genotypic (17.196 %) co-efficient of variation indicating moderate environmental effects on the character. Das and Mishra (1995) reported that length of pod showed moderate genotypic co-efficient of variation and phenotypic co-efficient of variation. Thaker *et al.*, (1981) and Lal *et al.* (1983) were also reported similar results of their study. The mean of this trait was 10.10 cm, which ranged from 7.190 (G_{10}) – 14.26 (G_{13}). The phenotypic variance (8.012 %) was double to the genotypic variance (3.02 %) i.e. environmental variance was half either of genotypic and phenotypic variances. This feature indicated that both environment and genetic factor had played equal significant role on the expression of the trait. The phenotypic coefficient of variation (28.00 %) was close to genotypic coefficient of variation (17.196 %) indicating little influence of environment. Estimation of heritability (37.718 %) for this trait was moderate. However, the genetic advance was moderate (21.756 %). So, selection based on this character would be moderate effective due to its genetic advance. A comparative pod shape and size of different okra has been presented in Plate 3.

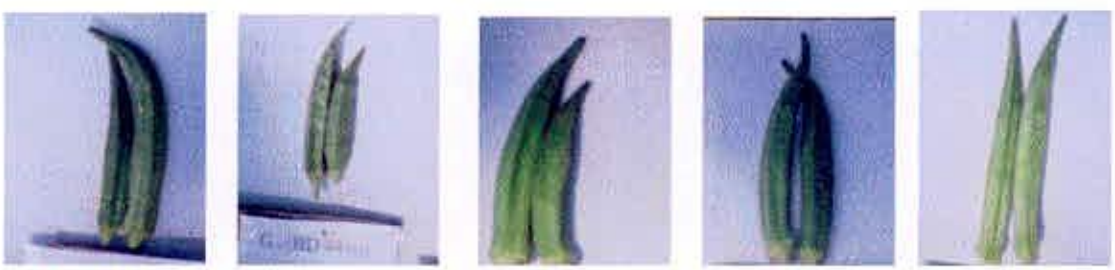
4.2.2.8 Diameter of pod (cm)

Highly significant mean sum of squares for the genotypes were estimated (Table 3). The mean was (1.59 cm) ranged from 1.25 cm (G_{10}) – 1.90 cm (G_5). The phenotypic variance (0.027%) was mostly close to genotypic variance (0.02%). Such result indicated all about total influence of genetic factor in controlling this trait. However, phenotypic coefficient of variation (10.295%) was also more close to genotypic coefficient of variation (9.293%) indicating high influence of genetic factor. Estimation of heritability (81.481%) for this trait was so high but the genetic advance

BD 9442 BD 9444 BD 9446 BD 9454 BD 9456

BD 9457 BD 9458 BD 9460 BD 9462 BD 9463

BD 9465 BD 9470 BD 9474 BD 9475 BD 9476



BD 9477 BD 9478 BD 9494 BD 9480 BARI Okra-1

Plate 3. Photographs represent the differences in pod shape and size of different genotypes of Okra

was very low (0.276%). It thus, may be concluded that the selection based on this character would be ineffective due to its low genetic advance. Reddy and Kumar (1998) reported significant variability on diameter of pod (cm).

4.2.2.9 Individual pod weight (gm)

Significant mean sum of squares due to genotypes for this trait indicated considerable difference among the genotypes studied (Table 5). The mean of individual pod weight was 12.75 gm and ranged from 6.99 gm (G_{10}) to 18.84 gm (G_{18}). The genotypic variance (9.19%) and phenotypic variance (1.234%). The character showed higher estimates of phenotypic (25.316%) and genotypic (23.770%) coefficient of variations. The character showed high heritability (88.159%) and moderate genetic advance (5.863%). Such results indicated that this trait had maximum genetic effect and high heritability and so, selection would be effective. Rao *et al.* (1989), and Singh and Singh (1978)) reported similar results on okra genotypes in their study.

4.2.2.10 Number of seeds per pod

Number of seeds per pod showed a highly significant mean sum of squares due to genotypes, which indicated considerable range of variation among the genotypes for this character (Table 5). The mean value was 54.80 that ranged from 32.90 (G_{10}) to 72.70 (G_5). The difference between phenotypic variance (138.201%) and genotypic variance (124.18%) was higher. Such result indicated maximum influence of environment on the expression of the trait and genetic factor had minimum significant role in controlling this trait. The phenotypic coefficient of variation (21.451%) was higher than genotypic coefficient of variation (20.331%) indicating influence of environment. Estimation of heritability (89.851%) for this trait was high. However,

the genetic advance was extreme (39.703%). So selection based on this character would be effective due to its additive gene action. Balakrishna *et al.* (1983) and Iftekharuddaula *et al.* (2001) also reported similar results in okra.

4.2.2.11 Yield per plant (g)

Highly significant estimation mean sum squares for this trait indicated considerable variation among the genotypes. There was a wide range of variation among the genotypes for yield (Table 5). The mean was 144.13 g per plant ranged from 80.90g (G_{10}) to 190.6g (G_7). The difference between phenotypic (1225.37) and genotypic variances (1199.64) was minimal for green pod yield per plant and seed yield per plant indicating least environmental effect for this trait (Table 5). It also observed that the difference between phenotypic (24.287%) and genotypic coefficient of variation (24.030%) was low. Lal and Srivastava (1973), Sing and Sing (1978), Sharman and Sharma (1984),Kumbhani et al. (1993), Das and Mishra (1995), Wankhade et al. (1995), Kumar (1999) reported and observed genotypic coefficient of variation for yield per plant. In case of heritability estimation this character showed higher heritability (97.899%) with moderate genetic advance (48.980%). So, selection based on this trait would be effective due to its high heritability and additive gene action. Similar findings were found by Kumar *et al.* (1998), Daysagar (1994), Sing and Mondal (1993), and Mehetre *et al.* (1998) while working with okra genotypes. Therefore, selection for this trait could bring about satisfactory improvement over the population.

4.2.3 Character association

Yield is complex products being influenced by several inter dependable quantitative characters. Thus selection for yield may not be effective unless the other yield components influence it directly or indirectly are taken into consideration. When selection pressure is exercised for improvement of any character associated with yield. It simultaneously affects a number of other correlated characters. Hence, knowledge regarding association of characters with yield among themselves provides guideline to the breeder for making improvement through selection *viz* . provide a clear understanding about the contribution in respect of establishing the association by genetic and non-genetic factor.

4.3 Genetic diversity of twenty okra genotype

The results of the genetic diversity of among the okra genotypes are represented in Table 4 to Table 12 and Figure 1 to 3.

4.3.1 Principal component analysis

The principal component analysis produces yielded eigen values of each principal component axes of coordination of genotypes in which the first axes accounting for the variation among the genotypes, while three these with eigen values above unity accounted for 97.55 %. The first two principal axes accounted for 93.17 % of the total variation among the 11 characters describing 20 genotypes (Table 6). Based on principal component scores I and II (Table 7); a two dimensional chart ($Z_1 - Z_2$) of the genotypes are presented in figure 1. The scattered diagram revealed that apparently there were mainly five clusters. Distantly located genotypes of different clusters were the genotype number 3, 7, 9, 10, 11, 12, 14, 16, 19, 20 etc.

Table 6: Eigen values and percentage of variation for corresponding 11 component characters in twenty okra genotypes

Principal component character	Eigen values	Percentage of total variation account for	Cumulative percentage
Day to 50% flowering	9.322	84.74	84.74
Days to edible maturity	0.928	8.43	93.17
Plant height (cm)	0.482	4.38	97.55
Height 1st node from the ground (cm)	0.154	1.40	98.95
Number of branches/plant	0.051	0.46	99.41
Number of pods/plant	0.029	0.27	99.68
Length of pod (cm)	0.018	0.16	99.84
Diameter of pod (cm)	0.007	0.07	99.91
Individual pod weight (g)	0.005	0.05	99.96
Number of seeds/pod	0.002	0.02	99.98
Yield/plant (g)	0.002	0.02	100.00

Table 7. Principal component scores (PCS) for twenty genotypes of okra

Genotypes	Score 1 (Z_1)	Score 2 (Z_2)
G_1	33.73	3.20
G_2	5.42	8.33
G_3	-23.90	3.83
G_4	28.45	4.38
G_5	-14.79	8.32
G_6	13.62	7.36
G_7	67.55	-14.19
G_8	-38.08	-6.13
G_9	50.02	-2.90
G_{10}	-76.34	2.72
G_{11}	56.77	-8.64
G_{12}	-54.15	-10.17
G_{13}	-1.17	4.68
G_{14}	40.95	3.09
G_{15}	-65.02	-10.49
G_{16}	-6.28	2.95
G_{17}	-32.37	8.11
G_{18}	45.69	-0.53
G_{19}	-49.58	-6.27
G_{20}	19.50	2.37

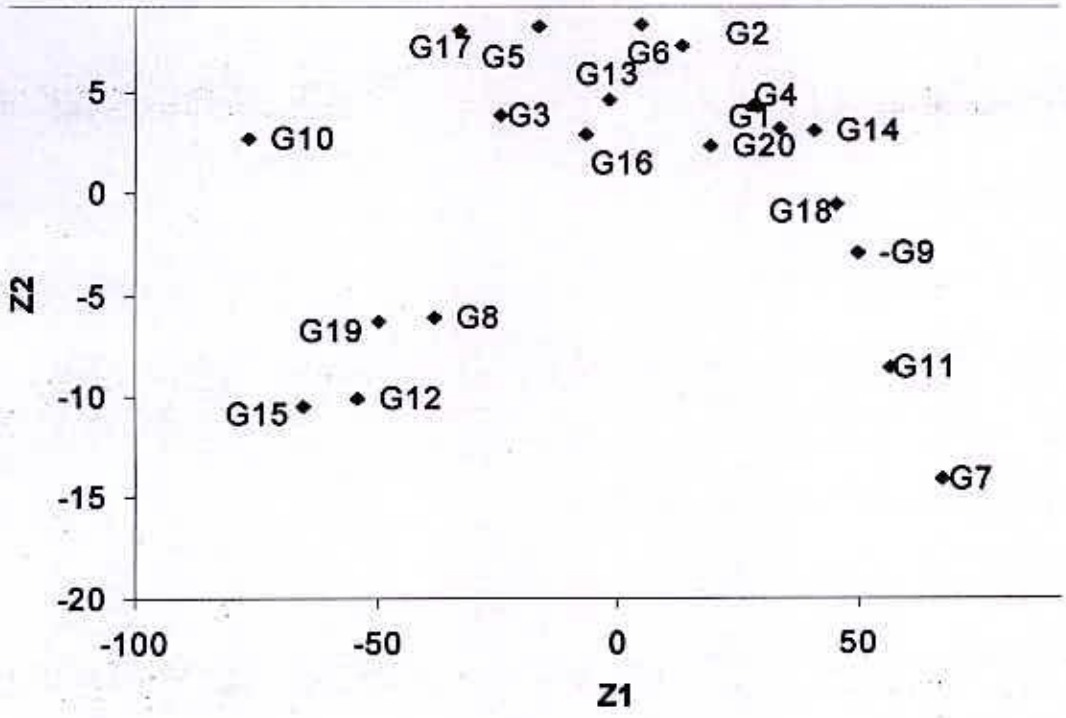


Figure 1. Scattered distribution of twenty okra genotypes based on their principal component scores (PCS)

4.3.2 Construction of a scatter diagram

Based on the values of principal component scores 2 and 1 obtained from the principal component analysis, a two dimensional scatter diagram ($Z_1 - Z_2$) using component score 1 as X- axis and component score 2 as Y-axis was constructed. the position of the genotypes in the scatter diagram was apparently distributed into five groups, which indicated that considerable for the 20 okra genotypes of different clusters revealed that the genotype number 7, 10, 8, 5, 1 were distantly located which suggesting more diverse from rest of the genotypes.

4.3.3 Principal Coordinate Analysis (PCO)

The inter-genotypic distances are obtained by principal coordinate analysis. The results showed that the highest distance was observed between the genotype number 7 and 10 (2.7319) followed by those of between 10 & 11 (2.3729), 9 and 10 (2.1152), 7 and 17 (2.0926) and the lowest distance was observed between 6 and 2 (0.1270) followed by 13 and 16 (0.1319), 3 and 5 (0.1570), 1 and 4 (0.1620). The difference between highest and lowest inter-genotypic distances indicated the prevalence of variability among 20 parental genotypes of okra studied (Table 8). The intra cluster distance was computed by the values of inter-genotypic distance matrix of PCO according to Singh and Choudhury (1985). Cluster II showed highest intra cluster distance (1.1262) composed of 2 genotypes and lowest distance in cluster I (0.2628) composed of 4 genotypes that indicated within group diversity of the genotypes was maximal in cluster II and minimum in cluster in I (Table 9).

Table 8. Ten of each lower and higher inter-genotypic distances between pairs of genotypes

Ten higher D^2 Values	Genotype Combination	Ten Lower D^2 Values	Genotype Combination
2.7319	G_7 & G_{10}	0.1270	G_2 & G_6
2.3729	G_{10} & G_{11}	0.1319	G_{13} & G_{16}
2.1152	G_9 & G_{10}	0.1570	G_3 & G_5
2.0926	G_7 & G_{17}	0.1620	G_1 & G_4
2.0857	G_7 & G_{15}	0.1903	G_1 & G_{14}
2.0101	G_{10} & G_{18}	0.2163	G_{14} & G_{18}
1.9678	G_7 & G_{12}	0.2420	G_4 & G_{20}
1.8938	G_7 & G_{19}	0.2484	G_1 & G_{20}
1.8624	G_{10} & G_{14}	0.2518	G_4 & G_6
1.8492	G_5 & G_7	0.2557	G_3 & G_{17}

Table 9. Distribution of twenty okra genotypes in five clusters

Cluster	Total no. of genotypes (entry no.)	Name of the genotypes with serial number
I	4(1, 4 ,6 ,20)	BD 9442 (G_1), BD 9454 (G_4), BD 9457 (G_6), BARI okra-1 (G_{20})
II	2 (10, 15)	BD 9463 (G_{10}), BD 9476 (G_{15})
III	5 (7, 9, 11, 14, 18)	BD 9458 (G_7), BD 9462 (G_9), BD 9465 (G_{11}), BD 9475 (G_{14}), BD 9480 (G_{18}),
IV	5 (2, 3, 5, 13, 16)	BD 9444 (G_2), BD 9446 (G_3), BD 9456 (G_5), BD 9474 (G_{13}), BD 9477 (G_{16})
V	4 (8, 12, 17, 19)	BD 9460 (G_8), BD 9470 (G_{12}), BD 9478 (G_{17}), BD 9494 (G_{19}),

4.3.4 Canonical Variate Analysis

Canonical variate analysis was performed to obtain the inter-cluster distances .The intra and inter-cluster distance (D^2) is presented below (Table 10). Statistical distances present the index of genetic diversity among the clusters. The inter-cluster distances were bigger than the intra cluster distances suggesting wider genetic diversity among the genotypes of different groups. Singh *et al.* (1990) obtained larger inter-cluster distances than the intra-cluster distances in a multivariate analysis in okra. Results indicated that the highest inter cluster distance was observed between cluster III and II (22.397) followed by the distance between cluster I and II (19.983), III and IV, (17.192), III and V (17.017). The higher inter-cluster distances between these clusters indicated to obtain wide spectrum of segregating population if parents chosen from these distant clusters are used in hybridization program. However, the highest inter-cluster distance was observed between clusters III and II indicated the genotypes in these clusters were far diverged than those of other clusters. The minimum values of inter-cluster distance indicated that the genotypes belonging to cluster IV were closely related to the cluster V, cluster IV to cluster I and cluster V to cluster I. These relationships were also reflected in the scattered diagram (Figure 1). The lowest inter-cluster distance was observed between cluster IV and V (2.190) followed by IV and I (5.469), I and V (6.832) suggesting a close relationship among these three clusters (Figure 2). Similar reports were also made by Mahajan *et al.* (1980), Mehtre *et al.* (1998), Rather *et al.* (2001), Soni *et al.* (1999), and Singh *et al.* (1996) on okra genotypes. The genotypes belonging to the cluster III and II having greater cluster distance are recommended for inclusion in hybridization programme as they are expected to produce good segregants. Thus it could be suggested that crosses should be made between genotypes belonging to the distant clusters for higher heterotic

Table 10: Average intra (Diagonal) and inter cluster distance (D^2) of five clusters formed by Tocher's method

Cluster no.	I	II	III	IV	V
I	**0.2628**	19.983	13.330	5.469	6.832
II		**1.1262**	22.397	16.592	14.402
III			**0.5490**	17.192	17.017
IV				**0.4763**	2.190
V					**0.7157**

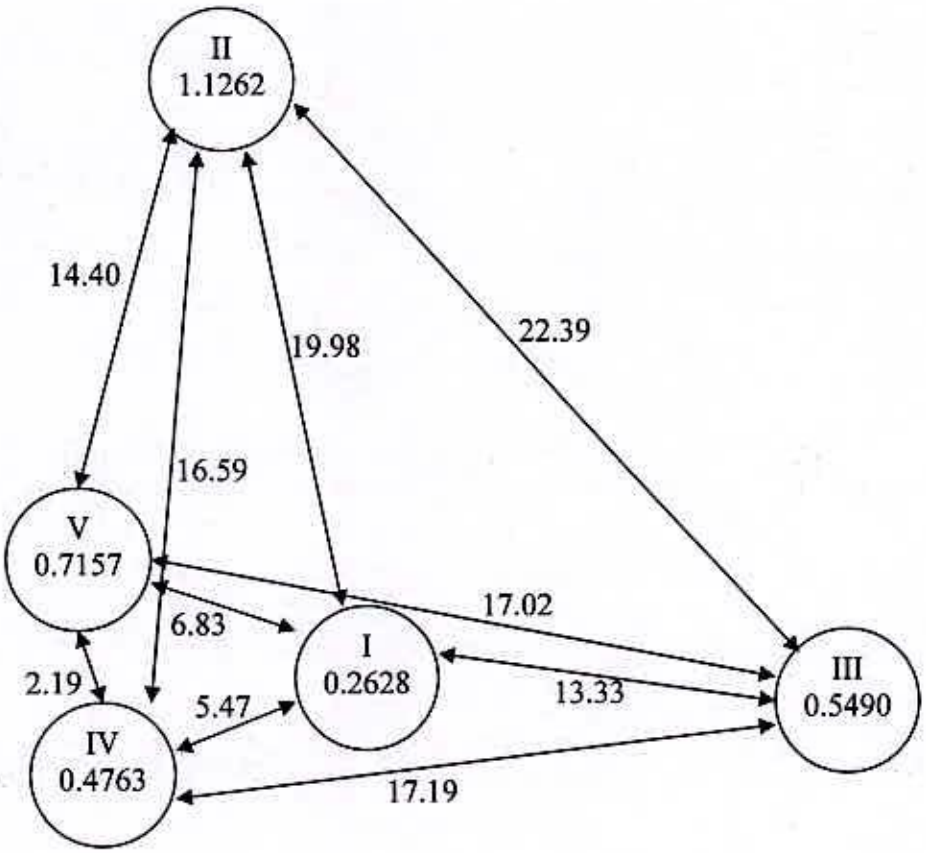


Figure 2: Diagram showing intra and inter-cluster distance of twenty okra genotypes

response. Singh *et al.* (1998) reported similar results in 42 genotypes. Sawant *et al.* (1995) reported that selection of parents from distantly placed clusters exhibited significant high heterosis in okra. Moderate type of inter-cluster distance has been existed between the cluster II and I. The promising genotypes grouped in cluster II and I (Table 10) could also be utilized in hybridization program considering genetic distances of the genotypes of different clusters. So the genotypes from these three cluster II, III and I if involved in hybridization may occur a wide spectrum of segregating population as genetic variation is very distinct among the group. The genotypes belonging to the distant clusters could be used in hybridization program for obtaining a wide spectrum of variation among the segregants. Similar reports were also made by Bansal *et al.* (2000), Pandey and Ghorai (1986), Pyene *et al.* (1989).

4.3.5 Non – hierarchical clustering

By application of non-hierarchical clustering using covariance matrix, the 20 genotypes of okra were grouped into five different clusters. These results confirmed the clustering pattern of the genotype according to the principal component of analysis Sawanta *et al.* (1995) reported that principal component analysis and cluster analysis in 75 genotypes and stated 75 varieties into 10 clusters. Roy and Panwar also carried out principal component analysis of 99 diverse okra genotypes using multivariate D^2 analysis, which grouped into 16 clusters. These results confirmed the clustering pattern of the genotypes according to the principal component analysis.

Composition of different clusters with their corresponding genotypes and origin included in each cluster are presented in Table 9. Cluster III and IV had maximum five (5) genotypes followed by cluster V and cluster I, and cluster II which had 4, 4 and 2 genotypes respectively. Cluster II had minimum two (2) genotypes namely G_{10},

G_{15}. Five genotypes number included in cluster III and IV thus are G_7, G_9, G_{11}, G_{14}, G_{18} and G_2, G_3, G_5 G_{13} and G_{16}, respectively. Cluster I and V was constituted of four namely G_1, G_4, G_6, G_{20} and G_8, G_{12}, G_{17}, G_{19} respectively.

4.3.6 Cluster mean value

An attempt was made to characterize the individual genotype in respect of their mean values for different characters with a view to get idea that weather genotypes having similar characteristics could be disseminated. The mean values for all the 11characters along with the marking of the highest (H) and the lowest (L) for each of the cluster are presented in Table 11. The data revealed that different clusters exhibited different mean values for almost all the characters.

The genotypes (G_1, G_4, G_6 and G_{20}) included in this cluster I produced the highest mean for diameter of pod (1.68 cm). The second highest mean for number of seeds/pod 60.90 and second highest Yield/plant (165.43g) and there were no lowest mean for the cluster.

From mean values the cluster II (G_{10} and G_{15}) it was observed that the highest mean was obtained for days to 50% flowering (77.00 days), days to edible maturity (96.50 days), height 1st node from the ground (17.45 cm), the lowest mean values for plant height (42.25 cm), number of pods/plant (6.95), length of pod (7.29 cm), diameter of pod (1.33 cm), number of seeds/pod (34.55), individual pod weight (7.28 g) and yield/plant (84.65 g). It revealed that genotypes included this cluster were early maturity type but low yielder.

Bases on the man values of inter-cluster distance will be used for initiating hybridization (Rather *et al.*, 2001).

Table 11: Cluster mean of 5 clusters for 11 characters in twenty okra genotypes

Characters	Cluster mean				
	I	II	III	IV	V
Day to 50% flowering	64.00	77.00 H	59.40 L	68.40	72.50
Days to edible maturity	77.50	96.50 H	72.80 L	82.00	88.50
Plant height (cm)	77.40	42.25 L	98.12 H	60.18	49.38
Height 1st node from the ground (cm)	15.50	17.45 H	10.48 L	16.74	11.90
Number of branches/plant	3.42	2.00	4.66 H	2.84	1.98 L
Number of pods/plant	10.50	6.95 L	13.66 H	9.34	7.53
Length of pod (cm)	10.42	7.29 L	12.90 H	9.17	8.06
Diameter of pod (cm)	1.68 H	1.33 L	1.67	1.66	1.47
Individual pod weight (g)	14.21	7.28 L	16.54 H	12.00	10.24
Number of seeds/pod	60.90	34.55 L	68.04 H	53.62	43.83
Yield/plant (g)	165.43	84.65 L	183.57 H	140.30	108.08

The genotypes (G_7, G_9, G_{11}, G_{14} and G_{18}) of cluster III group produced the highest mean for plant height (98.12 cm), number of branches per plant (4.66), number of pods per plant (13.66), length of pod (12.90 cm), individual pod weight (16.54 gm), number of seeds per pod (68.04) and yield per plant (183.57 gm). The lowest mean values of these cluster for days to 50% flowering (59.40 days), days to edible maturity (72.80 days) and height 1st node from the ground (10.48 cm). It revealed that genotypes included this cluster were late maturity type but high yielder.

The mean performance of the cluster means the cluster III are used for the future hybridization program (Rather *et al.*, 2001).

Cluster IV constituted five genotypes namely G_2, G_3, G_5, G_{13} and G_{16}. The genotype of these cluster produced no highest and no lowest mean value.

Cluster V constituted five genotypes namely G_8, G_{12}, G_{17} and G_{19}. The genotype of these cluster produced second highest value days to 50% flowering (72.50 days), days to edible maturity (88.50 days), second lowest mean value Height 1st node from the ground (11.90 cm) and the lowest value for the number of branches per plant (1.98).

The significant variations for the number of branches per plant and the cultivars from the cluster are used for initiating hybridization (Rather *et al.*, 2001).

The intra-cluster distance was computed by the values of inter-genotypic distance matrix of PCO according to Singh and Chaudhury (1985). There were not marked variations in intra-cluster distances, which ranged from 0.4763 to 1.1262 (Table 10). The highest intra-cluster distance was computed for cluster II (1.1262) indicating genotypes in this cluster is highly heterogeneous. The lowest intra-cluster distance

was computed for cluster IV (0.4763) composed of 5 genotypes indicating genotypes in this cluster is highly homogeneous. In 20 genotypes of okra the highest inter-cluster distance was observed (Table 10) between cluster III and II (22.397) followed by cluster II and I (19.983), III and IV (17.192) and the lowest inter-cluster distance was found between cluster IV and V (2.190) followed by cluster IV and I (5.469). The highest inter-cluster distance between clusters indicated that the genotypes belonging to each pair of clusters were genetically diverged. Similarly the lowest inter-cluster distance between clusters indicated that the genotypes belonging to each pair of clusters were genetically less diverged.

The clustering pattern of the genotypes revealed that varieties originating from country were grouped into different clusters (Table 9). This showed that geographic diversity is not always related to genetic diversity and therefore a single cluster, it is not adequate as an index of genetic diversity. Rao and Gomathinayagam (1998) stated that differential response of the genotypes to the environments has altered the clustering pattern between environments. Furthermore, there is a free exchange of seed material among the different region, as a consequence, the characters constellation that might be loose their individuality under human interferences associate with particular region in nature.

4.3.7 Contribution of characters towards diversity

The PCA revealed contribution of characters towards divergence (Table 12). The PCA revealed that in vector1 (Z_1) the important characters responsible for the genetic divergence in the major axis of differentiation were day to 50% flowering, days to edible maturity, plant height (cm), number of branches/plant, number of pods/plant, number of seeds/pod, yield/plant (g) having positive vector values. While in vector2

(Z_2) which was the second axis of differentiation day to 50% flowering, days to edible maturity, plant height (cm), number of pods/plant, individual pod weight (g), yield/plant (g) having positive vector values. On the other hand height 1st node from the ground (cm), individual pod weight (g), length of pod (cm) and diameter of pod (cm) in first axis differentiation had a minor role in the genetic divergence because of holding a negative signs. In second axis of differentiation of height 1st node from the ground (cm), number of branches/plant, diameter of pod (cm), number of seeds/pod had a minor role in the genetic divergence because of holding a negative signs. The values of vector 1 and vector 2 revealed that both the vectors had positive value only for the five characters of day to 50% flowering, days to edible maturity, plant height (cm), number of pods/plant, yield/plant (gm) among the eleven characters studied in this experiment. These results indicated that these five characters had the highest contribution towards the divergence among the 20 genotypes of okra. Singh *et al.* (1998) also reported similar response for the traits harvest index, total number of seeds/pod, number of fertile seeds/ pod and stability among 14 characters of 42 genotypes. Kumari and Rangasamy (1999) reported characters like seed yield per plant, pod length and plant height of 62 early varieties genotypes that made the largest contribution to total divergence. Mishra *et al.* (1994) reported that number of fertile seeds/plant, number of sterile seeds/plant and plant height was the highest contributors of Mahalanobis D^2 values among the 9 quantitative characters of 46 strains of okra. Chauhan and Chauhan (1994) reported that the contribution of 1000-grain weight was the highest in the genotypes.

Table 12: Latent vector values for 11 characters of twenty genotypes of okra

Sl no.	Characters	Vector 1	Vector 2
1	Day to 50% flowering	+2.373	+0.095
2	Days to edible maturity	+0.139	+0.044
3	Plant height (cm)	+0.719	+0.613
4	Height 1st node from the ground (cm)	-0.031	-0.079
5	Number of branches/plant	+2.822	-3.112
6	Number of pods/plant	+2.688	+0.220
7	Length of pod (cm)	-9.538	-4.912
8	Diameter of pod (cm)	-0.997	-7.413
9	Individual pod weight (gm)	-1.145	+0.589
10	Number of seeds/pod	+0.354	-0.358
11	Yield/plant (gm)	+0.296	+0.106

4.4 Comparison of results based on different multivariate (D^2) technique and principal component analysis

The cluster pattern of D^2 analysis through non-hierrachical clustering has taken care of simultaneous variation in all characters under study. Results combined from different multivariate techniques were superimposed in figure 3. It may be concluded from this figure that all techniques gave more or less similar results and one technique supplemented and confirmed the results of the other. The cluster pattern of D^2 analysis through non-hierarchical clustering has been taken care of simultaneous variation in all the traits under study. However, the distribution of genotypes in different clusters based on D^2 analysis has followed more or less similar trend of the component score 1 (Z_1) and component score 2 (Z_2) of the Principal Component analysis. The D^2 and PCA were found to be alternative methods in giving the information regarding the clustering pattern of genotypes. Nevertheless, the Canonical Vector Analysis (CVA) provides the information regarding the contribution of characters towards divergence of 20 okra genotypes. Mehetre *et al.*, (1998) reported that group constellation based on Tocher's method was fairly in good agreement with the scattered points of the Z_1-Z_2 graph as well as the clustering pattern obtained through dendograms.

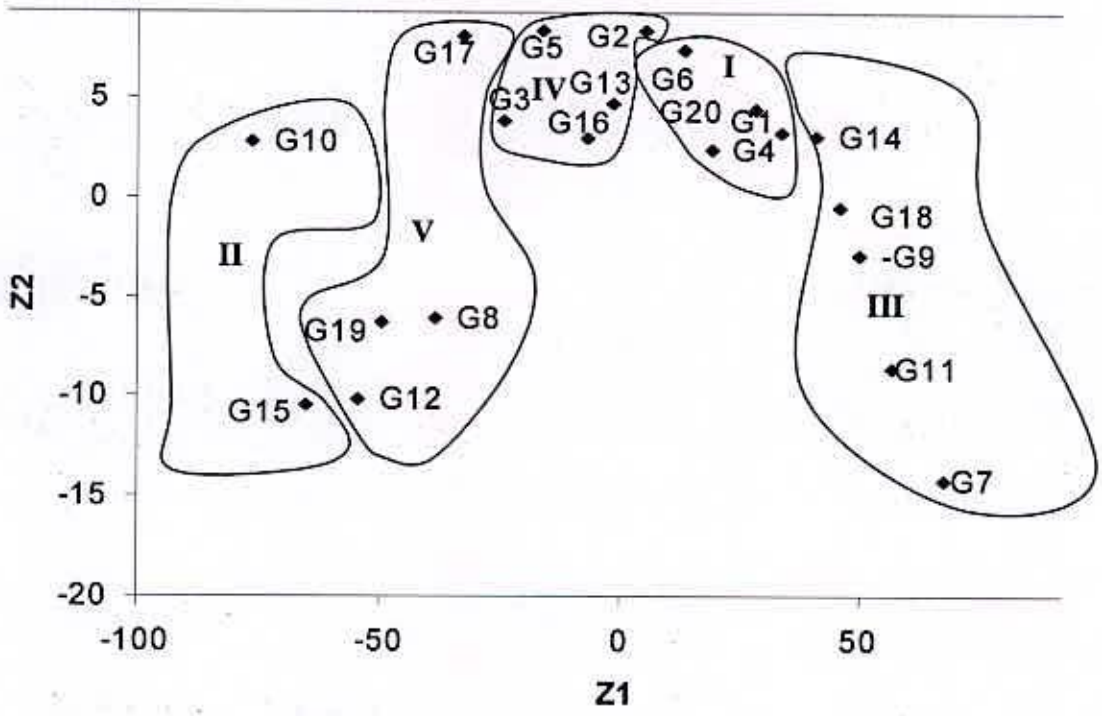


Figure 3. Scattered distribution of twenty okra genotypes based on their principalcomponent scores (PCS) superimposed with clustering

4.5 Selection of the genotypes for future hybridization programme

Genotypes are to be selected on the basis of specific objectives. Genetically distant parents usually are able to produce higher heterosis (Falconer, 1960). Considering magnitude of genetic distance, contribution of different characters towards the total divergence, magnitude of cluster means for different characters and per as performance the following genotypes were considered to perform better if used in hybridization program.

In 20 genotypes of okra the highest inter-cluster distance was between cluster II and III (22.397) followed by cluster I and II (19.983) and some other clusters were more or less intermediate. Intermediate diverse parents have the more chance to contribute heterosis in the subsequent generations. To select cluster for more heterotic genotypes, five pairs of clusters to be considered for this purpose, they are II and III, I and II, IV and III, IV and V. In an average cluster III was important for higher plant height, number of branches/plant, number of pods/plant, length of pod, individual pod weight, number of seeds and yield/plant. From cluster III genotype G_7 could be selected for higher number of pods/plant and yield/plant, genotype G_9 for plant height and number of branches/plant and genotype G_{18} for individual pod weight. So, genotype G_7 for maximum days for flowering and days to edible maturity. Cluster II was important for highest late maturity and height 1st node from the ground. In cluster II, genotype G_{10} could be selected for height 1st node from the ground and genotypes that take to maximum days to flowering and maturity (G_{10}) can be selected from cluster II. Cluster IV was important for diameter of pod, number of seeds/pod and semi dwarf type plant. From cluster IV genotype G_5 could be selected for the pod diameter and seed yield, and genotype G_3 for dwarf type plant.

It assumed that highest heterosis would be manifest in cross combination involving the genotypes belonging to divergent clusters. However for a practical plant breeder, the objective was not only high heterosis but also to achieve high level of production. Considering this, it appears that the cross between the genotypes belonging cluster III with cluster II, cluster III with cluster IV, cluster III with cluster V and cluster I with II might produce high heterosis in yield as well as earliness and better performance. So, selected the better performed genotype G_7 from cluster III, G_1 from cluster I, G_{10} from cluster II and G_5 from cluster IV were selected for future hybridization. Therefore, considering group distance and the agronomic performance, the inter genotypic crosses between G_7 and G_1, G_7 and G_5, G_7 and G_{10}, G_7 and G_{13}, G_9 and G_1, G_9 and G_5, G_9 and G_{10}, G_9 and G_{13}, G_{11} and G_1, G_{11} and G_5, G_{11} and G_{10}, G_{11} and G_{13}, G_1 and G_5, G_1 and G_{10}, G_1 and G_{13}, G_5 and G_{10}, G_{10} and G_{13} might be considered for efficient hybridization programme.

Chapter 5

Summary and Conclusion

CHAPTER 5

SUMMARY AND CONCLUSION

An investigation was conducted based on some parameters of okra at the SAU, Dhaka-1207, Bangladesh, during the period of November 2007 to April 2008 to study morphological characterization and genetic diversity of twenty okra genotypes. The experiment was conducted in a Randomized Complete Block Design (RCBD) with three replications. The performance of twenty okra genotypes in order to know the genetic parameter and variability of eleven quantitative characters and finally assessing the genetic diversity among these genotypes. The salient features of the present study are summarized below on the basis of the objectives studied.

Significant differences among the different genotypes for all characters were observed. From ANOVA it was observed that highly significant variation exist among the genotypes for all the characters. From the mean value BD 9458 (G_7) was early flowering and early maturing while BD 9463 (G_{10}) late flowering and late maturing, BD 9462 (G_9) was tallest and BD 9463 (G_{10}) dwarf type plant, BD 9463 (G_{10}) showed highest and BD 9458 (G_7) lowest height to 1st node from the ground, BD 9462 (G_9) produced highest and BD 9463 (G_{10}) lowest number of branches per plant, BD 9458 (G_7) produced highest and BD 9463 (G_{10}) lowest number of pods/plant, BD 9474 (G_{13}) produced highest and BD 9463 (G_{10}) lowest the length of pod, BD 9456 (G_5) produced highest and BD 9463 (G_{10}) lowest diameter of pod, BD 9442 (G_1) produced highest and BD 9463 (G_{10}) lowest individual pod weight, BD 9456 (G_5) produced highest and BD 9463 (G_{10}) lowest number of seeds/pod and BD 9458 (G_7) was high yielder and BD 9463 (G_{10}) low yielder/plant.

Incase of maximum characters wide range of variation was observed. The phenotypic variance was higher than the corresponding genotypic variance for most of the yield

contributing characters. The results indicated that the all characters greater influence on environment. High heritability (>60%) was observed for days to flowering, days to edible maturity, plant height, height to 1st node from the ground, number of branches per plant, number of pods/plant, diameter of pod, individual pod weight, number of seeds/pod and yield/plant. Low heritability (<40%) was also observed for length of pod only. High genetic advance in 5% of mean (>60%) was observed for plant height and height to 1st node from the ground. Low genetic advance in 5 % of mean (<40 %) was observed days to 50 % flowering, days to edible maturity, length of pod, diameter of pod and number of seeds per pod. Incase of high heritability and low genetic advance character of a genotypes may be done for more effective hybridization programme.

For knowing the genetic diversity of okra genotypes, multivariate analysis was performed through Principal Component Analysis, Principal Coordinate Analysis, Cluster Analysis, and Canonical Vector Analysis using Genstat 5 Release 4.1 (Copyright 1997, Lawes Agricultural Trust, Rothamasted Experimental Station, UK). As per PCA, D^2 and cluster analysis, the genotypes grouped into 5 clusters. Cluster I, II, III, IV and V composed of 4, 2, 5, 5 and 4 genotypes respectively. PCA showed 32.52% variation against first three eigen values. The highest intra-cluster distance (1.126) composed of 2 genotypes found in cluster II and lowest (0.2628) in cluster I among the five clusters. The highest inter-cluster difference was found between cluster II and III (22.397) followed by cluster I and II (19.983) while the minimum distance was in between cluster IV and V (2.190) followed by IV and I (5.469). The maximum values of inter-cluster distance indicated that the genotypes of cluster III was far diverged from those of cluster II. The highest inter-genotypic distance (2.731) was observed between the genotypes G_7 and G_{10} followed by genotypes G_{10} and G_{11}

(2.3729) and the least genotypes were G_6 and G_2 (0.1270) followed by G_{13} and G_6 (0.1319).

Cluster I included genotypes mainly with medium days to 50% flowering, days to edible maturity, plant height, number of branches/plant, length of pod and yield/plant. In cluster II genotypes with higher height to 1st node from the ground and low yield/plant. In cluster III rich with genotypes of higher days to 50% flowering, days to edible maturity, number of pods/plant and yield/plant were included. Cluster IV was dominated with genotypes of higher length of pod, diameter of pod and height to the 1st node from the ground. Where as those in cluster V was dominated with the days to 50% flowering, days to edible maturity, plant height, number of pods/plant, length of pod and yield. Genetic diversity was not always associated with geographic diversity.

The latent vector values for 11 characters among the genotypes showed characters like percentage of days to 50% flowering, days to edible maturity, plant height, number of branches per plant, number of pods/plant, number of seeds/pod and yield/plant divergence in vector 1 while in vector 2, days to flowering (+0.095), days to edible maturity, plant height, number of pods/plant, individual pod weight, yield/plant were important. Among the all characters days to flowering, days to edible maturity , plant height, number of branches per plant, number of pods/plant, length of pod, diameter of pod, individual pod weight, number of seeds/pod and yield/plant contributed maximum towards the genetic divergence among the 20 genotypes under study.

Considering cluster distance, inter-genotypic distance, cluster mean and agronomic performances ten genotypes such as BD 9458 (G_7), BD 9462 (G_9), and BD 9465 (G_{11}) from cluster III and BD 9442 (G_1) from cluster I and BD 9463 (G_{10}) from cluster II and BD 9456 (G_5) and BD 9474 (G_{13}) from cluster IV selected to be the better parents

for efficient hybridization progrm to obtain desirable segregants in respect of different yield contributing characters. However for a practical plant breeder, the objective is not high heterosis but also achive high level of production.

Therefore, considering group distance and the agronomic performance, the inter genotypic crosses between G_7 and G_1, G_7 and G_5, G_7 and G_{10}, G_7 and G_{13}, G_9 and G_1, G_9 and G_5, G_9 and G_{10}, G_9 and G_{13}, G_{11} and G_1, G_{11} and G_5, G_{11} and G_{10}, G_{11} and G_{13}, G_1 and G_5, G_1 and G_{10}, G_1 and G_{13}, G_5 and G_{10}, G_{10} and G_{13} might be considered to be better parent for efficient hybridization programme.

The following recommendations may be drawn from the findings in present study-

(i) Selection of okra germplasm should be continued for getting more variability and desired traits.

(ii) Inter-genotypic crossing should be possible for efficient hybridization program to get more production.

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CHAPTER 6

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Appendices

APPENDICES

Appendix I. Monthly average temperature, relative humidity, total rainfall and sunshine (hours/day) of the experimental site during the period from (November, 07 to April, 08)

Month	Average Temperature ^{0}C			RH% 9 am	Average Rainfall (mm)	Sunshine (hours/day)
	Minimum	Maximum	Mean			
November	19.90	29.00	24.45	69	111	5.5
December	15.00	25.80	20.40	73	00	5.6
January	12.50	24.70	18.60	67	00	5.8
February	16.80	27.20	22.00	67	31	5.8
March	19.70	31.50	25.60	55	12	8.3
April	23.81	33.74	28.78	61	188	8.5

Source: Bangladesh Metrological Department (Climate division), Agargaon, Dhaka-1207.

Appendix II: Range and mean with coefficients of variation for 11 characters in 20 okra genotypes

Characters	Minimum	Mean	Maximum	CV%
Day to 50% flowering	56.33	67.18	78.00	5.69
Days to edible maturity	68.00	81.70	101.00	5.52
Plant height (cm)	40.30	69.16	112.00	7.46
Height 1st node from the ground (cm)	5.367	14.02	26.47	21.85
Number of branches/plant	1.613	3.15	5.26	18.57
Number of pods/plant	6.867	10.00	17.04	6.72
Length of pod (cm)	7.190	10.10	14.26	21.10
Diameter of pod (cm)	1.250	1.59	1.90	4.47
Individual pod weight (g)	6.990	12.75	18.84	8.71
Number of seeds/pod	56.33	54.80	72.70	6.83
Yield/plant (g)	68.00	144.13	190.6	3.52