GENETIC DIVERGENCE AND RELATIONSHIP BETWEEN YIELD AND YIELD CONTRIBUTING CHARACTERS IN OKRA (*Abelmoschus esculentus* L.)

NAHID AHMED

DEPARTMENT OF GENETICS AND PLANT BREEDING

SHER-E-BANGLA AGRICULTURAL UNIVERSITY

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NAHID AHMED

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Approved By

.....	**.....**
(Prof. Dr. Md. Sarowar Hossain)	**(Prof. Dr. Jamilur Rahman)**
Supervisor	**Co-Supervisor**

……...…….
(Prof. Dr. Jamilur Rahman)
Chairman
Examination Committee

Dr. Md. Sarowar Hossain
Professor
Department of Genetics and Plant Breeding
Sher-e-Bangla Agricultural University
Sher-e-Bangla Nagar, Dhaka-1207, Bangladesh
Mobile Number: +8801552499169
E-mail: sarowargpb@sau.edu.bd
sarowargpb@gmail.com

CERTIFICATE

*This is to certify that the thesis entitled "**Genetic Divergence and Relationship Between Yield and Yield Contributing Characters in Okra (Abelmoschus esculentus)**" 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 **NAHID AHMED**, Registration No. **11-04359** under my supervision and guidance. No part of the thesis has been submitted for any other degree or diploma.*

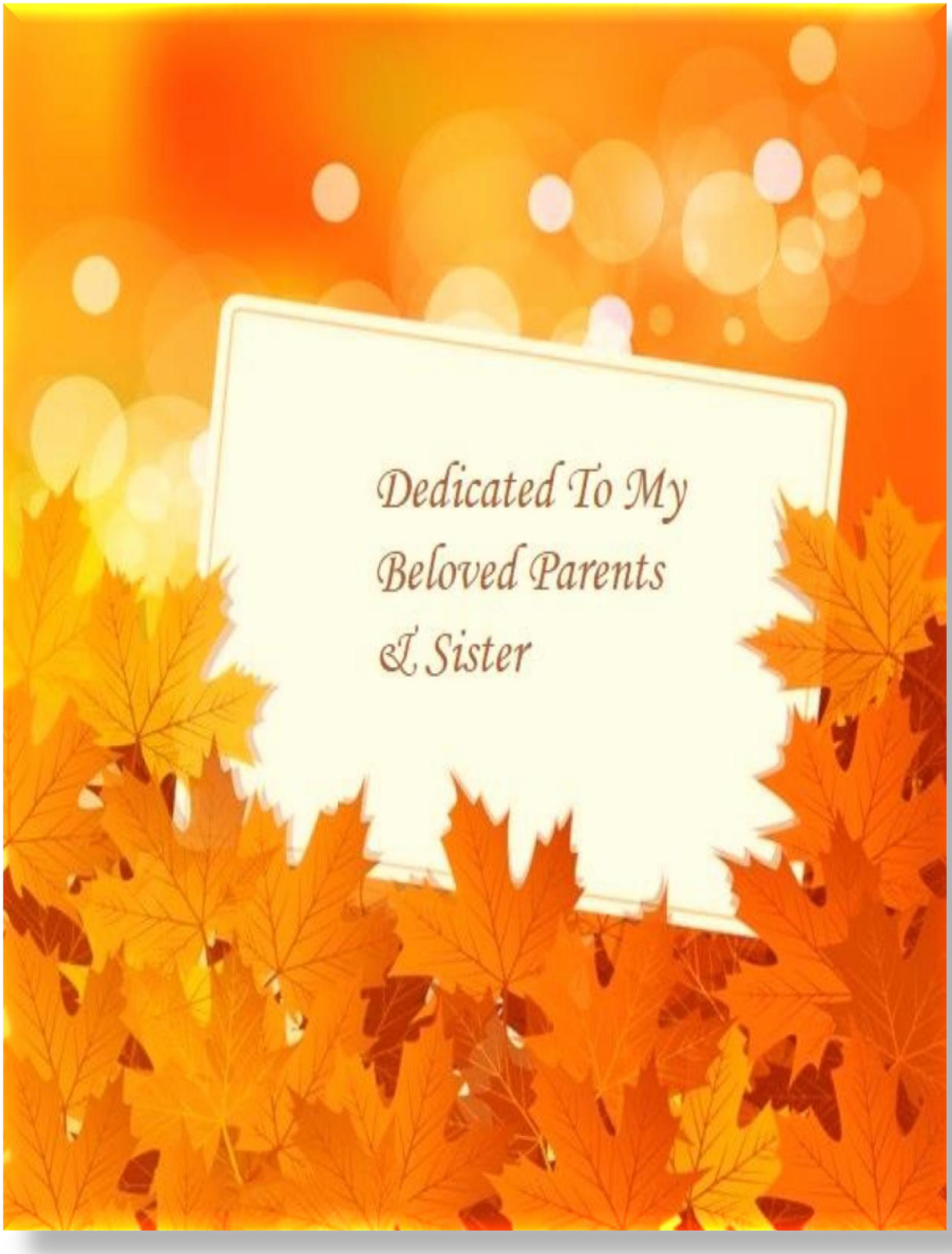
I further certify that such help or sources of information, as has been availed of during the course of this investigation has duly acknowledged.

Date: June, 2017

Place: Dhaka, Bangladesh

(Prof. Dr. Md. Sarowar Hossain)

Supervisor


Dedicated To My
Beloved Parents
& Sister

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SOME COMMONLY USED ABBREVIATION

FULL WORD		ABBREVIATION
At the rate	:	@
Analysis of Variance	:	ANOVA
Critical difference	:	C.D.
Degrees of Freedom	:	d.f.
Et al (And others or co-workers)	:	*et al.*
Genetic Advance	:	GA
Genotypic coefficient of variation	:	GCV
Phenotypic coefficient of variation	:	PCV
Mean Sum of Squares	:	M.S.S.
Standard error mean	:	SEm±
Yellow Vein Mosaic Virus	:	YVMV
Figure	:	Fig.
Percentage	:	%
Meter	:	M
Centimeter	:	Cm
Hectare	:	Ha
Kilogram	:	Kg
Metric ton	:	mt
Maximum	:	Max.
Minimum	:	Min.
Journal	:	J.

GENETIC DIVERGENCE AND RELATIONSHIP BETWEEN YIELD AND YIELD CONTRIBUTING CHARACTERS IN OKRA (*Abelmoschus esculentus* L.*)*

BY

NAHID AHMED

ABSTRACT

The present investigation was carried out to evaluate the genetic divergence and relationship between yield and yield contributing characters in nineteen genotypes of okra at the experimental field of Sher-e-Bangla Agricultural University. The seeds of 19 genotypes of okra were sown in Randomized Complete Block Design with three replications during kharif-I season of 2017. Results of analysis of variance indicated that significant differences among the genotypes were found for all the characters observed. The mean performance of the genotypes as the days to 1st flowering (41.58 days), number of flowers per plant (22.65), fruiting span (56.35 days), plant height (127.23 cm), number of fruits per plant (17.30), fruit length (12.93 cm), individual fruit weight (15.84 g) and fruit yield per plant (279.04 g) were recorded. High heritability coupled with high genetic advance was found in flowers per plant, fruits per plant, fruit diameter, individual fruit weight and fruit yield per plant. Such results revealed that these characters were controlled by additive gene action and selection based on these characters will be effective for the improvement of the crop. The correlation analysis revealed that the traits like flowers per plant (0.724), internodes per plant (0.712), fruits per plant (0.935), fruit length (0.708), fruit weight (0.591) and seeds per fruit (0.680) had positive and significant genotypic correlation with fruit yield. The diversity analysis grouped the nineteen genotypes into five different clusters. The cluster IV contains the maximum genotypes (6) and cluster III contains the minimum genotypes (2). Considering genetic variability, diversity and mean performance, genotype G14 and G15 could be selected from cluster IV for earliness whereas genotype G2 and G3 could be selected for more fruit per plant and high yield per plant from cluster III. The highest cluster distance was between cluster I & cluster III and lowest was between cluster IV and cluster V. So, divergent genotypes are recommended to use as parents in future hybridization program from more distant cluster I and cluster III.

CHAPTER I

INTRODUCTION

Okra [*Abelmoschus esculentus* (L.) Moench] has captured a prominent position among vegetables. It is a fruit vegetable grown in the tropical, subtropical and warm area of the world like Bangladesh, India, Africa, Turkey and other neighboring countries. Okra is grown extensively due to its wider adaptability, year round cultivation, highly nutritive along with medicinal value, export potential and good portability (Hammon and Van Sloten, 1989). In Bangladesh, okra is one of the most important vegetable crops grown for its tender green fruits during spring-summer and rainy seasons. Okra is known by many local names in different parts of the world. It is called lady's finger in England, Gumbo in U.S.A., Bhindi in India and Dherosh in Bangladesh.

Okra is an allopolyploidy, belongs to the family Malvaceae and a self-pollinated seed propagated crop. Occurrence of out crossing to an extent of 4 – 19 per cent with the maximum of 42.2 per cent is noticed with the insect assisted pollination. The number of chromosome of okra varies from species to species, but the reason of variation is unknown. The number of chromosome varies from 66 to 144 (Rashid, 1999). Besides, two wild species *Abelmoschus tuberculatus* (n= 29) and *Abelmoschus ficulenneus* (n=36) are amphidiploid (Joshi and Hardas, 1976). According to Vavilov, it was probably domesticated in the Ethopian region but according to Murdoc, it is in West Africa.

It is a multipurpose crop due to its various uses of the fresh leaves, buds, flowers, pods and stems, dry stems, pods and seeds (Martin, 1982; Kalra and Pruthi, 1984; Markose and Peter, 1990; Preston, 1998; Schippers, 2000). The green tender fruits of okra are good source of carbohydrates, protein, vitamins (A, B and C) and rich in calcium, potassium and other mineral matters. Its 100 g immature tender fruits contain 89.3 g moisture, 6.3 g carbohydrates, 1.8 g protein, 1 g fiber, 0.2 g fat, 6.9 mg sodium, 1.5 mg iron, 1.2 g minerals and 23 mg vitamin C. Being a rich source of iodine, it is used against goiter. Dry seeds of okra contain 18-20% oil and 20-23% crude protein. Seed of okra (Pusa makhmali) had the highest oil content 17.3% which is a nutritious

ingredient of cattle feed for more milk production. When the okra ripe, the black or brown white eyed seeds are roasted and used as substitute for coffee in Turkey (Bokshi, 1993). The roots and stems are used for cleaning of cane juice in the preparation of jiggery. Crude fiber obtained from mature fruits and stems are extensively being used in jute, textile and paper industry. The crude fiber of mature pods and stems is used in the paper industry. Its leaves are used for preparing a medicament to reduce inflammation. It is an excellent source of Iodine for control of goiter (Chadha, 2001). It is easily digestible and less input consuming vegetable. It can contribute much in solving the chronic nutritional problem of our people.

It is a hardy crop and can grow with considerable success on a wide range of soils and under variable environmental conditions. It can be grown in 21^0 to 42^0 C temperatures and can withstand drought to heavy monsoon during growing season. In the country, a large number of okra varieties are grown, the variation occurs with regards to quantitative and qualitative traits. The plant height, number of primary branches per plant, number of fruits per plant, size of fruit i.e. length as well as weight of fruits are the yield contributing characters while, color of fruit and fiber content determine the quality of fruit.

Vegetable production and supply is not uniform throughout the year in Bangladesh. Vegetables are abundant in winter but 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 season of the year resulted in the lowest per capita consumption of vegetable (25 g/head/day) in Bangladesh (Hossain *et al.*, 1990).

The foremost challenge to the existence of mankind has always been to produce adequate quantity of food form the available acreage to meet the requirements of ever expending world population. The rate of yield gain in crop improvement programme must match the rate of population growth so, as to avoid malnutrition and hunger.

The importance of genetic diversity for selecting parents in combination breeding of different autogamous crops to obtain transgressive segregants has been very well

emphasized by Khanna and Mishra (1977), Singh and Ramanujam (1981), Cox and Murphy (1990). Genetic diversity plays a significant role in plant breeding because hybrids between lines of diverse origin generally exhibit a great heterosis than those between closely related stains which permits to select the genetically divergent parents to get the desirable recombination of the segregating generations (Singh, 1983). Yield is complex character. Various morphological and physiological characters contribute to yield. It is crucial to have knowledge on variability of different characters for the yield improvement. The available variability in a population can be split 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).

A logical way to start any breeding programme is to survey the variation in the available materials. It is said that genetic variability is the "sine qua non" of any such programme. Genetic diversity is very vital factor for any hybridization programme aiming at genetic improvement of yield, especially in self-pollinating crops (Joshi and Dhawan, 1966). Selection is said to be effective in a population having large heritable variability. The genetic variability and its components are the genetic fractions of observed variability that provides measures of transmissibility of the variation and response to selection. The breeder's choice of the material for any improvement work consequently depends on the amount of genetic variability present. The phenotype is often not true indicator of its genotype. The phenotypic variability is the result of the effect of environment and genotype interaction.

Attempts have been made to determine the magnitude of heritable and non-heritable components and genetic parameters such as genotypic and phenotypic coefficient of variation, heritability and genetic advance as percentage of mean in some of the quantitative characters of okra. It is essential to have detail information on the association among different yield components and their relative contribution to yield. Association analysis of quantitative attributes would help in choosing component characters that are positively correlated. In addition, an understanding of association between the component characters is essential to judge their rational importance. Path coefficient analysis is also very useful in formulating breeding strategy to develop elite genotypes through selection in advanced generations. Thus, the nature and

magnitude of variability present in the gene pool for different characters and relationship with each other determine the success of genetic improvement of a character. Since the pattern of inheritance of quantitative characters is highly complex, therefore the present investigation was undertaken to study the association among different components and their direct and indirect contribution to fruit yield in okra. This may assist to scheme an efficient breeding programme for the development of new varieties of okra in Bangladesh.

In view of the above facts, the present study in okra entitled "Genetic Divergence and Relationship between Yield and Yield Contributing Characters in Okra (*Abelmoschus esculentus*)" has been carried out with the following objectives:

Objective of investigation:

1. To estimate genetic variability among okra genotypes for yield and its components,

2. To find out the interrelation among yield and its components at phenotypic and genotypic levels,

3. To find out the genetically divergent parents for future breeding programme.

CHAPTER II

REVIEW OF LITERATURE

The success of any plant improvement programme mainly depends on the right selection of material and its skillful management. It is only possible when we possess knowledge of previous work done in the concerned field. In okra substantial contribution has been made to the literature regarding its genetics and breeding in the recent years. The literature pertaining to the various aspects of the present study has been reviewed under the following heads:

2.1 Genetic variability

2.2 Heritability and genetic advance

2.3 Correlation coefficient analysis

2.4 Path analysis

2.5 Genetic diversity

2.1 Genetic variability

It is a known fact that genotypes within the species exhibit variation indifferent metric traits and components of yield. The genetic variation can only be useful for crop improvement with the help of partitioning variances. Plant breeders are able to determine the relative importance of genetic and environmental variances.

Hazra and Basu (2000) revealed that there was a wide range of variations for plant height (general mean 80.8 cm), leaves per plant (28.9),nodes per plant (14.9), days to first flower (49.9), fruit weight (15 g), fruits per plant (10), seeds per fruit (53.3), fruit yield per plant (155.7g), moderate variations for primary branches per plant (2.9) and fruit length (12.9 cm) and lesser variations for node at first flower (4.8) and ridges per fruit (5.1). Primary branches per plant, which showed a moderate range of variation, recorded the highest genotypic coefficient of variation (GCV; 35.5%). However, plant height (14.3%), leaves per plant (16.6), fruit weight (20%), fruits per plant (16.9%), seeds per fruit (23%), and fruit yield per plant (17.7%) recorded a moderate GCV.

Prakash *et al.* (2001) reported that Arka Abhay was best for high seed yield per plant (62.89g), capsule length (12.64cm) and capsule weight (15.66g) whereas Parbhani Kranti registered as a superior parent for number of capsules per plant (16.60) and days to first flowers (44.90). Among the F_1 hybrids, PK X Arka Abhay showed high capsule weight (20.20g).

Hamed *et al.* (2003) reported that Balady green recorded the highest number of days to first flower (71.78) and number of nodes of first flower (11.31). Gold coast had the highest number of pods per main stem (8.41), plant height (131.95cm) and yield per plant (90.50g). MNH 1999 had the highest number of branches per plant (12.59), number of early pods per plant (7.78) and total number of pods per plant (20.93).

Duzyaman *et al.* (2003) reported that the numerous okra genotypes of American, African, Indian, European & Turkish origin were examined for their pod properties and nutritive values. Pod thickness was considerably high in the genetic material from Africa with up to 2.84cm in diameter in the case of line 1051 from Togo. However, pods of the improved cultivars from the USA and India had a more attractive appearance with diameters varying between 1.15 and 1.50 cm.

Bendale *et al.* (2003) showed a wide range of genetic variability for yield and yield-contributing characters first flowering node, days to first harvest, pod length, pod weight, plant height, nodes per plant, intermodal length, number of branches per plant, fruiting period, number of pods per plant and yield per plant). The phenotypic variance (PCV) for all the 15 characters was higher than the genotypic variance (GCV). The number of branches per plant, yield per plant and number of pods per plant showed high GCV and PCV estimates. All the characters recorded medium to high and high heritability.

Zulfeghar and Patil (2004) reported that the Arka Anamika recorded the lowest disease incidence (0.80%) and the highest yield (23.00t/ha), while the susceptible control Pusa Sawani recorded the highest disease incidence (74.99%) and the lowest yield (7.90t/ha). None of the genotypes was immune to the disease. Arka Anamika, Hybrid 8 and Hybrid 10 were resistant, while Soumya F_1 and Reshma were moderately resistant

Verma *et al*. (2004) reported that the highly significant differences between genotypes were recorded for all the characters. While higher (168.33g/plant) fruit yield was observed in JAE-12 followed by JAE-4 (165.66g/plant) whereas, the lowest fruit yield was noted in JAE-15 (41.33 g/plant). The maximum range of mean value was observed for yield per plant and the minimum for branches per plant. High degree of variability was observed for branches per plant and yield per plant. High estimate of heritability and genetic advance were observed for seeds per fruit and plant height.

Kumar and Kuwar (2005) reported that the genotype Punjab-8 had the tallest plant (89.8cm) and produced significantly high number of primary branches (2.53) as compared to other genotypes. The maximum number of fruits per plant (11.6) was recorded in Arka Abhay and Punjab Padmini.

Singh and Singh (2006) reported that the considerable amount of genetic variation was exhibited by number of branches per plant, fruit yield per plant, tapering length, plant height and fruit length. The closer magnitude of genotypic and phenotypic coefficients of variation indicated that a greater magnitude was played by genotype rather than environment.

Manivannan *et al.* (2007) revealed that the analysis of variances revealed significant differences among parents and crosses for all the characters except fruit diameter. The highest coefficient of variation (PCV24.63 and GCV 23.95) was observed for 100-seed weight.

Naidu *et al.* (2007) reported that highly significant differences between genotypes were recorded for all the characters. While higher (221.0g/plant) fruit yield was observed in JAE-14 followed by JAE-18 (199.5g/plant) whereas, the lowest fruit yield was noted in JAE-4 (98.0g/plant). The maximum range of mean value was observed for yield per plant and the minimum for number of ridges per fruit. High degree of variability was observed for plant height, number of fruits per plant, fruit weight and fruit yield per plant.

Udengwu (2008) reported in okra with deep green skin color are considered more mucilaginous than others and okra consumers show appreciable preference for them.

The results confirmed that fruit skin color in okra is monogenically controlled and the recessive genes involved forma multiple allelic series. The genotypes of the genes involved are suggested as well as their dominance hierarchy.

Jindal *et al.* (2009) revealed that the mean squares for genotypes were highly significant for all the characters indicating presence of genetic variability among the genotypes.

Saifullah and Rabbani (2009) reported that the significant variations among the genotypes were observed for different characters studied. The GCV and the PCV were very close in most of the characters which indicated less environmental influence on the expression of those characters.

Shantha kumar and Salimath (2010) studied in an experiment undertaken to study phenotypic and genotypic coefficients of variation, heritability and genetic advance in three double crosses and four single crosses F_2 population of okra. The analysis of variance revealed highly significant differences for the populations under study for the characters. The estimate of phenotypic and genotypic coefficients of variation were moderate to high for all the characters except days to first flowering, stem diameter (in double cross), fruit length and 100 seed weight.

Somashekhar and Salimath (2011) reported that the wider range of variation as evidence by high PCV and GCV values for number of branches per plant, number of fruits per plant, average fruit weight (g), fruit length, and fruit yield per plant (g).

Oppong-Sekyere *et al.* (2011) revealed that the variation in petal color, pubescence of the leaf and stem, fruit shape, anthocyanin pigmentation and number of days to 50% flowering.

Prashant Kumar *et al.* (2011) found that the analysis of variance (mean square) revealed significant differences among genotypes for all the characters under study. The results based on GCV and PCV indicated considerable genetic variability among the genotypes for height at first fruiting node, number of node at first pod appearance, plant height, number of nodes per plant, number of pods per plant and pod yield per plant.

Senapati *et al.* (2011) reported that the analysis of variance exhibits a wide spectrum of variability among the characters of the hybrids. The largest variability was recorded in fruit yield (58.163-125.077 q/ha) followed by plant height (138.800-182.267 cm). In general phenotypic coefficients of variation (PCV) were greater than genotypic coefficients of variation (GCV) in all quantitative traits due to environmental influence.

Chaukhande *et al*. (2011) revealed that the highest genotypic coefficient of variation as well as phenotypic coefficient of variation was observed for incidence of yellow vein mosaic virus. The maximum difference between GCV and PCV was noted for inter nodal length.

Nagre *et al*. (2011) reported that the highest genotypic coefficient of variation as well as phenotypic coefficient of variation was observed for leaf area followed by number of nodes per plant, length of fruit, number of leaves per plant, yield per plant, and inter-nodal length.

Singh and Jain (2012) reported that the significant differences were recorded for all the characters except stem girth. The plant height was ranged 90.9 to 134.0 cm. It was highest in SOHO-2 and lowest in HIHBO-90, more number of branches per plant was recorded in SOHO-2 and DVR-1(5.1) and the minimum in RHROH-1 (3.7). DVR-1 was found early among all the cultivars. The number of pods per plant was ranged from 9.2 (Arka Anamika) to 22.2 (SOH-5), the weight of pods per plant ranged from 175.0 g to 327 g. It was greater in SOH-5 and the lowest in HIHBO-83 as compared to checks. The longest pods were harvested from RHROH-1 (16.8 cm) and the smallest from Arka Abhay (13.3 cm), thick pods were recorded in HIHBO-90 (5.87 cm), and thin pods in Vijaya (4.35 cm), the minimum infestation of fruit borer was observed in DVR-2 (10.8%) and it was higher in HIHBO-83 (29.6%), Hybrid/cultivars namely DVR-1, DVR-2, RHROH-1, HIHBO-68, and HIHBO-90were found free from YVMV up to 90 days after seed sowing. The highest infection of YVMV was recorded in HIHBO-90 (17.3%) followed by Vijaya (16.0%) and SOH O-2 (14.7%) than check cvs. Parbhani Kranti (6.3%) and Arka Anamika (5.60%), at 90 days after seed sowing. The hybrid cultivars viz.DVR-2, SOH-5 and HIHBO-83 were topper in

fruit yield. They produced189.97, 183.70 and 147.65% higher pod yield over Arka Anamika and 30.28,27.46 and 11.27% over Parbhani Kranti, respectively.

Nwangburuka *et al*. (2012) reported that the twenty-nine okra accessions from different agro-ecological regions in Nigeria were grown during the rainy and dry seasons, between 2006 and 2007 at Abeokuta (derived savanah) and Ilishan (rainforest). There was high genotypic coefficient of variability in traits such as plant height (26.2), fresh pod length (23.9), fresh pod width (23.9), mature pod length (28.6), branching per plant (29.3) and pod weight per plant (33.9).

Rajkumar *et al.* (2014) reported that estimates of mean sum of square due to genotypes were highly significant for all the characters, indicating the presence of genetic diversity in the existing material. The variation was highest for fruit yield per plant, followed by fruit yield per hectare, plant height at 120 DAS, plant height at 90 DAS, plant height at 60 DAS and fruiting span.

Mihretu Yonas *et al.* (2014) reveled that analysis of variance showed significant differences ($p<0.01$) among the accessions for all quantitative characters measured. Estimate of phenotypic and genotypic coefficients of variation also showed the presence of variability among the accessions for the majority of the character. High heritability (96.76 and 96.50%) coupled with high genetic advance as percent of mean (106.32 and 97.25%) were recorded for internodes length and plant height, respectively.

Grewal *et al.* (1972 and 1973) examined the effect of four characters on the yield and quality of okra seeds cv. Pusa Swani. They suggested 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) experimented on hybrid vigour among II 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) experimented on the F_1 and F_2 populations of 25 female lines *Abelmoschus esculentus* with 5 testers and revealed 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) reported that the additive component was the chief determinant of genetic variance in fruit yield per plant, single fruit weight and fruit length. Non-additive components administrated the number of fruits per plant.

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

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

Akorada (1986) experimented with 22 field plots differing with regard to genotype (12 cultivars), field site and cultivation regime for seed and fruit production. Plants that are 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 since there were fewer flowers and lower fruit setting. Of the number of floral buds noticeable on the day of first flowering, 70 % formed edible fruits in fruit plants but only 46 % in seed plants. Mature sun dried pods confined 57 % by weight of plantable seeds.

Ariyo (1987) experimented 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 noteworthy genotype x environment interaction for number of days to flowering and number of branches per plants. Additive environment effects were significant for all the characters. The cultivar UI 313 was steady for pod yield per plant and edible pod weight. A genotype grouping technique presented that the breeding line U 122-77 had below average coefficient of variation for pod yield per plant and above average yield.

Adetunji and Chheda (1989) worked 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 revealed 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 showed that the mean differences among environments, the varieties and their interactions were highly significant. The results recommended 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) experimented 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 PS1O, a mutant of Pusa Swani, was significantly better for number of branches per plant, pod number per plant and pod yield. Both 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) revealed that in case of yield contributing characters like high variability for number of pods per plant of okra. For the characters like days to maturity, plant height and pod length, the phenotypic coefficient of variability was higher than genotypic coefficient of variability

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

Patel and Dalal (1992) worked on the variability of okra for nine yield components in seven *Abelmoschus esculentus* genotypes and their F1 hybrids. They revealed significant variation among the genotypes for all the traits.

Khanobdee and Lertsilpmongkol (1993) conducted a trial at Laxnpang, 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 exposed that average number of pods per plant was 8.5, seed weight per plant 20.7-24.1 g and number of ridges per 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) experimented on heterosis among 8 diverse parents and 28 different hybrids. They found significant differences for plant height, inter-nodal length, pod length, pod girth, number of pods per plant and yield/plant.

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

Gondane and Bhatia (1995) worked with fifty genotypes of *Abelmoschus esculentus* for11 yield-related trails in the rainy and summer seasons of 1987 at Pantnagar. They revealed that all the genotypes responded differently to the environments. They also found significant and marked variation in the yield components, particularly for yield per plant, plant height, pods per plant and nodes to first pod.

Hossain (1997) evaluated the performance of okra for 9 characters in 4 genotypes ("IPSA Resistant", Parbhani Kranti, SL-44 and SL-46) and their 3 hybrids. He reported 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 determined that there was considerable genetic variability in the materials.

Reddy and Kumar (1998) observed 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 exhibited maximum contribution to total variability.

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

2.2 Heritability and genetic advance

Heritability (broad sense) is an index of transmitting a character from the parents to the offspring. It is of great importance for both breeders and geneticists. Lush (1940) defined the broad sense heritability as the ratio of the total genotypic variance to the

total phenotypic variance which provides a measure of the overall importance of hereditary determination of a trait. Characters bearing high heritability values could be improved directly through selection since they are less affected by environment. It indicates the effectiveness in which selection of genotypes can be based on phenotypic performance. Heritability could be more desirably utilized in assembly with the selection differential in predicting genetic gain.

2.2.1 Heritability

Hazra and Basu (2000) revealed that the plant height, fruit weight, ridges per fruit and seeds per fruit were highly heritable (above 80% heritability) while primary branches per plant, leaves per plant, days to first flower, fruit length, fruits per plant and fruit yield per plant were moderately heritable (60-75% heritability). Primary branches per plant, seeds per plant, seeds per fruit and fruit weight had high heritability values with above average to high genetic advance.

Dhankar and Dhankar (2002) reported that the fruit yield, number of fruits per plant and plant height showed high to moderate heritability in both the years.

Sureshbabu *et al*. (2004) reported that the high value of genotypic coefficient of variation combined with high heritability for the characters like fruits per plant, yield per plant, number of ribs on the fruit and height of the plant.

Singh and Singh (2006) expressed that the heritability estimates were high for days to first flowering, first fruiting node length.

Magar and Medrap (2009) reported that Heritability estimates were of high magnitude for fruit length, total fruit yield per plant indicating major role of genotype with less environmental influence.

Senapati *et al.* (2011) investigated that the high heritability estimates were obtained in YVMV disease incidence (98.02%), fruit yield (93.92%), edible maturity (90.98%) and days to 50% flowering (89.02%) indicating that these characters might be heritable and less influenced by environment.

Chaukhande *et al.* (2011) revealed that the character plant height exhibited high heritability (broad sense) percentage.

Nagre *et al.* (2011) reported that the highest estimate of heritability was recorded for leaf area followed by number of leaves per plant, yield per plant, length of fruit, number of nodes per plant, chlorophyll content of leaves and number of fruits per plant.

Nwangburuka *et al.* (2012) found that the twenty-nine okra accessions from different agro-ecological regions in Nigeria were grown during the rainy and dry seasons, between 2006 and 2007 at Abeokuta (derived savanah) and Ilishan (rainforest). There was high % broad-sense heritability in traits such as plant height (90.7), fresh pod length (98.5), fresh pod width (98.5), mature pod length (98.5), branching per plant (82.3) and pod weight per plant (90.0).

Singh and Singh (1978) crossed 25 female lines of okra with 5 testers and observed the 1-1 and 1:2 populations. They reported heritability for number of days to flowering, plant height, fruit length, number of fruits per plant and yield per plant.

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

Wright (1992) revealed 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) tested on heterosis of okra on 28 hybrids derived from 8 x 8 diallel cross and reported significant differences between parents and hybrids for all characters studied. They observed 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 per plant, pod length, pod girth, plant height and inter-nodal length.

Mandal and Dana (1993) experimented on the IF, 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 exhibited significant heritability for earliness, while two crosses, Sel 10x Punjab Padmini shows significant heritability for both plant height and fruits per plant.

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

Dayasagar (1994) evaluated on heterosis of 9 yield components in 6 cultivars and their 15 F1 hybrids. He reported highest heritability for yield per plant in the cross Pusa Sawani x Parhhani Kranti.

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

Poshiya and Vashi (1995) evaluated on heritability in okra and noticed highest heritability of 27.32 % for Fruit yield. The hybrids exhibited significant heterosis for fruit yield and for most of the other characters studied.

Mehetre *et al.* (1998) observed heritability estimation of eight okra varieties and reported that estimates of heritability ranges from 89.60% (plant height) to 32.45% (stability).

2.2.2 Genetic advance

Patil *et al*. (1996) expressed that relatively high genetic advance was observed for characters such as plant height, number of good pods per plant and weight of good pods per plant, indicative of the likely effectiveness of selection for such characters.

Dhall *et al.* (2000) reported that heritability and genetic advance as a percentage of the mean was higher for fruit length, plant height, number of fruits per plant and virus incidence.

Dhankar and Dhankar (2002) found that the fruit yield, number of fruits per plant and plant height showed high to moderate heritability in both the years. The genetic advance was found medium to low for all traits which indicates that there is limited scope for improvement through selection procedures.

Mehta *et al*. (2006) reported that The GCV, heritability and genetic advance as percentage of mean were higher for fruit yield, average fruit weight, plant height and fruit length, which might be attributed to additive gene action resulting their inheritance.

Chaukhande *et al*. (2011) revealed that the highest genetic advance was recorded for yellow vein mosaic virus while lowest for fruit diameter.

Nagre et al. (2011) reported that the highest genetic advance was also observed for the characters leaf area followed by yield per plant, plant height and number of leaves per plant.

Nwangburuka *et al*. (2012) investigated that the high genetic advance in traits such as plant height (51.5), fresh pod length (48.8), fresh pod width (48.8), mature pod length (52.3), branching per plant (54.8) and pod weight per plant (63.3).

2.2.3 Heritability with genetic advance

Chandra *et al.* (1996) noted that the estimates of heritability and genetic advance for pod yield, plant height and number of seeds per pod which were high in magnitude.

Panda and Singh (1997) reported high heritability estimates coupled with high genetic advance for plant height, number of pods and total pod yield per plant and suggested to improve these traits through selection schemes.

Verma *et al.* (2004) observed that the high estimate of heritability and genetic advance were observed for seeds per fruit and plant height.

Singh and Singh (2006) suggested that the genetic advance and heritability suggested that the characters such as first fruiting node length, number of branches per plant, tapering length and fruit yield per plant were under additive gene effects.

Naidu *et al.* (2007) observed that high estimate of heritability and genetic advance were obtained in number of nodes to first flower, number of fruits per plant, number of seeds per fruit and fruit yield per plant. These characters are governed by additive gene action.

Manivannan *et al.* (2007) revealed that the high heritability (94.5%) and highest genetic advance as percent of mean (1.870) were observed for 100-seed weight.

Saifullah and Rabbani (2009) noted that the high heritability estimates along with considerable genetic advance were noticed in days to first flowering, plant height, number of primary branches per plant, number of internodes per plant, number of fruits per plant, fruit weight, number of seeds per fruits and fruit yield per plant provided the basis for selection for development of new variety of okra based on phenotypic performance.

Shantha kumar *et al.* (2010) observed that the heritability and genetic advance were also high for all the characters indicating the involvement of additive type of gene action in controlling these characters, hence, selection could be effective.

Prashant Kumar *et al*. (2011) found that the heritability coupled with genetic advance indicated considerable genetic variability among the genotypes for height at first fruiting node, number of node at first pod appearance, plant height, numbers of node per plant, number of pods per plant and pod yield per plant.

Senapati *et al.* (2011) reported that the high heritability estimates coupled with high genetic advance were obtained for characters such as fruit yield (93.92, 38.89%) and YVMV incidence (98.06, 30.64%).

Umesh *et al.* (2013) recorded that high to moderate heritability and genetic advance were estimated for the characters viz., yield per plant (g), length of internode, height of plant (cm), days to flowering, number of 13 nodes per plant, while length of internode showed high heritability and high genetic advance but yield per plant showed high heritability and moderate genetic advance and also number of branches showed high heritability and low genetic advance. These two characters viz., yield per plant and length of internode indicated the involvement of non-additive gene action.

The heritability for these traits was only due to favorable environmental condition. The characters mentioned above except these two traits had high heritability coupled with high genetic advance and assured that there was preponderance of additive gene action, and selection for these traits was reliable for development of high yielding cultivars of okra.

Rajkumar *et al*. (2014) reported that high heritability coupled with high genetic advance as percentage of mean for traits like fruit yield per plant and fruit yield per plot suggested that the preponderance of additive genes. It also indicated higher response for selection of high yielding genotypes as these characters are governed by additive gene actions.

Reddy and Sridevi (2014) obtained High estimates of heritability coupled with high genetic advance obtained for fruit yield per plant indicating presence of additive gene effects which indicated the effectiveness of selection for these traits. Presence of high heritability coupled with low genetic advance for average fruit weight, plant height and fruit diameter revealed that straight selection has limited scope for further improving these traits. The results exhibited that four lines were highly resistant to yellow vein mosaic virus, ten lines showed moderate resistant, 26 lines tolerant, 10 lines moderate susceptible, 6 susceptible and one highly susceptible. The highest yield per hectare was found in the DBh-25 (21.98 t/ha) followed by DBh-33(19.9 t/ha) and DBh-7 (19.54 t/ha).

Balakrishna *et al.* (1983) tested 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 founded for number of pods per plant (39.5%) followed by plant height (3 1.29%) and number of seeds per pod (24.50%). The lowest genetic advance was observed for pod length (7.20%).

Lal *et al.* (1983) reported 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 founded 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) revealed 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).

Dc and Suriya (1986) observed 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 exhibited higher genetic advance in percent of mean but 1000- seed weight showed high heritability with very low genetic advance in percent of mean.

Oornathinayagam *et al*. (1991) revealed moderate heritability (54.78%) for plan theight but high heritability for days to maturity (98.88%). Genetic advance in percent of mean was high for pods/ plant but low for days to maturity and plant height.

Loknath *et al.* (1991) experimented 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.

Rajeswari and Nadarajan (1993) reported 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 observed for plant height, pod length and 1000- seed weight.

Akanda *et al.* (1995) revealed 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) tested on 20 okra varieties and observed high heritability for total number of pods followed by seed yield per plant and 1000- seed weight. They also reported that Genetics advances in percent of mean were higher for seed yield per plant followed by pod weight and total number of pods.

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

Shanthakumar *et al.* (1996) observed 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) revealed that thirty six genotypes of okra were evaluated in by and among the different characters and observed high genetic advance along with moderate to high heritability and genetic coefficient of variation was found for number of seeds per pod and 100- seed weight.

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

Yousuf *et al.* (1998) observed 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 noted for seed yield per plant (17.65) and 1000- seed weight (7.98). But pod length exhibited high heritability with moderate genetic advance in percentage of mean.

Paul and Sarmah (1999) noticed 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 higher for plant height and number of filled grains per pod and moderate for number of primary branch and harvest index.

Iffekhrauddaula *et al.* (2002) observed moderate value of heritability for number of pods per plant. They also reported that plant height; number of seeds per pod and1000- seed weight had high heritability with moderate genetic advance in percentage of mean.

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

2.3 Correlation coefficient analysis:

The study of correlation coefficient between various economic traits of crop plant is very important to display the degree of union between characters.

Hazare and Basu (2000) reported that fruit yield per plant was significantly and positively associated with plant height, whereas days to first flowering showed negative association with number of fruits per plant.

Gandhi *et al.* (2002) noted that the dry fruit yield was highly and significantly dependent on the number of nodes per plant, inter nodal length, number of fruits per plant and yield per plant.

Nimbalkar *et al*. (2002) observed that the dry fruit yield exhibited positive and significant correlation with number of days to maturity, plant height, seed yield per plant and number of fruits per plant, seed yield recording the highest correlation (r=0.667) with dry fruit yield. Regression studies showed that seed yield per plant contributed 62.8% genetic variability to the total 71.1% variability of the cultivars examined.

Niranjan and Mishra (2003) found that the genotypic correlations were higher than the corresponding phenotypic correlation for all the character combinations. Fruit yield was positively and significantly correlated with edibility period of fruits, number of fruits per plant, fruit length, number of seeds per fruit, fruit weight, plant height and number of branches per plant at both genotypic and phenotypic level. Associations were significant at the genotypic level only between edibility period of fruits and number of branches per plant. All characters had positive and significant association among each other at both level.

Bendale *et al.* (2003) reported that the pod length, pod weight, plant height, nodes per plant and number of pods per plant were positively correlated with the yield.

Duzyaman *et al*. (2003) investigated that pod weight and diameter were positively correlated with total yield. Early flowering was negatively correlated with total yield. Pod weight and pod number per plant were highly associated with flowering behavior

and pod composition on the first year. Pod weight per plant was associated with average pod weight, pod width and flesh thickness, whereas pod number per plant was correlated with dry matter content only. Significant correlation was observed among pod weight, pod width and flesh thickness.

Jaiprakash Narayan and Mulge (2004) reported that total yield per plant was positively and significantly correlated with number of fruits per plant, average fruit weight, number of nodes on main stem, fruit length, plant height 15 (at 60 and 100 DAS) and number of leaves (at 45 and 100 DAS), but negatively and significantly correlated with number of locules per fruit, number of nodes at first flowering and first fruiting.

Patro and Ravishankar (2004) observed that fruit yield per plant have significant and positive correlation with number of branches per plant, fruit length and fruit weight. Significant negative correlation of fruit yield per plant was recorded with plant height and number of days taken to first pod setting.

Sureshbabu *et al.* (2004) noted that the significant phenotypic and genotypic correlation with yield was shown by fruit length and fruits per plant.

Subrata *et al.* (2004) reported in his studies that, in 25 genotypes of okra fruit yield had significant positive correlation with number of fruits per plant and fruit weight.

Bhalekar *et al*. (2005) found that fruit length, inter nodal length, number of fruits per plant and number of branches per plant had positive and strong correlation with fruit yield.

Ghosh (2005) reported that fruit yield per plant was recorded significantly positively correlated with fruiting span, inter nodal length, number of seeds per fruit, plant height at maturity and weight of fruit.

Pawar (2005) reported that the yield per plant was recorded significantly positively correlated with number of fruits per plant, fruit weight, fruit length and fruit girth.

Sankaran *et al*. (2005) observed that the fruit length (0.977), fruit girth (0.922), fruit weight (0.984), crude fiber (0.973), total sugar (0.875) and acidity (0.993) had higher positive correlation with advancement of maturity.

Choudhary (2006) reported that the yield per plant showed positively significant association with number of fruits per plant, fruit weight, length of fruit, number of seeds per fruit, plant height, fruiting span, fruit girth and number of branches per plant.

Akinyele and Osekita (2006) observed that the seed yield per plant showed significant positive correlation with number of pods per plant, height at flowering, pod width and weight of hundred seeds.

Verma *et al.* (2007) reported that yield per plant exhibited positive and significant correlation with fruits per plant, fruit weight, fruit length, and fruit girth. Negative correlation was found in 100 seed weight, days to 50% flowering and days to first flowering with yield per plant.

Adeniji and Aremu (2007) observed the significant differences among the segregating population for pods per branch, seeds per pod, inter node distance, seeds per ridge, branch length, height at flower bud initiation and height at flowering. A positive correlation was recorded for number of pods per plant and seed weight, height at maturity, ridges per pod and seeds per ridge. The seed weight recorded a positive correlation coefficient with edible pod width, seeds per ridge and pods per plant.

Osekita and Akinyele (2008) noticed that there is a strong relationship between pod length and pod width with the number of seeds per pod.

Shazia Ali *et al.* (2008) reported that the Correlation coefficients were estimated among parents, F_1 hybrids and F_2 population separately at genotypic and phenotypic correlation coefficients. The correlation coefficients were consistently significant and positive in all the three population between fruit yield per plant and number of fruits per plant at both genotypic and phenotypic levels. The consistency was also observed in F_1 and F_2 generations between fruit yield per plant and plant height at both genotypic and phenotypic levels. Fruit yield per plant showed significant and positive

correlation between length of fruit and width of fruit at genotypic level in both F_1 and F_2 generations.

Kumar *et al.* (2009) revealed that the magnitudes of genotypic correlation coefficient were invariably higher than phenotypic correlation coefficient, suggesting therefore a strong inherent trait. The most important trait, no. of flower per plant was positively and significantly correlated with no. of leaves per plant, diameter of stem and no. of days to flower at genotypic and phenotypic levels. The data also revealed that no. of fruits per branch, no. of fruits per plant and no. of days to flower were positively and significantly correlated at genotypic and phenotypic levels.

Sharma and Prasad (2010) reported that the positive significant correlation for days to 50% flowering with days to first harvest, number of pod per plant with pod yield per plant and pod yield per plot and pod yield per plant with pod yield per plot and negative correlation was observed for pod weight with number of pod per plant.

Nagre *et al.* (2011) investigated that the yield per plant was closely associated positively and significantly with number of nodes per plant, number of fruits per plant, length of fruit, weight of fruit, leaf area, chlorophyll content of leaves plant height and number of primary branches per plant. The characters like number of leaves per plant, number of lobes per leaf, inter-nodal length, node at which first fruit appears and ascorbic acid content of fruits exhibited positive, however non-significant correlation with yield per plant. The characters diameter of fruit was negatively and significantly correlated with yield per plant. Number of ridges per fruit also showed negative but non-significant correlation with yield per plant.

Chaukhande *et al.* (2011) revealed that the yield per plant exhibit positive and significant correlation with plant height number of flowering nodes on main stem, number of fruits per plant and average weight of fruit.

Senapati *et al.* (2011) reported that the correlation studies exhibited that the genotypic estimates were higher than the phenotypic ones for the most of the traits, indicated a strong inherited association between the characters. Fruit yield is the most important

economic trait showed positive and significant association with number of nodes per plant, number of fruits per plant and fruit length.

Nwangburuka *et al.* (2012) expressed that the positive and significant phenotypic and genotypic correlation between plant height at maturity, fresh pod width, seeds per pod and pods per plant, branches per plant with seed weight per plant and pod weight per plant, suggests that selection on the basis of the phenotype of these characters will lead to high seed and pod yield in okra.

Mihretu Yonas *et al*. (2014) found that Correlation study between various quantitative characters highlighted significant association among18characters. Fruit yield was positive and highly significant genotypic correlation with fruit length (r=0.74), average fruit weight (r=0.62), fruit diameter (r=0.61), seed per pod (r=0.56), hundred seed weight (r=0.68) and number of pod per plant (r=0.66).

Balai *et al*. (2014) revealed that average weight of edible pod (0.943) had highest positive direct effect followed by number of pods per plant (0.372) and number of leaves per plant (0.125) on yield per plant. The study suggested that plant height, length of pod, average weight of edible pod and number of seeds per pod are important traits which should be used as selection criteria to develop high yielding varieties in okra.

2.4 Path analysis

Dhall *et al*. (2000) reported that path coefficient analyses in 48 advanced generation lines of okra were conducted. Significant differences among genotypes were observed for all the characters evaluated, except for virus incidence. Path analysis revealed that the marketable yield per plant, number of fruits per plant, fruit weight, fruit length and plant height had the highest direct effect on the total yield, indicating that emphasis should be given on such characters to improve the yield potential.

Subrata *et al.* (2004) found that twenty-five genotypes of okra were grown in Nadia, West Bengal, India, during kharif 2001 to study the genetic variability of important growth and fruit characters and their relationships. Path coefficient analysis with partitioning of phenotypic correlation revealed that number of fruits per plant and fruit

weight had positive and high direct effect on fruit yield, indicating their importance as reliable selection criteria for improvement of yield in okra.

Sarkar *et al.* (2004) investigated that path coefficient analysis with partitioning of phenotypic correlation revealed that number of fruits per plant and fruit weight had positive and high direct effect on fruit yield, indicating their importance as reliable selection criteria for improvement of yield in okra.

Mehta *et al.* (2006) revealed that fruit girth had the maximum direct effect followed by fruit length towards fruit yield. Thus, the fruit yield in okra can be improved by selecting for higher fruit length, fruit girth and average fruit weight simultaneously.

Magar and Mendrep (2009) reported that 41 genotypes of okra path co-efficient study revealed that number of fruits per plant had the maximum direct contribution towards total yield followed by fruit weight, plant height and days to first flowering. These important traits may be viewed in selection programme for the further improvement of okra.

Ramanjinappa *et al*. (2011) revealed that in path coefficient analysis, number of fruit per plant had the highest direct influence towards fruit yield per plant followed by number of seed per fruit, harvest index and number of nodes per plant.

Senapati *et al.* (2011) found in path coefficient analysis that the number of fruits/plant (0.242), fruit girth (0.218) and fruit length (0.058) exhibited the maximum direct effects on fruit yield as phenotypic level. On the basis of above findings, it was concluded that the number of fruits/plant and fruit length would be considered for improvement of fruit yield of okra hybrid and among the genotypes, JOH 05-9 was found the most promising hybrid followed by HOK 152 and AOH-23.

Sibsankar *et al.* (2012) reported in path coefficient analyses, that the top priority should be given to selection based on numbers of fruit per plant and fruit weight for yield improvement and could be considered while formulating selection indices in the improvement of okra.

Gangashetti *et al.* (2013) reported that path analysis depicted high effect on number fruit per plant, fruit weight, plant height, and number of branches per plant with fruit yield per plant. To release importance of fruit yield, direct selection can be practiced for the characters.

Mihretu Yonas *et al.* (2014) reported that path coefficient analysis at genotypic level revealed that internodes number had high positive direct effect on fruit yield (p=6.90) followed by average fruit weight (p=6.89) which had positive genotypic correlation with yield. The present study indicated a considerable amount of variability for majority of quantitative characters in okra for exploration.

2.5 Genetic diversity

The wide diversity of genotypes attained from 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 Mahalanohis (1963) is an influential 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) calculated 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) experimented 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 assembled into 5 clusters. Mostly the cultures in a cluster derived from the same cross. The geographical diversity was accompanied with genetic diversity to some extent. Seven cultures were recognized with genetic diversity, high yield component and multiple resistances to be utilized as parent's in future breeding program.

Kanwal *et al*. (1983) studied genetic divergence on 100 strain using Mahalanohis's D^2 statistics and canonical variate analysis and reported that fruit weight, number of days to maturity, height and fruit size contributed most towards divergence. The strains

were gathered into nine clusters, which were not correlated with geographical diversity.

Naskar *et al.* (1985) revealed that when cluster analysis was applied to 9 characters in 22 diverse Indian genotypes in 1981 and 1982, all genotypes were assembled 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) used in crosses to give promising sergeants. It was suggested high heterosis could be achieved by crosses between members of distant clusters.

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

Digby *et al.* (1989) studied 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 whereas PCO is used to calculate the minimum distance straight line between each pair of points.

Pyene *et al.* (1989) studied 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 recommended non-hierarchical classification, as an alternative approach to optimize some suitability choosing criteria directly from the data matrix. They also observed that the squared distance between means were Malialanobis's D^2 statistics when all the dimensions were used, could be computed using Principal Coordinate Analysis (FCC). They also suggested the canonical vector analysis (CVA) for discriminatory purpose.

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

with 817 parents grouped into as many as 9 clusters. Direct relationship between genetic distance and heterobeltiosis did not occur but parental diversity looks to play a significant role in expressing the positive heterobeltiosis. Most of the crosses did not express any relationship with divergence estimates.

Ibrahim *et al.* (1992) reported that the genetic divergence in okra population comprising nine morphologically different genotypes over the different environment (E) has been measured through Mahalanohis's D^2-statistics. The analysis exposed considerable genetic divergence among genotypes. The genotypes under study fall into 3 arrangements in E1, E2 and E3 in D^2. Poongar, an indigenous short duration tall stature genotype, consistently happened either in the same or closely related cluster in both stress (E2 and E3) and non-stress conditions (B1).

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

Chauhan and Chauhan (1994) observed 12 clusters through using D^2 statistics while studying genetic diversity. Thousand-grain weight expressed maximum to total divergence. Other traits with appreciable contribution to total divergence were days to 50% flowering, pod weight and seeds per pod.

Mishra *et al.* (1994) revealed that the multivarianec of divergence for 9 quantitative traits among 46 strains of okra divided the genotypes into 5 clusters. The first cluster hold 35 genotypes, the second 5, while the third 3, fourth and fifth cluster each contained 1 genotype. Number of fertile seeds per plant, number of sterile seeds per plant and plant height were the highest contributors of Mahalanobis D^2 values.

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

Sarawgi and Shrivastava (1996) conducted 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 assembled into 7 and 15 clusters, respectively, under irrigated

and rainfed conditions.

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

Sardana *et al*. (1997) revealed 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 gathered into 18 clusters, of which cluster I with 15 genotypes was the largest. The genetic diversity was because of genetic drill, selection in peculiar topography and diverse agro-climatic condition of Tripura. Numbers of pods per plant, leaf area, seed weight per plant and seed yield per plant were the foremost components contributing to the genetic diversity.

Rao and Gomathinayagarn (1998) analyzed genetic divergence separately by using Mahalanobis's 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 transformed the clustering pattern between environments. Favorable environment yielded in lesser number of clusters by manipulating high genetic potential of different traits expressed by genotypes. Genotypes with steady genotype environment interaction in the expression of different traits were tending to cluster together in one cluster in both the environments.

Singh *et al.* (1998) studied 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 congregated into four clusters. No relationship between geographic origin and genetic diversity was found. The four characters, that are, harvest index, total number of seeds per pod, number of fertile seeds per pod and stability accounted 92.65 % of the total divergence.

Kumari and Rangasamy (1999) analyzed the genetic divergence using Mahalanobis's D^2-statistics in 62 early okra genotypes. Based on eight important yield-contributing characters, these genotypes were assembled into six clusters. Cluster I was the largest, containing 85% of genotypes, Cluster II, III, IV and V had two genotypes in each. Cluster VI contained only one genotype.

Soni *et al.* (1999) revealed 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 designated the existence of significant amount of variability among the genotypes for the quality trials. Higher order of divergence was observed between clusters VI and VII. Based on mean performance, genetic distance and clustering pattern, hybridization involving selected 10 genotypes are likely to give required segregants for seed quality.

Bansal *et al.* (2000) evaluated the genetic assessing of 36 okra stocks using Mahalanobis's D^2 statistics. Thirty four genotypes belonging to seven countries were grouped into 15 clusters. The patterns of sharing 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 generating wider variability for early maturity, dwarf and high yielding segregants.

Rather *et al.* (2001) assessed 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 reported among cultivars. The highest mean value for harvest index and the lowest plant height were found. Based on the mean performance for plant height, maturity, seed yield and inter-cluster distance, cultivars from clusters II and IV may be utilized for initiating hybridization.

CHAPTER III

MATERIALS AND METHOD

This chapter comprises the details about the materials used and the methods adopted during the course of present investigation entitled "Genetic divergence and relationship between yield and yield contributing characters in okra (*Abelmoschus esculentus*)" which was carried out in Kharif-I season during the year 2017.

3.1 Experimental site

The experiment was carried out at the experimental field of Sher-e-Bangla Agricultural University (SAU), Sher-e-Bangla Nagar, Dhaka. The location of the site was situated at 23º41´ N latitude 90º22´ E longitude and 8.6 m above from the sea level. It felled under sub-tropical climate. The field views of experimental plot are presented in Plate 1.

3.1.1 Soil

The soil of the experimental site lies in Agro-ecological region of "Madhupur Tract" (AEZ No. 28). Its top soil was clay loam in texture and olive gray with common fine to medium distinct dark yellowish brown mottles. The pH was 4.47 to 5.63 and organic carbon content was 0.82%. The physical and chemical characteristics of initial soil (0-15 cm depth) of the experimental site are presented in the Appendix I.

3.1.2 Climate and weather conditions

The experimental site had sub-tropical climate. It was characterized by high temperature accompanied by moderate high rainfall during kharif season (April to September) and low temperature in the Rabi season (October to March). Details of the metrological data including the maximum and the minimum mean monthly temperature (^{0}C), relative humidity and sunshine (hours/day) for growing season was collected from the Bangladesh Metrological Department (Climate division), Agargaon, Dhaka-1207, which is presented in Appendix II.

a) Field view at early stage

b) Field view at flowering and fruiting stage

Plate 1: Field view of Experimental site

3.2 Experimental material

The experimental material for this study comprised of 19 genotypes *Abelmoschus esculentus*. The germination percentage was above 92. The genetically pure and physically healthy seeds of these genotypes were collected from the Plant Genetic Resources Center (PGRC), BARI, Horticulture Research Center (HRC). The name and source of the genotypes are presented in Table 1.

3.3 Experimental details

3.3.1 Design of experiment

The experiment was laid out in Randomized Complete Block Design (RCBD) with 19 treatments in three replications. The plot size was 3 × 22 square meter. The row to row distance was 50 cm and plant to plant distance was 40 cm. the number of row per plot was 38 and number of plants per row was 6. Distance between each replication was 1 m. five plants were randomly selected for data collection.

3.3.2 Land preparation

In order to bring good tilth, the experiment plot was prepared by several ploughing and cross ploughing followed by laddering and harrowing with tractor and power tiller in the first week of May 2017. Weeds and other stables were collected and removed carefully from the experimental plot and leveled properly.

3.3.3 Fertilizer application

A dose of 150kg N, 110kg P_2O_5 and 80kg K_2O/ha along with 2.5 ton cowdung/ha was applied. One third nitrogen and entire quantity of P, K and cowdung was applied prior to sowing. Remaining dose of nitrogen was applied in two splits at 30 and 60 days after sowing.

3.3.4 Sowing

The seeds were soaked overnight into water before sowing. Seeds were dibbled at about 1.5 cm depth in the soil. Two seeds were placed in each hole.

Table 1. Name and Source of nineteen okra genotypes used in the present study

Sl. No.	Genotypes	Source
1	G1	PGRC, BARI
2	G2	PGRC, BARI
3	G3	PGRC, BARI
4	G4	PGRC, BARI
5	G5	PGRC, BARI
6	G6	PGRC, BARI
7	G7	PGRC, BARI
8	G8	PGRC, BARI
9	G9	PGRC, BARI
10	G10	PGRC, BARI
11	G11	HRC, BARI
12	G12	HRC, BARI
13	G13	HRC, BARI
14	G14	HRC, BARI
15	G15	HRC, BARI
16	G16	HRC, BARI
17	G17	HRC, BARI
18	G18	HRC, BARI
19	G19	HRC, BARI

3.3.5 Thinning and gap filling

After two weeks of sowing, thinning and gap filling was carried out to maintain uniform plant population. All the recommended package of practices was followed to raise healthy crop.

3.3.6 Irrigation

The moisture was not sufficient in the soil that's why pre-sowing irrigation was given in the experimental field. Then the irrigation was given when required.

3.3.7 Weeding and earthing up

The experimental plots were kept weed free. Hand weeding was done as and when needed. Earthing up was done especially to prevent water logged condition.

3.3.8 Plant protection

The crop was sprayed with Ripcord @ 0.5 ml/liter of water and Marshal @ 0.5 ml/liter of water for eight times at an interval of 12 days to keep the crop free from pest during crop growth period. As a preventive measure against different fungal disease and foot rot, Ridomyl Gold @ 0.2 % was sprayed five times at an interval of 10 days. Both the insecticide and fungicide were sprayed in the evening.

3.3.9 Sampling

Sampling was done after 30 days to harvest time for growth analysis. Five plants were randomly selected from each genotype for the study.

3.4 Observation

The data recorded on various parameters were subdivided into three categories during the period of experimentation.

(A) Morphological parameters

3.4.1 Plant height (cm)

Height of plant was recorded from the base just above the soil surface to growing point of the plant with the help of meter scale. The height was recorded after final harvesting.

3.4.2 Number of flower per plant

Numbers of flower of five randomly selected plants were counted and mean data was recorded.

3.4.3 Branches per plant

Number of branches of selected plants was counted and average was worked out at 60 days after sowing and 90 days after sowing.

3.4.4 Number of internodes per plant

Total numbers of internodes of five randomly selected plants were counted and their mean data was recorded.

(B) Phenological parameters

3.4.5 Days to 50% flowering

Average number of days required to 50% flowering in each genotype was recorded separately and their mean data was noted.

3.4.6 Fruiting span

Fruiting span means the duration between first and last picking was recorded to know the fruiting span of each genotypes.

(C) Yield parameters

3.4.7 Number of fruits per plant

The number of fruits harvested from five randomly selected plants in each genotype wascollected during each picking counted and totaled together and average fruits per plant were calculated.

3.4.8 Fruit length (cm)

The length of fruit was measured from randomly selected five fruits from every genotype with the help of scale and then average was recorded.

3.4.9 Fruit diameter (cm)

The diameters of the randomly selected fruits were recorded with the help of Vernier calipers and average was worked out.

3.4.10 Fruit weight (g)

The weight of five fruits was recorded separately with the help of weighing balance and average was worked out for each genotypes.

3.4.11 Number of seed per fruit

Mean numbers of seed of fruits of five randomly selected plants was recorded.

3.4.12 Fruit yield per plant

Total yield of the selected plants was measured in gram and mean data was recorded.

3.5 Statistical analysis

The data obtained in respect of all the characters has been subjected to the following statistical analyses.

3.5.1 Mean

It was calculated by using following formula.

$$\text{Mean} = \frac{\Sigma x}{n}$$

Where,

Σx = The sum of all the observations
n = Number of observations

3.5.2 Analysis of variance

The data based on the mean of individual plants selected for observations were statistically analyzed to find out overall total variability present in the material under study for each character and for all the populations. The first and foremost step is to carry out analysis of variance to test the significance of differences among the populations. The analysis of variance was carried out as per methods suggested by Panse and Sukhatme (1967). The skeleton of analysis of variance used is as follows:

ANOVA for Randomized Completely Block Design:

Source of Variation	df	Sum of Square	Mean sum of square	F value	F_t 5% or 1%table value
Replications	r-1	RSS	RMS	RMS/EMS	-
Genotypes	g-1	GSS	GMS	GMS/EMS	-
Error	(r-1)(g-1)	ESS	EMS	-	-
Total	rg-1	TSS	-	-	-

Where,

r = Number of replications

g = Number of genotypes

df = Degree of freedom

RSS = Replication sum of squares

GSS = Genotype sum of squares

ESS = Error sum of squares

TSS =Total sum of squares

RMS = Replication mean sum of squares

GMS = Genotype mean sum of square

EMS = Error mean sum of square

A significant value of F test indicates that the test entries differ significantly among themselves, which require the computing of CD

$$CV = \frac{\sqrt{EMS}}{GM} \times 100$$

$$SEm \pm = \frac{\sqrt{EMS}}{r}$$

$$SE\ diff = \frac{\sqrt{2EMS}}{r}$$

CD at 5% prob. Level = SE diff x t5% table value at error d.f.

Where,

CV % = Coefficient of variation

SEm± = Standard error of means

SE diff = Standard error of difference of mean

GM = Grand mean

CD = Critical difference

t 5% = table value of t at 5% probability level at error df

Estimation of components of variance, phenotypic, genotypic and environmental coefficient of variation, heritability, genetic advance and genetic advance as percentage of mean:

The component of variance was calculated as follows:-

Source of Variation	MSS.	Expected MSS
Replication	-	-
Genotypes	M_i	$\sigma^2_{ei} + r.\ \sigma^2_{gi}$
Error	E_i	σ^2_{ei}

$$\sigma^2_{gi} = M_i - E_i$$

$$\sigma^2_{ei} = E_i$$

$$\sigma^2_{pi} = \sigma^2_{ei} + \sigma^2_{gi}$$

where,

σ^2_{gi} = Genotypic variance for i^{th} character.

σ^2_{ei} = Environmental variance for i^{th} character.

σ^2_{pi} = Phenotypic variance for i^{th} character.

Phenotypic and genotypic coefficient of variation (expressed in %) were calculated by using the formula given by Burton (1952). Genotypic coefficient of variation (GCV) was calculated as below:

$$GCV\% = \frac{\sqrt{\sigma^2 g_i}}{X_i} \times 100$$

Phenotypic coefficient of variation (PCV)

$$PCV\% = \frac{\sqrt{\sigma^2 P_i}}{X_i} \times 100$$

Where,

Xi =General mean of the i^{th} character under consideration.

σ^2_{gi} and σ^2_{pi} = Genotypic and phenotypic variances of the i^{th} character respectively.

3.5.3 Heritability and genetic advance

Heritability (broad sense) which is ratio of genotypic variance to the total phenotypic variance is symbolized as h^2 (BS) and expressed in percentage. Estimation of heritability was done as per the formula given by Hanson *et al.* (1956).

$$h^2 (BS) = \frac{\sigma^2 g_i}{\sigma^2 p_i} \times 100$$

Or

$$= \frac{\text{Genotypic variance of the ith character}}{\text{Phenotypic variance of the ith character}}$$

Expected genetic advance was calculated by using the method suggested by Johnson *et al.* (1955) at 5% selection intensity.

Genetic advance (GA) = K. P_i .h^2_i

Genetic advance as percentage of mean was calculated as follows:

$$\frac{Genetic\ advance}{\bar{x}}$$

Where,

K= Selection intensity its value at 5% selection level is 2.06.

P_i = Phenotypic standard deviation of the i^{th} character.

h^2_i = Broad sense heritability (fraction) of the i^{th} character.

$\bar{X}_i$ = General mean of the i^{th} character under consideration.

3.5.4 Correlation coefficients

Correlation coefficients were calculated in all possible combination staking all the characters into consideration at genotypic, phenotypic and environmental levels by using the formula as proposed by Miller *et al.* (1958).

$$r = \frac{\sum xy - \frac{\sum xy}{n}}{\sqrt{(\sum x^2 - \frac{(\sum x)^2}{2})\ (\sum y^2 - \frac{(\sum y)^2}{2})}}$$

Where,

r = Correlation coefficient

n = Number of treatments

x and y = Characters under study

Genotypic, phenotypic and environmental correlations were computed by substituting corresponding variance and covariance in the following formula:

$$r_G\,(X_i\ X_j) = \frac{Cov\ G\ (Xi\ Xj)}{\sqrt{VG\ (Xi).\ VG\ (Xj)}}$$

$$r_P (X_i X_j) = \frac{\text{Cov P (Xi Xj)}}{\sqrt{\text{VP (Xi). VP (Xj)}}}$$

$$r_E (X_i X_j) = \frac{\text{Cov E (Xi Xj)}}{\sqrt{\text{VE (Xi). VE (Xj)}}}$$

Testing of correlation coefficient

The phenotypic correlations were tested for their significance by using the following formula based on "t" test:

$$t = \frac{r}{\sqrt{(1-r^2)}} \sqrt{n-2} \text{ at (n-2) d. f.}$$

Where,

n= Number of treatments.

r= phenotypic correlations coefficient.

The calculated value of "t" is compared with table of "t" at (n-2) d. f. If the calculated value is equal to or greater than table value, it is significant at given probability level. If $t_c < t_T$, it is non-significant.

3.5.5 Path coefficient analysis

Path coefficient are standardized partial regression coefficient and as such these provide the means to direct influence of one character upon another character upon another character and also permit portioning of correlation coefficient into direct and indirect effect via other character. The direct indirect contribution of various independent characters on a dependent character yield were calculated through path coefficient analysis as suggested by Wright (1921) and elaborated by Dewey and Lu (1959). The following set of simultaneous equation were formed and used for the estimation of direct and indirect effects.

$r_{1y} = p_{1y} + r_{12}\, p_{2y} + r_{13}\, p_{3y} +$ ---------- $r_{1y}\, p_{1y}$

$r_{2y} = r_{2y}\, p_{1y} + r_{2y} + r_{23}\, p_{3y} +$ ---------- $r_{21y}\, p_{1y}$

$r_{ky} = r_{ki}\, p_{1y} + r_{k-1}\, p_{2y} + r_{k3} p_{3y} +$ ---------- p_{ky}

$r_{xky} = r_{xk1}\, p_{1y} + r_{xk2}\, p_{2y} + r_{xk3}\, p_{3y} +$ ---------- p_{xky}

Where,

r_{xky} = Coefficient correlation between independent character

P_{iy} to P_{3y} = Direct effect of character 1 to 3 character y

Direct effect

The direct effects were calculated as follows:

$$P_{ky} = \sum_{i=1}^{k} C_{krik}\, Y$$

Indirect effect

Indirect effect of any independent traits on the dependent one (=yield) via other independent traits are computed by multiplying the direct effects (P_{ky}) of that independent variables with the corresponding correlation coefficient as follows:

$$K^{th} \text{ traits via } (n\text{-}1) = rk\ (n\text{-}1)\ P\ (n\text{-}1)\ Y$$

3.5.6 Cluster analysis (CA)

Cluster analysis separated the genotypes of a data set into some number of mutually exclusive groups. Clustering was done by using non-hierarchical classification. In GenStat program, the algorithm is used to search for optimal values of chosen criterion proceeds as follows. Starting from some preliminary 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 observed 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.

3.5.6.1 Calculation of D^2 values

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

$$D^2 = \sum_i^x d^2{}_i = \sum_j^x (Y^j{}_i - Y^k{}_j) \quad (j \neq k)$$

Where,

Y = Uncorrelated variable (character) which varies from i = I ----------to x

x = Number of characters.

Superscript j and k to Y = A pair of any two genotypes.

3.5.6.2 Computation of average intra-cluster distances

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

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

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.

3.5.6.3 Computation of average inter-cluster distances

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

Average inter-cluster distances $= \frac{\sum D_{ij}^2}{n_i \times nj}$

Where,

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

n_i = Number of populations in cluster i.

n_j = Number of populations in cluster j.

3.5.6.4 Cluster diagram

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

3.7 Selection of varieties for future hybridization program

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

a) Selection of cluster from which genotypes are chosen for use as parent (s)
b) Identification of particular genotype(s) from the selected cluster(s)
c) Relative contribution of the characters to the total divergence
d) Other significant characters of the genotypes (per se performance)

CHAPTER IV

RESULTS AND DISCUSSIONS

The present investigation was carried out on 19 genotypes of okra (*Abelmoschus esculentus* L. Moench) to study the genetic diversity and relationship between yield and yield contributing characters. Further, selection of most suitable and high yielding genotype(s) for fruit yield would be based according to mean performance of genotypes and existence of genetic variability and diversity for yield components. The observations were recorded on the characters such as days to first flowering, number of flowers per plant, number of internodes per plant, number of primary branches per plant, fruiting span, plant height (cm), number of fruits per plant, fruit length (cm), fruit diameter (cm), individual fruit weight (g), number of seeds per plant and fruit yield per plant (g).

The results obtained after analysis of data are presented in this chapter under following heads:

4.1 Analysis of variance
4.2 Mean performance of genotypes
4.3 Genetic divergence analysis
4.4 Variability study in genotypes
4.5 Correlation among the component traits
4.6 Path coefficient analysis

4.1 Analysis of Variance

The results of analysis of variance for 12 characters of 19 okra genotypes are presented in Table 2. Mean square for most of the characters studied revealed highly significant ($P< 0.01$) differences for all the traits studied. This was revealed that existence of a good deal of variation for all the traits among the population. This could be exploited through selection to improve the crop for desired traits. This results is in agreement with Hazem *et al.* (2013) and Amoatey *et al.* (2015) who reported that significant differences among

Table 2. Analysis of variance for different characters in okra genotypes

Characters	Mean sum of square		
	Replication (r-1) = 2	Genotype (g-1) = 18	Error (r-1)(g-1) = 36
Days to 1st flowering	11.84**	6.40**	1.08
No. of flower per Plant	49.17**	88.64**	0.30
No. of internodes per plant	30.94**	73.71**	0.55
No. of primary branches per plant	3.43**	4.99**	0.27
Fruiting span (days)	0.43	21.09**	1.90
Plant height (cm)	2.62	1,063.81**	24.03
No. of fruits per plant	29.80**	91.32**	1.23
Fruit length (cm)	19.10**	4.54**	0.52
Fruit diameter (cm)	0.29**	0.12**	0.001
Individual fruit weight (g)	102.68**	18.63**	1.86
No. of seeds per fruit	145.59**	295.52**	1.59
Fruit yield per plant (g)	68,711.47**	30,216.53**	1,021.52

** Denote Significant at 1% level of probability

the tested okra genotypes for most of the studied traits. This study results also supported by Salesh *et al.* (2010) and found highly significant differences. A wide range of variations for yield contributing traits was also observed by Gandhi *et al.* (2002). Replication was also highly significant different for all the traits studied except fruiting span and plant height.

4.2 Mean Performance of Okra Genotypes

4.2.1 Days to 1st flowering

Days to first flowering varied significantly among the genotypes (Table 2). Days to first flowering ranged from 38.67 to 43.33 days with a general mean of 41.58 days (Table 3). Early flowering was observed in the genotype G16 (38.67 days) followed by G15 (39.00), G14 (39.33 days) and G1 (39.67 days). The late first flowering was observed in the three genotypes G9, G10 & G19 (43.33 days) followed by G12 (43.00 days). Six genotypes expressed better values i.e. lower the days to first flowering compared to population mean (41.58 days). From these genotypes early varieties could be selection for further study.

4.2.2 Number of flowers per plant

Number of flowers per plant varied significantly among the genotypes (Table 2). Number of flowers per plant ranged from 14.33 to 30.67 with a general mean of 22.65 (Table 3). Nine genotypes expressed better values as compared to population mean (22.65). The genotype expressing the maximum value was in G10 (30.67) and the minimum was recorded in G4 (14.33).

4.2.3 Number of internodes per plant

Number of internodes per plant varied significantly among the genotypes (Table 2). Number of internodes per plant ranged from 18.33 to 34.67 with a general mean of 26.95 (Table 3). More number of internodes per plant was recorded in G16 (34.67) followed by G10 (32.67) and G14 (32.33) (Table 4). Nine genotypes expressed better values compared to population mean (26.95). These findings may be due to greater plant height, and more number of primary branches per plant may be because of

Table 3. Range, mean, CV (%) and standard deviation of 19 okra genotypes

Parameters	Range		Mean	CV (%)
	Min	Max		
Days to 1st flowering	38.67	43.33	41.58	2.50
No. of flower per Plant	14.33	30.67	22.65	2.44
No. of internodes per plant	18.33	34.67	26.95	2.77
No. of primary branches per plant	1.33	6.00	3.09	16.89
Fruiting span (days)	52.33	62.67	56.35	2.45
Plant height (cm)	102.00	164.43	127.23	3.85
No. of fruits per plant	7.67	25.33	17.30	6.42
Fruit length (cm)	9.50	14.33	12.93	5.59
Fruit diameter (cm)	1.62	2.24	1.87	3.74
Individual fruit weight (g)	10.10	19.53	15.84	8.61
No. of seeds per fruit	33.33	70.67	56.56	2.23
Fruit yield per plant (g)	77.87	441.73	279.04	11.45

CV (%) = coefficient of variation

getting more space for plant canopy development.

4.2.4 Number of primary branches per plant

Number of primary branches per plant varied significantly among the genotypes (Table 2). Number of primary branches per plant ranged from 1.33 to 6.00 with a general mean of 3.09 (Table 3). Nine genotypes expressed better values as compared to population mean (3.09). The results of the present study were also in conformity with Gondane (1989). The genotype expressing the maximum value was in both G1 & G2 (6.00) and the minimum was recorded in G18 (1.33) (Table 4). The general mean of primary branches per plant were recorded as 2.9 and 1.57 by Hazra and Basu (2000); Alam and Hossain (2008), respectively.

4.2.5 Fruiting span (days)

Fruiting span varied significantly among the genotypes (Table 2). Number of days of fruiting span ranged from 52.33 days to 62.67 days with a general mean of 56.35 days (Table 3) More number of days of fruiting span was recorded in G15 (62.67 days) followed by G14 (60.00 days) and G10 (59.33) (Table 4). Eight genotypes expressed better values compared to population mean (56.35 days).

4.2.6 Plant height (cm)

Plant height is usually a good index of plant vigour, which may contribute towards greater production of fruit yield in okra. Plant height varied significantly among the genotypes (Table 2). Plant height ranged from 102.00 cm to 164.43 cm with a general mean of 127.23 cm (Table 3).

The maximum plant height was recorded in G10 (164.43 cm) and minimum was observed in G1 (102.00 cm) (Figure 1) (Table 4). When compared to population mean (127.23 cm), ten genotypes exhibited better plant height. Rest of the genotypes showed lower plant height than population mean. Significant differences for plant height were reported by Singh *et al.* (1993 and 1996) also reported the tallest plants during rainy season in their experiments. Hazra and Basu (2000) observed low general value for plant height (80.8 cm).

Table 4. Mean performance of different characters of 19 okra genotypes

G	DFF	FP	IPP	PBP	FS	PH	FPP	FL	FD	IFW	SPF	FYP
1	39.67	28.33	30.67	6.00	52.33	102.00	22.00	13.00	1.94	13.70	55.67	304.33
2	41.67	30.33	32.00	6.00	55.00	138.93	24.67	13.50	2.05	16.73	60.00	413.20
3	42.33	28.00	31.67	4.67	54.67	118.30	22.33	13.83	1.74	19.53	70.67	441.73
4	41.67	14.33	18.33	2.33	55.67	126.10	10.67	13.17	1.77	17.07	61.67	186.80
5	42.00	23.33	28.33	3.33	55.00	115.27	17.33	13.50	1.68	19.23	59.67	337.43
6	42.00	18.33	21.67	3.33	54.33	102.40	15.67	12.00	1.64	13.13	56.67	206.77
7	42.33	20.33	24.33	3.00	57.00	146.77	17.00	13.00	1.71	16.50	65.00	282.50
8	40.67	19.67	23.33	3.33	56.67	129.00	22.33	12.33	1.88	13.83	52.67	310.70
9	43.33	28.00	31.67	2.33	58.33	139.23	25.33	12.67	2.13	15.27	57.33	387.00
10	43.33	30.67	32.67	3.33	59.33	164.43	15.67	13.17	2.24	18.13	68.00	285.37
11	41.33	20.33	25.00	2.33	58.33	136.40	14.33	13.17	1.62	15.97	49.00	233.40
12	43.00	17.00	22.33	2.33	55.33	104.20	13.00	14.33	1.95	18.87	54.33	246.60
13	42.33	18.67	24.67	1.67	56.33	133.77	19.67	12.67	1.68	18.23	47.33	361.70
14	39.33	27.00	32.33	3.33	60.00	150.90	20.33	14.17	2.11	16.13	67.33	308.07
15	39.00	24.67	30.67	3.33	62.67	151.17	20.67	14.17	2.06	14.40	65.00	308.00
16	38.67	29.33	34.67	1.67	58.67	131.40	22.00	14.17	2.13	16.10	64.67	360.27
17	42.00	18.33	23.00	2.67	53.67	114.90	9.67	10.50	1.88	12.33	33.33	115.13
18	42.00	19.00	24.67	1.33	53.00	105.57	7.67	9.50	1.69	10.10	41.00	77.87
19	43.33	14.67	20.00	2.33	54.33	106.67	8.33	12.83	1.63	15.67	45.33	134.97

DFF : days to 1st flowering, FP : No. of flower per plant, IPP : no. of internodes per plant, PBP : no. of primary branches per plant, FS : fruiting span (days), PH : plant height (cm), FPP : no. of fruits per plant, FL : fruit length (cm), FD : fruit diameter (cm), IFW : Individual fruit weight (g), SPF : no. of seeds per fruit and FYP : Fruit yield per plant (g).

4.2.7 Number of fruits per plant

Number of fruits varied significantly among the genotypes (Table 2). Number of fruits per plant ranged from 7.67 to 25.33 with a general mean of 17.30 (Table 3). More number of fruits per plant was recorded in G9 (25.33) followed by G2 (24.67) and G3 & G8 (22.33) (Table 4). Ten genotypes expressed better values compared to population mean (17.30). These findings may be due to greater plant height, and more number of branches per plant may be because of getting more space for fruit development. Singh and Jain (2002) reported that 'Pant Bhindi-1' produced more number of fruits per plant out of eleven cultivars a performance trial of okra. Singh and Jain (2006) also recorded high values for number of fruits per plant in PB 31-1 (18.7) and PB- 226 (17.0). Hazra and Basu (2000), Singh *et al.* (1996) and Mohapatra *et al.* (2007) were reported significant differences for this trait.

4.2.8 Fruit length (cm)

The fruit length varied significantly among the genotypes (Table 2). Fruit length ranged from 9.50 cm to 14.33 cm with a general mean of 12.93 cm (Table 3). The maximum fruit length was recorded in G12 (14.33 cm) followed by G14, G15 & G16 (14.17 cm) (Table 4). As compared to population mean (12.93 cm), ten genotypes exhibited higher fruit length. This result may be due to environment influence and/or varietal characteristics of the genotypes as also reported by Wankhede *et al.* (1995), Singh *et al*. (1996) and Mohapatra *et al*. (2007).

4.2.9 Fruit diameter (cm)

The fruit diameter varied significantly among the genotypes (Table 2). Fruit diameter ranged from 1.63 cm to 2.24 cm with a general mean of 1.87 cm (Table 3). The maximum fruit diameter was recorded in G10 (2.24 cm) followed by G16 (2.13 cm) and G14 (2.11 cm) (Table 4). As compared to population mean (1.87 cm), Nine genotypes exhibited higher fruit diameter. Genotype G19 recorded the minimum fruit diameter (1.63 cm). Plate 2(a) and Plate 2(b) are showing variation in fruit shape and size of different genotypes of okra.

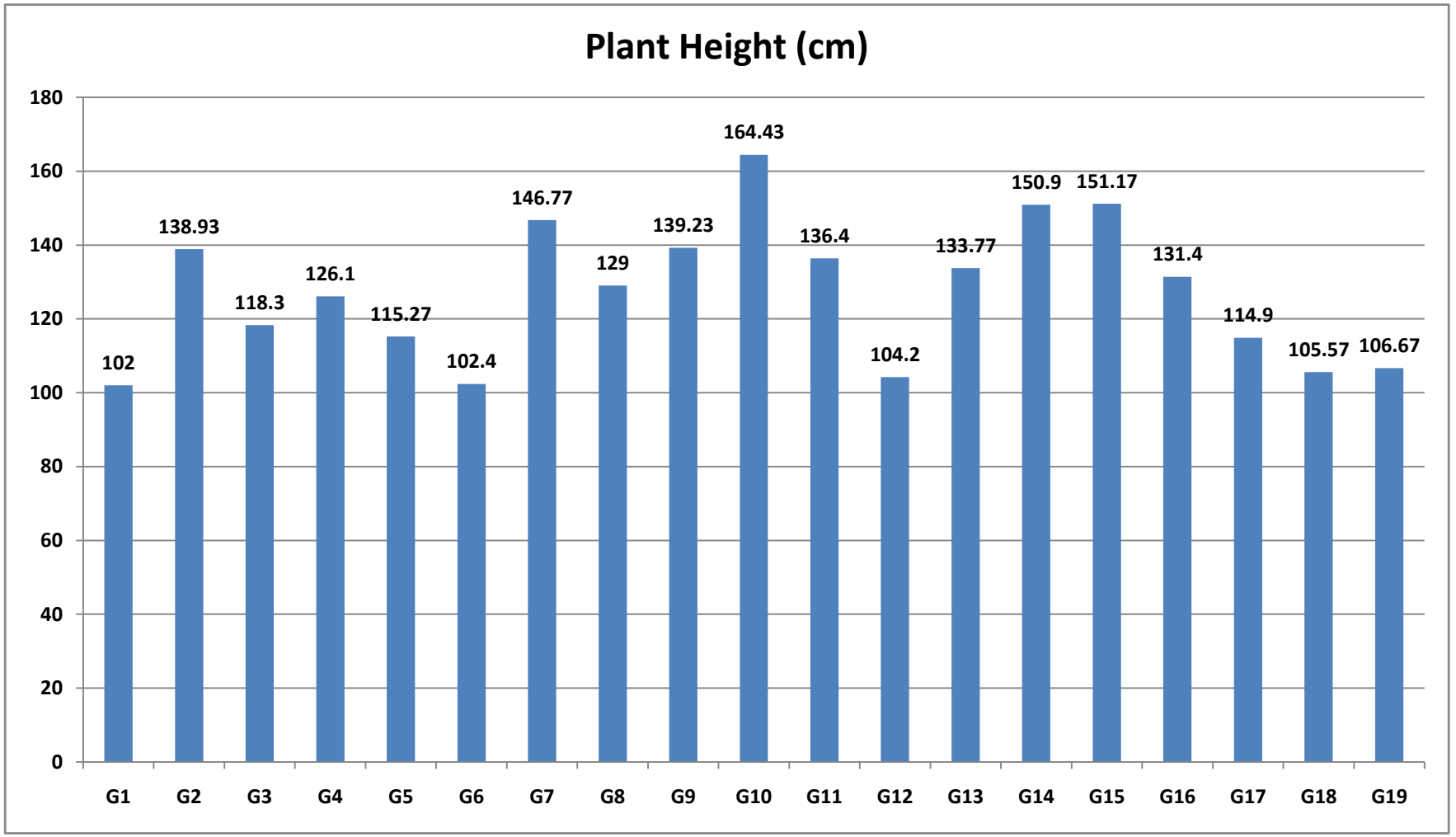


Figure 1. Representing the plant height of 19 okra genotypes

4.2.10 Individual Fruit weight (gm)

Statistically significant variation was found in terms of individual fruit weight of okra (Table 2). The highest individual fruit weight (19.53 g) was found in G3, while the lowest was (10.10 g) recorded in G18 (Table 4). The general mean of individual fruit weight was 15.84 g and more than 50% lines gave more than that general mean fruit weight (Figure 2). Due to different plant height, length of fruit and other morphological structure of different lines the mean fruit weight of different lines were varied from each other. Mishra *et al.* (1996) and Hazra and Basu (2000) reported that genotypes differed significantly for Individual fruit weight.

4.2.11 Number of seeds per fruit

Number of seeds per pod ranged from 33.33 to 70.67 with a general mean of 56.56. Number of seeds per fruit varied significantly among the genotypes. More number of seeds per fruit was recorded in G3 (70.67) followed by G10 (68.00) and G14 (67.33) (Table 4). Ten genotypes expressed higher values compared to population mean (56.56). The least value was recorded in G17 (33.33) followed by G18 (41.00) and G20 (45.33). Similar significant differences for this trait were also noted by Arvind Kumar (2009). Hazra and Basu (2000) also reported similar general mean for seeds per fruit (53.3).

4.2.12 Fruit yield per plant (g)

Performance of genotypes differed significantly for fruit yield per plant (Table 2). Fruit yield per plant ranged from 77.87 g to 441.73 g with a general mean of 279.04 g (Table 3). Maximum fruit yield was exhibited by G3 (441.73 g) followed by G2 (413.20 g) (Table 4). Among all the genotypes, twelve genotypes exhibited higher fruit yield per plant compared to population mean (279.04 g). Minimum fruit yield per plant was observed in G18 (77.87 g) (Figure 3). Gondane (1989) recorded highest fruit yield per plant (418 g). This higher fruit yield per plant maybe due to higher fruit length and more number of fruits per plant showing genetic response of genotypes to environmental conditions as also reported by earlier workers viz., Muhammad *et al.* (2001) and Mohapatra *et al.* (2007).

G-1

G-2

G-3

G-4

G-5

G-6

G-7

G-8

G-9

Plate 2(a). Photographs represent the variation in fruit shape and size of different genotypes of Okra

G-10

G-11

G-12

G-13

G-14

G-15

G-16

G-17

G-18

G-19

Plate 2(b). Photographs represent the variation in fruit shape and size of different genotypes of Okra

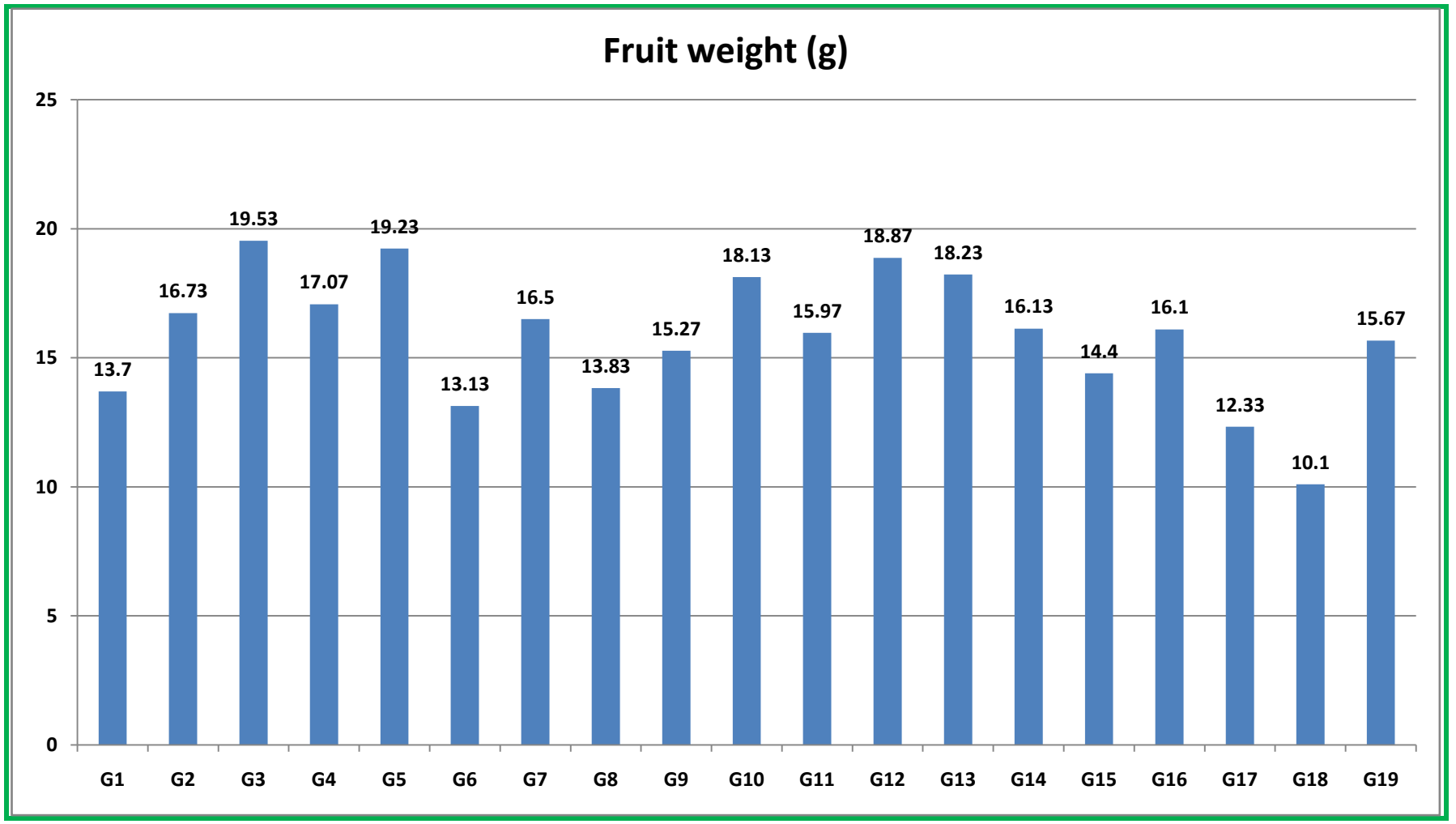


Figure 2. Mean performance of fruit weight of 19 okra genotypes

4.3 Variability Estimates in Okra Genotypes

Estimated variability components viz. phenotypic and genotypic variance, phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV), heritability in broad sense and genetic advance as percent of means (GA%) for 12 characters are presented in Table 5.

Variability in the genotypes of crop species can be studied in different ways in light of modern genetics and plant breeding principles but the measurement of differences in performance of genotypes for growth pattern and various quantitative traits under particular environment has been the base of the crop improvement programme. Data collected from the investigation were analyzed to partition the total variation into magnitude of genotypic and phenotypic variation of 19 genotypes of okra. A perusal of results pertaining to existence of variation at genotypic and phenotypic level and studies of environmental effects on genotypes for the yield attributing characters has been presented in bellow.

4.3.1 Phenotypic and genotypic variances

Estimation of variance and coefficients of variation at genotypic and phenotypic levels in a population is decisive factor for scope and efficiency of selection of individuals for future breeding programme in crop species. The 19 genotypes of okra in present investigation were grown to estimate the variability parameters for eleven characters comprising yield and yield attributing traits.

The highest phenotypic variances were calculated for fruit yield per plant (10753.19) followed by plant height (650.99) and seed per fruit (99.57) while the lowest value was recorded for fruit diameter (0.05) followed by primary branches per plant (1.85) and fruit length (1.86) (Table 5). The genotypic variance ranged from 0.04 (fruit diameter) to 9731.67 (fruit yield per plant). Consistence result was reported by Mehta *et al*. (2006); Pradip *et al.* (2010) for fruit yield per plant, plant height, number of seeds per fruit and number of tender fruit per plants. This result is in agreement with Ehab *et al.* (2013**)** who reported that phenotypic variances were higher than the corresponding genotypic variances indicating predominance of environmental

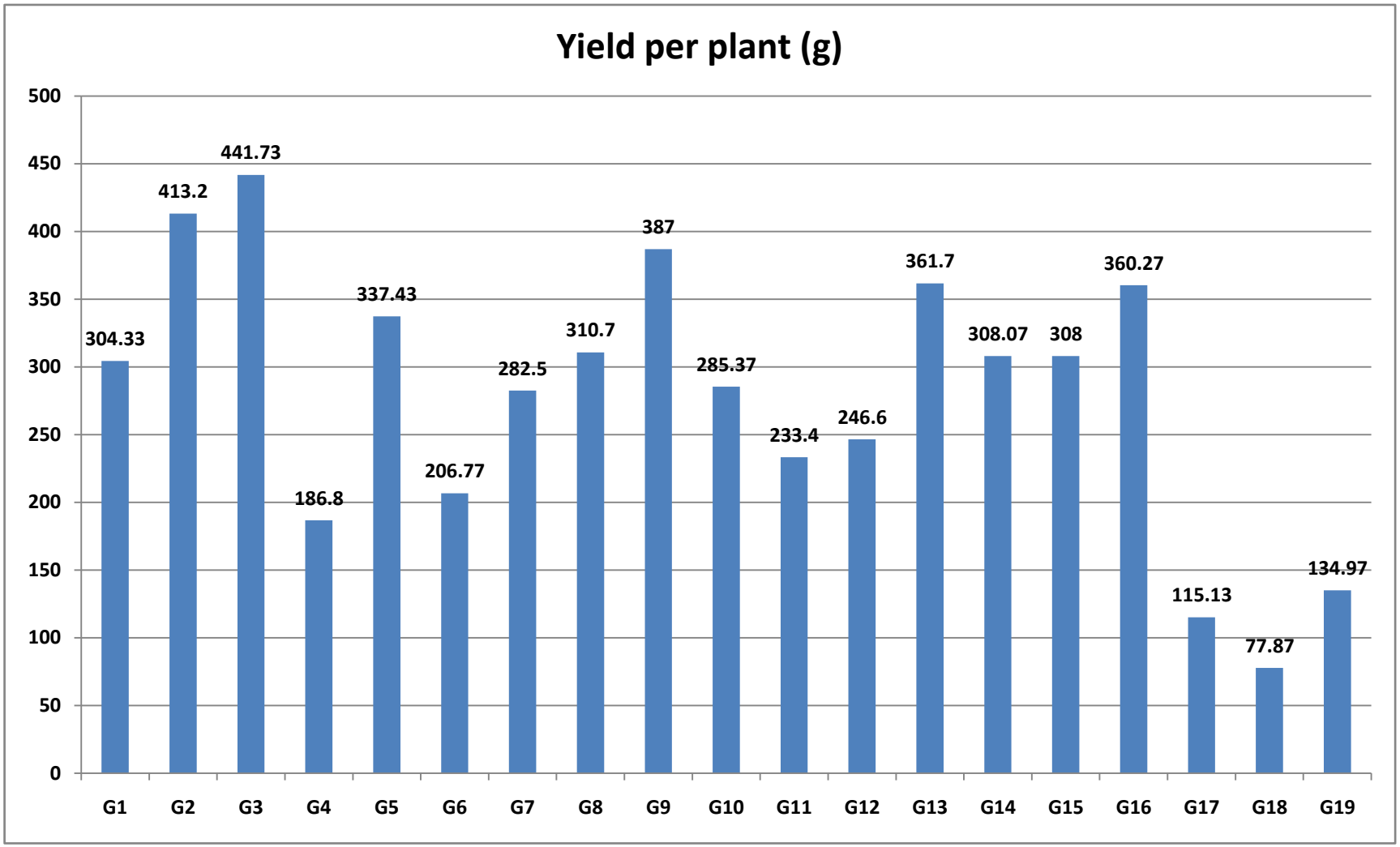


Figure 3. Mean performance of yield per plant of 19 okra genotypes

Table 5. Estimation of variance parameters for different characters in okra genotypes

Parameters	$\sigma^2 p$	$\sigma^2 g$	$\sigma^2 e$	PCV	GCV	ECV
Days to 1st flowering	2.86	1.77	1.08	4.06	3.20	2.50
No. of flower per Plant	29.75	29.45	0.31	24.08	23.96	2.44
No. of internodes per plant	24.94	24.38	0.56	18.53	18.33	2.77
No. of primary branches per plant	1.85	1.57	0.27	44.00	40.63	16.89
Fruiting span (days)	8.30	6.40	1.90	5.11	4.49	2.45
Plant height (cm)	650.99	299.83	351.15	20.05	13.61	14.73
No. of fruits per plant	31.27	30.03	1.23	32.32	31.68	6.42
Fruit length (cm)	1.86	1.34	0.52	10.55	8.95	5.59
Fruit diameter (cm)	0.05	0.04	0.00	11.35	10.72	3.74
Individual fruit weight (g)	7.45	5.59	1.86	17.24	14.93	8.61
No. of seeds per fruit	99.57	97.97	1.60	17.64	17.50	2.23
Fruit yield per plant (g)	10753.19	9731.67	1021.52	37.16	35.35	11.45

$\sigma^2 p$: Phenotypic variance PCV: Phenotypic coefficient of variation
$\sigma^2 g$: Genotypic variance GCV: Genotypic coefficient of variation
$\sigma^2 e$: Environmental variance ECV: Environmental coefficient of variation

effects on the expression of these studied characters. This study result showed that the traits exhibited phenotypic variances higher than their respective genotypic variances thus revealing the great significant influence of environmental factors in the expressions of the traits in okra genotypes and the apparent variation is not only due to the genotypes but also due to the influence of environment. This result supported by Adeoluwa and Kehinde (2011), Nwangburuka *et al.* (2012), Thirupathi *et al.* (2012) and Adekoya *et al.* (2014) who reported that most of the traits exhibited highly phenotypic variance higher than their respective genotypic variances.

4.3.2 Phenotypic and genotypic coefficient of variation

The phenotypic coefficient of variation (PCV) ranged between 4.06% (days to first flowering) and 44.00% (primary branches per plant) while genotypic coefficient of variation (GCV) ranged between 3.20 (days to first flowering) and 40.63% (number of primary branches per plant) (Table 5). Similar results were reported by Ehab et al. (2013) and Mihretu *et al.* (2014) in okra. According to Sivasubramaniah and Meron (1973**)** PCV and GCV values greater than 20% are regarded as high, values between 10% and 20% to be medium whereas values less than 10% are considered to be low. Based on this delineation PCV and GCV recorded in this study, days to first flowering (4.06% and 3.20%), fruiting span (5.11% and 4.49%) had low values (<10%) for both phenotypic and genotypic coefficient of variations. Sibsankar *et al.* (2012) reported that low PCV and GCV values for days to first flowering. The low PCV and GCV value of traits suggests the higher influence of environment on these traits thus; selection on the phenotypic basis would not be effective for the genetic improvement (Bharathiveeramani *et al.* 2012; Sankara and Pinaki 2012; Thirupathi *et al.* 2012; and Ehab *et al.* 2013).

Moderate PCV and GCV were found in number of internodes per plant (18.53 and 18.33%), fruit diameter (11.35% and 10.72%), individual fruit weight (17.24% and 14.93%) and number of seeds per fruit (17.64% and 17.50%) (Table 5). Medium PCV and GCV value suggested that these characters were controlled more by the genetic factors. Hence, these characters amenable to selection for further improvement. This result was in agreement with the finding of Das *et al*. (2012), Thirupathi *et al*. (2012)

and Ehab *et al.* (2013) who reported medium PCV and GCV values of characters.

Among all characters exhibiting high degree of genotypic and phenotypic coefficients of variation were in number of flowers per plant (24.08% and 23.96%), number of primary branches per plant (44.00% and 40.63%), number of fruits per plant (32.32% and 31.68%) and fruit yield per plant (37.16% and 35.35%), respectively (Figure 4). The closer magnitude of genotypic and phenotypic coefficients of variation indicated that a greater role was played by genotypes rather than environment. The results of the present investigation were agree with Hazra and Basu (2000), Dhall *et al.* (2001), Gandhi *et al.* (2001), Ravindra *et al.* (2004) and Singh and Singh (2006).

The results of this study suggested that traits with high PCV and GCV were amenable for selection whereas hardly possible to improve traits contrarily to those traits with low phenotypic and genotypic coefficient of variations. The research findings of Bharathiveeraman *et al.* 2012, Nwangburuka *et al.* 2012 and Swati *et al.* 2014 who suggested that the high phenotypic and genotypic coefficient of variation is an indication of the less influence of environmental factors in the expression of such traits and the higher possibility to improve them through selection breeding. The high PCV and GCV value with low magnitude of differences between the two genetic parameters indicates that the less environmental influence on the phenotypic expression. Hence, selection of desired character uses phenotypic value may be effective in improving the character.

4.3.3 Estimate of heritability

The estimate of heritability in broad sense ranged from 46.06% for plant height to 98.97% for number of flowers per plant (Table 6). According to Robinson *et al.* (1955) heritability was categorized as low (0-30%), moderate (31-60%) and high > 60%. Accordingly, heritability estimate in broad sense was high (>60%) for days to first flowering (62.08%), number of flowers per plant (98.97%), number of internodes per plant (97.76%), number of primary branches per plant (85.27%), fruiting span (77.08%), number of fruits per plant (96.06%), fruit length (71.97%), fruit diameter (89.17%), individual fruit length (75.03%), number of seeds per fruit (98.40%) and fruit yield per plant (90.50%).

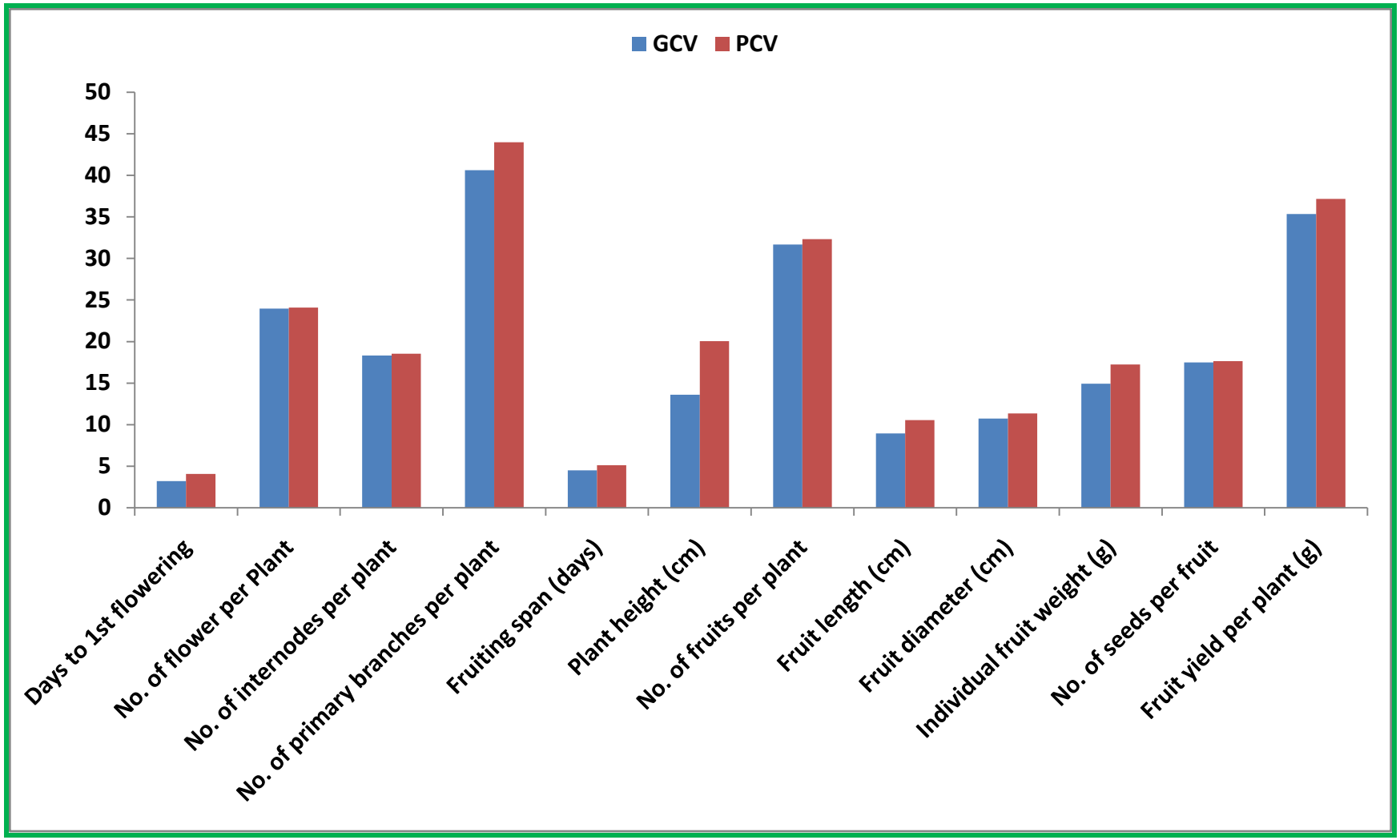


Figure 4. Representing of genotypic and phenotypic coefficient of variation of okra

Table 6. Estimation of heritability and genetic advance of different parameters of okra

Parameters	Heritability	GA (5%)	GAM
Days to 1st flowering	62.08	2.16	5.20
No. of flower per Plant	98.97	11.12	49.10
No. of internodes per plant	97.76	10.06	37.32
No. of primary branches per plant	85.27	2.39	77.29
Fruiting span (days)	77.08	4.57	8.12
Plant height (cm)	46.06	24.21	19.03
No. of fruits per plant	96.06	11.06	63.96
Fruit length (cm)	71.97	2.02	15.64
Fruit diameter (cm)	89.17	0.39	20.86
Individual fruit weight (g)	75.03	4.22	26.64
No. of seeds per fruit	98.40	20.23	35.76
Fruit yield per plant (g)	90.50	193.32	69.28

GA (5%): Genetic advance
GAM: Genetic advance (% of mean)

This result was agreement with Mihretu *et al.* (2014) who reported high heritability estimates for fruit yield per plant, average fruit weight, plant height and number of branches per plant; Pradip *et al.* (2010) who reported high broad sense heritability for plant height; Hazem *et al.* (2013) for days to flowering and Simon *et al.* (2013b) high heritability for tender fruit yield per plant. If heritability of a character is very high around 80% or more, selection for such character is fairly easy. This is because there would be a close correspondence between the genotypic and phenotypic variations due to relatively small contribution of the environment to the phenotype expression of the trait (Singh *et al.*, 1990).

Moderate heritability values (31- 60%) were registered for plant height (46.06%). These results were in agreement with the finding of Pradip *et al.* (2010) for the traits with moderate heritability but disagreed with the results of low heritability. Sudip *et al.* (2014) reported moderate heritability for days to 50% flowering. Very low heritability revealed the ineffectiveness of direct selection for the improvement of the traits while moderate heritability suggests improvement through selection. Snowder *et al.* (2005) had also reported that when the heritability of a trait is medium to high, selection based on the individual level of performance allows relatively rapid rate of improvement.

4.3.4 Estimate of expected genetic advance

The genetic advance as the percentage of the mean (GAM) at 5% selection intensity is presented (Table 6). In this study, genetic advance ranged between 5.20% for days to first flowering to 77.29% for number of primary branches per plant. Different result by Nwangburuka *et al.* (2012) who reported genetic advance had ranged from 15.13% for pod width at maturity to 66.30% for pod weight per plant, Mihretu *et al*. (2014b) also reported genetic advance in the ranged between 5.94% for number of epicalyxes to 198.15% for number of primary branches. The observed differences in results of different studies may be due to the different genotypes used in each experiment and the environmental differences where the genotypes were grown.

Genetic advance as percent mean was categorized as high (≥20%), moderate (10-20%) and low (0-10%) (Johnson *et al.*, 1955). As per this suggestion, the highest (≥20%)

genetic advance was observed for number of flower per plant (49.10), number of internodes per plant (37.32), number of primary branches per plant (77.29), number of fruits per plant (63.96), fruit diameter (20.86), individual fruit weight (26.64), number of seeds per fruit (35.76) and fruit yield per plant (69.28). Consistence result was reported by Hazem *et al.* (2013) for plant height, number of seeds per pod, yield per plant. Pradip *et al.* (2010) also reported high genetic advance for plant height and number of fruits per plant. This indicated that these traits are controlled more of by additive genes (Panse, 1957).

Moderate genetic advance (10-20%) was registered for plant height (19.03%) and fruit length (15%). On the other hand, low (<10%) genetic advance was recorded for days to first flowering (5.20%) and fruiting span (8.12%). Similar result was reported by Hazem *et al.* (2013) for the traits that exhibited low genetic advance. This study result disagreed with finding of Ehab *et al.* (2013) for the traits that exhibited moderate and low genetic advance for different traits.

Johnson *et al.* (1955) suggested that heritability estimates along with genetic advance were more useful in predicting the effect of selecting the best individual. High heritability along with high genetic advance as percent of the mean was obtained for number of flower per plant (98.97% and 49.10%), number of internodes per plant (97.76% and 37.32%), number of primary branches per plant (85.272% and 77.29%), number of fruits per plant (96.06% and 63.96%), fruit diameter (89.39% and 20.86%), individual fruit weight (75.03% and 26.64%), number of seeds per fruit (98.40% and 35.76%) and fruit yield per plant (90.50% and 69.28%). Consistent result was reported by Ikram *et al.* (2010) for average fruit weight, plant height and fruit yield, Ehab *et al.* (2013) who also reported high heritability and genetic advance for plant height and tender fruit yield, Mihretu *et al*. (2014b) who reported similarly for fruit weight, plant height and fruit yield and Sudip *et al.* (2014) for fruit yield per plant. This result indicates that these characters are controlled by additive gene action and phenotypic selection is effective for the improvement of the characters. As discussed earlier by Johnson *et al.* (1955), Panse (1957), Pradip *et al.* (2010) and Sibsankar *et al.* (2012) high heritability estimates along with genetic advance were more useful in predicting the effect of selecting the best individual. It provides better information than each

parameters alone and also an expression of additive gene action and amenable for selection (Mehta, 2006; Bozokalfa *et al.,* 2010; Salesh *et al.*, 2010; Sibsankar *et al.*,2012).

High heritability along with moderate genetic advance in fruit length while moderate values for both heritability and genetic advance for fruit diameter (89.17% and 20.86%). This result is in dis-agreement with Jagan *et.al.* (2013) who reported that moderate heritability and genetic advance for stem diameter. Akbar *et al.* (2003), Ali *et al.* (2008), Bozokalfa *et al.* (2010) and Jagan *et al*. (2013) reported that traits showed moderate values both of heritability and genetic advance might be amenable for selection and improvement of such traits.

Hazra and Basu (2000), Gandhi *et al.* (2001), Dhall *et al.* (2003), Ravindra *et al.* (2004), Subrata *et al.* (2004), Indurani and Veeraragavathatham (2005), Singh *et al.* (2006), Singh and Singh (2006) and Yadav *et al.* (2007) also recorded moderate to high heritability with high genetic advance and suggested that selection for these characters would improve fruit yield in okra for exploiting full potential of any genotype.

Both heritability and genetic advance values were low for fruit length (77.08% and 8.12). This result disagreed with Jagan *et al.* (2013) who reported that low value for both on pods weight and fruit diameter. Contrarily current study result agreed with Akbar *et al.* (2003), Ali *et al*. (2008) and Bozokalfa *et al.* (2010) who reported that selection is hardly possible to improve traits which exhibited low values both for heritability and genetic advance or moderate and low values combinations. This may be due to the higher influence of environment on the expression of the characters and limit the scope of improvement by selection due to the presence of non-additive (dominant and/or epistatic) type of gene action. Characters those possessing low heritability in association with low genetic advance special approaches i.e. hybridization or recurrent selection should be followed (Sankara and Pinaki, 2012; Jagan *et al.*, 2013).

4.4 Correlation coefficient

Pearson`s correlation coefficient was carried out in this study. Mutual association of characters is often expressed in phenotypic and genotypic with direction and magnitude of correlation coefficients among yield and yield related traits. Phenotypic and genotypic correlations of all possible combinations of 12 traits of 19 okra genotypes are presented in Table 7 and Figure 5.

In Pearson correlation fruit yield has shown positive and significant correlations with flowers per plant (0.710), number of internodes per plant (0.700), primary branches per plant (0.466), fruits per plant (0.922), fruit length (0.655), fruit weight (0.594) and average seeds per fruit (0.665), respectively. Fruit yield per plant has also shown negatively and insignificantly correlated with days to first flowering (-0.193) (Table 7).

Analysis result of phenotypic correlation coefficient ranged in values from -0.141 (days to flowering with primary branches per plant) to 0.966 (number of flower per plant with internodes per plant) and genotypic correlation coefficient ranged in values from -0.171 (days to first flowering with plant height) to 0.976 (number of flowers per plant with internodes per plant) (Table 8). Traits with positive and significant genotypic correlation coefficients were higher in magnitude than the corresponding phenotypic correlations coefficient. Earlier studies also reported similar results of higher magnitude of genotypic correlation for most of the characters than their corresponding phenotypic correlation coefficient indicating that genotype is superior but its expression influenced by environment (Ashraful *et al.*, 2006; Nwangburuka *et al.*, 2012; Sibsankar *et al*., 2012; Ahiakpa *et al.*, 2013). Even though, significant and positive genotypic correlation coefficients were observed between traits higher than their corresponding phenotypic correlation, the difference between the two was low in magnitude for most of these traits, similar results were reported by Mehta *et al.* (2006) and Sibsankar *et al.* (2012).

This result is consistence with Mehta *et al.* (2006) and Pradip *et al.* (2010) who indicating presence of inherent or genetic association among these characters. Genes governing two positive and significantly correlated traits were similar and

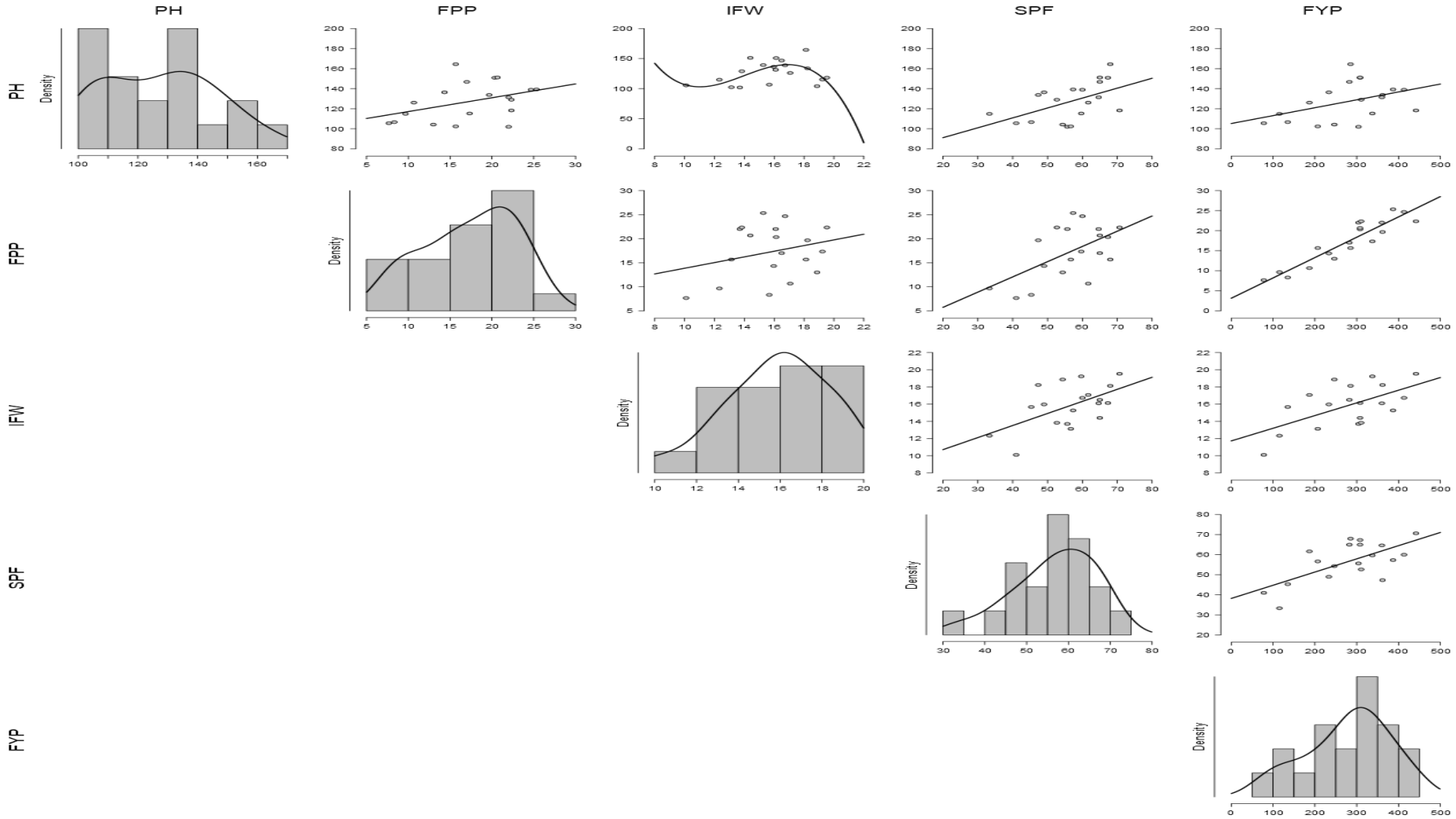
Table 7. Pearson correlation coefficient for different traits of Okra

	DFF	FP	IPP	PBP	FS	PH	FPP	FL	FD	IFW	SPF
FP	-0.324										
IPP	-0.404	0.972**									
PBP	-0.189	0.540*	0.401								
FS	-0.367	0.342	0.434	-0.201							
PH	-0.165	0.476*	0.490*	0.006	0.836**						
FPP	-0.380	0.743**	0.721**	0.519*	0.363	0.404					
FL	-0.293	0.388	0.417	0.287	0.527*	0.378	0.510*				
FD	-0.314	0.709**	0.701**	0.219	0.534*	0.553*	0.495*	0.367			
IFW	0.257	0.199	0.202	0.123	0.214	0.280	0.266	0.746**	0.068		
SPF	-0.261	0.593**	0.570*	0.375	0.513*	0.520*	0.569*	0.752**	0.432	0.559*	
FYP	-0.193	0.710**	0.700**	0.466*	0.343	0.419	0.922**	0.655**	0.397	0.594**	0.665**

** = Significant at 1%

* = Significant at 5%

DFF : days to 1st flowering, FP : No. of flower per plant, IPP : no. of internodes per plant, PBP : no. of primary branches per plant, FS : fruiting span (days), PH : plant height (cm), FPP : no. of fruits per plant, FL : fruit length (cm), FD : fruit diameter (cm), IFW : Individual fruit weight (g), SPF : no. of seeds per fruit and FYP : Fruit yield per plant (g).



PH : plant height (cm), FPP : Fruits per plant, FW : Fruit weight (g), SPF : Seeds per fruit and FYP : Fruit yield per plant (g).

Figure 5. Correlation coefficient among PH, FPP, FW, SPF and FYP in Okra

Table 8. Genotypic (G) and phenotypic (P) correlations among different pairs of traits for different genotype of okra

	Attribute	FP	IPP	PBP	FS	PH	FPP	FL	FD	IFW	SPF	FYP
DFF	G	-0.351	-0.433	-0.223	-0.424	-0.171	-0.427	-0.339	-0.367	0.312	-0.288	-0.213
	P	-0.286	-0.365	-0.141	-0.288	-0.155	-0.313	-0.230	-0.241	0.184	-0.223	-0.165
FP	G	-	0.976**	0.556*	0.361	0.484*	0.751**	0.412	0.729**	0.209	0.596**	0.724**
	P	-	0.966**	0.511*	0.308	0.460*	0.726**	0.349	0.676**	0.185	0.587**	0.683**
IPP	G		-	0.416	0.462	0.497*	0.728**	0.438	0.720**	0.214	0.573*	0.712**
	P		-	0.373	0.387	0.475*	0.710**	0.384	0.672**	0.185	0.564*	0.677**
PBP	G			-	-0.202	-0.002	0.534*	0.316	0.235	0.137	0.389	0.491
	P			-	-0.199	0.019	0.491*	0.245	0.200	0.101	0.349	0.422
FS	G				-	0.897**	0.378	0.593**	0.571*	0.236	0.544*	0.361
	P				-	0.736**	0.337	0.426*	0.472*	0.179	0.463*	0.313
PH	G					-	0.411	0.400	0.569*	0.307	0.526*	0.438
	P					-	0.390	0.341	0.521*	0.235	0.507*	0.384
FPP	G						-	0.540*	0.512*	0.280	0.575*	0.935**
	P						-	0.464*	0.470*	0.245	0.558*	0.899**
FL	G							-	0.370	0.857**	0.799**	0.708**
	P							-	0.363	0.582**	0.677**	0.571*
FD	G								-	0.095	0.439	0.418
	P								-	0.025	0.423	0.367
IFW	G									-	0.590**	0.591**
	P									-	0.508*	0.601**
SPF	G										-	0.680**
	P										-	0.637**

** = Significant at 1%

* = Significant at 5%

DFF : days to 1st flowering, FP : No. of flower per plant, IPP : no. of internodes per plant, PBP : no. of primary branches per plant, FS : fruiting span (days), PH : plant height (cm), FPP : no. of fruits per plant, FL : fruit length (cm), FD : fruit diameter (cm), IFW : Individual fruit weight (g), SPF : no. of seeds per fruit and FYP : Fruit yield per plant (g).

environmental factors played a small part in the expression of these traits that justified the possibility of correlated response to selection.

The negative correlations observed at phenotypic and genotypic level were observed between days to first flowering and internodes per plant, days to first flowering and primary branches per plant, days to first flowering and flowers per plant, days to first flowering and number of fruits per plant.

This suggests that selection of traits negatively correlated will favor one trait while depressing others negatively associated of traits. This is supported by Akinyele and Osekita (2006), Nwangburuka *et al.* (2012), Ahiakpa *et al.* (2013) who reported that negative association of traits was difficult or practically impossible to improve through simultaneous selection of those traits. The pairs of traits showed non-significant genotypic and phenotypic correlations indicating they were independent each another and that they could be selected separately for specific purpose.

4.4.1 Days to first flowering

Days to first flowering was exhibited positively and insignificantly correlated with fruit weight (0.312 and 0.184) and negatively insignificantly associated with flowers per plant (-0.351 and -0.286), flowers per plant (-0.424 and -0.288), plant height (-0.171 and -0.155), fruits per plant (-0.427 and -0.313), fruit length (-0.339 and -0.230) at both genotypic and phenotypic levels. In the contrary, Nwangburuka *et al.* (2012) reported that significant and positive correlation of days to flowering with plant height at phenotypic and genotypic level.

4.4.2 Flowers per plant

Flowers per plant had positive and significant genotypic and phenotypic correlation with internodes per plant (0.976** and 0.966**), primary branches per plant (0.556* and 0.511*), plant height (0.484* and 0.460*), fruits per plant (0.751** and 0.726**), fruit diameter (0729** and 0.676**), seeds per fruit (0.596** and 0.587**) and fruit yield per plant (0.724 ** and 0.683**) at genotypic and phenotypic level.

4.4.3 Internodes per plant

Internodes per plant have positive significant correlation with plant height (0.497* and 0.475*), fruits per plant (0.728** and 0.710**), fruit diameter (0.720 ** and 0.672**), seeds per fruit (0.573* and 0.564*) and fruit yield per plant (0.712 ** and 0.677**) at both levels. It has positive correlation with fruiting span (0.361 and 0.308), fruit length (0.349 and 0.438) and fruit weight (0.214 and 0.185) at both levels.

4.4.4 Primary branches per plant

Number of primary branches per lant had positive and significant genotypic and phenotypic correlation with flowers per plant (0.556* and 0.511*), fruits per plant (0.534* and 0.491*). It has positive insignificant correlation with internodes per plant (0.416 and 0.373), fruit length (0.316 and 0.245), fruit diameter (0.235 and 0.200), fruit weight (0.137 and 0.101) and seeds per fruit (0.389 and 0.349. Negative insignificant correlation of number of primary branches per plant was observed with days to first flowering (-0.223 and -0.141), fruiting span (-0.202 and -0.199). Saitwal *et al.* (2011) reported that positive and significant phenotypic and genotypic correlation with number of fruit per plant. In the contrary, Medagam *et al.* (2013) reported that negative significant correlation with plant height and number of fruit per plant.

4.4.5 Fruiting span

Fruiting span had significant positive correlation with plant height (0.897 ** and 0.736**), fruit length (0.593* and 0.426*), fruit diameter (0.571* and 0.472*) and seed per fruit (0.544* and 0.463*). It was positively correlated with flower per plant (0.361 and 0.308), internodes per plant (0.462 and 0.387), fruits per plant (0.378 and 0.337), fruit weight (0.236 and 0.179) and fruit yield per plant (0.361 and 0.313).

4.4.6 Plant height

Plant height had positive and significant phenotypic and genotypic correlation with flowers per plant (0.484* and 0.460*), internodes per plant (0.497* and 0.475*), fruiting span (0.897** and 0.736**), fruit diameter (0.569* and 0.521*) and seeds per

fruit (0.526* and 0.507*) but insignificant positive correlation with fruits per plant (0.411 and 0.390), fruit length (0.400 and 0.341) and fruit weight (0.307 and 0.235). Almost similar result reported by Saitwal *et al.* (2011) and Medagam *et al.* (2013) that positive and significant phenotypic and genotypic correlation with number of fruit per plant. Plant height was exhibited negative insignificant correlation with days to first flowering (-0.171 and -0.155) (Table 8). In the contrary, Medagam *et al.* (2013) who reported that negative correlation of plant height with number of branches per plant.

4.4.7 Number of fruits per plant

Number of fruits per plant had positive and significant genotypic and phenotypic correlation with flowers per plant (0.751** and 0.726**), internodes per plant (0.728** and 0.710**), primary branches (0.534* and 0.491*), fruit length (0.540* and 0.464*), fruit diameter (0.512* and 0.470*), seeds per fruit (0.575* and 0.558*) and fruit yield per plant (0.935** and 0.899**) but negative insignificant correlation with days to first flowering (-0.427 and -0.313). Result reported by Dhankhar and Dhankhar (2002) on number of fruits per plant showed significant and positive association with plant height that support this finding. Medagam *et al.* (2013) who reported that positive and significant correlation with plant height and negative significant correlation with number of branches per plant.

4.4.8 Fruit length (cm)

Fruit length had significant positive phenotypic and genotypic correlation with fruiting span (0.593** and 0.426*), fruits per plant (0.540* and 0.464*), fruit weight (0.857** and 0.582**), seeds per fruit (0.799** and 0.677**) and fruit yield per plant (0708** and 0.571*).

4.4.9 Fruit diameter (cm)

Fruit diameter had positive and significant phenotypic and genotypic correlation with flower per plant (0.729** and 0.676**), internodes per plant (0.720** and 0.672**), fruiting span (0.571* and 0.472*) and number of fruit per plant (0.512* and 0.470*).

4.4.10 Fruit weight (g)

Fruit weight had positively significant correlated with fruit length (0.857** and 0.582**), number of seeds per fruit (0.590** and 0.508*) and fruit yield per plant (0.591** and 0.601**).

4.4.11 Fruit yield per plant (g)

Analysis revealed that fruit yield has shown positive and significant genotypic and phenotypic correlations with flowers per plant (0.724** and 0.683**), number of internodes per plant (0.712** and 0.677**), fruits per plant (0.935** and 0.899**), fruit length (0.708** and 0.571*), fruit weight (0.591** and 0.601**) and average seeds per fruit (0.680** and 0.637**), respectively. Fruit yield per plant has also shown negatively and insignificantly correlated with days to first flowering (-0.0213 and -0.165). The findings of positive correlation are also confirmatory with Chhatrola and Monpara (2005), Alam and Hossain (2006), Mehta *et al.* (2006) and Pal *et al*. (2008 and 2010). The results in respect of negative correlations were in accordance with Jaiprakashnarayan and Ravindra (2004). Mihretu *et al.* (2014) also reported positive and significant genotypic correlation of fruit yield with fruit length, fruit weight, fruit diameter, number internodes and number of fruit per plant.

On other hand, fruit yield showed positive and non-significant genotypic and phenotypic correlation with primary branches per plant (0.491 and 0.422), flowers per plant (0.361 and 0.313) and plant height (0.438 and 0.384) but fruit yield per plant exhibited negative and non-significant correlation coefficient with days to first flowering (-0.213 and -0.165). This result in consistent with Dhankhar and Dhankhar (2002) who reported positive and significant phenotypic correlation of fruit yield with number of fruits per plant, number of branches per plant and plant height, Mihretu *et al.* (2014b) who reported that positive and significant phenotypic correlation of tender fruit yield with number of internodes and number of fruit per plant. Simon et al. (2013a) and Mehta *et al.* (2006) also reported that fruit yield was negatively correlated with plant height, number of branches per plant and days to 50% flowering. Selection of characters that exhibit positive significant genotypic and phenotypic correlation will automatically increase fruit yield per plant (Nwangburuka *et al.*, 2012; Simon *et*

al., 2013a).

This study results revealed that phenology, growth and fruit characters showed positive and significant phenotypic and genotypic correlation between other traits indicated that selection one character directly affects the others and may increase chances for all traits that were positively correlated but declines for characters that are negatively correlated. On other hand, non-significant correlation between them suggests independence of association that would be possible to select independently for the two characteristics for diverse directions. This suggestion is supported by Mihretu *et al.* (2014) who reported the same as above stated. Selection for a single character may increase chances for all traits that are positively correlated but declines for characters that are negatively correlated (Oppong-Sekyere *et al.*, 2011). This study results is supported by the finding of Akinyele and Osekita (2006) who reported that negative and significant correlations both at phenotypic and genotypic correlation with one another will be difficult to select for in characterization of desirable traits and those with negative association but insignificant correlation would be disregarded in selection for crop improvement.

4.5 Path coefficient analysis

A critical perusal of path coefficient analysis has been presented in Table 9. Number of fruits per plant (0.816) had highest positive direct effects on fruit yield per plant followed by fruit weight (0.478) and internodes per plant (0.225). The indirect positive effects were recorded in number of flower per plant (0.606), internodes per plant (0.588), primary branches (0.424), fruiting span (0.295), plant height (0.330), fruit length (0.416), fruit diameter (0.404), fruit weight (0.217) and seeds per fruit (0.454) via fruits per plant. Same trend was observed for seeds per fruit (0.267), fruit length (0.356), fruits per plant (0.127) and plant height (0.134) via fruit weight. The direct positive effect of number of fruits per plant on yield in okra was also observed by Dhankhar and Dhankhar (2002b), Jaiprakashnarayan and Ravindra (2004), Bali *et al.* (2005). Hence, direct selection for average number of fruits per plant was suggested to improve yield.

Table 9. Partitioning of genotypes into direct (bold) and indirect effects of eleven traits by path analysis of okra

	DFF	FP	IPP	PBP	FS	PH	FPP	FL	FD	IFW	SPF
DFF	**-0.011**	0.037	-0.091	0.000	-0.031	0.016	-0.310	0.057	0.020	0.123	-0.010
FP	0.004	**-0.115**	0.219	0.001	0.029	-0.046	0.606	-0.075	-0.046	0.095	0.022
IPP	0.004	-0.112	**0.225**	0.001	0.037	-0.048	0.588	-0.081	-0.046	0.097	0.021
PBP	0.002	-0.062	0.090	**0.002**	-0.017	-0.001	0.424	-0.056	-0.014	0.059	0.014
FS	0.004	-0.039	0.098	0.000	**0.085**	-0.081	0.296	-0.102	-0.035	0.102	0.019
PH	0.002	-0.055	0.110	0.000	0.071	**-0.097**	0.330	-0.073	-0.036	0.134	0.019
FPP	0.004	-0.085	0.162	0.001	0.031	-0.039	**0.816**	-0.099	-0.032	0.127	0.021
FL	0.003	-0.045	0.094	0.001	0.045	-0.037	0.416	**-0.194**	-0.024	0.357	0.028
FD	0.003	-0.082	0.158	0.000	0.045	-0.054	0.404	-0.071	**-0.065**	0.033	0.016
IFW	-0.003	-0.023	0.045	0.000	0.018	-0.027	0.217	-0.145	-0.004	**0.478**	0.021
SPF	0.003	-0.068	0.128	0.001	0.044	-0.050	0.464	-0.146	-0.028	0.267	**0.037**

Residual effect: 0.157

DFF : days to 1st flowering, FP : No. of flower per plant, IPP : no. of internodes per plant, PBP : no. of primary branches per plant, FS : fruiting span (days), PH : plant height (cm), FPP : no. of fruits per plant, FL : fruit length (cm), FD : fruit diameter (cm), IFW : Individual fruit weight (g), SPF : no. of seeds per fruit.

Direct negative effect was observed for days to first flowering (-0.011), flowers per plant (-0.115), plant height (-0.097), fruit length (-0.194) and fruit diameter (-0.065) on fruit yield per plant. The results of present investigation are in conformity with Chhatrola and Monpara (2005) suggesting that direct sharing of plant height and primary branches with its important indirect contributors are a good indices of selection for improved pod yield.

4.6 Genetic Diversity

The genetic divergence was estimated by Mahalanobis D^2 statistic as described by Rao (1952). The analysis of variance revealed significant difference among all 19 genotypes for all the characters. Based on D^2 values, the constellation of genotypes into clusters was done following Tocher's method (Rao, 1952).

4.6.1 Clustering Pattern of the Genotypes

The clustering pattern of all genotypes has been presented in Table 10. All 19 genotypes grouped into five clusters on the basis of yield components studied. The cluster I comprised three genotypes including G17, G18 and G19. Cluster II contained four genotypes namely, G4, G6, G11, G17 and G12. Cluster III consisted of two genotypes viz., G2 and G3. Cluster IV comprised highest six genotypes viz., G1, G7, G8, G10, G14 and G15. Cluster V includes four genotypes namely G5, G9, G13 and G16. Figure 6 is showing the distribution of genotypes in scattered diagram. Clustering of genotypes on the basis of genetic diversity would help the breeder for selecting diverse plants for using in hybridization under further breeding programme. Clustering pattern was not influenced by geographical distribution of genotypes. Patro and Ravisankar (2004) studied cluster analysis and revealed considerable variation among forty one genotypes of okra, which were grouped into eight clusters. Dhaduk *et al.* (2004) studied the genetic diversity of 22 genotypes of okra and grouped them into nine clusters. Patel *et al.* (2006) grouped 26 genotypes of okra into six clusters. Singh and Jain (2006) studied genetic divergence of 70 genotypes of okra and classified them into 18 clusters.

Table 10. Distribution of 19 genotypes in different clusters

Cluster no.	Genotypes	No. of Genotypes
I	G17, G18, G19	3
II	G4, G6, G11, G12	4
III	G2, G3	2
IV	G1, G7, G8, G10, G14, G15	6
V	G5, G9, G13, G16	4
	Total	19

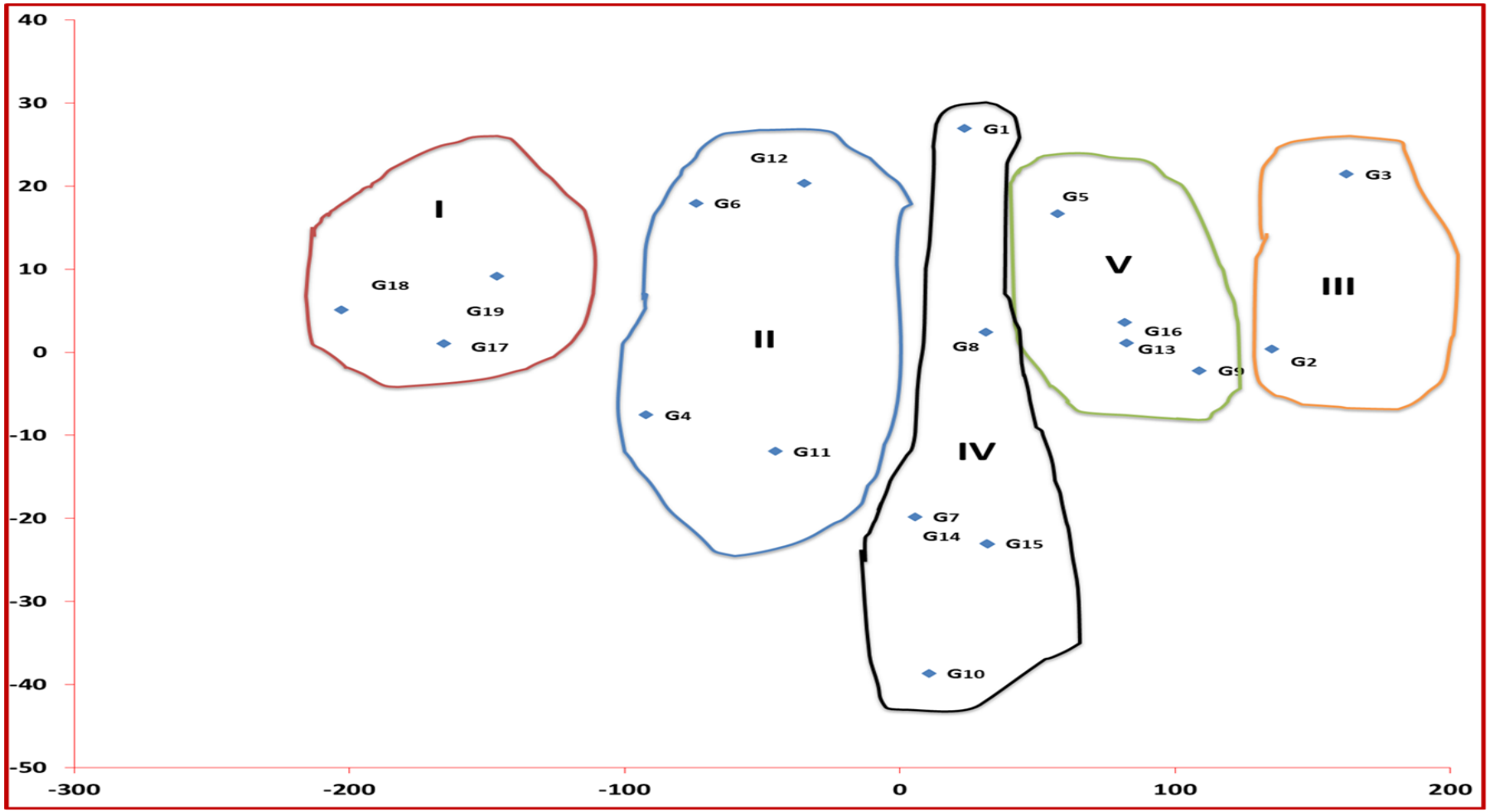


Figure 6: Distribution of genotypes in scattered diagram

4.6.2 Contribution of different characters to total diversity

The relative contribution of twelve different characters intakes in the evaluation of 19 genotypes towards the expression of genetic divergence is given in Table 11. The percent contribution of component characters ranged from 0.03 to 50.50 percent. The studies revealed that more or less contributions of similar characters towards total divergence was also been discussed by Dhaduk *et al.* (2004), Mamta and Choudhury (2006), Patel *et al*. (2006) and Singh and Jain (2006).

4.6.3 Principal Component Analysis

Principal components analysis (PCA) results of 12 traits are presented. The PCA analysis results includes the factor scores of each character among the 19 okra genotypes, eigen values, percentage total variance accounted for by twelve principal components (PCs). This principal component analysis resulted in twelve principal components (PC1 to PC11) with eigen values ranged from 0.003 to 6.006 (Table 11). The twelve principal components accounted varied percentage of total variance ranged from 0.02 to 50.50%. Cumulative percent of total variation up to PCA three with eigen value more than unity accounted 78.63%. Ahiakpa (2012), Nwangburuka *et al.* (2011) and Mihretu *et al.* (2014a) who reported that principal component axes contributed 64.32%, 78.51% and 83% variation, respectively. The first three components were retained in analysis because eigen values are greater than 1. The others factors having eigen value < 1 were ignored. These were ignored due to Gutten's lower bound principle that eigen values <1 should be ignored (Kumar *et al.*, 2011). The first three principal components PC1, PC2 and PC3 with values of 50.50%, 14.17% and 13.96%, respectively, contributed more to the total of 78.63% variation. Similar result was reported by Amoatey *et al.* (2015) and Ahiakpa (2012) that the first principal component (PC1) recording the highest (32.44%) variance. According to Chahal and Gosal (2002), characters with largest absolute values closer to unity with in the first principal component influence the clustering more than those with lower absolute values closer to zero.

Table 11. Eigen values (latent roots) and yield percent contribution of 12 characters of 19 genotypes

Principal component axes	Eigen values	Percent variation	Cumulative % of Percent variation
I	6.060	50.50	50.5
II	1.701	14.17	64.67
III	1.675	13.96	78.63
IV	0.899	7.49	86.12
V	0.537	4.48	90.6
VI	0.449	3.74	94.34
VII	0.315	2.63	96.97
VIII	0.220	1.83	98.8
IX	0.112	0.93	99.73
X	0.023	0.19	99.92
XI	0.006	0.05	99.97
XII	0.003	0.02	100

4.6.4 Intra and inter cluster divergence

The intra cluster and inter cluster divergence (average D^2 values) of all clusters have been presented in Table 12 & 13. Intra cluster average D^2 values ranged from 0.00 to 1.98. It recorded maximum (1.98) in cluster I with three genotypes followed by 0.96 in cluster II with four genotypes. Inter cluster average D^2 values were higher (56.42) between cluster I and cluster III followed by 41.92 between cluster II and cluster III. The minimum inter cluster value for all the characters were as 3.88 between cluster IV and cluster V. Singh and Jain (2007) found highest intra cluster distance (22.46) in cluster-IV and inter cluster distance (101.93) between cluster-XIV and XVII in the germplasm they studied.

4.6.5 Cluster mean

The cluster wise mean for all the characters are presented in Table 14. A close perusal of these cluster mean for different characters indicated considerable genetic differences among the clusters for all the characters. Cluster I showed highest mean values for days to first flowering (42.44). On the other hand it had low cluster mean for number of flower per plant (17.33), primary branches per plant (2.11), fruiting span (53.67), plant height (109.05), fruits per plant (8.56), fruit length (10.94), fruit diameter (1.73), fruit weight (12.70), seeds per fruit (39.89) and fruit yield per plant (109.32). Cluster II had none of highest mean values but lowest value for internodes per plant (21.83). Cluster III had shown the high mean values for number of flowers per plant (29.17), internodes per plant (31.83), primary branches (5.34), fruits per plant (23.50), fruit length (13.66), fruit weight (18.13), seeds per fruit (65.33) and fruit yield per plant (427.47). None of the lowest value was found in cluster III. Cluster IV had shown high mean values for fruiting span (58.00), plant height (140.71) and fruit diameter (1.99). Apart from observing high cluster mean, low mean values were also envisage for its important in getting early that was recorded in cluster IV for the character viz., days to first flowering (40.72). Among all clusters, cluster V had none of highest and lowest value. A substantial variation in cluster mean observed for various characters in okra was also reported by Hazra *et al.* (2002), Bendale *et al.* (2003), Ghai *et al.* (2004) and Singh and Jain (2006).

Table 12. Intra (Bold) and inter cluster distances (D^2) for 19 genotypes

Cluster	I	II	III	IV	V
I	**1.98**	15.21	56.42	31.86	35.73
II		**0.96**	41.92	16.96	20.77
III			**0.00**	25.05	21.43
IV				**0.56**	3.88
V					**0.85**

Table 13. The nearest and farthest clusters from each cluster between D^2 values in okra

Cluster	Nearest Cluster with D^2 values	Farthest Cluster with D^2 values
I	II (15.21)	III (56.42)
II	I (15.21)	III (41.92)
III	V (21.43)	I (56.42)
IV	V (3.88)	I (31.86)
V	IV (3.88)	I (35.73)

Table 14. Cluster mean for 12 yield and yield related characters in 19 okra genotypes

Characters	I	II	III	IV	V
Days to 1st flowering	42.44**	42.00	42.00	40.72*	41.58
No. of flower per Plant	17.33*	17.50	29.17**	25.11	24.83
No. of internodes per plant	22.56	21.83*	31.83**	29.00	29.83
No. of primary branches per plant	2.11*	2.58	5.34**	3.72	2.25
Fruiting span (days)	53.67*	55.92	54.83	58.00**	57.08
Plant height (cm)	109.05*	117.27	128.61	140.71**	129.92
No. of fruits per plant	8.56*	13.42	23.50**	19.67	21.08
Fruit length (cm)	10.94*	13.17	13.66**	13.31	13.25
Fruit diameter (cm)	1.73*	1.74	1.89	1.99**	1.90
Individual fruit weight (g)	12.70*	16.26	18.13**	15.45	17.21
No. of seeds per fruit	39.89*	55.42	65.33**	62.28	57.25
Fruit yield per plant (g)	109.32*	218.39	427.47**	299.83	361.60

* Lower value
** Higher value

4.6.6 Genetic distance

Genetic distance among 19 okra genotypes was measured using Euclidean distance based on 12 traits and the result is presented in Table 15. Euclidean distance developed by Sneath and Sokal (1973) has been used to classify the divergent genotypes into different groups. The genetic distances for all possible pairs of 19 okra genotypes ranged from 0.16 to 2.44. The most distant genotypes were G2 and G18 (2.44) followed by G3 and G18 (2.40), G9 and G18 (2.13)**,** G1 and G18 (2.11) and G16 and G18 (2.04**)**.

The lowest genetic distance was exhibited between G14 and G15 (0.16) followed by G10 and G14 (0.34), G9 and G16 (0.35), G2 and G3 (0.39) and G5 and G7 (0.41) (Table 15). This suggested that the higher chance of improving the crop production through collection, evaluation and selection or hybridization of okra genotypes from different regions even from other countries. The extent of diversity present between genotypes determines the extent of improvement gained through selection and hybridization. The more divergent the two genotypes are the more would be the probability of improving through selection and hybridization. This result is supported by Prakash *et al.* (2011), Kamalpreet *et al.* (2013) who reported that presence of genetic diversity for okra genotype. Figure 7 is showing the genetic distance by constructing tree.

Genetic distance or diversity of genotypes is considered as a good start in plant breeding to improve crops either by means of hybridization or direct selection of genotypes for their desirable traits. The high yielding varieties in okra has been developed by exploiting the genetic diversity available in the crop. Genetic diversity is importance for selecting parents in combination breeding of different autogamous crops to obtain transgressive segregants (Pradip *et al.*, 2010). Shujaat *et al.* (2014) who suggested that genetic variations is an important feature to get together the diversified goals of plant breeding including higher yield resistance to diseases, advantageous qualities and wider adaptations. Mihretu *et al*. (2014) also suggested that crossing of genotypes not genetically diverse or with little genetic diversity might not give higher heterotic value in F_1 and narrow range of variability in the segregating

Table 15. Genetic Euclidean distances and mean Euclidean distance of 19 genotypes based on 12 traits

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18
2	0.50																	
3	0.62	0.39																
4	1.42	1.62	1.49															
5	0.69	0.73	0.52	1.02														
6	0.89	1.20	1.13	0.64	0.72													
7	0.86	0.91	0.79	0.78	0.41	0.58												
8	0.70	0.81	0.78	1.01	0.51	0.60	0.42											
9	0.87	0.76	0.68	1.38	0.61	1.06	0.69	0.61										
10	0.84	0.78	0.73	1.15	0.56	0.95	0.55	0.79	0.68									
11	1.04	1.19	1.10	0.62	0.61	0.52	0.43	0.61	0.87	0.73								
12	1.13	1.31	1.15	0.49	0.64	0.54	0.57	0.75	1.04	0.92	0.43							
13	1.17	1.16	1.01	1.01	0.63	0.90	0.60	0.60	0.64	0.92	0.60	0.68						
14	0.69	0.63	0.58	1.19	0.46	0.88	0.48	0.57	0.47	0.34	0.73	0.91	0.80					
15	0.69	0.67	0.64	1.14	0.49	0.81	0.43	0.47	0.48	0.45	0.69	0.89	0.76	0.16				
16	1.05	0.99	0.84	1.35	0.68	1.11	0.76	0.80	0.35	0.69	0.86	1.01	0.68	0.54	0.58			
17	1.58	1.91	1.91	0.93	1.45	0.94	1.30	1.37	1.72	1.49	0.97	1.07	1.47	1.56	1.51	1.71		
18	2.11	2.44	2.40	1.28	1.93	1.40	1.75	1.87	2.13	1.91	1.42	1.50	1.88	1.99	1.95	2.04	0.71	
19	1.63	1.92	1.83	0.54	1.33	0.85	1.17	1.33	1.71	1.45	0.87	0.80	1.35	1.52	1.48	1.66	0.55	0.88

Min.	0.16
Max.	2.44

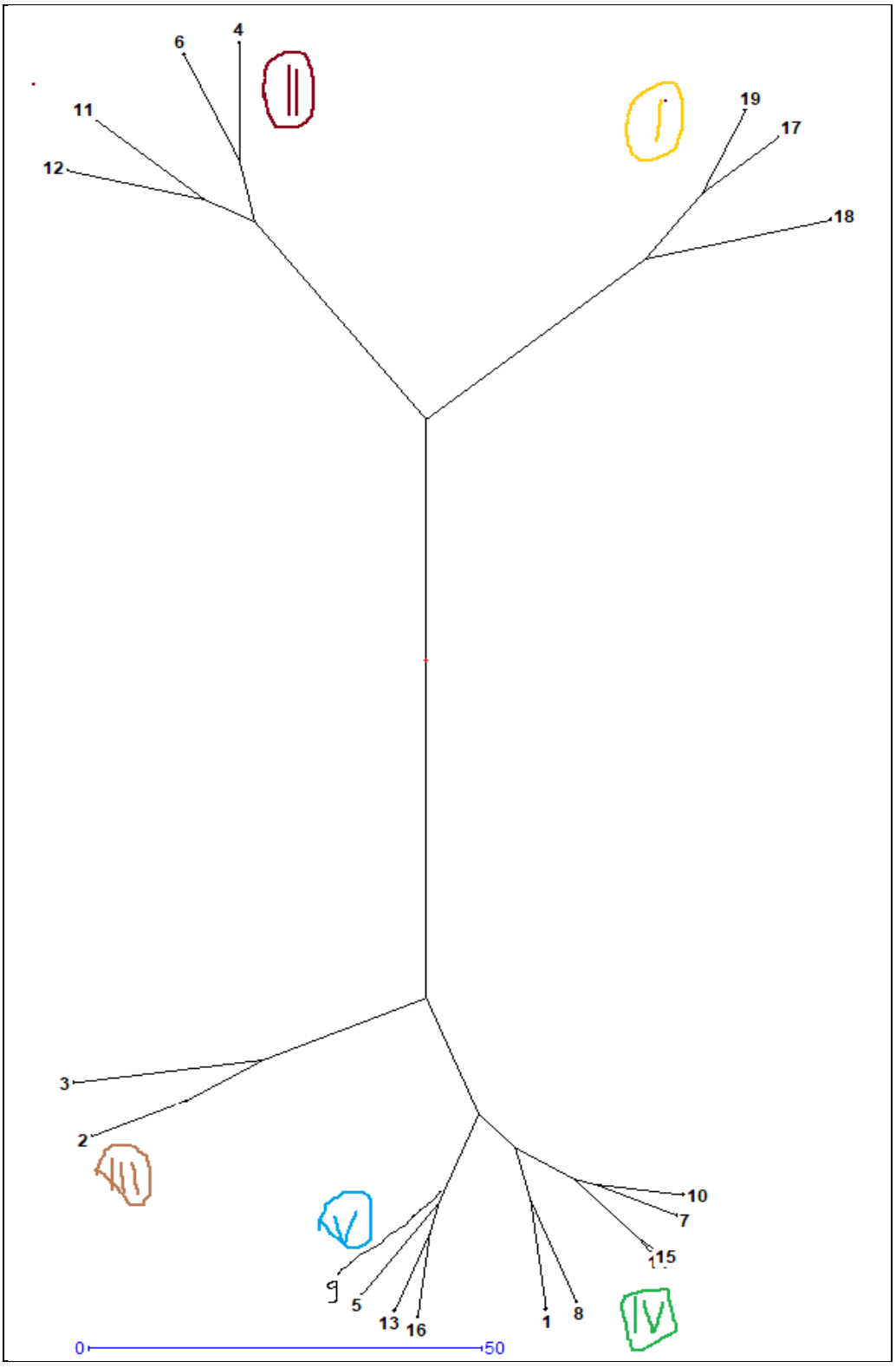


Figure 7. Construction of tree using genotypes

F_2 population.

Thus, selection of genotypes for hybridization between the genetically diverse parents in further breeding programs may produce large variability and better recombinants in the segregating generations. Therefore, the observed genetic distance among okra collections that grouped as most distant and close to others is suggesting the higher possibility of improving the crop either through selection or crossing of distant genotypes.

4. 7 Selection of genotypes

The selection for desirable types should not only be based on yield, the other yield components should also be considered. Direct selection for yield is often misleading in okra because vegetable pod yield is polygenically controlled. Thus, knowledge about the degree of interrelationship, that exists among different component characters and with vegetable pod yield is important for devising an efficient selection criterion for fruit yield and a basis for planning and efficient breeding programme. Considering diversity, variability and all agronomic traits the genotypes G14 and G15 could be selected from cluster IV for earliness and high plant height (Table 16). Genotypes G2 and G3 could be selected from cluster III for high number of fruits per plant and high fruit yield per plant and genotype G17 for less seeds per fruit from cluster I.

Table 16. Finally selected genotypes for important traits

Sl No.	Selection traits	Genotypes	Cluster No.
01	Days to flowering (earliness), fruiting span, plant height	G14, G15	IV
	Number of fruits per plant, fruit yield per plant	G2, G3	III
02	Less seeds per fruit	G17	I

CHAPTER V

SUMMARY AND CONCLUSION

The present investigation "Genetic divergence and relationship between yield and yield contributing characters in okra (*Abelmoschus esculentus* L.)" was carried out during kharif season of 2017 at experimental field of Genetics and Plant Breeding Department, Sher-e-Bangla Agricultural University, Dhaka-1207. The experimental material for the present investigation was comprised of 19 genotypes of okra. These genotypes were sown in Randomized Complete Block Design with three replications. Observations were recorded on the basis of five random competitive plants selected from each genotype separately for morphological, phonological, yield and other parameters were evaluated as per standard procedure. The variance components and coefficient of variation were determined according to Burton (1952). The heritability (broad sense) and genetic advance was worked out by Hanson *et al.* (1956) and Johnson *et al.* (1955). Correlation coefficient and path coefficient analysis were computed by the formula suggested by Miller *et al.* (1958) and Wright (1921) Dewey and Lu (1959). On the basis of results, the present investigation is summarized as follows:

5.1 Summary

Significant differences were observed among the genotypes for all the traits viz. days to first flowering, no. of flower per plant, no. of internodes per plant, no. of primary and secondary branches per plant, fruiting span, plant height, no. of fruits per plant, fruit length, fruit diameter, individual fruit weight, no. of seeds per fruit and fruit yield per plant. Lowest days to first flowering were recorded in G16 (38.67) and highest in G9, G10 & G19 (43.33 days). The minimum number of flowers per plant was observed in G4 with 14.33 while in G10 is maximum with 30.67. The range of number of internodes per plant was recorded from 18.33 to 34.67. The highest number of primary branches produced by the genotype G1 & G2 (6.00) and lowest number in the genotype G18 (1.33).

The genotype G9 (25.33) represented the maximum number of fruits per plant. The Maximum fruit length was found in genotype G12 (14.33 cm). The genotype G3 (19.53 g) represented the maximum fruit weight and the minimum was observed by the genotype G18 (10.10 g). The maximum number of seeds per pod was produced by the genotype G3 (70.67) and minimum in the genotype G17 (33.33). Genotype G3 (441.73 g) produced the highest fruit yield per plant and genotype G18 (77.87 g) produced the lowest yield per plant.

Genotypic coefficient of variation ranged from 4.06% (days to first flowering) to 44.00% (primary branches per plant) while phenotypic coefficient of variation was range between 3.20 (days to first flowering) to 40.63% (number of primary branches per plant). Though, phenotypic coefficient of variation values was greater than genotypic coefficient of variation. The magnitudinal differences were medium to low in PCV and GCV for days to first flowering (4.06 and 3.20), no. of flowers per plant (24.08% and 23.96%), no. of internodes per plant (18.53% and 18.33%), fruiting span (5.11% and 4.49%), number of fruits per plant (32.32% and 31.68%), fruit diameter (11.35% and 10.72%), no. of seeds per fruit (17.64% and 17.50%) and fruit yield per plant (37.16% and 35.35%) suggesting the little role of environment in the expression of these traits. On the other hand high difference PCV and GCV for primary branches per plant (44.00% and 40.63%), plant height (20.05% and 13.61%), and fruit weight (17.24% and 14.93%) suggested a highly significant influence of environment on the expression of these traits.

Heritability in broad sense ranged from 46.06% for plant height to 98.97% for number of flowers per plant and genetic advance as percent of mean (GAM) ranged from 5.20% for days to first flowering to 77.29% for number of primary branches per plant. The traits number of flower per plant (98.97% and 49.10%), number of internodes per plant (97.76% and 37.32%), number of primary branches per plant (85.272% and 77.29%), number of fruits per plant (96.06% and 63.96%), fruit diameter (89.39% and 20.86%), individual fruit weight (75.03% and 26.64%), number of seeds per fruit (98.40% and 35.76%) and fruit yield per plant (90.50% and 69.28%) showed high heritability along with high genetic advance in percent of mean revealed that such

characters are controlled by additive gene action and selection based on these characters will be effective. High h^2_b along with moderate GA for the character fruit length suggested that this trait is most probably controlled by both additive and non-additive gene action. Moderate h^2_b with moderate GA revealed the possibility of predominance of both additive and non-additive gene action in the inheritance of the trait fruit diameter (89.17% and 20.86%). Both heritability and genetic advance values were low for fruit length (77.08% and 8.12). The results of genetic variation components suggested that most of the traits were highly heritable and the expression of the traits were more of controlled by genetic factor with less influence of environmental factors which allow breeders to improve the crop yield and other desirable traits through selection.

Data analysis revealed that number of internodes per plant had the highest genotypic and phenotypic correlation coefficient. The correlation coefficient showed numbers of internodes per plant serve as most important selection indices of fruit yield. Genotypic correlations were higher in magnitude than phenotypic correlation.
Moreover, the traits flowers per plant (0.724 and 0.683), number of internodes per plant (0.712 and 0.677), fruits per plant (0.935 and 0.899), fruit length (0.708 and 0.571), fruit weight (0.591 and 0.601) and seeds per fruit (0.680 and 0.637) had positive and significant genotypic and phenotypic correlations with fruit yield. This suggested selection of genotypes for high performance of these characters also leads the increment of fruit yield. The results suggested traits controlled by the genetic factors with positive association among the traits indicating the possibility of simultaneous selection of traits.

Path analysis revealed number of fruits per plant (0.816), fruit weight (0.478), internodes per plant (0.225), seeds per fruit (0.037) and primary branches per plant (0.002) had direct positive effect on pod yield per plant, indicating these are the main contributors to fruit yield per plant. The highest positive indirect effects on fruit yield per plant were obtained by flowers per plant (0.606), internodes per plant (0.588), and primary branches per plant (0.424) via number of fruits per plant.

Genetic diversity among 19 genotypes was performed through Principal Component Analysis (PCA), Cluster Analysis using GENSTAT software. The first three components with eigen value were greater than unity contributed a total of 78.63% variation towards the divergence. As per PCA, D^2 and Cluster Analysis, the genotypes were grouped into five different clusters. Cluster IV, I and III composed of six, three and two genotypes, respectively. Cluster II & V were consisted of both four genotypes. The highest inter-cluster distance was observed between clusters I and III (56.42) indicating diverse genotypes from these two clusters, if involved in hybridization may produce a wide spectrum of segregating population while the lowest inter-cluster distance was observed between cluster IV and V (3.88) .

5.2 Conclusion

Results of the present studies indicated significant variation among the genotypes for all the characters studied. Internodes per plant, fruits per plant and fruit weight contributed maximum towards fruit yield improvement. Nineteen okra genotypes formed five different clusters. Considering genetic variability, diversity and other agronomic performance selection of genotypes G14 and G15 could be selected for from cluster IV for earliness; genotypes G2 and G3 selected for more fruit per plant and high yield per plant from cluster III; cluster I is performed for all the traits are less value. So, from cluster I genotype G17 and G19 are selected for crossing with distance cluster III. So, divergent genotypes are recommended to use as parents in future hybridization program from more distant cluster I and cluster III.

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APPENDICES

Appendix I: Physical and chemical characteristics of initial soil (0-15 cm depth) of the experimental site

A. Physical composition of the soil

Soil separates	%
Sand	36.90
Silt	26.40
Clay	36.66
Texture class	Clay loam

B. Chemical composition of the soil

Sl. No.	Soil characteristics	Analytical data
1	Organic carbon (%)	0.82
2	Total N (kg/ha)	1790.00
3	Total S (ppm)	225.00
4	Total P (ppm)	840.00
5	Available N (kg/ha)	54.00
6	Available P (kg/ha)	69.00
7	Exchangeable K (kg/ha)	89.50
8	Available S (ppm)	16.00
9	pH (1:2.5) soil to water	5.55
10	CEC	11.23

Source: Central library, Sher-e-Bangla Agricultural University

Appendix II: Monthly average temperature, relative humidity, total rainfall and sunshine (hours/day) of the experimental site during the period from May to September, 2017.

Month	Average Temperature ^{0}C			RH%	Average Rainfall (mm)	Sunshine (Hours/Day)
	Minimum	Maximum	Mean			
May	26.00	34.05	30.03	78	158.3	8.8
June	27.23	31.34	29.29	67	168.5	8.6
July	25.31	34.23	29.77	81	175.5	8.2
August	26.23	33.45	29.84	79	163.4	8.7
September	25.67	32.31	28.99	63	146.5	8.1

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

Appendix III: Range and mean with coefficients of variation for 12 characters in 19 okra genotypes.

Characters	Range		Mean	CV%
	Minimum	Maximum		
Days to 1st Flowering	38.67	43.33	41.58	2.50
No. of Flower per Plant	14.33	30.67	22.65	2.44
No. of Internodes per Plant	18.33	34.67	26.95	2.77
No. of Primary Branches/Plant	1.33	6.00	3.09	16.89
Fruiting Span	52.33	62.67	56.35	2.45
Plant Height	102.00	164.43	127.23	3.85
No. of Fruits per Plant	7.67	25.33	17.30	6.42
Fruit Length	9.50	14.33	12.93	5.59
Fruit Diameter	1.62	2.24	1.87	3.74
Individual Fruit Weight	10.10	19.53	15.84	8.61
No. of Seeds per Fruit	33.33	70.67	56.56	2.23
Fruit Yield per Plant	77.87	441.73	279.04	11.45

Appendix IV: Geographical position of the experimental site.