CHARACTER ASSOCIATION AND DIVERSITY ANALYSIS OF OKRA (*Abelmoschus esculentus* L. Moench)

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*This is to certify that thesis entitled, "**CHARACTER ASSOCIATION AND DIVERSITY ANALYSIS OF OKRA (Abelmoschus esculentus L. Moench)**" 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 bona fide research work carried out by **KHALID SYFULLAH**, Registration No. **10-03916** 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 source of information, as has been availed of during the course of this investigation has duly been acknowledged.

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Place: Dhaka, Bangladesh

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CHARACTER ASSOCIATION AND DIVERSITY ANALYSIS OF OKRA (*Abelmoschus esculentus* L. Moench)

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ABSTRACT

A field experiment was conducted at the experimental farm of Sher-e-Bangla Agricultural University with twenty eight Okra (*Abelmoschus esculentus* L. Monech) genotypes during 'Kharif' season (March 2017 to July 2017).Eleven characters were studied to find out the genetic variability, heritability and genetic advance, correlation coefficient analysis, path coefficient analysis and genetic divergence. The genotypes varied significantly ($p< 0.01$) for all of the characters studied. High genotypic and phenotypic coefficient of variation were observed for primary branches (43.91 and 33.64) and fruit yield per plant (37.51 and 32.48). Accordingly high heritability accompanied with high genetic advance in percent of mean observed in plant height (97.32 and 29.98), number of fruits per plant (88.55 and 50.44), fruit yield per plant (74.99 and 57.94), seed per fruit (73.02 and 34.00) and primary branches (58.70 and 53.10) suggested that these characters would be considered for varietal selection. The correlation studies revealed that fruit yield per plant showed significant positive correlation with number. of average fruit weight (0.569 and 0.629) number of fruit per plant (0.879 and 0.796), plant height (0.699 and 0.618) and significantly negative correlation with seed per fruit (-0.021 and -0.065) at genotypic and phenotypic level. These characters would be considered when selection a good variety. Path analysis revealed days to 50% flowering (0.0070), plant height (0.370), number of fruits per plant (0.7560), average fruit weight (0.5380) had direct positive effect on pod yield per plant, indicating these traits are the main contributors to fruit yield per plant. The studied genotypes were clustered into five groups with highest of inter-cluster distance between clusters I and V (20.07).This indicates 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 II and IV (5.34). The greater divergence in the genotypes due to different morph genic characters would offer a great scope in okra breeding.

TABLE OF CONTENTS

CHAPTER	TITLE	PAGE
	ACKNOWLEDGEMENT	i
	ABSTRACT	ii
	TABLE OF CONTENTS	iii-v
	LIST OF TABLES	vi
	LIST OF FIGURES	vii
	LIST OF PLATES	vii
	LIST OF APPENDICES	vii
	SOME COMMONLY USED ABBREVIATIONS	viii-x
I	**INTRODUCTION**	**1-3**
II	**REVIEW OF LITERATURE**	**4-36**
	2.1 Origin and Distribution	4
	2.2 Importance Of Okra	5-6
	2.3 Ecological Requirement	6
	2.4 Phenology and Growth	7-9
	2.4.1 Vegetative Growth	7
	2.4.2 Reproductive Growth	8-9
	2.5 Genetic of Okra	9
	2.6 Breeding of Okra	9-10
	2.7 Performance of Genotypes	10-12
	2.8 Genetic Variance	12-22
	2.8.1 Genetic variability	12-17
	2.8.2 Heritability and genetic advance	18-22
	2.9 Correlation of Quantitative Traits	22-28
	2.10 Path analysis	28-31
	2.11Genetic divergence	31-36

TABLE OF CONTENTS (Cont'd)

CHAPTER	TITLE	PAGE
III	**MATERILAS AND METHODS**	**37-52**
	3.1 Site of Experiment	37
	3.2 Soil and Climate of the Experimental Site	37
	3.3 Description of Experimental Materials	38
	3.4 Experimental Design	38
	3.5 Details of the Experiment	39
	3.6 Field Managements	39-43
	3.6.1 Land preparation	39
	3.6.2 Manures and fertilizers	39
	3.6.3 Bed preparations	39
	3.6.4Seed Sowing	39
	3.6.5 Thinning of excess seedlings	40
	3.6.6 Cultural Practices	40
	3.6.7 Observations recorded	40-41
	3.6.8 Fruit character and yield	41-42
	3.7 Statistical Analysis	45-50
	3.7.1 Analysis of Variance	45
	3.7.2 Contribution of different characters towards divergence	45
	3.7.3 Phenotypic and Genotypic Variability	46
	3.7.4 Heritability and Genetic Advance	47-52
IV	**RESULT AND DISCUSSION**	53-92
	4.1 Analysis of Variance	53-54
	4.2 General performance of genotypes	56-
	4.2.1 Germination (%)	56
	4.2.2 Days to 1st flowering	56
	4.2.3 Days to 50% flowering	56

TABLE OF CONTENTS (Cont'd)

CHAPTER	TITLE	PAGE
	4.2.4 Plant height (cm)	60
	4.2.5 Number of primary branches per plant	60
	4.2.6 Number of fruits per plant	60
	4.2.7 Fruit length (cm)	61
	4.2.8 Fruit diameter (cm)	61
	4.2.9 Average fruit weight (gm)	61
	4.2.10 Number of seeds per fruit	61
	4.2.11 Fruit yield per plant (g)	62
	4.3 Variability study in genotypes	64-73
	4.3.1 Phenotypic and genetic variances	64
	4.3.2 Phenotypic and genetic coefficient of variation	65-68
	4.3.3 Estimate of heritability	69
	4.3.4 Estimate of expected genetic advance	72-73
	4.4 Correlation coefficient	74-81
	4.4.1 Phenotypic and genotypic correlation coefficients	74-78
	4.4.2 Correlation of fruit yield with other traits	78
	4.4.3 Correlation among other characters	79-81
	4.5 Path coefficient analysis	81-83
	4.6 Genetic divergence analysis	84-97
	4.6.1 Clustering Patterns of the Genotypes	84
	4.6.2 Contribution of different characters to total diversity	88
	4.6.3 Principal component analysis	84
	4.6.4 Intra and inter cluster divergence	90
	4.6.5 Cluster Mean	90
	4.6.6 Genetic distance	94-97

TABLE OF CONTENTS (Cont'd)

CHAPTER	TITLE	PAGE
V	**SUMMERY AND CONCLUSION**	99-101
	REFERNCES	102-115
	APPENDICES	116-120

TABLE No.	LIST OF TABLES	PAGE
1	Details of experiential materials	38
2	Mean sum of square of different characters of 28 okra genotypes	55
3	Range, mean and CV (%) of 28 okra genotypes	57
4	Mean performance of eleven characters of 28 okra genotypes	58-59
5	Estimation of variance parameters for eleven characters in okra genotypes	66
6	Estimation of heritability and genetic advance of different parameters of okra	70
7	Pearson correlation coefficient for different traits	75
8	Genotypic (G) and phenotypic (P) correlations among different pairs of traits for different genotype of okra	76
9	Partitioning of genotypics into direct (bold) and indirect effects of eleven traits by path analysis of okra	82
10	Distribution of 28 genotypes in different clusters	85
11	Eigen values and yield percent contribution of 11 characters of 28 genotype	89
12	Intra (Bold) and inter cluster distances (D2) for 28 genotypes	91
13	The nearest and farthest clusters from each cluster between D2 values in okra	92
14	Cluster mean for 11 yield and yield related characters in 28 okra genotypes	93
15	Genetic Euclidean distances and mean Euclidean distance of 28 genotypes based on 11 traits	95-96
16	Finally selected genotypes for important traits	98

LIST OF FIGURES

FIGURE No.	TITLE	PAGE
1	Performance of okra genotypes for fruit yield per plant (g)	63
2	Genotypic and phenotypic coefficient of variation	67
3	Heritability and genetic advance in percent of mean	71
4	Scatter diagram of okra genotypes of based on their principal component scores	86
5	Cluster diagram showing genotypes grouping in different clusters of 28 genotypes of okra	87

LIST OF PLATES

PLATE No.	TITLE	PAGE
1	Experimental Plot	43
2	Seed sowing	43
3	Fruit with flower	43
4	Fruits of different Okra genotypes	44

LIST OF APPENDICES

APPENDICES	TITLE	PAGE
I	Analysis of variance for yield and yield contributing traits of 28 Okra genotypes	116
II	Appendix 2. Principal component score I and II	117
III	Map showing the experimental site under the study	118
IV	Morphological, physical and chemical characteristics of initial soil (0-15 cm depth) of the experimental site	119
V	Monthly average record of air temperature, rainfall, relative humidity, sunshine hours of the experimental site during study period from March 2017 to July 2017.	120

SOME COMMONLY USED ABREVIATIONS

FULL WORD	ABREVIATION
At the rate	@
Agro Ecological Zone	AEZ
Agriculture	Agric
Agricultural	Agril.
Analysis of variance	ANOVA
And others	et al.
Average fruit weight	AFW
Bangladesh Agricultural Research Institute	BARI
Bangladesh Bureau of Statistics	BBS
Bangladesh	BD
By way of	Via
Cultivars	cv
Centimeter	CN
Canonical Variate Analysis	CVA
Degree Celsius	0c
Degrees of Freedom	df
Days to 50% flowering	D50%F
Days After Sowing	DAS
Days first flowering	DFF
Duncan`s Multiple Range Test	DMRT
Etcetera	etc.
Environmental variance	σ^2_e
Food and Agricultural Organization	FAO
Fruit length	FL
Fruit diameter	FD
Fruit yield per plant	FYPP
Genetics and Plant Breeding	GEPB
Germination %	G%
Genotypic variance	σ^2_g
Gram	Gm

SOME COMMONLY USED ABREVIATIONS (Cont'd)

FULL WORD	ABREVIATION
Genotype	G
Genetic Advance	GA
Genotypic coefficient of variation	GCV
Genetic Advance	GA
Harvest Index	HI
Heritability in broad sense	h^2_b
International Center for Agricultural Research in Dry Areas	ICARDA
Indian Agricultural Research Institute	IARI
Journal	J.
Kilogram	Kg.
Meter	M
Mean sum of square	MS
Murate of Potash	MP
Ministry of Agriculture	MOA
Number	No.
Namely	Viz.
Number of fruit per plant	NFPP
Number of primary branches	NPB
Principal Component Analyais	PCA
Principal Coordinate Analysis	PCO
Phenotypic coefficient of variantion	PCV
Percent	%
Phenotypic variance	σ^2_p
Percentage of Coefficient of Variation	CV%
Plant height	Ph
Residual Effect	R
Randomized Complete Block Design	RCBD
Science	Sci.
Standard Error	SE
Seeds per fruit	SPF
Square meter	m2

SOME COMMONLY USED ABREVIATIONS (Cont'd)

FULL WORD	ABREVIATION
Sher-e-Bangla Agricultural University	SAU
Saturated fatty acid	SFA
Triple Super Phosphate	TSP
The third generation of a cross between two dissimilar homozygous parents	F3
University	Uni.
Variety	Var

CHAPTER I

INTRODUCTION

Okra [*Abelmoschus esculentus* (L.) Monech] is a polyploid, belonging to the family Malvaceae with 2n = 2x =72 or 144 chromosome. It is the only vegetable crop in the Malvaceae family (Santos, 2012). It is self-pollinated crop; occurrence of out crossing to an extent of 4 to 19% with the maximum of 42.2% is noticed with the insect assisted pollination (Kumar, 2006). This self-pollinating crop is an example that requires a separation between varieties to maintain purity (Tripathi *et al.,* 2011). It is an important vegetable crop grown in the tropical and sub-tropical parts of the world (Raju *et al.*, 2008) and commonly known as "lady's finger" (Anwar *et al.,* 2011). It is a warm season vegetable (Voss and Bell, 2007; Reddy *et al*., 2012) and can tolerant more heat and drought (Phathizwe and Ekpo, 2011).

Okra is native to North Eastern Africa in the area of Ethiopia and Sudan (Santos, 2012). It is cultivated in various tropical, subtropical and Meditterean regions of the world (Kamalpreet *et al.*, 2013). It is cultivated since ages, and extensively disseminated from Africa to Asia, Southern Europe and America and currently grown in many countries. It is grown for fresh table use or for processing (Voss and Bell, 2007; Reddy *et al.*, 2012), its tender green fruits for consumption as a fried or boiled vegetable (Pradip *et al.*, 2010, Anwar *et al.*, 2011). It is an important source of nutrients and vitamins for the rural population. It is extensively cultivated for its tender immature fruits, which are largely used as fresh vegetable. Okra fruits contain water (89 g), protein (2-4 g), fat (0.3), carbohydrate (7.6 g), calcium (92 mg), phosphorus (51 mg), iron (0.6 mg) and potassium (249 mg) per 100 gram fresh weight. It is also a rich source of iron and vitamin A, B and C (Aykroyd, 1966).

The fruits have various medicinal properties too. It is useful in fever, chronic dysentery, and irritable states of genitero. It is good for people suffering from renal colic, leucorrhoea, spermatorrhoea, chronic dysentery and general weakness. Due to high iodine content fruits are considered useful for control of goiter. The stem of the

plant is used for cleaning of sugarcane juice and for the extraction of fibres in paper mills (Choudhury, 1979). Okra is specially valued for its tender and delicious fruits in different part of the country. However, to a limited extent, it is canned, dehydrated to preserve, and also used as in frozen form. Kharif season is the main growing season for cultivation of okra. During this season the plants showed luxurious growth and bears more number of pods that contribute to high yield per unit area.

Now-a-days large number of commercial cultivars including hybrids of okra is available in the market but all these are not adapted and suited to all the regions of the country. Further, no specific recommendation about the suitability of genotypes for a particular area is available. Farmers face problems in selecting genotypes/cultivars for commercial cultivation in a particular area. Considering the above mentioned facts, there is a need to compare some of the available genotypes/cultivars to select high yielding, better adaptable genotypes/cultivars for commercial cultivation in Bangladesh.

Knowledge of genetic diversity among okra germplasm will play significant role in breeding program as it helps to develop varieties with desired traits. It is a prerequisite to develop high yielding okra varieties. This is important for selecting parents in combination breeding and to obtain transgressive segregants (Prakash *et al.*, 2011). The knowledge of pattern of inheritance of various characters are important consideration while, determining the most approximate breeding procedures applicable to any particular crop.

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. These studies along with the association analysis will be more useful in the estimation of inter-relationship among the yield contributing components.

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. In view of the above facts, the present studies in okra entitled character association and diversity analysis of okra genotypes has been carried out with the following objectives:

Objectives:

i. To study the genetic variability, heritability, genetic advance of yield and yield contributing traits in different okra genotypes;

ii. To study the character association for quantitative attributes of different okra genotypes;

iii. To study the genetic divergence in okra genotypes.

CHAPTER II

REVIEW OF LITERATURE

2.1 Origin and Distribution

Okra originated in Ethiopia around Nile River (Torkpo *et al*., 2006) and was cultivated by the ancient Egyptians by the 12th century BC. Its cultivation spread throughout Middle East and North Africa (Vavilov, 1951; Sorapong, 2012; Reddy *et al.*, 2012). Ethiopia as center of origin for okra, collection of genotypes in the country is expected to be diverse and rewarding in breeding to improve the crop (Ren *et al.*, 1995). It is found all around the world from equatorial areas to Mediterranean Sea as may be seen from the geographical distribution of cultivated and wild species. Cultivated and wild species of okra clearly showed overlapping in Southeast Asia, which is considered as the center of diversity (Sorapong, 2012).

It is believed that originated from Africa and is currently being grown in most subtropical and tropical regions of the world (Tattanakorn and Prabhat, 2004; Phathizwe and Ekpo, 2011). There are two hypotheses concerning the geographical origin of *A. esculentus*. Some scientists argue that one putative ancestor (*A. tuberculatus*) is native from Northern India, suggesting that the species originated from this geographic area. On the basis of ancient cultivation in East Africa and the presence of the other putative ancestor (*A. ficulneus*), others suggest that the area of domestication is Ethiopia or North Egypt, but no definite proof is available (Sorapong, 2012).

Okra was previously included in the genus *Hibiscus*. Later, it was designated to *Abelmoschus*, which is distinguished from the genus Hibiscus (Sorapong, 2012). It was earlier included in the genus *Hibiscus*, section *Abelmoschus* in the family Malvaceae. The *Abelmoschus* was subsequently proposed to be raised to the rank of distinct genus. The wider use of *Abelmoschus* was subsequently accepted in the taxonomic and contemporary literature. This genus is distinguished from the genus *Hibiscus* by the characteristics of the calyx, spathulate, with five short teeth, connate to the corolla and caduceus after flowering (Charrierl, 1984; Tripathi *et al.*, 2011).

2.2 Importance of Okra

Okra is an economically important vegetable crop grown in tropical and sub-tropical parts of the world. This crop is suitable for cultivation as a garden crop as well as on large commercial farms (Tattanakorn and Prabhat, 2004). It has potential for cultivation as an oilseed crop because its mature pods contain high quantity of seeds containing considerable amount of oil which could be characterized and utilized for commercial purposes (Anwar *et al.*, 2011). Industrially, okra mucilage is usually used for glace paper production and also has a confectionery use (Sorapong, 2012; Lengsfeld *et al.*, 2004; Adetuyi *et al.*, 2008). It is exported in two forms i.e. fresh and frozen (Tattanakorn and Prabhat, 2004). Its flowers can be very attractive and sometimes are used in decorating the living room. Additionally, dry okra pods can be used as naturals for crafting (Maurya *et al.*, 2013).

Okra is nutritionally rich vegetable which provides carbohydrates, protein, vitamins A, B_1, calcium, potassium, dietary fiber, and mineral matters; hence it plays a vital role in the human diet (Tripathi *et al.*, 2011; Maurya *et al.*, 2013). It plays an important role in meeting nutritional demand when other vegetables supplies are scarce in the market (Maurya *et al*, 2013). Young immature pods are important fresh fruit vegetables that can be consumed in many different forms; raw, steamed, boiled or fried (Maurya *et al.*, 2013; Sorapong, 2012).

Okra fruits are used as boiled, sliced vegetable or fried. It is mainly grown by many farmers because of its tender texture which is highly mucilaginous and useful in soup thickening (Akanbi *et al.*, 2010). Its ripe seeds are roasted, ground and used as a substitute for coffee in some countries. Mature fruits and stems containing crude fiber are used in the paper industry. The seeds from fully mature and ripened okra pods are sometimes used for chicken feed. On a small scale it has also been used edible oil production (Anwar *et al.*, 2011). The greenish yellow edible oil has a pleasant taste and odor, and is high in unsaturated fats such as oleic acid and linoleic acid. The oil content of the seed is quite high about 40% (Tripathi *et al.*, 2011).Okra has medical application as a plasma replacement or blood volume expander (Sorapong, 2012). Its medicinal value has also used in curing ulcers and relief of hemorrhoids. It is useful against spermatorrhoea; chronic dysentery and genito urinary disorders (Rajendra *et al.*, 2013). Its high dietary fibers help stabilize blood sugar and help to reduce

cholesterol by binding along with bile acids which usually carry the toxins which the body should eliminate.

The alkaline pH of okra could also contribute to its effect in gastro-intestinal ulcers by neutralizing the digestive acids. So eating okra is good for health and digestion. Its mucilage is suitable for medicinal applications (Sorapong, 2012; Lengsfeld *et al*., 2004; Adetuyi *et al.*, 2008; Ahiakpa *et al.*, 2013). The mucilaginous property is comparable to statins. Statins are drugs that are doctors prescribed for treating of high cholesterol or high fat in the blood (Okra, 2008. http://healthypage-info.blogspot.com)

2.3 Ecological Requirement

Okra is tolerant to a wide range of climatic condition (Akanbi *et al.*, 2010). It requires a long, warm and humid growing environment. It can be successfully grown in hot humid areas (Tripathi *et al.*, 2011). The crop grows well in hot weather, especially in the regions with warm nights (>20^{o}C) (Anwar *et al.*, 2011). It is sensitive to frost at in its all growth stage and injured below 10^{o}C (Voss and Bell, 2007; Tripathi *et al.*, 2011). It is a short day plant, but its wide geographical distribution indicates that cultivars differ markedly in sensitivity. The shortest critical day length reported is 12.30 hours for flower initiation and flowerings are hardly affected by day length in popular subtropical cultivars (Sorapong, 2012).

Okra needs an average optimum temperature of 20°C to 35°C (Voss and Bell, 2007, Sorapong, 2012, Tripathi *et al.*, 2011) with 15^{o}C and 42^{o}C minimum and maximum temperature respectively (Voss and Bell, 2007). For faster plant growth still higher temperature helps though it delays fruiting but at temperatures beyond 40 – 42°C, flowers may desiccate and drop, causing yield losses. For seed germination, optimum soil moisture and a temperature between 25°C and 35°C and fastest germination observed at 35°C. Beyond this range the germination will be delayed and weak seeds may not germinate (Tripathi *et al.*, 2011). Okra tolerates poor soils, but prefers well drained sandy loams, with pH 6-7 and a high content of organic matter. Okra requires a moderate rainfall of 80-100 cm well distributed throughout the growing season to produce its young edible fruits (Sorapong, 2012).

2.4 Phenology and Growth

Okra is an upright annual, herbaceous 91 to 244 cm tall plant with a hibiscus like flower. It is a tropical direct sown vegetable with duration of 90-100 days (Tripathi *et al.*, 2011). Different genotypes have different growth habits, as a result of selection or a natural adaptation mechanism. The common growth habit among all the landraces observed indeterminate with erect growth appearance (Oppong-Sekyere *et al.* 2011). Flower buds are initiated at 22-26 days and the first flower opened 41-48 days after sowing. Once initiated, flowering continues for 40-60 days (Tripathi *et al.* 2011). Growth and yield of okra depends upon many factors including seed quality, soil nutrition, climatic conditions and cultural practices (Kusvuran, 2012).

Anthesis and stigma receptivity are influenced by genotype and climatic factors like temperature and humidity. Anthesis is observed between 6 AM and 10 AM. Anthers dehisce before flower opening and hence self-pollination may occur at anthesis. The dehiscence of anthers is transverse and complete dehiscence occurs in 5-10 minutes. Pollen fertility is maximized in the period between an hour before and an hour after opening of the flower. The stigma is receptive on the day of (90-100%) flowering, day before (50-70%) and the day after (1-15%) flowering. Flowers open only once in the morning and close after pollination on the same day (Tripathi *et al*., 2011). Flowers are very attractive to bees and the plants are cross-pollinated. Cross pollination up to 4-19% with maximum of 42.2% has been reported. The extent of cross-pollination in a particular place will depend upon the cultivar, competitive flora, insect population and season (Tripathi *et al*., 2011).

2.4.1 Vegetative Growth

Okra's stem is semi woody and sometimes pigmented with a green or reddish color. It is erect, variable in branching, with many short branches that are attached to thick semi woody stem. The stem attains height from 91 cm in dwarf varieties to 244 cm in height (Tripathi *et al*., 2011). The woody stem bears leaves that are lobed and hairy. Leaf is cordate (heart-shaped), simple, usually palmately 3-7 lobed and veined. It is subtended by a pair of narrow stipules and alternate and usually palmately five lobed, whereas the flower is axillary and solitary. The leaf is dark green in color and resembles a maple leaf (Tripathi *et al.*, 2011).

Okra has a strong deep taproot system which penetrates almost vertically downward up to 160 cm with a diameter of 0.5 cm (Tripathi *et al.*, 2011). A total of 24 to 35 laterals ran horizontally from just beneath the soil surface to a depth of 41 cm. A maximum spread of 46 cm is reached at the 13 cm level. A few of the deeper laterals pursued an obliquely down ward course (Okra http://www.soilandhealth.org/01alb rary /010 137vegroots/010137tochtm).

2.4.2 Reproductive Growth

Okra has perfect flowers (male and female reproductive parts in the same flower) and it is self-pollinated. Its flowers are 4-8 cm in diameter, with five white to yellow petals, often with a red or purple spot at the base of each petal and the flower withers within one day. Flower structure is hermaphrodite and self-compatible. Flower bud appears in the axil of each leaf, above 6th to 8th leaf depending upon the cultivar. The plant usually bears its first flower one to two months after sowing (Tripathi *et al.*, 2011). Flower bud initiation and flowering are influenced by genotype and climatic factors like temperature and humidity (Tripathi *et al.*, 2011). Flowering is continuous but highly dependent upon biotic and a biotic stress. Flowering and fruiting is continuing for an indefinite time, depending upon the variety, the season and soil moisture and fertility (Tripathi *et al.*, 2011). Flower initiation and flowerings are delayed as temperatures increase (positive correlation between temperature and number of vegetative nodes (Sorapong, 2012).

The fruit is an elongated, conical or cylindrical capsule and containing ovules. It is long pod and generally ribbed, developing in the leaf axil and spineless in cultivated kinds. Its color varies from normally yellowish green to green. Sometimes purple or whitish green colored fruit exists. The fruit is a capsule and grows quickly after flowering. The greatest increase in fruit length and diameter occurs during 4th to 6th day after pollination. At this stage fruit is most often plucked for consumption. Its fruits are harvested when immature and high in mucilage but before becoming highly fibrous. Generally the fiber production in the fruit starts from 6th day onwards of fruit formation and a sudden increase in fiber content from 9th day is observed (Tripathi *et al.*, 2011). Pods older than 7 days are considered to be low in quality mainly due to excessive increase in crude fiber, gradual reduction of moisture and important

components of the table quality. Crude protein and starch contents are also reduced by late harvest while crude oil content increased (Duzyaman and Vural, 2003).

Okra fruit contains numerous ovals, smooth, striated and dark green to dark brown seeds (Tripathi *et al.*, 2011). The easiest way to keep the seed is to leave it in the pod. Seed weight varies from 30 to 80 g 1000^{-1} seeds. Okra seeds contain about 20% protein and 20% oil. The dried seeds are a nutritious material that can be used to prepare vegetable curds, or roasted and ground to be used as coffee additive or substitute (Sorapong, 2012).

2.5 Genetic of Okra

The numbers of chromosome in okra is 2n= 6x=72, 9x=108, 10x=120, 11x=132 and 12x=144 are in regular series of polyploid with n=12. The most frequently observed somatic chromosome number of okra is 2n=130 (Sorapong, 2012). Additive and nonadditive variance components are important in the genetic control of yield and its associated traits. In okra a set of half-diallel crosses elicit information about the nature and magnitude of gene action and combining ability effects for yield and its components. This will help to formulate suitable breeding strategy and isolate potential parents and promising crosses for further exploitation (Reddy *et al.*, 2012).

2.6 Breeding of Okra

The main goal of most of the plant breeding program is to increase the yielding ability of crop plants. Information on various quantitative traits, particularly those that contribute to yield will be useful for breeding program (Weerasekar, 2006). 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). Selection of parents on the basis of phenotypic performance alone is not a sound procedure, since phenotypically superior lines may not lead to expected degree of heterosis in generation or generate superior transgressive segregants in segregating generations (Thirupathi *et al*., 2012; Reddy *et al.*, 2012).

Generally the success of crop improvement program largely depends on the magnitude of genetic variability, genetic advance, character association, direct and indirect effects on yield and yield attributes (Mehta *et al.*, 2006, Nwangburuka *et al.*, 2012). In plant breeding program, assessment of parental divergence is important. Breeding would be very effective in the event of strong positive associations of major yield characters. Greater coefficient of variations in traits give credence to the relevance of these characters in selecting accessions for yield improvement since they possess greater variability for exploitation of desirable traits for overall yield and productivity (Ahiakpa *et al.*, 2013).

2.7 Performance of genotypes

Hazra and Basu (2000); observed that there was a wide range of variation for plant height (general mean=80.8 cm), days to first flower (49.9), fruit weight (15.0 g), fruits per plant (10), seeds per fruit (53.3), fruit yield per plant (155.7 g), moderate variations for primary branches per plant (2.9) and fruit length (12.9 cm) and narrow variation for node at first flower (4.8), ridges per fruit (5.1) and dry weight of fruit (1.5 g). Lal *et al.* (2001); studied the performance of three okra varieties viz., Parbhani Kranti, Pusa Sawani and Punjab-7 under three sowing dates. Parbhani Kranti produced maximum green pod yield (5.99 q/ha) followed by Pusa Sawani (80.49 q/ha) and Punjab-7 (72.5 q/ha). Punjab-7 was least effected by yellow vein mosaic virus and Pusa Sawani was worst effected with 41.1% (plant showing infection). They also observed taller plant in Parbhani Kranti with maximum fresh weight of plant as well as dry weight of plant. Among all the three varieties, Parbhani Kranti took minimum days to first fruit appearance, more number of green pods per plant and low infection of yellow vein mosaic virus as compared to Pusa Sawani and Punjab-7.

Muhammad *et al.* (2001); reported four okra cultivars, namely Pusa Sawani, Parbhani Kranti, hybrid Sakshi and Krisma-51, which were evaluated for their performance in comparison to a local cultivar, Sabz Pari, in a field experiment. Sabz Pari ousted all the cultivars for average weight per green pod (16.08 g) and green pod yield per plant (332.53 g) and per hectare (23.41 tones). The highest number of seeds per pod, 1000-seed weight and seed yield per plant (42.06 g) and per hectare (2959.3 k g) were also recorded in Sabz Pari.

Tiwari (2001), studied the performance of okra hybrids in tarai region of U.P in rainy season. She observed maximum plant height at 30, 60 and 90 days after seed sowing in SPHV-316 (7.26) and VLC-1 (6.26) as against Parbhani Kranti, the hybrid cultivars viz., SPHV-316 and HOE-301. She observed maximum pod yield in SPHP-316, AROH-10, SOH-54, DBR-3 and DBR-4. HOH-24 and Varsha produced significantly more number of pods per plant than Parbhani Kranti. The hybrid varieties namely SPHB-316, DVR-3 and AROH-10 produced significantly higher pod yield per hectare as compared to Parbhani Kranti. She observed the minimum incidence of fruit borer in KOH-5 (0%), Vijaya (3.3%) and AROH-21 (4.76%) and minimum YVMV infection in SPHB-316 (21.11%), followed by AROH-9 (21.85%), AROH-10 (23.33%) and VLC-1 (24.44%).Mohapatra *et al.* (2007) evaluated twenty three genotypes of okra for resistant to yellow vein mosaic virus as well as yield component. Pusa Makhmali exhibited higher level of resistance towards yellow vein mosaic virus followed by Mahyco-10 and Japani Jhaar which showed resistance behavior.

Alam and Hossain (2008); assessed the variability of growth contributing characters of 50 okra accessions and their interrelation effects on the yield of green pods. The experiment was undertaken at the Horticulture Farm of Bangladesh Agricultural University, Mymensingh during the period from February to May, 2002. There was a wide range of variation for height of plant (80.90 cm) contrasting lesser variation for number of primary branches per plant (1.57) was observed. The yield of green pod varied significantly and ranged from 4.39 t/ha (Accession No. 19) to 12.77 t/ha (Accession No. 69) with the average value of 7.86 t/ha.

Arvind Kumar (2009); carried out a trial in India with 12 genotypes of okra. Significant differences recorded in all the quantitative characters such as plant height, branches/plant, number of pods/plant, pod length, pod weight as well as pod yield/plant, number of seeds/pod, weight of seeds/pod, and test weight. The tallest plants were observed in PB-236 and dwarfest Vivek-1. More branches/plant was observed in Pusa Sawni. The genotypes, PB-27-1 and PB-174 were found earliest for flowering and fruit picking. The pod length was recorded maximum in PB-195, it was lowest in Pusa Sawni and Vivek-1. More number of pods/plant was observed in PB-520 followed by PB-236 and Prabhani Kranti.

The number of seeds/pod was noted maximum in PB-31-1 whereas weight of seeds/pod was higher in PB-520, PB-31-1 and PB-236. Test weight was higher in Pusa Sawni and lowest in Vivek-1. The pod weight/plant as well as pod yield/ha were greater in PB-520 followed by PB-31-1 and PB-236. PB-520 and PB-57 were found free from YVMV up to 60 days after sowing. The minimum infection of virus was noted in PB-520 (12.9%), PB-236 (13.79%), and PB-57 (15.38%) at 90 DAS. The genotype, PB-520 produced significantly higher pod yield (188.86 q/ha) and found best among all the genotypes.

Singh and Jain (2012), evaluated eleven cultivars of okra for yield and other characters. They found that pod length was greater in Parbhani Kranti and it was minimum in Pusa Sawani (12.8 cm). Tallest plants were found in PB-266 and DARL-601. They also found that PB-266 (96.6 q/ha), PB-1 (83.0 q/ha) PB-2018 (82.4q/ha) and PB 31-1 (81.2 q/ha) were top yielder than check cultivars Punjab-7 (48.0 q/ ha) and Pusa Sawani (62.3 q/ha). More number of fruits per plant was harvested from PB-266, PB-2018 and PB 31-1. Mishra *et al*. (2015); observed the wide variations for fruit weight (12.23g to 23.40g), first flowering nodes (4.90 to 7.77), and fruit yield per plant (192.26g to 433.34g). Similarly, fruit yield per plant had the highest mean of 290.90g followed by plant height (160.62 cm) whereas; the lowest mean was observed for first flowering node.

2.8 Genetic Variance

2.8.1 Genetic Variability

Genetic variability is an important attribute in breeding program (Oppong-Sekyere *et al.,* 2011). It is pre-requisite for any breeding program (Azam *et al*., 2013). To improve the yield and other characters, information on genetic variability among different traits is necessary. The ratio of GCV and PCV indicate that some of the characters were influenced by the environment (Simon *et al.,* 2013b).Variability in the various traits studied gives ample scope for manipulation of okra and its components for higher economic returns (Ahiakpa *et al.,* 2013). Characterized okra genotypes showed broad variation for most traits which allows identification of promising accessions for breeding (Oppong-Sekyere *et al.*, 2011).

Two major classes of okra, the conventional and unconventional type are present major production area. The conventional *Abelmoschus esculentus* is a native of Asia, and the unconventional *Abelmoschus callei* is a native of Africa (Adeoluwa and Kehinde, 2011). Hazra and Basu (2000), reported that the primary branches per plant, which the highest genotypic coefficient of variation (GCV; 35.5%). However, plant height (14.3%), fruit weight (20%), fruits perplant (16.9%), seeds per fruit (23%), and fruit yield per plant (17.7%) recorded a moderate genotypic coefficient of variation. These characters proved the existence of justifiable genetic distance among the different cultivars. An investigation carried on genotypes showed highly significant mean squares for all the traits. This suggests the presence of genetic variation for the performance of traits (Azam *et al*., 2013). The significant differences among the accessions for all quantitative characters measured and estimate of phenotypic and genotypic coefficients of variation showed the presence of genetic variability among okra accessions for the majority of the character (Mihretu *et al.*, 2014b).

Detection of significant genetic variability indicates that genetic variance exists in the genotypes but tells nothing about the range of genetic variability within a particular population (Jindal *et al.*, 2010; Pradip *et al.*, 2010). Dhall *et al.* (2001); studied genetic variability, heritability and genetic advance for some of the quantitative characters, i.e. days to first flowering, total yield per plant, marketable yield per plant, number of fruits per plant, fruit length, fruit weight, plant height and virus incidence, were evaluated in 48 okra genotypes in 1997 in India. Significant differences among genotypes were observed for all characters except for virus incidence. Estimates of phenotypic and genotypic coefficients of variation were found to be high for plant height, total yield per plant, marketable yield per plant, number of fruits per plant and virus incidence.

Gandhi *et al.* (2001); evaluated forty-four genotypes of okra to study the variability for 13 characters. The treatment mean squares were significant for all the characters studied. The characters viz., number of branches per plant, dry fruit yield per plant and height at first fruit set showed high genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) estimates. High magnitude of differences between GCV and PCV were observed for characters like number of branches per plant and seed yield per plant, indicating the role of environment in the expression of

characters. Dhankhar and Dhankhar (2002a) estimated the extent of variability of fruit yield and its components (number of fruits per plant, days to 50% flowering, number of branches per plant and plant height) in 15 advance lines of okra. All the characters had relatively low genotypic and phenotypic coefficients of variation in both years.

Dhankhar and Dhankhar (2002b), evaluated 62 lines of okra for genetic variation in yield and yield components. Higher range of variation was recorded for the number of fruits per plant, days to 50% flowering, and number of branches per plant during the rainy season, and for fruit yield and plant height during the spring-summer season. The non-significant variation between phenotypic and genotypic coefficients of variation for fruit yield and plant height indicated that the environment did not significantly affect the expression of these traits. The coefficient of variation at phenotypic and genotypic levels was high for the number of branches and fruits per plant, fruit yield, and plant height, suggesting that selection may be based on these traits. Ghai *et al.* (2004); carried out the investigations on the induced variability of economic traits with Pusa Sawani and Punjab-7. They found that Punjab-7 was significantly superior to Pusa Sawani for fruit length, number of fruits per plant, total yield, marketable yield and virus incidence.

Ravindra *et al.* (2004); studied on genetic variability for fruit and yield parameters in okra. The genotypic and phenotypic coefficients of variations (GCV and PCV, respectively) were high for total yield per plant and number of seeds per fruit. Moderate GCV and PCV were observed for number of ridges per fruit, number of fruits per plant, fruit length, fruit diameter and average fruit weight. Subrata *et al.* (2004); evaluated twenty-five genotypes of okra, grown at Nadia, West Bengal, India, during kharif season of 2001. They observed genetic variability of important growth and fruit characters and their relationships. Days to 50% flowering, plant height, number of ridges per fruit, fruit length, fruit width and fruit weight, number of fruits per plant and fruit yield per plant varied significantly among the genotypes. Fruit yield per plant, number of fruits per plant, fruit weight showed high values of genetic coefficient of variation and phenotypic coefficient of variation.

Indurani and Veeraragavathatham (2005), assessed genetic variability for eight characters (plant height at first flower bud appearance, number of fruits per plant, fruit weight, fruit length, fruit girth, plant height at final harvest, number of branches per plant and yield per plant) in 33 okra hybrids and their seven parents in 1998, in India. Significant differences were observed among genotypes for all characters studied. Phenotypic variance was highest for yield per plant, followed by plant height at final harvest. Genotypic variance was also highest for yield per plant, followed by plant height at final harvest and number of fruits per plant.

Jaiprakashnarayan and Ravindra (2006), conducted field experiments in Karnataka, India, during 2002-2003, to study the genetic variation among 69 okra genotypes for different growth and earliness characters. High genotypic (GCV) and phenotypic coefficients of variation (PCV) were observed for number of branches per plant and plant height at 100 DAS. Days to first flowering and days to 50% flowering exhibited low GCV and PCV. Singh *et al.* (2006); studied the genetic variability of 15 quantitative characters in 19 okra genotypes in 2002 in India. Significant differences among genotypes were observed for all the characters under study. Estimates of phenotypic and genotypic coefficient of variation were high for number of branches per plant, number of fruits per plant, number of seeds per pod and fruit yield per plant.

Singh and Singh (2006); conducted a field experiment in Uttar Pradesh, India, to estimate the range of genetic and phenotypic variation in 64 okra genotypes based on days to first flowering, plant height, number of branches per plant, fruit length, fruit width, number of fruits per plant and fruit yield per plant. A considerable amount of genetic variation was exhibited by number of branches per plant, fruit yield per plant, 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. Krushna *et al.* (2007**)**; conducted a field trial during kharif season of 2003, in India. Studies indicated the presence of considerable amount of genetic variability in eight genotypes of okra as well as the occurrence of genotypic and phenotypic variation among the various yield-related characters studied. The magnitude of difference between PCV and GCV estimate was maximum for fruit length, number of fruits/plant and fruit girth, suggesting the influence of environment on these traits.

Manivannan *et al.* (2007) observed the experimental material comprising the parental lines of okra, viz., Pusa A-4, Punjab Padmini, Pusa Makhmali, Pusa Sawani, Arka Anamika, VRO-4, VRO-5, VRO-6 and IIVR-10 for plant height, days to 50% flowering, fruit length, fruit diameter, number of ridges per fruit, 100-seed weight and yield per plant. Analysis of variances revealed significant differences among parents and crosses for all the characters except fruit diameter. The highest coefficient of variation (PCV=24.63, GCV=23.95) associated with high heritability (94.5%) and highest genetic advance as percent of mean (1.870) were observed for 100-seed weight.

Alam and Hossain (2008); assessed the variability of growth contributing characters of 50 okra accessions. Number of primary branches per plant, which showed a lesser range of variation, recorded the highest genotypic co-efficient of variation (26.56%) and also the highest phenotypic co-efficient of variation (32.37%). These characters suggested the existence of justifiable genetic and phenotypic distance among different accessions.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 .Somashekhar *et al.* (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). Kumar *et al.* (2011); found that the analysis of variance (mean sum of squares) 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, and 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 the 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 were observed for leaf area followed by number of nodes per plant, length of fruit, number of leaves per plant, yield per plant, and internodal length. 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). Patel *et al.* (2014); found that estimates of mean sum of squares due to genotypes were highly significant for all the characters, indicating the presence of genetic diversity in the existing material. The variation was the 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 et al. (2014) revealed that the 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 characters. High heritability (96.76 and 96.50%) coupled with high genetic advance as percent of mean (106.32 and 97.25%) were recorded for internodal length and plant height, respectively.

Sharma and Prasad (2015); investigated that the phenotypic variance and coefficient of variation were higher than their respective genotypic variance and coefficient of variation for all the traits indicated the environmental effects on their expression. The differences between GCV and PCV were high for fruit diameter (FD) followed by number of branches per plant (NB), days to 50% flowering (DF), fruit weight (FW) and days to first harvest (FH) indicating the vulnerability of traits to environmental influences reflects the possibilities of varietal improvement.

2.8.2 Heritability and Genetic Advance

Estimation of heritability serves as a useful guide to breeder for determination of variation that is due to genotypic broad sense heritability or narrow sense heritability effects (Khanorkar and Kathiria, 2010). If broad sense heritability of a character is very high, selection for the character will be fairly easy. This is because there would be a close correspondence between the genotype and phenotype due to relatively smaller contribution of the environment to phenotype. A character with low heritability, selection may be considerably difficult or virtually impractical due to the masking effect of the environment on genotypic effects (Khanorkar and Kathiria, 2010). The information on heritability alone may be misleading but when used in combination with genetic advance, the utility of heritability estimate increases. Broad sense heritability estimate provides information on relative magnitude of genetic and environmental variation in germplasms pool (Jindal *et al.*, 2010, Pradip *et al.*, 2010).

A character with high heritability in association with high genetic advance (in % mean) is an expression of additive gene action. Characters without such combination are controlled by non-additive gene action (Mehta *et al.*, 2006). High heritability estimates along with high genotypic coefficient of variation and genetic advance is usually more useful in predicting the response of an individual to selection than heritability values alone (Das *et al.*, 2012). High heritability accompanied with low genetic advance for the characters suggests that these characters are influenced by environment rather than genotypes (Das *et al.*, 2012). High heritability and high genetic advance for characters revealed that such characters are controlled by additive gene action and selection based on these characters will be effective (Mihretu *et al.*, 2014b). Thus, estimates of heritability are useful in predicting the transmission of characters from the parents to their offspring.

Hazra and Basu (2000), studied on heritability and found that plant height, fruit weight, ridges per fruit and seeds per fruit were highly heritable (above 80% heritability) while primary branches 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.

Dhall *et al.* (2001); studied genetic variability, heritability and genetic advance for some of the quantitative characters, i.e. days to first flowering, total yield per plant, marketable yield per plant, number of fruits per plant, fruit length, fruit weight, plant height and virus incidence, were evaluated in 48 okra genotypes in 1997 in India. The characters fruit length, plant height, number of fruits per plant and virus incidence exhibited high heritability along with high genetic advance, indicating the dominance of additive factors.

Gandhi *et al.* (2001); evaluated forty-four genotypes of okra to study the variability for 13 characters. Medium to high and high heritability was recorded for all the characters studied. Fruit length (64.4%), plant height at first fruit set (55.88%) and fruit girth (43.60%) showed high heritability estimates, however, these characters were coupled with varied genetic advance, i.e. high, medium and low, respectively, and suggesting complexity of genetic mechanism in expression of those characters. The additive genetic variance was reported by characters like plant height, height at first fruit set, inter-nodal length, fruit length, number of fruits per plant and number of branches per plant.

Dhankhar and Dhankhar (2002a), estimated the extent of heritability and genetic advance of fruit yield and its components (number of fruits per plant, days to 50% flowering, number of branches per plant and plant height) in 15 advance lines of okra. 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 too low for all the characters. Dhankhar and Dhankhar (2002b), evaluated 62 lines of okra for heritability and genetic advance in yield and yield components. High genetic advance coupled with high heritability was recorded for all characters except days to 50% flowering during the spring-summer season. Fruit yield can be improved through selection for higher number of fruits and branches, and medium plant height.

Dhall *et al.* (2003); studied the heritability and genetic advance in 48 advanced generations of okra. Fruit length, plant height, number of fruits per plant and virus incidence exhibited high heritability and high genetic advance. Patro and Ravisankar (2004), observed high heritability for number of branches per plant, yield per plant, and high genetic advance for yield per plant and plant height. Highest genetic advance

as percentage of mean was recorded for number of branches per plant indicating that the trait is more reliable for improvement through selection. Ravindra *et al.* (2004); studied on heritability for fruit and yield parameters in okra. High heritability with high genetic advance over mean (GAM) was observed for total yield per plant, number of seeds per fruit, number of ridges per fruit and number of fruits per plant.

Subrata *et al.* (2004**)**; evaluated heritability on twenty-five genotypes of okra, grown at Nadia, West Bengal, India, during kharif season of 2001. High heritability coupled with high genetic advance was recorded for number of fruits per plant, fruit weight and dry weight as well as fruit yield per plant, indicating that these characters are controlled by additive action of poly genes. Indurani and Veeraragavathatham (2005), assessed the heritability and genetic advance for eight characters in 40 genotypes during 1998, in India. High heritability coupled with high genetic advance was recorded for plant height at first flower bud appearance, number of fruits per plant, fruit weight and yield per plant. Thus, these characters should be given importance in selection program.

Singh *et al.* (2006); studied the heritability and genetic advance of 15 traits in 19 okra genotypes in 2002 in India. The characters, number of seeds per pod, number of branches per plant, fruit yield per plant, number of fruits per plant, plant height and 100-seed weight exhibited high heritability along with high genetic advance, which indicated that there was more number of additive factors and, therefore, further improvement could be brought about by selection.

Singh and Singh (2006); conducted a field experiment in India, to estimate the heritability and genetic advance in 64 okra genotypes. The heritability estimates were high for days to first flowering. The genetic advance and heritability suggested that the characters such as number of branches per plant and fruit yield per plant were under additive gene effects.

Jaiprakashnarayan and Ravindra (2006), conducted field experiment in India in the year of 2002-2003 to study the heritability and genetic advance with 69 okra genotypes. High heritability with high genetic advance as percent of mean was observed for plant height at 100, and 45 DAS, high heritability with low GAM was

observed for days to first flowering and days to 50% flowering. Krushna *et al.* (2007); conducted a field trial during kharif season of 2003, in India. High heritability (bs) coupled with high genetic advance was observed for fruit yield/plant and plant height, indicating the importance of additive gene action in the expression of these traits. The estimates of heritability (bs) were of high magnitude for green fruit yield /plant, plant height at harvest and days to maturity indicating the major role of genotype and ultimately less of environmental influence.

Yadav *et al.* (2007); studied on 51 treatments in 15 okra parents, KS-423, KS-440, KS-447, KS-441, KS-453, KS-455, KS-420, BO-2, KS-437, KS-448, KS-439, KS-427, Prabhani Kranti, KS-10 and KS-404. High heritability coupled with high genetic advance was observed for the number of fruits per plant, yield per plant and number of branches per plant, indicating that most likely, heritability is due to additive gene effects and selection may be effective. The maximum value of genetic advance in percent of mean was observed for the number of fruits per plant followed by fruit length, plant height, days to flowering and width of fruit.

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 and highest genetic advance was observed for the characters leaf area followed by yield per plant, plant height and number of leaves 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). High genetic advance was observed 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).

2.9 Correlation of Quantitative Traits

Correlation coefficient measures the mutual association between a pair of variables independent of other variables to be considered (Akinyele and Osekita, 2006). The correlation coefficients among the quantitative traits in the accessions of okra selection for a single character may increase the traits value which are positively correlated characters and decline the values for negatively correlated traits (Ahiakpa *et al.*, 2013). The higher genotypic correlation coefficient over phenotypic correlation coefficient observed in characters suggests very strong inherent association between various characters at genetic level and indicate the masking action of genes on the influence of environment in the expression of characters indicating the association is largely due to genetic effect (Nwangburuka *et al*., 2012).

When there is positive association of major yield characters, component breeding would be very effective but when these characters are negatively associated, it would be difficult to exercise simultaneous selection for them in developing a variety. The result of correlation is of great value in the determination of the most effective procedures for selection of superior genotypes (Akinyele and Osekita, 2006). The positive and significant phenotypic and genotypic correlation of tender fruit yield with yield related traits suggests that selection on the basis of the phenotype of these characters will lead to high seed and tender fruit yield in okra (Nwangburuka *et al*., 2012, Mihretu *et al.*, 2014b).

Dhall *et al.* (2001) studied the correlation in 48 advanced lines of okra. From the findings, marketable yield per plant, fruit weight, fruit length, number of fruits per plant and plant height were positively and significantly correlated with the total yield per plant.

Dhankhar and Dhankhar (2002b); studied the correlation between the yield and yield attributes of 62 advance lines of okra. Crop yield showed strong positive association with number of fruits and branches per plant. Plant height and number of days to 50%

flowering had positive association with yield. The number of fruits per plant had positive relationship with number of days to 50% flowering and number of branches per plant. Yadav and Dhankhar (2001); studied correlation between field parameters and seed yield and quality of okra cv. Varsha Uphar. Seed yield of okra cv. Varsha Uphar was positively and significantly correlated with plant height, number of branches, number of fruits per plant, fruit length and fruit girth. Seed yield was negatively correlated with days to 50% flowering and days to fruit maturity. Positive and significant correlations were observed between plant height and number of branches per plant.

Nimbalkar *et al*. (2002); studied the correlation and regression coefficients between dry fruit yield and yield-contributing characters of 44 okra cultivars to identify the relative contributions of these characters to the total variability in the yield of the cultivars examined. 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, with seed yield recording the highest correlation (r=0.667) with dry fruit yield.

Niranjan and Mishra (2003); conducted a trial on 27 genotypes to study the correlation analyses. They found that the genotypic correlations were higher than the corresponding phenotypic correlations for all the character combinations. They also noted that fruit yield was positively and significantly correlated with 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 levels. Jaiprakash narayan and Ravindra (2004);carried out correlation in 69 okra genotypes using growth, earliness and yield traits in an experiment conducted in Karnataka, India. The results indicated the inverse relationship between growth and earliness characters, but strong association between growth and yield characters. Total yield per plant was positively and significantly correlated with number of fruits per plant, average fruit weight, fruit length, plant height at 60 and 100 days after sowing (DAS) and number of leaves at 45 and 100 DAS, but negatively and significantly correlated with first fruiting.Bali *et al.* (2005); studied the correlation analysis in okra and they found that the number of fruits per plant and plant height had the highest significant correlation with total yield per plant.

Chhatrola and Monpara (2005); studied correlation in okra on 68 advanced breeding lines and their seven parents and a standard control Pusa Sawni. Yield revealed a high significant and positive genotypic and phenotypic correlation with plant height, fruits per plant and 10-fruit weight. Genotypic and phenotypic correlations were roughly equal for the character combinations of days to 50% flowering with days to first picking and fruits per plant, plant height with 10-fruit weight and fruit length with 10-fruit weight, implying that these characters were less under the influence of environmental conditions. Character combinations like plant height with primary branches, fruits per plant with fruit yield per plant, and primary branches with fruits per plant showed highly significant and positive correlations but the values of phenotypic correlation were higher than those of genotypic correlation.

Shekhavat *et al.* (2005); studied on okra cultivars Azad Ganga, KS-313, KS-375, KS-405, KS-410, KS-412, P-7, BO-2, Prabhani Kranti and Pusa Sawani, were crossed in a diallel fashion excluding reciprocals during kharif 2000 at Kanpur, Uttar Pradesh, India. Correlation studies were performed using 100 genotypes, i.e. 45 F_1, 45 F_2 and 10 parents. Data were recorded for days to flowering, plant height and number of branches per plant, length of first fruiting node, length and width of fruits, number of fruits per plant and weight of fruits per plant (yield per plant). The genotypic correlation coefficients were higher than the corresponding phenotypic correlation coefficients, indicating an inherent association among characters. This further indicated that selection for number of fruits per plant may result in significant yield improvement in fruit yield.

Akinyele and Osekita (2006); studied NH47-4 cultivar of okra grown in two locations for two years in Nigeria. Correlation coefficients were calculated for seed yield per plant and its components from data collected over two years. Seed yield per plant showed significant positive correlation with number of pods per plant, height at flowering, pod width and weight of hundred seeds. Alam and Hossain (2006); conducted a field experiment in Mymensingh, Bangladesh, during February to May 2002 to assess the variability of 10 yield contributing characters in 50 okra accessions and their interrelation effects on green pod yield. Correlation coefficients indicated that yield of green pods had a highly significant positive association with weight of green pods per plant and weight of individual green pods.

Mehta *et al.* (2006); studied the correlation analyses in 22 diverse genotypes of okra for fruit yield and its component traits during the 2003 summer season in India. The fruit yield was significantly and positively correlated with fruit length and average fruit weight.Kumar *et al*. (2007); studied the correlation coefficient analysis in 15 parents along with 36 F_1s of the crop to select superior okra genotypes to make substantial improvement of the crop. Highly significant positive association was found between yield per plant and length of fruit at the phenotypic level. Plant height was highly significant and positively correlated with length of fruit, girth of fruit and yield per plant at both genotypic and phenotypic levels. Number of branches per plant was highly significant and positively correlated with the length of fruit, number of fruits per plant and yield per plant at the phenotypic level and genotypic level. The length of fruit had highly significant and positive associated with girth of fruit, number of fruits per plant and yield per plant at both genotypic and phenotypic levels.

Mohapatra *et al.* (2007); evaluated 23 genotypes of okra for plant height (cm), number of primary branches per plant, days to first flowering, days to 50 percent flowering, height to first fruiting (cm), node at first flowering, fruit length (cm), fruit girth (cm), 1000 seed weight (g), number of seeds per fruit, number of fruits per plant, total yield per plant (g), inter-nodal length (cm), average fruit weight (g). These characters indicated that total fresh yield per plant was having positive and significant phenotypic correlation with number of fruits per plant, fruit girth, inter-nodal length and fruit weight. The same set of characters expressed in a similar manner under genotypic correlation. Most of the genotypes were highly variable based on individual traits as well as divergent based on character constellation.

Pal *et al.* (2008); studied correlation analysis for yield and yield components (plant height, number of primary branches per plant, number of days to flowering, number of fruits per plant, number of ridges per fruit, fruit length, fruit diameter and fruit weight) of 27 okra genotypes grown in India, during 2001 and 2002. In general, the genotypic correlation was more pronounced than the phenotypic correlation. The number of fruits per plant had significant and positive correlation with marketable fruit yield per plant at both levels. Fruit length showed significant positive association with fruit diameter and weight at the phenotypic and genotypic levels. The number of fruits per plant and marketable fruit yield per plant were negatively associated with number of days to flowering at both levels.

Pal *et al.* (2010); observed genotypic correlations higher in magnitude as compared to their corresponding phenotypic correlations for most of the character combinations. Edible fruit yield was found to be positively and significantly correlated with plant height and number of fruits per plant in parents, F_1 and F_2 population levels. This indicated that any selection based on these characters would enhance the performance and improve the edible fruit yield in okra. 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 *et al.* (2014); found that Correlation study between various quantitative characters highlighted significant association among characters. 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 (0.943g) 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.

Saryam *et al.* (2015); reported that Yield plant-1 had highly significant positive phenotypic correlation with viz., number of fruits per plant (0.803), fruit diameter (0.376), fruit length (0.349), number of seeds fruit-1 (0.316), days to maturity (0.301), fruit weight (0.274) leaf blade width (0.219),100 seed weight (0.219), flower diameter (0.154), fruiting span (0.152), petiole length (0.151), and stem diameter (0.150). Highly negative non-significant association was observed with incidence of YVMV (-0.389), days to 50 per cent flowering (-0.319) and node at first flower appears (-0.307) this correlation study indicated that close interrelationship between genotypic and phenotypic correlation co-efficient and magnitude of genotypic correlation were higher than their corresponding phenotypic correlation for most of the traits.

Mishra *et al.* (2015); observed that wide variability was found for different traits in Okra. Invariably, higher values were observed for phenotypic coefficient of variation with respect to corresponding genotypic coefficient of variation indicating the impact of environmental factors towards trait expression. The presence of moderate to high heritability coupled with moderate genetic advance for fruit weight, days to 50% flowering, fruits per plant as well as fruit yield per plant indicated their possibility of improvement with simple selection procedure in okra. Similarly, highly significant and positive correlation of fruit yield per plant with plant height, nodes per plant and fruits per plant was observed.

Ahamed *et al.* (2015); revealed that the highest range of variation was recorded in average fruit weight (18.25- 25.41g), followed by yield per plant (98.90 – 1650.00g). The highest GCV (46.70%) and PCV (47.72%) were recorded for fruit yield per plant while both were lowest for days to maturity (8.07 % and 8.25 %).Sreenivas *et al.* (2015); found that fruit length had significant positive correlation with fruit girth, fruit weight, number of fruits per plant and duration. Fruit girth had significant positive correlation with fruit length, fruit weight and number of fruits per plant. Fruit weight

had significant positive correlation with fruit length, fruit girth, number of fruits per plant and duration. Number of fruits per plant had significant positive correlation with all characters.

2.10 Path Analysis

Dhall *et al.* (2001); studied the path coefficient analyses in 48 advanced lines of okra. 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. Dhankhar and Dhankhar(2002b); studied the path analysis among the yield and yield attributes of 62 advance lines of okra. The number of fruits per plant and days to 50% flowering had the highest direct effect on fruit yield.

Niranjan and Mishra (2003); conducted a trial on 27 genotypes to study the path coefficient analyses. They reported that fruit weight exerted the highest positive direct effect (0.507) and the highest genotypic correlation value (0.975**).** Jaiprakash narayan and Ravindra (2004); carried out path analysis in 69 okra genotypes using growth, earliness and yield traits in an experiment conducted in Karnataka, India. Path analysis revealed that average fruit weight and number of fruits per plant had high direct effect on total yield per plant. Hence, direct selection for average fruit weight and number of fruits per plant was suggested to improve yield.

Bali *et al.* (2005); studied the path analysis in okra and they found that number of fruits per plant, average fruit weight and plant height had the highest positive direct effect on total yield per plant. Chhatrola and Monpara (2005); studied path analyses in okra on 68 advanced breeding lines and their 7 parents and a standard control Pusa Sawni. In path analysis, primary branches showed the highest direct contribution to fruit yield (0.62), followed by plant height (0.50) and nodes per plant (0.47). These were not only the important direct sharing characters but also were important indirect contributors through the characters among them. Although fruits per plant showed high correlation with yield, the direct contribution of this trait to fruit yield was negligible. Despite its large negative direct effect, plant height was significantly and positively correlated with fruit yield.

Akinyele and Osekita (2006); studied NH47-4 cultivar of okra grown in two locations for two years in Nigeria. Path coefficient analysis revealed that number of pods per plant and height at flowering had the highest direct effect on seed yield. This suggested that the two attributes have strong influence on seed yield. Hence, number of pods per plant and height at flowering are the main determinants of seed yield per plant in the variety studied. Alam and Hossain (2006); conducted a field experiment in Mymensingh, Bangladesh in 2002 to assess the path analysis of 10 yield contributing characters in 50 okra accessions. Path coefficient analysis showed that the weight of green pods per plant and weight of individual green pods were directly contributed towards the yield of green pods.

Mehta *et al.* (2006); studied the path coefficients analyses in 22 okra genotypes for fruit yield and its component traits in 2003 in India. Path coefficients 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 madrep (2009); reported that 41 genotypes of okra path coefficient study the 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 program 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 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); investigated 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 practices for the characters. Mihretu *et al.* (2014b); reported that path coefficient analysis at genotypic level revaled 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.

Saryam *et al.* (2015); found that Phenotypic path coefficient analysis revealed traits viz., number of fruits plant-1(0.733) followed by number of seeds fruit-1 (0.165), number of branches plant-1(0.147), fruit diameter (0.133), fruit weight (0.097), days to maturity (0.058), fruiting span (0.056), 100 seed weight (0.055), stem diameter (0.027) and plant height (0.023) have positive and high direct effects with fruit yield per plant. Number of fruits plant1, fruit diameter, fruit length, plant height, number of seeds fruit-1, days to maturity, fruit weight, and stem diameter indicating importance of these characters and can be strategically used for selection criteria to develop and improve high yielding okra varieties.

Ahamed *et al.* (2015); revealed that significantly positive correlation was between 100-seed weight and yield per plant (r = 0.44), 100-seed weight and leaf length (r =0.42), 100-seed weight and leaf diameter (0.38), number of leaves per plant and 100-seed weight (r = 0.28), 100-seed weight and plant height(r =0.40), 100-seed weight and fruit length (r =0.28). Significantly positive correlations were also observed for plant height and number of fruits per plant, number of leaves per plant and yield per plant. The path coefficient analysis was done to determine direct and indirect effects of traits on fruit yield. Direct significant positive and negative effect of number of fruits per plant (-0.091), 100-seed weight (0.174), number of seeds per plant (-0.213), average fruit yield (-0.310) towards yield.

Sreevivas *et al.* (2015); found that number of fruits per plant had the maximum direct contribution (0.698) towards total yield followed by fruit weight (0.467), fruit girth (0.075) duration (0.042) and plant height (0.014). However, days to first flowering and fruit length exhibited negative direct effect. Hence, selection should be practiced for these characters in order to isolate superior plant types for improvement of fruit yield.

Sharma and Prasad (2015**)**; reported that number of fruits per plant (NP) and fruit weight (FW) contributed major direct positive effect to fruit yield per plot, whereas, number of branches per plant (NB) and days to first harvest (FH) showed highest negative direct effect on yield component. Plant height, however, showed the highest positive indirect effect via number of fruits per plant and negative indirect effect via fruit weight. Number of branches (NB) showed positive indirect effect via number of fruits per plant (0.7655) and plant height (0.2728) and negative indirect effect via fruit weight (-0.2830). The estimated residual effect found was 0.0118 indicated about 98.82% of variability in fruit yield was contributed by yield affecting characters studied.

2.11 Genetic Divergence

Mahalanobis' generalized distance (D^2)

Information on the genetic diversity in okra collections can give breeders and geneticists' important information on the allelic diversity present in gene bank materials and may help to identify genetically diverse pools for use in cross combinations to improve important agronomic traits or to exploit heterosis (Naser, 2014a). Information about the nature and magnitude of genetic divergence would help selection of diverse parents which upon hybridization might lead to effective gene recombination (Pradip *et al.*, 2010). Genomic diversity is the basis of evolutionary change in nature underlying the evolution of biodiversity at the level of genes, genomes, populations, species and ecosystems (Henry, 2005). Diversity based on morphological characters usually varies with environments and evaluation of traits requires growing the plants to full maturity prior to identification of diverse genotypes (Prakash *et al.*, 2011).

The value of a germplasm collection depends not only on the number of accessions it contains, but also upon the diversity present in those accessions. Knowledge of genetic diversity and relationships among okra germplasm may play significant role in breeding program of okra. Characterization and quantification of genetic diversity has long been a major goal in evolutionary biology. Information on the genetic diversity within and among closely related crop varieties is essential for a rational use of plant genetic resources (Aladele, 2009; Prakash *et al.*, 2011). In okra, pod yield and related traits are polly genetically determined. Availability of genetically based variation for yield and its component traits is a prerequisite for the development of new cultivars of okra.

Okra breeders all over the world have been utilizing the available genetic resources to modify the varieties (Reddy *et al.*, 2012). Ghai *et al.* (2005); studied the genetic diversity in thirty genotypes of okra collected from various ecological regions of India. Data were collected on nine nutritional and six agronomic traits. Mahalanobis D^2 analysis was applied to evaluate the genetic divergence and Tocher's method (Rao, 1952) was used to form the clusters. The clustering pattern revealed that there was no parallelism between genetic and geographic divergence as the types chosen from same eco-geographic region were found scattered in different clusters.

Canonical variate analysis

Dhaduk *et al.* (2004); studied the genetic diversity for nine characters in 22 genotypes of okra in 2003 in India. Inter-cluster distance was highest between cluster II and V followed by cluster II and III. Intra-cluster distance was highest in cluster IV, followed by cluster I. Clusters II, IV, V and VII were suitable for use in plant breeding. Among the characters, fruit weight, girth and length, days to 50% flowering, and fruit yield contributed more than 83% of the total diversity.

Singh *et al.* (2007) studied genetic divergence of 70 genotypes of okra. Based on Mahalanobis D^2values and canonical vector analysis the genotypes were classified into 18 clusters. Characters like plant height, number of branches/plant, pod length, pod girth, inter nodal length, yield/plant, number of pods/plant and node at which first flower appeared contributed maximum to total divergence.

Inter and intra cluster divergences indicated variations in the parameters (Pradip *et al.*, 2010). On the basis of inter cluster distance cluster means and characters with high contribution to genetic distance values, genotypes could be selected as parents for future hybridization program and among them, the two exhibited highest distance and accordingly could be utilized for obtaining heterobeltiosis (Pradip *et al.*, 2010).

Bendale *et al.* (2003); studied 25 okra genotypes by using Mahalanobis D^2 statistical analysis to understand the nature of divergence and to assess the importance of a set of quantitative characters related to economic yield in genetic differentiation. The characters such as ascorbic acid content and yield per plant had the largest contribution to divergence.

Patel *et al.* (2006); estimated the genetic distance for 26 genotypes of okra by using D^2 statistics. The highest inter-cluster distance was observed between cluster V and VI, followed by cluster II and V, cluster II and VI, and cluster IV and V, which may serve as potential parents for hybridization program. Among the traits studied (days to 50% flowering, plant height, number of branches per plant, inter nodal length, fruit length, fruit girth, number of fruits per plant, 10-fruit weight and fruit yield), more than 86% of total divergence was contributed by five traits, i.e. fruit yield, days to 50% flowering, fruit girth, fruit length and inter node length.

Principal component analysis (PCA)

Principal component analysis (PCA) is multivariate statistical techniques which is a powerful tool for investigating and summarizing underlying trends in complex data structures (Legendre and Legendre 1998). Principal component analysis reflects the importance of the largest contributor to the total variation at each axis for differentiation (Sharma, 1998). Individual contributions of traits to variations observed in okra accessions as well as their contributions to seed yield in the accessions. The factor scores of quantitative characters among the accessions of okra, eigen values and percentage total variance accounting for the principal component axes.

Ahiakpa *et al.* (2013) who reported four Principal Components (PC) accounted for 82.97% of total variance with the first principal component (PC1) contributing the highest (46.62%). The Eigen value gives the relative discriminating power of the principal axes with (5.128) for PC1 and as low as (1.031) for PC4. Mihretu *et al.* (2014a)who reported that 6 principal components PC1, PC2, PC3, PC4, PCA5 and PCA6 with Eigen value 10.65, 30.4, 2.41, 1.7, 1.62 and 1.32, respectively, have accounted for 83% of the total variation.

Mamta and Choudhury (2006); evaluated forty genotypes of okra for genetic variation for yield and yield components. The yield components, fruit length had the greatest effect on divergence (43.08%), followed by fruit yield per plant (23.72%) during the rainy season, whereas fruit yield per plant had the greatest effect on divergence (68.85%), followed by number of primary branches (20.0%), during the summer. The results suggested that greater emphasis should be given to fruit yield per plant, fruit length, and number of primary branches during selection for high-yielding genotypes of okra.

Clustering of the genotypes

Hazra *et al.* (2002); evaluated twenty two genotypes of okra for 13 fruit yield and other related characters to determine their genetic divergence. Following D^2analysis, the genotypes were grouped into five clusters with the highest of 16 genotypes in cluster I. Most of the genotypes were not much divergent based on character constellation but were highly variable for individual characters. Patro and Ravisankar (2004), studied cluster analysis and revealed considerable variation among the genotypes. Forty one genotypes were grouped into eight clusters. Among all the clusters, cluster IV had a maximum number (eight) of genotypes. D^2 values ranged from 205.03 to 32666.9.

Ghai *et al.* (2005); studied the genetic diversity in thirty genotypes of okra collected from various ecological regions of India. The genotypes were classified into 13 discrete clusters and the entire collection was allocated to different clusters. Patel *et al.* (2006**)**; estimated the genetic distance for 26 genotypes of okra by using D^2 statistics. The 26 genotypes were grouped into six clusters (I-VI). Cluster I had the maximum number of genotypes (18). Cluster I and IV had two genotypes each, while cluster V and VI had solitary entries.

Singh *et al.* (2007) studied genetic divergence of 70 genotypes of okra. Based on Mahalanobis D^2values and canonical vector analysis the genotypes were classified into 18 clusters. Cluster II had maximum of 12 genotypes followed by cluster IV with 10 genotypes.

Singh *et al.* (2007) studied genetic divergence of 70 genotypes of okra. Based on Mahalanobis D^2values and canonical vector analysis the genotypes were classified into 18 clusters. The mean intra and inter cluster distance (D) revealed that cluster IV had highest intra cluster distance (22.46), while the inter cluster distance was maximum between cluster XIV and XVII (101.93).

Principal coordinate analysis (PCO)

Hazra *et al.* (2002); evaluated twenty two genotypes of okra for 13 fruit yield and other related characters to determine their genetic divergence. On the basis of high yield, important yield components and fruit quality, four diverse and desirable genotypes (MDO-10, LORM-1, KS-410 and MDO-6) were selected. It was proposed that these genotypes may be involved in a multiple crossing programme to recover transgressive segregants with high genetic yield potential.

Cluster mean analysis

Bendale *et al.* (2003); studied 25 okra genotypes by using Mahalanobis D^2 and revealed that a substantial variation in cluster means was observed for plant height. Crosses among genotypes of clusters IV, VII and VIII were recommended to develop desirable high yielding okra cultivars. Dhaduk *et al.* (2004); studied the genetic diversity for nine characters (fruit length, girth and weight, plant height, inter-node length, number of branches per plant, number of fruits per plant, days to 50% flowering and fruit yield) in 22 genotypes of okra during spring summer of 2003 in India. Mahalanobis D^2 analysis grouped the genotypes into seven clusters. Cluster I contained 13 genotypes. Clusters II, II and IV had two genotypes each, while clusters V, VI and VII had one genotype each.

Patro and Ravisankar (2004), studied the cluster analysis with forty one genotypes. The cluster mean values revealed that plant height, yield per plant and germination percentage contributed towards divergence. Ghai *et al.* (2005); studied the genetic diversity in thirty genotypes of okra collected from various ecological regions of India. There was sustained variation in cluster means for all the characters studied. The inter-cluster D^2 values indicated that crosses among the genotypes from distant clusters VIII, XII and IV should give rise to a high heterotic hybrids and wide spectrum of variability in subsequent segregating generations.

Singh *et al.* (2007) studied genetic divergence of 70 genotypes of okra. Based on Mahalanobis D^2values and canonical vector analysis the genotypes were classified into 18 clusters. Depending upon the inter cluster distance and higher cluster means crossing of genotypes from cluster I (having flowering at early node), VIII (having shorter inter nodal length), X (having tall plants), XV, XVI and XVIII (having more number of pods/plant, long pods and higher yield) is expected to give maximum heterosis and opportunity to isolate progenies with higher yield in okra.

Akotkar *et al.* (2010) evaluated the genetic variability of some yield contributing characters, and the genetic diversity in fifty genotypes of okra collected from the NBPGR New Delhi, India. On the basis of D^2 analysis, the 50 genotypes could be grouped into five clusters. Cluster I had the highest number of genotypes (45) followed by cluster II (2). Remaining clusters were mono genotypic.

Akotkar *et al.* (2010) evaluated the genetic diversity in fifty genotypes of okra in India. Plant height had the highest contribution towards the total genetic divergence. The highest intra-cluster distance was recorded in cluster I followed by cluster II. The maximum inter-cluster distance was recorded between cluster IV and cluster II, followed by cluster V and cluster II.

Akotkar *et al.* (2010) evaluated the genetic diversity in fifty genotypes of okra in India. Among the 50 genotypes, IC-332454 showed the highest cluster mean for fruit yield per plant and number of fruits per plant. The genotypes which were in the cluster V, III and II also exhibited significant performance for fruit yield per plant, number of fruits per plant and plant height sequentially. On the basis of groupings of individual genotypes into different clusters, contribution of individual character towards total genetic divergence, inter-cluster distance and cluster mean, the genotypes such as IC-9856B, IC-331157, IC-342075, IC-332453 and IC-43736 were found promising for using in the hybridization program.

CHAPTER III
MATERIALS AND METHODS

A field experiment was conducted at the experimental field of Genetics and Plant Breeding Department of Sher-e-Bangla Agricultural University, Dhaka Bangladesh during March 2017 to July 2017 to study on the inter genotypic variability, genetic divergence and path coefficient in Okra. The materials and methods of this experiment are presented in this chapter under these following headings:

3.1 Site of Experiment

The research work was conducted at the experimental farm of Sher-e-Bangla Agricultural University, Dhaka. The experimental site was at $90^0$22′ E longitude and $23^0$41′N latitude at an altitude of 8.6 meters above the sea level.

3.2 Soil and Climate of the Experimental Site

The experimental area was under the sub-tropical monsoon climate zone, which was characterized by heavy rainfall, high humidity, high temperature and relatively long day during the *Kharif* season while hardly rainfall, low humidity, low temperature and short day during the Rabi season. Rabi season is favorable for okra cultivation but it also be cultivated as summer crops in kharif-1 season. The land belongs to agro-ecological region of‘ Madhupur Tract’ (AEZ28) of Nodda soil series. The soil was sandy loam in texture having pH 5.47-5.63. The mean temperature of the growing period was 26.43°C with average maximum and minimum being 36°C and 20.54°C, respectively. Details of the meteorological data in respect of temperature, rainfall, relative humidity, total sun shine and soil temperature during the period of experiment were collected from the weather station, Dhaka, Bangladesh.

3.3. Description of Experimental Materials

The experimental material for this study consisted of 28 genotypes of Okra. The Okra genotypes were collected from Bangladesh Agricultural Research Institute (BARI), Gazipur, and HRC: Horticulture Research Center, local market.

Table 1: Details of Experimental Materials

GENOTYPES SL NO	SOURCE
G1	PGRC, BARI
G2	PGRC, BARI
G3	PGRC, BARI
G4	PGRC, BARI
G5	PGRC, BARI
G6	PGRC, BARI
G7	PGRC, BARI
G8	PGRC, BARI
G9	PGRC, BARI
G10	PGRC, BARI
G11	PGRC, BARI
G12	PGRC, BARI
G13	PGRC, BARI
G14	PGRC, BARI
G15	PGRC, BARI
G16	PGRC, BARI
G17	PGRC, BARI
G18	HRC
G19	HRC
G20	HRC
G21	HRC
G22	HRC
G23	HRC
G24	HRC
G25	HRC
G26	HRC
G27	HRC
G28	HRC

3.4 Experimental Design

Twenty eight genotypes were used to conduct the experiment. Genotypes were evaluated at experiment field of Sher-e-Bangla Agricultural University. The experiment was conducted in randomized complete block design with three replications. In each block, each genotype was planted in one row of 8.4 m length and 1 m width, maintaining a plant to plant spacing of 0.6 m and accommodated 14 plants

per plot. Two seeds per hill was sown at 1 x 0.60 m and thinned to one plant per hill when plants reached 3-4 leaves stage. Data for different plant parameters were recorded from 10 plants of each genotype. Mature fruit seed characteristics were measured from the two plants in each row.

3.5 Details of the Experiment

For this study, the experiment was conducted during kharif-1, 2017. The experiment was carried out to study the genetic variability and diversity. The experiment was laid out in a Randomized Complete Block Design (RCBD). Seed of each genotype were sown with a spacing 60 cm x 30 cm in three replications. The plants were trained onto an inverted 'V' structure. A pictorial view of experimental plot is shown in Plate 1.

3.6 Field Managements

3.6.1 Land preparation

The experimental area was thoroughly ploughed and brought to a fine tilth on 15 Mar 2017. Final land was prepared on 23.03.2017. One ton of FYM and the recommended basal dose of fertilizers were incorporated in the soil before final harrowing. The entire plot was divided in to three blocks. All treatments were placed randomly in each replication. Okra plants were established by direct seeding in the field.

3.6.2 Manures and Fertilizers

The recommended dosage of Urea, TSP, MP was applied in field at the rate of 150, 100, 150 Kg/ha respectively. Nitrogen was applied in three splits, the first dose at 20 DAS, second dose applied at 40 DAS and last split dose at 60 days after sowing. The entire dose of phosphorus was applied at the time of as basal dose application. Potash fertilizer was applied in four installments at the time of base dose application and other three with the three top dressed of urea fertilizer in equal amount.

3.6.3 Bed preparation

Lay out preparation was done on 29.03.2017. The bed was made on 30.03.2017 for seed sowing.

3.6.4 Seed Sowing

After the lay out, the genotypes were assigned to different plots in each replication by using random numbers. The seeds of each genotype were sown on 31.03.2017 by

dibbling two to three seeds per hill. The gap filling was done by re-sowing within a week after germination. A pictorial view of seed sowing in experimental plot is shown in Plate 2.

3.6.5 Thinning of excess seedlings

The weak seedlings were thinned out leaving only one vigorous seedling per hill after 20 days of sowing. The first top dressed of nitrogen and potash was applied at 20 days after sowing. All recommended cultural practices were followed to raise a good okra crop.

3.6.6 Cultural practices

Irrigation was applied once a week at emergence and every two weeks at flowering and pod production and started on 28.04.2017. Cultural practices were done for weed control on 12 April 2018. Chemical (Sevine, Marshal and deltanet) and cultural practices (hand picking and remove infected plant part) were applied to control insect pest (feel beetle, mealybug, aphid). The immature tender fruit and mature fruit were harvested for different parameters. Tender fruits were harvested two times per week to estimate fruit yield while mature fruits were harvested when fruits turned to loss green color and dry pods for seed yield parameter.

3.6.7 Observations recorded

Observations were recorded on five plants in each genotype in each replication for all the characters studied. The mean values of five plants were averaged and expressed as mean of the respective characters. The details of data recorded are as follows.

Days to first flowering

The number of days taken from the date of sowing to onset of first flower appears on the plant in each plot.

Days to 50% flowering

The number of days taken from the date of sowing to the day on which 50% of the plants in each plot produce flower.

Days to maturity

The average number of days from sowing to the date of first harvest of 10 sample plants of the plot was recorded. A pictorial view of fruit with flower is shown in Plate 3.

Plant height (cm)

The plant height was measured at final harvesting from the ground level to the growing tip of plant with the help of a meter scale. The average height per plant was calculated in centimeters.

Number of primary branches per plant

The number of primary branches per plant was counted at the time of final harvesting in each genotype in each replication and average number of branches per plant was calculated.

3.6.8 Fruit character and yield

Fruits were harvested two times per week and number and weight of all tender fruits were recorded in each harvest. Five randomly tender fruits from each harvest in each plot which a totally not less than fifty tender fruits from each plot were used to record tender fruit characteristics while mature pods which produced between the 6th and 20th nodes were harvested at the end of the growing season to estimate mature fruit length, seed number/pod and 100 seed weight. A pictorial view of fruits of different okra genotypes is shown in Plate 4.

Fruit length (cm)

The length of five tender fruits per plot in each harvest was measured from the base of calyx to the tip of the fruit. The average was calculated by dividing the sum of all tender fruits length by the total number of fruits measured. Five edible fruits were selected randomly in each genotype in each replication and the length of these fruits, excluding fruit stalk was measured in centimeters and the mean length per fruit was computed. The length was taken from the fruits of third picking.

Fruit diameter (mm)

The five tender fruits per plot which fruit length was measured as indicated above was also used to measure tender fruits diameter of with the help of a venire caliper at the center of the fruit and the average was calculated like that of the fruit length.

Average fruit weight (g)

Each of five tender fruits per plot that was used to measure fruit length and width was weighed using sensitive balance and the average weight of tender fruit was calculated and recorded accordingly.

Number of tender fruits per plant

Fruits of ten plants in each plot at each harvest was counted and summed at the end of the harvest and the average number of tender fruits per plant was calculated and considered for statistical analysis. The number of edible pods harvested from the five tagged plants in each entry and over all the picking was added and the average number of pods per plant was calculated.

Number of seeds per pod

Ten fully matured and dried pods were collected randomly from the two plants in each plot as indicated above and seeds were extracted, counted and average number of seeds per pod computed. The five dry pods were randomly taken for seed extraction. The seeds were counted and average was calculated by dividing with five.

Hundred seed weight (g)

Seeds extracted from ten matured pods as indicated above were kept in open air under sun and the dried 100 seeds were randomly counted and weighted to estimate 100 seeds weight. The100-seeds of each entry in each replication were taken and measured their weight and multiplied with 10 to calculate the 1000 seed weight and their average was worked out.

Fruit yield per plant (g)

Weight of tender fruits from five selected plants in each replication and average was counted. It is denoted as g.

Plate 1. Experimental field

Plate 2.Seed sowing

Plate 3. Fruit with flower

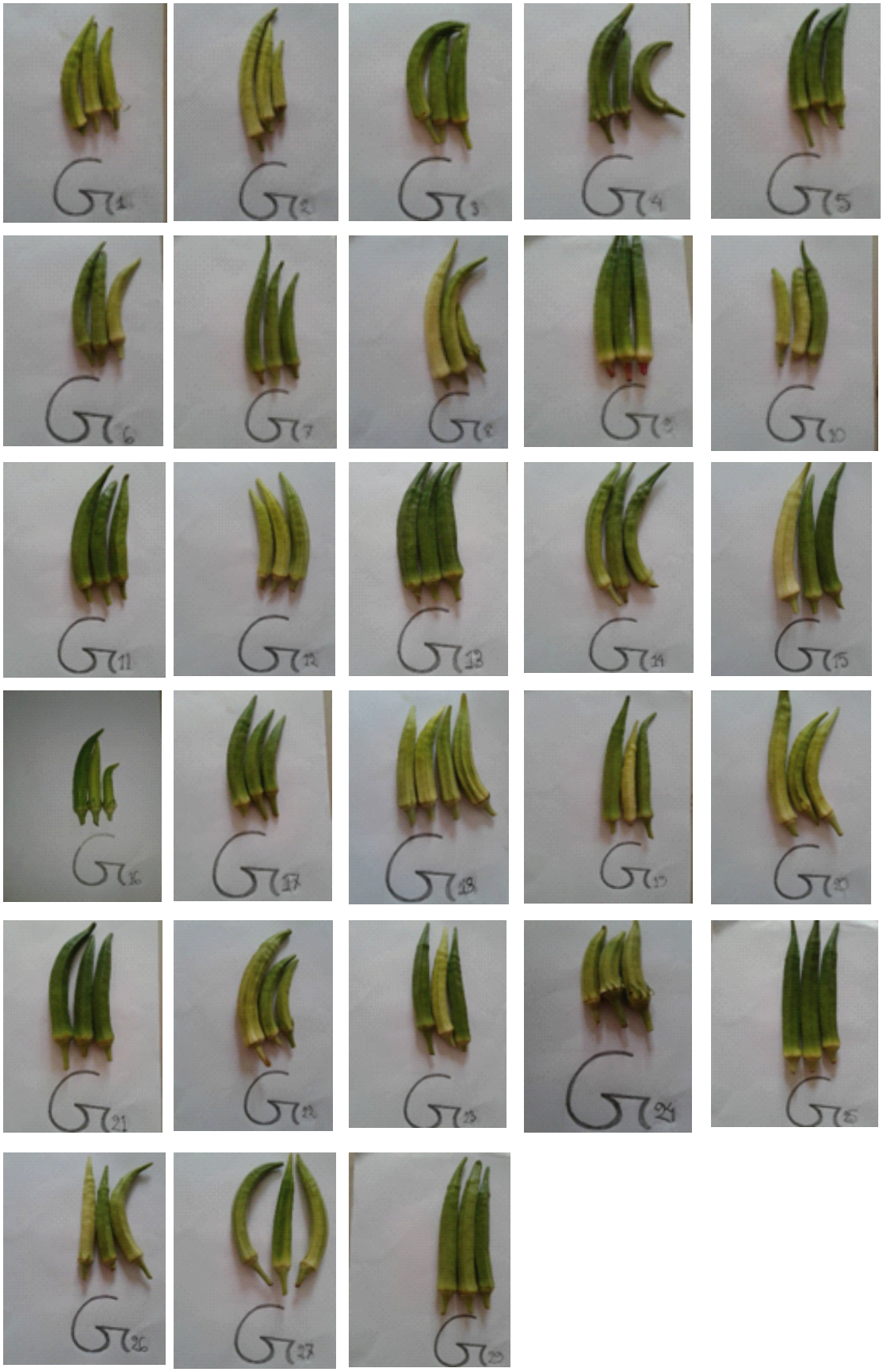

Plate 4. Fruits of different Okra genotypes

3.7 Statistical Analysis

3.7.1 Analysis of Variance

Genotypic and phenotypic variance was estimated by the formula used by Johnson *et al*. (1955). Heritability and genetic advance were measured using the formula given by Singh and Chaudhary (1985) and Allard (1960). Genotypic and phenotypic coefficient of variation was calculated by the formula of Burton (1952). Genotypic and phenotypic correlation coefficient was obtained using the formula suggested by Miller *et al.* (1958), Johnson *et al*. (1955) and Hanson et al. (1956); path coefficient analysis was done following the method outlined by Dewey and Lu (1959). Multivariate analysis viz., Principal Component Analysis (PCA), Principal Coordinate Analysis (PCO), Cluster Analysis (CA) and Canonical Vector Analysis (CVA) were done by using GENSTAT 5.13 and Microsoft Excel 2007 software.

3.7.2 Contribution of different characters towards divergence

The relative contribution of different characters to the total D^2 between each pair of genotypes was given a score of total number of characters based on the magnitude of the D^2 value due to each character. The percent contribution of characters towards divergence was calculated by the formula given below.

$$\text{Percent contribution of character 'X'} = \frac{N(x)}{n\,(n-1)/2}$$

Where,

N (x) = Number of genotypic combinations, which were ranked first for character 'X' out of total genotypic combinations of n(n-1)/2.

Data of eleven characters were subjected to analysis of variance (ANOVA) using MSTATC software program to test the presence of significant differences among accessions for the traits measured. It was also measure of mean, range, CV, standard deviation by this software. Phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), broad-sense heritability (h^2) and expected genetic advance as percentage to mean (GAM) were computed. Diversity analysis was estimated from measured quantitative traits. Duncan's Multiple Range (DMRT) was employed to identify genotypes that are significantly different from each other. Descriptive statistic was used for qualitative traits data.

3.7.3 Phenotypic and Genotypic Variability

The variability of each quantitative trait was estimated using mean, range, standard deviation, phenotypic and genotypic variances and coefficients of variation. The phenotypic and genotypic coefficient of variation was computed using the formula suggested by Burton and de Vane (1953) as follows:

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

Where,

GMS = Genotypic mean sum of square

EMS = Error mean sum of square

r = number of replications

Phenotypic variance (σ^2_p)=σ^2_g + σ^2_e

Where,

σ^2_g = Genotypic variance

EMS = Error mean sum of square

σ^2_e = Error variance

Genotypic and phenotypic co-efficient of variation

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

Where,

σ^2_g = Genotypic variance

$\bar{x}$ = Population mean

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

Where,

σ^2_p = Phenotypic variance

$\bar{x}$ = Population mean

PCV and GCV values were categorized as low, moderate, and high values as indicated by Sivasubramaniah and Menon (1973) as follow:

0 - 10% = Low

10 – 20 = Moderate

> 20 = High

3.7.4 Heritability and Genetic Advance

Broad sense heritability values were estimated using the formula adopted by Falconer and Mackay (1996) as follows:

Heritability, $h^2{}_b\% = \frac{\sigma^2{}_g}{\sigma^2 p} \times 100$

Where,

$h^2{}_b$ = Heritability in broad sense

$\sigma^2{}_g$ = Genotypic variance

$\sigma^2{}_p$ = Phenotypic variance

The heritability percentage was categorized as low, moderate and high as suggested by Robinson et al. (1955):

0 - 30% = Low,

30 – 60 = Moderate and

> 60 = High

Genetic advance

Genetic advance in absolute unit (GA) and percent of the mean (GAM), assuming selection of superior 5% of the genotypes were estimated in accordance with the methods illustrated by Johnson et al. (1955) as:

Genetic advance, $GA = K.\ h^2.\ \sigma_p$

Or Genetic advance, $GA = K.\ \frac{\sigma^2{}_g}{\sigma^2 p}.\sigma_p$

Where,

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

σ_p = Phenotypic standard deviation

h^2_b= Heritability in broad sense

σ^2_g = Genotypic variance

σ^2_p = Phenotypic variance

Genetic advance mean's percentage

$$\text{Genetic advance (\% of mean)} = \frac{\text{Genetic Advance}}{\text{Population mean}} \text{ X } 100$$

The GA as percent of mean was categorized as low, moderate and high as suggested by Johnson et al.(1955) as follows.

0 - 10% = Low

10 – 20 = Moderate

> 20 = High

Genotypic and phenotypic correlation co-efficient

The calculation of genotypic and phenotypic correlation co-efficient for all possible combinations through the formula suggested by Johnson *et al.* (1955) and Singh and Chaudhury (1985). The genotypic co-variance component between two traits and have the phenotypic co-variance component were derived in the same way as for the corresponding variance components. The co-variance components were used to compute genotypic and phenotypic correlation between the pairs of characters as follows:

$$\text{Genotypic correlation, } r_{gxy} = \frac{GCOVxy}{\sqrt{GVx.GVy}} = \frac{\sigma_{gxy}}{\sqrt{(\sigma^2_{gx}.\sigma^2_{gy})}}$$

Where,

σ_{gxy} = Genotypic co-variance between the traits x and y

σ^2_{gx} = Genotypic variance of the trait x

σ^2_{gy} = Genotypic variance of the trait y

$$\text{Phenotypic correlation } (r_{pxy}) = \frac{PCOVxy}{\sqrt{PVx.PVy}} = \frac{\sigma_{pxy}}{\sqrt{(\sigma^2_{px}.\sigma^2_{pv})}}$$

Where,

σ_{pxy} = Phenotypic covariance between the trait x and y

σ^2_{px} = Phenotypic variance of the trait x

σ^2_{py} = Phenotypic variance of the trait y

Path co-efficient

The phenotypic and genotypic correlation coefficients obtained from correlation study, were further partitioned into direct and indirect effects with the help of path coefficient analysis as suggested by Wright (1921) and applied in plant breeding by Dewey and Lu (1959). Pod yield per plant was considered as dependent variable (y) as factors assumed to be influenced by the other characters called independent variables(x1…xi) as causes. The path coefficient was estimated by solving following sets of simultaneous equations indicating the basic relationship between correlation and path coefficients.

r1y = P1y + r12 P2y + r13 P3y +…… + r1iPiy

r2y = P2y + r21P1y + r23 P3y +...……..…….. + r2i Piy

r3y = P3y + r31 P1y + r32 P2y +….....+ r3i Piy

riy = Piy + ri1 P1y + ri2 P2y + ……....…….+ ri (i-1) Piy

Where,

r1y to riy = coefficient of correlation between independent variables (1…i) with dependent character y

r12, ri1 to ri (i -1) = coefficient of correlation among all possible combination of causal factors (independent variables), and

P1y to Piy = direct path effects of independent variables (1 to i) on the dependent variable y

Multivariate analysis

The genetic diversity among the genotypes was assessed by Mahalanobis's (1936) general distance (D^2) statistic and its auxiliary analyses. The parents' selection in hybridization programme based on Mahalanobis's D^2 statistic is more reliable as requisite knowledge of parents in respect of a mass of characteristics is available prior to crossing. Rao (1952) suggested that the quantification of genetic diversity through biometrical procedures had made it possible to choose genetically diverse parents for a hybridization programme. Multivariate analysis viz. Principal Component analysis,

Principal Coordinate analysis, Cluster analysis and Canonical Vector analysis (CVA), which quantify the differences among several quantitative traits, are efficient method of evaluating genetic diversity. These are as follows:

Principal component analysis (PCA)

Principal component analysis, one of the multivariate techniques, is used to examine the inter-relationships among several characters and can be done from the sum of squares and products matrix for the characters. Thus, PCA finds linear combinations of a set variate that maximize the variation contained within them, thereby displaying most of the original variability in a smaller number of dimensions. Therefore, Principles components were computed from the correlation matrix and genotypes scores obtained for first components (which has the property of accounting for maximum variance) and succeeding components with latent roots greater than unity. Contribution of the different morphological characters towards divergence is discussed from the latent vectors of the first two principal components.

Principal coordinate analysis (PCO)

Principal coordinate analysis is equivalent to PCA but it is used to calculate inter unit distances. Through the use of all dimension of p it gives the minimum distance between each pair of the n points using similarity matrix.

Cluster analysis (CA)

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

Canonical vector analysis (CVA)

Canonical vector analysis (CVA) finds linear combination of original variability's that maximize the ratio of between group to within group variation, thereby giving

functions of the original variables that can be used to discriminate between the groups. Thus, in this analysis a series of orthogonal transformations sequentially maximizing of the ratio of among groups to the within group variations. The canonical vector are based upon the roots and vectors of WB, where W is the pooled within groups covariance matrix and B is the among groups covariance matrix.

Calculation of D^2 values

The Mahalanobis's distance (D^2) values were calculated from transformed uncorrelated means of characters according to Rao (1952), and Singh and Chaudhury (1985). The D^2 values were estimated for all possible combinations between genotypes. In simpler form D^2 statistic is defined by the formula

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

Where,

Y = Uncorrelated variable (character) which varies from i = 1 ------to x

x = Number of characters.

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

Intra-cluster distances

Average intra-cluster distances were calculated by the following formula as suggested by Singh and Chuadhury (1985).

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

Where,

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

n = Number of all possible combinations between the populations in cluster

Inter-cluster distances

Average inter-cluster distances were calculated by the following formula as suggested by Singh and Chuadhury (1985).

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

Where,

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

n_i = Number of populations in cluster i

n_j = Number of populations in cluster j

Cluster diagram

Using the values of intra and inter-cluster distances ($D = \sqrt{D^2}$), a cluster diagram was drawn as suggested by Singh and Chuadhury (1985). It gives a brief idea of the pattern of diversity among the genotypes included in a cluster.

CHAPTER IV

RESULTS AND DISCUSSIONS

The present investigation was carried out with 28 genotypes of okra (*Abelmoschus esculentus* L. Moench) to study the genetic variability among genotypes for different characters, character association and direct and indirect effects of component traits on fruit yield and finally genetic diversity analysis. 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 germination (%), days to first flowering, days to 50% flowering, plant height (cm), number of primary branches, number of fruit's per plant, fruit length (cm), fruit diameter (cm), average fruit weight (g), seed's per fruit 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 General performance of genotypes

4.3 Variability study in genotypes

4.4 Correlation among the component traits

4.5 Path coefficient analysis

4.6 Genetic divergence analysis

4.1 Analysis of variance

The results of analysis of variance of 11 quantitative characters for 28 okra genotypes are presented (Table 2). Mean square of most of the characters studied revealed that genotypes showed 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 result is in agreement with Akinyele and Osekita (2006), Hazem *et al.* (2013) and Amoatey *et al.* (2015) who reported significant differences among the tested okra genotypes for most of the studied traits. This study results also supported by Salesh *et al.* (2010). A wide range of variations for yield contributing traits was also observed by Hazra and Basu (2000) and Gandhi *et al.* (2002).

Table 2. Mean sum of square of different characters of 28 okra genotypes

Characters	Mean sum of square		
	Replication (r-1) = 2	**Genotype (g-1) = 27**	**Error (r-1)(g-1) = 54**
Germination (%)	17.76	157.86**	8.16
Days to 1st flowering	8.37	12.38**	2.21
Days to 50% flowering	13.58	14.54**	2.50
Plant height (cm)	8.56	775.61**	7.05
Primary branches	0.06	2.71**	0.51
No. of fruit per plant	7.58	61.92**	2.56
Fruit length (cm)	0.08	5.09**	2.37
Fruit diameter (cm)	0.08	0.06**	0.02
Average fruit weight (gm)	1.35	28.10**	5.02
Seed per fruit	506.18	245.78**	26.96
Fruit yield per plant (g)	114.19	30528.76**	3054.35

** Indicates significant at 1% level of probability

4.2 General performance of genotypes

4.2.1 Germination (%)

Germination% is a good index of plant uniformity. Germination% varied significantly among the genotypes (Table 2). It was ranged from 60.67% to 88.00% with a general mean of 75.40%. The coefficient of variation was 3.79% for this trait (Table 3). The maximum germination was recorded in G5 (88.00%) and minimum was observed in G28 (60.67%). When compared to population mean (75.40%) (Table 4). Fifteen genotypes exhibited better germination percentage. Rest of the genotypes showed lower germination% than population mean.

4.2.2 Days to 1st flowering

Days to first flowering varied significantly among the genotypes (Table 2). Days to first flowering ranged from 29.67 to 36.00 days with a general mean of 32.74 days (Table 3). Early flowering was observed both in the genotypes G1 and G8 (29.67 days) followed by G12 (30.00 days) and G4 (30.33 days). The late first flowering was observed in the genotype G23 (36.00 days) followed by G17 (35.67 days) and G11 (35.33 days) (Table 4). Fourteen genotypes expressed better values i.e. lower the days to first flowering compared to population mean (32.74 days). From these genotypes early varieties could be selection for further study.

4.2.3 Days to 50% flowering

Days to 50% flowering varied significantly among the genotypes (Table 2). Days to 50% flowering ranged from 36.00 to 43.00 days with a general mean of 39.27 days (Table 3). Early 50% flowering was observed in the genotype G13 (36.00 days) followed by G1, G8, G24 and G26 (36.67 days). The late 50% flowering was observed in the genotype G19 (43.00 days) followed by G17 (42.67 days) and G3 (42.33 days) (Table 4).Thirteen genotypes expressed better values i.e. lower the days to 50% flowering compared to population mean (39.27 days). From these genotypes early varieties could be selected for further study.

Table 3. Range, mean and CV (%) of 28 okra genotypes

Parameters	Range		Mean	CV (%)
	Min.	Max.		
Germination (%)	60.67	88.00	75.40	3.79
Days to 1st flowering	29.67	36.00	32.74	4.54
Days to 50% flowering	36.00	43.00	39.27	4.02
Plant height (cm)	79.83	152.67	108.48	2.45
Primary branches (cm)	1.50	6.00	2.54	28.22
No. of fruit's per plant	10.33	26.33	17.10	9.36
Fruit length (cm)	10.21	16.46	12.92	11.93
Fruit diameter (cm)	1.07	1.60	1.35	10.42
Average fruit weight (gm)	10.67	25.33	17.07	13.12
Seed's per fruit	24.00	58.67	44.21	11.74
Fruit yield per plant (g)	124.00	535.33	294.65	18.76

CV (%) = coefficient of variation

Table 4. Mean performance of eleven characters of 28 okra genotypes

Genotypes	G (%)	DFF	D50%F	PH	PB	NFP	FL	FD	AFW	SPF	FYP
G1	78.67	29.67	36.67	152.67	2.00	26.33	12.77	1.27	18.67	47.00	481.00
G2	71.67	33.00	40.00	124.43	1.67	21.33	12.02	1.50	20.00	40.67	428.00
G3	66.67	35.33	42.33	102.53	3.33	20.33	12.47	1.50	19.33	29.67	402.33
G4	82.33	30.33	37.33	110.27	1.80	20.67	14.29	1.37	17.33	31.67	369.67
G5	88.00	34.67	41.67	118.77	2.33	20.00	14.50	1.17	16.50	54.67	312.67
G6	74.00	33.33	40.33	108.17	3.00	19.67	12.81	1.50	14.67	24.00	293.33
G7	73.33	35.00	42.00	114.27	1.70	23.33	13.89	1.13	16.00	44.33	381.33
G8	76.67	29.67	36.67	87.07	2.33	11.67	16.46	1.27	16.67	31.00	193.67
G9	80.00	32.33	39.33	123.97	2.67	22.67	11.45	1.30	14.00	37.33	328.33
G10	80.67	31.00	38.00	98.83	2.67	16.67	11.84	1.37	17.20	42.33	285.20
G11	68.00	35.33	37.00	117.10	2.33	23.00	13.19	1.30	19.33	55.33	429.67
G12	86.67	30.00	41.33	107.27	1.62	17.00	14.30	1.27	21.67	52.67	358.00
G13	83.33	34.67	36.00	111.73	3.00	20.33	11.26	1.07	15.33	46.33	321.33
G14	84.00	31.67	40.67	79.83	3.67	11.00	13.94	1.60	21.67	45.00	228.00

G (%): Germination (%), DFF: Days to 1st flowering, D50%F: Days to 50% flowering, PH: Plant height (cm), PB: Primary branches, NFP: No. of fruit's per plant, FL: Fruit length (cm), FD: Fruit diameter (cm), AFW: Average fruit weight (gm), SPF: Seed's per fruit and FYP: Fruit yield per plant (g)

Table 4. Mean performance of eleven characters of 28 okra genotypes (Contn'd)

Genotypes	G (%)	DFF	D50%F	PH	PB	NFP	FL	FD	AFW	SPF	FYP
G15	61.67	34.67	37.33	110.70	1.53	18.00	12.27	1.27	14.33	41.67	258.67
G16	64.33	32.00	40.33	103.03	2.00	12.00	13.87	1.47	14.33	51.00	171.67
G17	67.00	35.67	42.67	108.90	2.67	16.33	13.39	1.30	15.00	47.67	245.00
G18	72.00	33.00	40.00	121.57	3.33	19.67	12.08	1.33	25.33	51.33	535.33
G19	75.00	35.00	43.00	120.90	2.33	13.67	13.48	1.10	15.33	58.67	207.33
G20	75.33	31.67	38.00	115.03	2.67	17.00	11.41	1.57	18.33	30.67	297.00
G21	80.33	34.33	41.33	127.43	1.50	21.33	11.27	1.33	15.00	51.67	328.00
G22	82.00	31.00	38.00	97.10	2.67	10.33	12.23	1.27	20.00	49.67	208.67
G23	80.67	36.00	42.00	116.40	3.67	14.33	13.19	1.57	13.00	36.33	191.33
G24	76.67	31.00	36.67	108.77	3.00	13.00	12.70	1.37	17.00	39.00	221.00
G25	76.33	30.67	37.33	99.77	2.67	14.33	14.37	1.17	17.00	46.33	248.00
G26	75.33	30.67	36.67	87.00	1.50	11.67	13.30	1.43	15.33	57.33	186.33
G27	70.00	31.67	37.67	82.67	6.00	11.33	12.75	1.43	19.00	46.67	215.33
G28	60.67	33.33	39.33	81.30	1.50	11.67	10.21	1.47	10.67	48.00	124.00

G (%): Germination (%), DFF: Days to 1st flowering, D50%F: Days to 50% flowering, PH: Plant height (cm), PB: Primary branches, NFP: No. of fruit's per plant, FL: Fruit length (cm), FD: Fruit diameter (cm), AFW: Average fruit weight (gm), SPF: Seed's per fruit and FYP: Fruit yield per plant (g)

4.2.4 Plant height (cm)

Plant height is usually a good index of plant vigor, which may contribute towards greater production of fruit yield in okra. Plant height varied significantly among the genotypes (Table 2). Plant height ranged from 79.83 cm to 152.67 cm with a general mean of 108.48 cm. The coefficient of variation was 2.45% for this trait (Table 3). The maximum plant height was recorded in G1 (152.67 cm) and minimum was observed in G14 (79.83 cm) (Table 4).When compared to population mean (108.48 cm), sixteen 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).They also reported the highest plants height during rainy season in their experiments. Hazra and Basu (2000) observed low general value for plant height (80.8 cm).

4.2.5 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 1.50 to 6.00 with a general mean of 2.54 (Table 3). Fourteen genotypes expressed better values as compared to population mean (2.54). The results of the present study were also in conformity with Gondane (1989). The genotype expressing the maximum value was in G27 (6.00) and the minimum was recorded in G21 (1.50). The general mean of primary branches per plant were recorded as 2.9 and 1.57 by Hazra and Basu (2000); and Alam and Hossain (2008), respectively.

4.2.6 Number of fruits per plant

Number of fruits varied significantly among the genotypes (Table 2). Number of fruits per plant ranged from 10.33 to 26.33 with a general mean of 17.10 (Table 3). More number of fruits per plant was recorded in G1 (26.33) followed by G7 (23.33) and G11 (23.00) (Table 4). Thirteen genotypes expressed better values compared to population mean (17.10). 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.

4.2.7 Fruit length (cm)

The fruit length varied significantly among the genotypes (Table 2). Fruit length ranged from 10.21 cm to 16.46 cm with a general mean of 12.92 cm (Table 3). The maximum fruit length was recorded in G8 (16.46 cm) followed by G5 (14.50 cm) and G25 (14.37 cm) (Table 4). As compared to population mean (12.92 cm), fifteen genotypes exhibited higher fruit length. Genotype G28 recorded the minimum fruit length (10.21 cm). 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).

4.2.8 Fruit diameter (cm)

The fruit diameter varied significantly among the genotypes (Table 2). Fruit diameter ranged from 1.07 cm to 1.60 cm with a general mean of 1.35 cm (Table 3). The maximum fruit diameter was recorded in G20 and G23 (1.13 cm) (Table 4).As compared to population mean (1.35 cm), thirteen genotypes exhibited higher fruit diameter. Genotype G13 recorded the minimum fruit diameter (1.07 cm).

4.2.9 Average fruit weight (gm)

Statistically significant variation was found in terms of average fruit weight of okra (Table 2). The highest average fruit weight (25.33 g) was found in G18, while the lowest (10.67 g) was recorded in G28. The general mean of average fruit weight was 17.07 g and around 50% lines gave more than that general mean fruit weight. 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.

4.2.10 Number of seeds per fruit

Number of seeds per pod ranged from 24.00 to 58.67 with a general mean of 44.21. Number of seeds per fruit varied significantly among the genotypes. More number of seeds per fruit was recorded in G19 (58.67) followed by G26 (57.33) and G11 (55.33) (Table 4). Seventeen genotypes expressed higher values compared to population mean (44.21). The least value was recorded in G6 (24.00) followed by G3 (29.67), G8 (31.00) and G4 (31.67) (Table 4). Similar significant differences for this trait were also noted by Arvind Kumar (2009). Hazra and Basu (2000) also reported similar general mean (53.3) for seeds per fruit.

4.2.11 Fruit yield per plant (g)

Performance of genotypes differed significantly for fruit yield per plant (Table 2). Fruit yield per plant ranged from 124 g to 535.33 g with a general mean of 294.65 g (Table 3). Maximum fruit yield was exhibited by G18 (535.33 g) followed by G1 (481.00 g) and G11 (429.67 g) (Table 4 and Fgure1). Among all the genotypes, thirteen genotypes exhibited higher fruit yield per plant compared to population mean (294.65 g). Minimum fruit yield per plant was observed in G28 (124.00 g). 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).

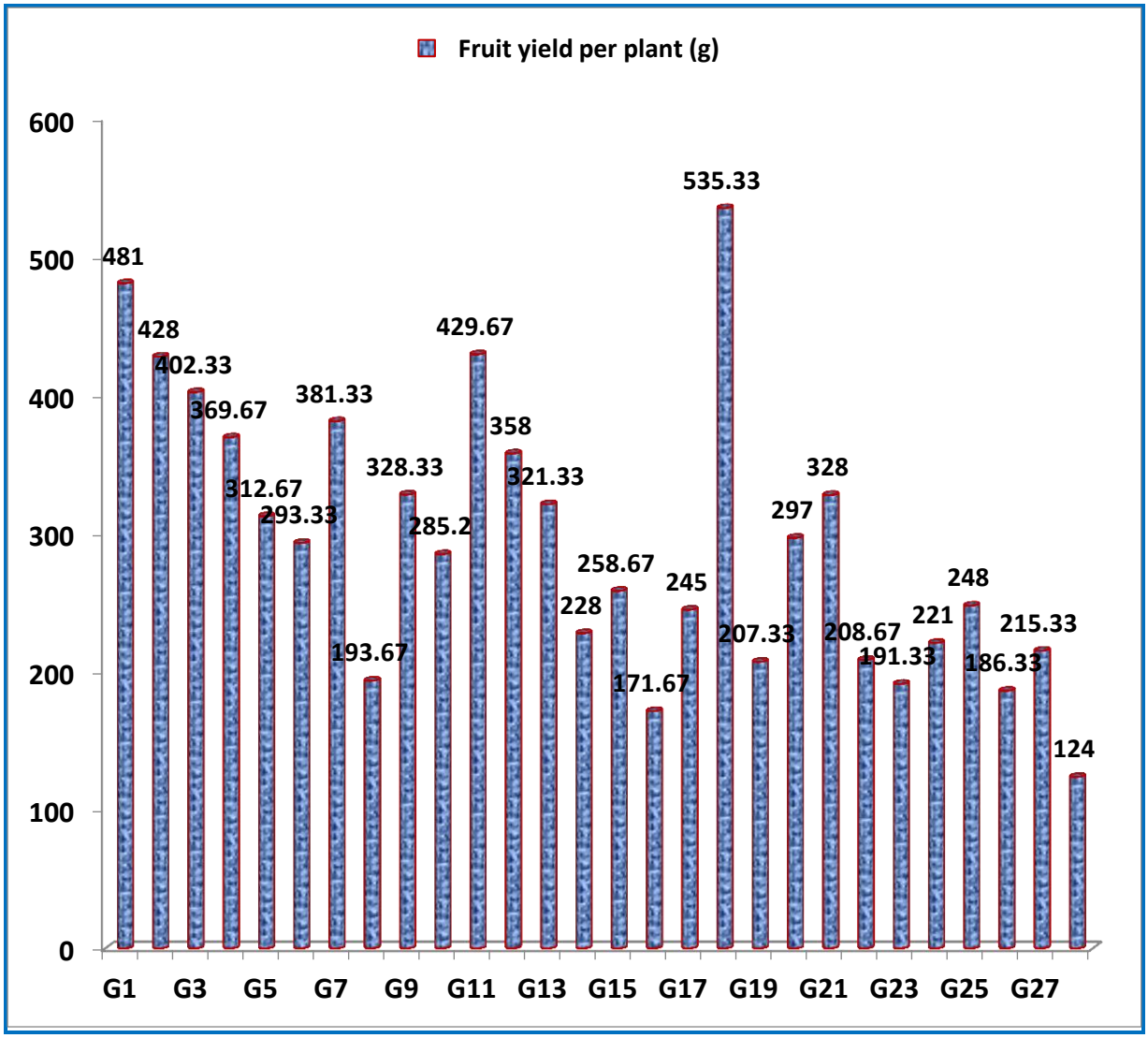

Figure 1. Performance of okra genotypes for fruit yield per plant (g)

4.3 Variability study in 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 11 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 program. Data collected from the investigation were analyzed to partition the total variation into magnitude of genotypic and phenotypic variation of 28 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 genetic 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 program in crop species. The 28 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 (12212.49) followed by plant height (263.24) and seed per fruit (99.90) while the lowest value was recorded for fruit diameter (0.03) followed by primary branches per plant (1.25) and fruit length (3.28). The genotypic variance ranged from 0.01 (fruit diameter) to 9158.14 (fruit yield per plant). Consistent 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 the result of Ehab *et al.* (2013) who reported that phenotypic variances were higher than the corresponding genotypic variances indicating predominance of environmental 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 genetic coefficient of variation

The phenotypic coefficient of variation (PCV) ranged between 6.50% (days to 50% flowering) to 43.91% (primary branches per plant) while genotypic coefficient of variation (GCV) ranged between 5.10 (days to 50% flowering) to 33.64% (number of primary branches per plant) (Table 5 and Figure 2). Similar results were reported by Ehab *et al.* (2013), Mihretu *et al.* (2014) for 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 (7.23% and 5.62%), days to 50% flowering (6.50% and 5.10%) had low values (<10%) for both phenotypic and genotypic coefficient of variations and it was low in case of genotypic level for fruit length (7.36%) and fruit diameter (8.91%). 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; Das *et al.* 2012; Sankara and Pinaki 2012; Thirupathi *et al.* 2012; and Ehab *et al*. 2013).

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

Parameters	$\sigma^2 p$	$\sigma^2 g$	$\sigma^2 e$	PCV	GCV	ECV
Germination (%)	58.06	49.90	8.16	10.10	9.37	3.79
Days to 1st flowering	5.60	3.39	2.21	7.23	5.62	4.54
Days to 50% flowering	6.51	4.02	2.50	6.50	5.10	4.02
Plant Height (cm)	263.24	256.19	7.05	14.96	14.75	2.45
Primary branches (cm)	1.25	0.73	0.51	43.91	33.64	28.22
No. of fruit's per plant	22.35	19.79	2.56	27.65	26.02	9.36
Fruit length (cm)	3.28	0.90	2.37	14.02	7.36	11.93
Fruit diameter (cm)	0.03	0.01	0.02	13.71	8.91	10.42
Average Fruit weight (gm)	12.71	7.69	5.02	20.89	16.25	13.12
Seed per fruit	99.90	72.94	26.96	22.61	19.32	11.74
Fruit yield per plant (g)	12212.49	9158.14	3054.35	37.51	32.48	18.76

$\sigma^2 p$: 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

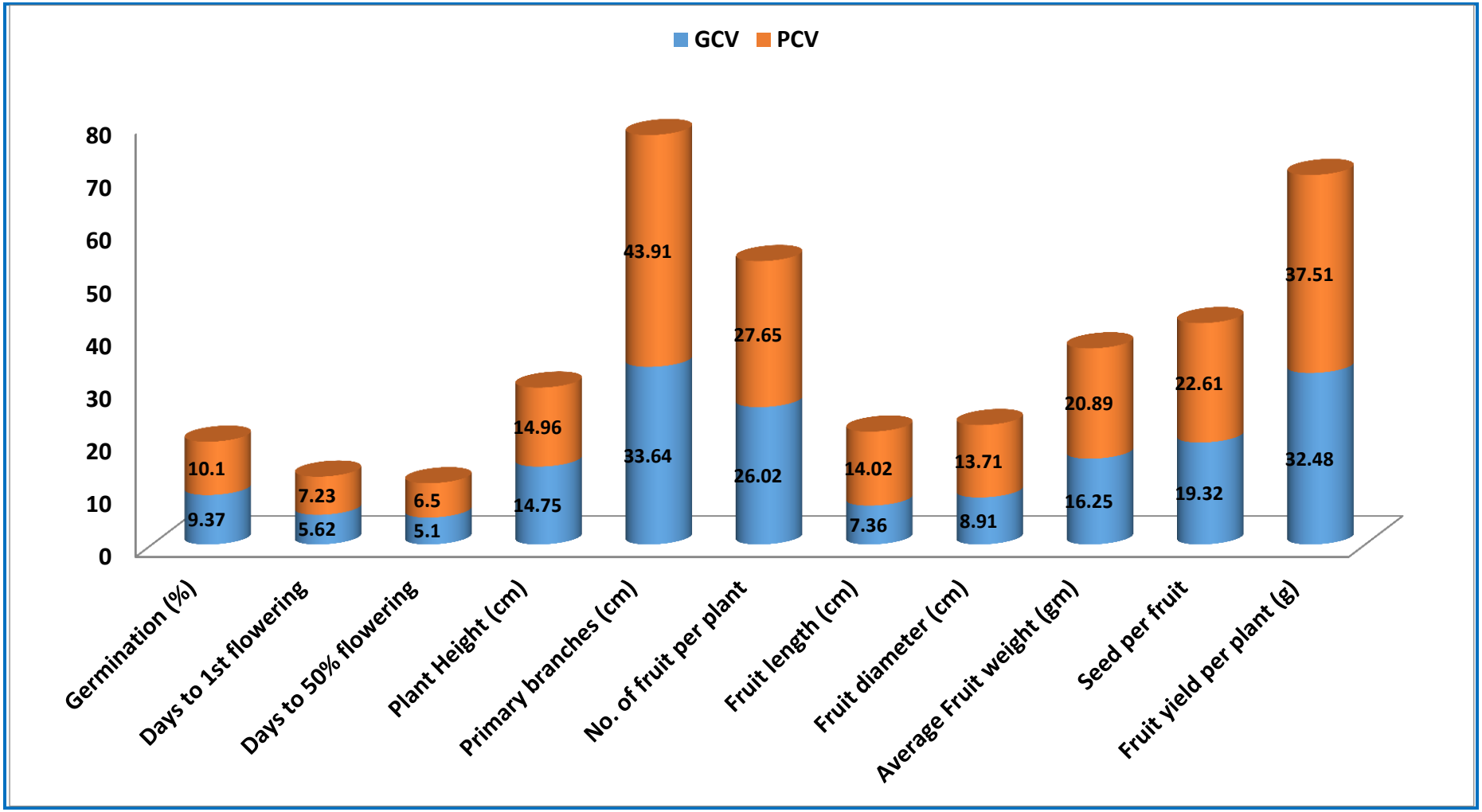

Figure 2. Genotypic and phenotypic coefficient of variation

Moderate GCV and PCV were found in germination% (9.375 and 10.10%), plant height (14.75% and 14.96%) and average fruit weight (16.25% and 20.89%) (Table 5). Medium PCV and GCV value suggests that these characters are controlled more of by the genetic factors. Hence, these characters amenable to selection for further improvement. This result is 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 primary branches per plant (33.64% and 43.91%), number of fruits per plant (26.02% and 27.65%), seed per fruit (19.32% and 22.61%) and fruit yield per plant (32.48% and 37.51%), respectively. 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 are 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 suggests that traits with high PCV and GCV are 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

In this study estimate of heritability in broad sense ranged from 27.58% for fruit length to 88.55% for fruits per plant (Table 6 and Figure 3). According to Robinson *et al.* (1955) heritability is categorized as low (0-30%), moderate (31-60%) and high > 60%. Accordingly, heritability estimate in broad sense was high (>60%) for germination% (85.95%), days to 50% flowering (61.66%), plant height (97.32%), number of fruits per plant (88.55%), seed per fruit (73.02%) and fruit yield per plant (74.99%). This result is 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 days to first flowering (60.55%), average fruit weight (60.51%), primary branches per plant (58.70%), fruit diameter (42.23%). On the other hand, low broad sense heritability value was recorded for fruit length (27.58%). These results are 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 reveals 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.

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

Parameters	Heritability	Genetic advance (5%)	Genetic advance (in % of mean)
Germination (%)	85.95	13.49	17.89
Days to 1st flowering	60.55	2.95	9.02
Days to 50% flowering	61.66	3.24	8.25
Plant height (cm)	97.32	32.53	29.98
Primary branches (cm)	58.70	1.35	53.10
No. of fruit's per plant	88.55	8.62	50.44
Fruit length (cm)	27.58	1.03	7.96
Fruit diameter (cm)	42.23	0.16	11.93
Average fruit weight (gm)	60.51	4.44	26.04
Seed's per fruit	73.02	15.03	34.00
Fruit yield per plant (g)	74.99	170.72	57.94

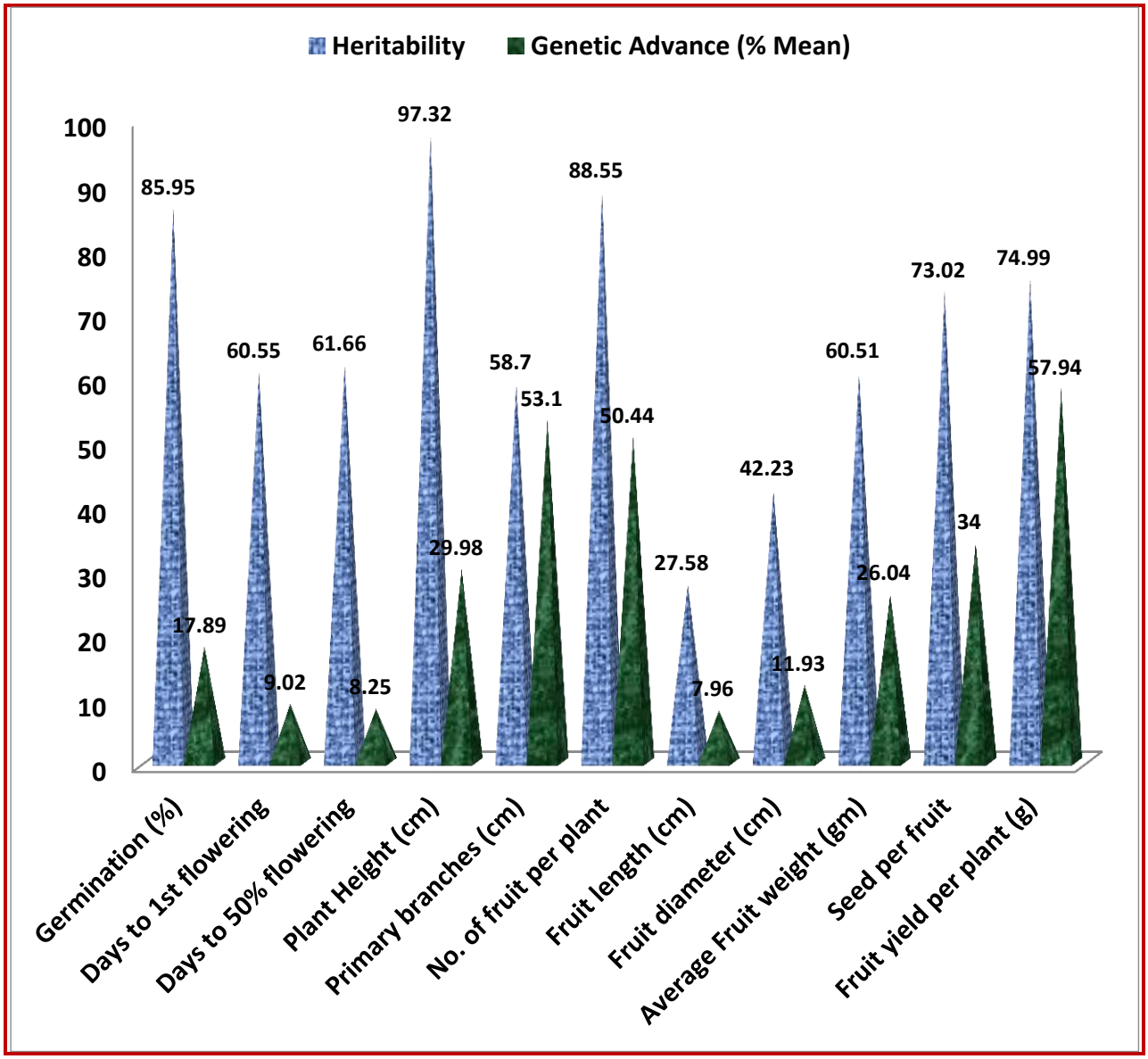

Figure 3: Heritability and genetic advance in percentage of mean

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 (in % of mean) ranged between 7.96% for fruit length to 57.54% for fruit yield 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 branches, number of fruit per plant, plant height, average fruit weight, seed per fruit and fruit yield per plant. 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 germination% (17.89%) and fruit diameter (11.93%). This result is in agreement with Pradip *et al.* (2010) who reported moderate heritability for days to first flowering and fruit diameter. On the other hand, low (<10%) genetic advance was recorded for days to first flowering (9.02%), days to 50% flowering (8.25%) and fruit length (7.96%). 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 plant height (97.32% and 29.98%), fruits per plant (88.55% and 50.44%), seeds per fruit (73.02% and 34.00%), average fruit weight (60.51% and 26.04%) and fruit yield per plant (74.99% and 57.94%). 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 germination% (85.95% and 17.89%) while moderate values for both heritability and genetic advance for fruit diameter (42.43% and 11.93%). 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 geneticadvance 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 (27.58% and 7.96%). 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 and presented in Table 7. 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 11 traits of 28 okra genotypes are presented in Table 8.

Magnitude of genotypic coefficients of correlation was high compared to their corresponding phenotypic coefficient values indicating that there was an inherent association among various traits studied (Table 8).

Fruit yield has shown positive and significant phenotypic and genotypic correlations with plant height (0.699 and 0.618), number of fruits per plant (0.879 and 0.796), and average fruit weight (0.569 and 0.629), respectively and only positive correlation with germination percentage (0.137 and 0.101), days to first flowering (0.104 and 0.047). Fruit yield per plant has also shown negatively and insignificantly correlated with number of seeds per pod (-0.021 and -0.065), fruit length (-0.198 and -0.030), fruit diameter (-0.169 and -0.162) and also only negative phenotypic correlation with days to 50% flowering (-0.002). The findings of positive correlation are also confirmatory with Dhall *et al.* (2001), Dhankhar and Dhankhar (2002b), Nimbalkar *et al.* (2002), Niranjan and Mishra (2003), Jaiprakashnarayan and Ravindra (2004), 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).

4.4.1 Phenotypic and genotypic correlation coefficients

Analysis results of phenotypic and genotypic correlation coefficient ranged in values from -0.302 to 0.796 and -0.571 to 0.879 respectively between germination% with days to first flowering, number of fruits per plant with fruit yield per plant; fruit diameter with seeds per fruit and number of fruits per plant with fruit yield per plant (Table 8). Traits with positive and significant genotypic correlation coefficients were higher in magnitude than the corresponding phenotypic correlations coefficient except few traits. 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 (Dhankhar and

Table 7. Pearson correlation coefficient for different traits

Traits	G (%)	DFF	D50%F	PH	PB	NFP	FL	FD	AFW	SPF	FYP
G (%)	**1.000**	-0.323*	-0.024	0.169	0.047	0.095	0.248	-0.223	0.252	0.033	0.123
DFF	-0.323*	**1.000**	0.568**	0.231	0.043	0.281	-0.254	-0.105	-0.314*	0.101	0.080
D50%F	-0.024	0.568**	**1.000**	0.143	-0.013	0.071	0.072	0.090	-0.053	0.103	0.032
PH	0.169	0.231	0.143	**1.000**	-0.290	0.792**	-0.178	-0.300	0.067	0.051	0.668**
PB	0.047	0.043	-0.013	-0.290	**1.000**	-0.283	-0.019	0.255	0.274	-0.197	-0.105
NFP	0.095	0.281	0.071	0.792**	-0.283	**1.000**	-0.193	-0.269	0.111	-0.130	0.847**
FL	0.248	-0.254	0.072	-0.178	-0.019	-0.193	**1.000**	-0.207	0.160	0.003	-0.107
FD	-0.223	-0.105	0.090	-0.300	0.255	-0.269	-0.207	**1.000**	0.058	-0.436**	-0.169
AFW	0.252	-0.314*	-0.053	0.067	0.274	0.111	0.160	0.058	**1.000**	0.105	0.594**
SPF	0.033	0.101	0.103	0.051	-0.197	-0.130	0.003	-0.436**	0.105	**1.000**	-0.039
FYP	0.123	0.080	0.032	0.668**	-0.105	.847**	-0.107	-0.169	0.594**	-0.039	**1.000**

G (%): Germination (%), DFF: Days to 1stflowering, D50%F: Days to 50% flowering, PH: Plant height (cm), PB: Primary branches, NFP: No. of fruit's per plant, FL: Fruit length (cm), FD: Fruit diameter (cm), AFW: Average fruit weight (gm), SPF: Seed's per fruit and FYP: Fruit yield per plant (g).

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

Traits		DFF	D50%F	PH	PB	NFP	FL	FD	AFW	SPF	FYP
G (%)	G	-0.339*	-0.001	0.169	0.062	0.101	0.350*	-0.299	0.292	0.037	0.137
	P	-0.302	-0.059	0.169	0.025	0.084	0.171	-0.147	0.196	0.027	0.101
DFF	G		0.536**	0.260	0.055	0.337*	-0.331*	-0.151	-0.392*	0.110	0.104
	P		0.607**	0.191	0.029	0.204	-0.200	-0.048	-0.219	0.088	0.047
D50%F	G			0.164	0.003	0.084	0.094	0.145	-0.040	0.095	0.056
	P			0.114	-0.033	0.055	0.056	0.045	-0.070	0.113	-0.002
PH	G				-0.319*	0.809**	-0.256	-0.361*	0.069	0.055	0.699**
	P				-0.252	0.761**	-0.115	-0.236	0.066	0.045	0.618**
PB	G					-0.307	0.044	0.351*	0.322*	-0.235	-0.109
	P					-0.251	-0.069	0.167	0.219	-0.147	-0.098
NFP	G						-0.271	-0.319*	0.130	-0.128	0.879**
	P						-0.132	-0.211	0.083	-0.134	0.796**
FL	G							-0.112	0.163	0.056	-0.198
	P							-0.278	0.162	-0.043	-0.030
FD	G								0.123	-0.571**	-0.169
	P								-0.001	-0.284	-0.162
AFW	G									0.150	0.569**
	P									0.047	0.629**
SPF	G										-0.021
	P										-0.065

G (%): Germination (%), DFF: Days to 1st flowering, D50%F: Days to 50% flowering, PH: Plant height (cm), PB: Primary branches, NFP: No. of fruit per plant, FL: Fruit length (cm), FD: Fruit diameter (cm), AFW: Average fruit weight (gm), SPF: Seed per fruit and FYP: Fruit yield per plant (g).

Dhankhar,2002; 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), Nwangburuka et al. (2012) 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 environmental factors played a small part in the expression of these traits that justified the possibility of correlated response to selection. This study result also showed positive and significant phenotypic correlations higher in magnitude than genotypic correlations coefficients of days to first flowering with days to 50% flowering and days to 50% flowering with seeds per fruit The negative and significant correlations observed at phenotypic and genotypic level were observed between germination and days to first flowering, plant height and primary branches per plant, days to first flowering and fruit length, plant height and fruit diameter, number of fruits per plant and fruit diameter, days to first flowering and fruit weight. 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.

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4.4.2 Correlation of fruit yield with other traits

Analysis revealed that fruit yield per plant had positive and significant phenotypic and genotypic correlation coefficient with plant height (0.699 and 0.618), number of fruits per plant (0.879 and 0.796) and average fruit weight (0.569 and 0.629) (Table 8). This suggests that the characters are more related phenotypically than genotypically. Similar result reported by Nwangburuka *et al.* (2012) and Mihretu *et al.* (2014b), conversely Simon *et al.* (2013a) reported positive and significant genotypic correlations of most traits with fruit yield. Saitwal *et al.* (2011) reported positive and significant genotypic correlation of fruit yield with number of fruit per plant and plant height. Mihretu *et al.* (2014b) 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 germination% (0.137 and 0.101), days to first flowering (0.104 and 0.047), but fruit yield per plant exhibited negative and non-significant correlation coefficient with primary branches per plant (-0.109 and -0.098), fruit length (-0.198 and -0.030) and fruit diameter (-0.169 and -0.162). 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 epicalyx, 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).

4.4.3 Correlation among other characters

This study result showed phenology, growth and fruit related traits showed positive and significant phenotypic and genotypic correlation coefficient between them (Table 8). Three phenology traits (germination, days to first flowering and 50% flowering), five growth traits (plant height, number of primary branches,) and six fruit related traits (number of fruit per plant, fruit length, fruit diameter, fruit weight, seeds per fruit, fruit yield per plant) were studied for correlations coefficients.

Germination% was exhibited positively and significantly with fruit length (0.350) and and negatively significantly associated with days to first flowering (-0.339) at genotypic level. It was positively non-significant correlation with plant height (0.169 and 0.169), primary branches per plant (0.062 and 0.025), number of fruits per plant (0.101 and 0.084), fruit weight (0.292 and 0.196), seeds per fruit (0.037 and 0.027).

Days to first flowering had positive and significant phenotypic and genotypic correlation with days to 50% flowering (0.536 and 0.607) and with number of fruit per plant (0.337) at genotypic level. Similarly days to first flowering were showed positive and non-significant phenotypic and genotypic correlation with plant height (0.260 and 0.191), primary branches (0.055 and 0.029), seeds per fruit (0.110 and 0.088). In other hand, negative and significant genotypic correlation observed with fruit length (-0.331) and fruit weight (-0.392). Nwangburuka *et al.* (2012) reported that significant and positive correlation of days to flowering with plant height at phenotypic and genotypic level.

Days to 50% flowering has no significant correlation with other yield contribution traits except days to first flowering (0.536 and 0.607) at both levels. It has positive correlation with plant height (0.164 and 0.114), number of fruits per plant (0.084 and 0.055), fruit length (0.094 and 0.056), fruit diameter (0.145 and 0.045) and seeds per fruit (0.095 and 0.113) at both levels. On the other hand, days to 50% flowering exhibited negative genotypic and phenotypic correlation with fruit weight (-0.040 and -0.070).

Plant height had positive and significant phenotypic and genotypic correlation with number of fruits per plant (0.809 and 0.761) but only insignificant positive correlation with fruit weight (0.069 and 0.066) and seeds per fruit (0.055 and 0.045). 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 significant correlation with primary branches (-0.319 and -0.252), fruit diameter (-0.361 and -0.236) and insignificant with fruit length (-0.256 and -0.115) (Table 8). Medagam *et al.* (2013) who reported that negative correlation of plant height with number of branches per plant.

Number of primary branches per plant had positive and significant genotypic correlation with fruit diameter (0.351) and fruit weight (0.322). It has positive insignificant correlation with germination (0.062 and 0.025) and days to first flowering (0.055 and 0.029). Negative significant correlation of number of primary branches per plant was observed with plant height (-0.319 and -0.252); and insignificant with number of fruit per plant (-0.307 and -0.251) and seeds per fruit (-0.235 and -0.147). Similar findings found by Medagam *et al.* (2013) who reported that negative significant correlation with plant height and number of fruit per plant. In the contrary, Saitwal *et al.* (2011) reported that positive and significant phenotypic and genotypic correlation with number of fruit per plant.

Number of fruit per plant had positive and significant phenotypic and genotypic correlation with plant height (0.809 and 0.761) and days to first flowering (0.337 and 0.204) but negative significant genotypic correlation with fruit diameter (-0.319). 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.

Fruit length had positive phenotypic and genotypic correlation with fruit weight (0.163 and 0.162), germination (0.350 and 0.171) and seeds per fruit (0.056 and 0.056).

Fruit diameter had negative and significant phenotypic and genotypic correlation with seeds per fruit (-0.571 and -0.284), germination (-0.299 and -0.147), days to first flowering (-0.151 and -0.048), plant height (-0.361 and -0.236), number of fruit per plant (-0.319 and -0.211) and fruit length (-0.112 and -0.278).

Fruit weight had positively correlated with number of seeds per fruit (0.150 and 0.047), number of primary branches (0.332 and 0.219) and fruit length (0.163 and 0.162).

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 Ahiakpa (2012) and Mihretu *et al.* (2014b) 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 will be disregarded in selection for crop improvement.

4.5 Path coefficient analysis

The path coefficient analysis was used to partition the correlations of all the component characters with fruit yield into their direct and indirect effects. Since the mutual relationship of component characters might vary both in magnitude and direction it may tend to probe the association of fruit yield with its attributes. Thus, it is necessary to partition the correlations into direct and indirect effects of each other characters on fruit yield per plant.

A critical perusal of path coefficient analysis has been presented in Table 9. Number of fruits per plant (0.756) had highest positive direct effects on fruit yield per plant followed by fruit weight (0.538) and plant height (0.037). The indirect positive effects were recorded of number of fruits per plant via plant height (0.0293), fruit weight (0.0597), primary branches per plant (0.0062) and fruit length (0.0046). 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.

Days to first flowering showed negative direct effect on fruit yield (-0.011). It had indirect positive effect via germination (0.0287), days to 50% flowering (0.004), plant height (0.0085), number of fruit per plant (0.2124), fruit length (0.0061) and fruit diameter (0.0008).

Days to 50% flowering showed positive direct effect on fruit yield (0.007). It was positive indirect effect through germination (0.0021), plant height (0.0053) and number of fruits per plant (0.0537).

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

Traits	G (%)	DFF	D50%F	PH	PB	NFP	FL	FD	AFW	SPF
G (%)	**-0.0890**	0.0036	-0.0002	0.0063	-0.0010	0.0718	-0.0060	0.0018	0.1356	-0.0001
DFF	0.0287	**-0.0110**	0.0040	0.0085	-0.0009	0.2124	0.0061	0.0008	-0.1689	-0.0003
D50%F	0.0021	-0.0062	**0.0070**	0.0053	0.0003	0.0537	-0.0017	-0.0007	-0.0285	-0.0003
PH	-0.0150	-0.0025	0.0010	**0.0370**	0.0064	0.5988	0.0043	0.0024	0.0360	-0.0002
PB	-0.0042	-0.0005	-0.0001	-0.0107	**-0.0220**	-0.2139	0.0005	-0.0020	0.1474	0.0006
NFP	-0.0085	-0.0031	0.0005	0.0293	0.0062	**0.7560**	0.0046	0.0022	0.0597	0.0004
FL	-0.0221	0.0028	0.0005	-0.0066	0.0004	-0.1459	**-0.0240**	0.0017	0.0861	0.0000
FD	0.0198	0.0012	0.0006	-0.0111	-0.0056	-0.2034	0.0050	**-0.0080**	0.0312	0.0013
AFW	-0.0224	0.0035	-0.0004	0.0025	-0.0060	0.0839	-0.0038	-0.0005	**0.5380**	-0.0003
SPF	-0.0029	-0.0011	0.0007	0.0019	0.0043	-0.0983	-0.0001	0.0035	0.0565	**-0.0030**

Residual effect: 0.144 ** = Significant at 1%. * = Significant at 5%.

G (%): Germination (%), DFF: Days to 1st flowering, D50%F: Days to 50% flowering, PH: Plant height (cm), PB: Primary branches, NFP: No. of fruit's per plant, FL: Fruit length (cm), FD: Fruit diameter (cm), AFW: Average Fruit weight (gm), SPF: Seed's per fruit and FYP: Fruit yield per plant (g).

Plant height had positive direct phenotypic and genotypic effects on pod yield (0.037). The indirect positive effects of plant height on pod yield were recorded via days to 50% flowering (0.001), primary branches (0.0064), number of fruits per plant (0.5988), fruit length (0.0043), and fruit diameter (0.0024) and fruit weight (0.036).

The direct effects of number of primary branches per plant on fruit yield were recorded negative. Its indirect effects via number of pods per plant were found negative. 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.

Fruit length showed negatively direct effects on fruit yield (-0.024). Its indirect effects through fruit weight (0.0861), fruit diameter (0.0017), days to first flowering (0.0028) and days to 50% flowering (0.0005) were positive. The findings of the present study are also in accordance with the results as reported by Niranjan and Mishra (2003), Jaiprakash narayan and Ravindra (2004), Bali *et al.* (2005), Alam and Hossain (2006).

The direct effect of fruit diameter (-0.008) on fruit yield per plant as recorded negative, whereas it had positive indirect effect on fruit yield via fruit weight (0.0312), fruit length (0.005), germination (0.0198) and days to first flowering (0.0012). It had indirect negative effect through number of fruits per plant (-0.2034), plant height (-0.0111) and primary branches per plant (-0.0056).

The direct effect of fruit weight on fruit yield per plant was recorded positive (0.538). Its indirect contribution towards fruit yield per plant via number of fruits per plant (0.0839), days to first flowering (0.0035) and plant height (0.0025) was also positive. It had negative indirect effect via germination (-0.0224), primary branches (-0.0060) and days to 50% flowering (-0.0004).

The direct effect of seeds per fruit on fruit yield per plant was recorded negative (-0.003), whereas its indirect effects via fruit weight (0.0565), fruit diameter (0.0035), primary branches per plant (0.0043) and days to 50% flowering (0.0007) were positive. It had indirect negative effect through (number of fruits per plant (-0.0983), germination (-0.0029) and days to first flowering (-0.0011).

4.6 Analysis of 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 the 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 and Figure 4 & 5). All 28 genotypes grouped into five clusters on the basis of yield components studied. The cluster I comprised two genotypes including G1 and G18. Cluster II contained six genotypes namely, G6, G10, G15, G17, G20 and G25. Cluster III consisted of five genotypes viz., G2, G3, G4, G7 and G11. Cluster IV comprised five genotypes viz., G5, G9, G12, G13 and G21. Cluster V includes highest ten genotypes namely G8, G14, G16, G19, G22, G23, G24, G26, G28 and G30. Clustering of genotypes on the basis of genetic diversity would help the breeder for selecting diverse plants for using in hybridization under further breeding program. 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 28 genotypes in different clusters

Cluster no.	Genotypes	No. of populations
I	G1, G18	2
II	G6, G10, G15, G17, G20, G25	6
III	G2, G3, G4, G7, G11	5
IV	G5, G9, G12, G13, G21	5
V	G8, G14, G16, G19, G22, G23, G24, G26, G27, G28	10
	Total	**28**

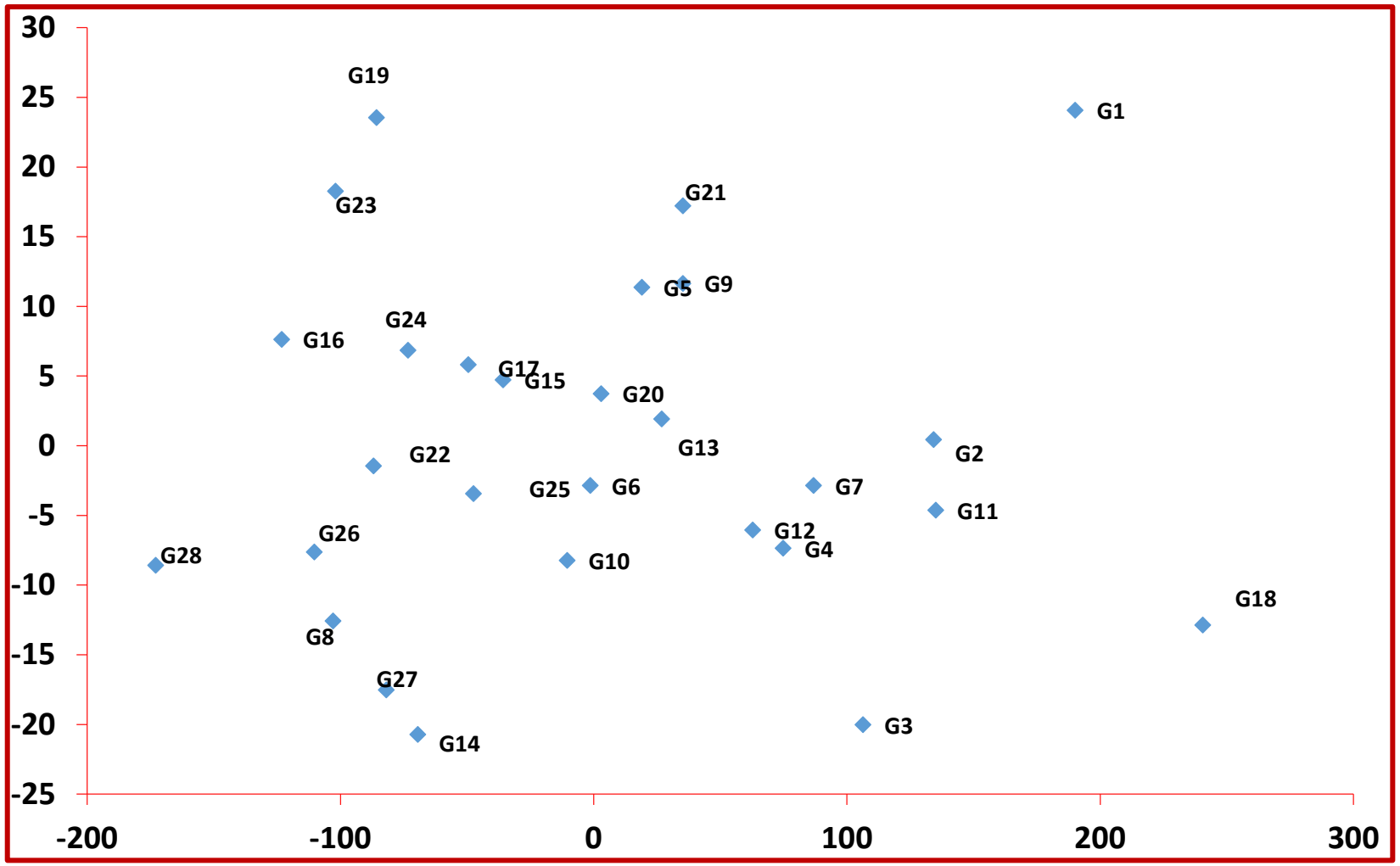


Figure 4. Scatter diagram of Okra genotypes of based on their principal component scores

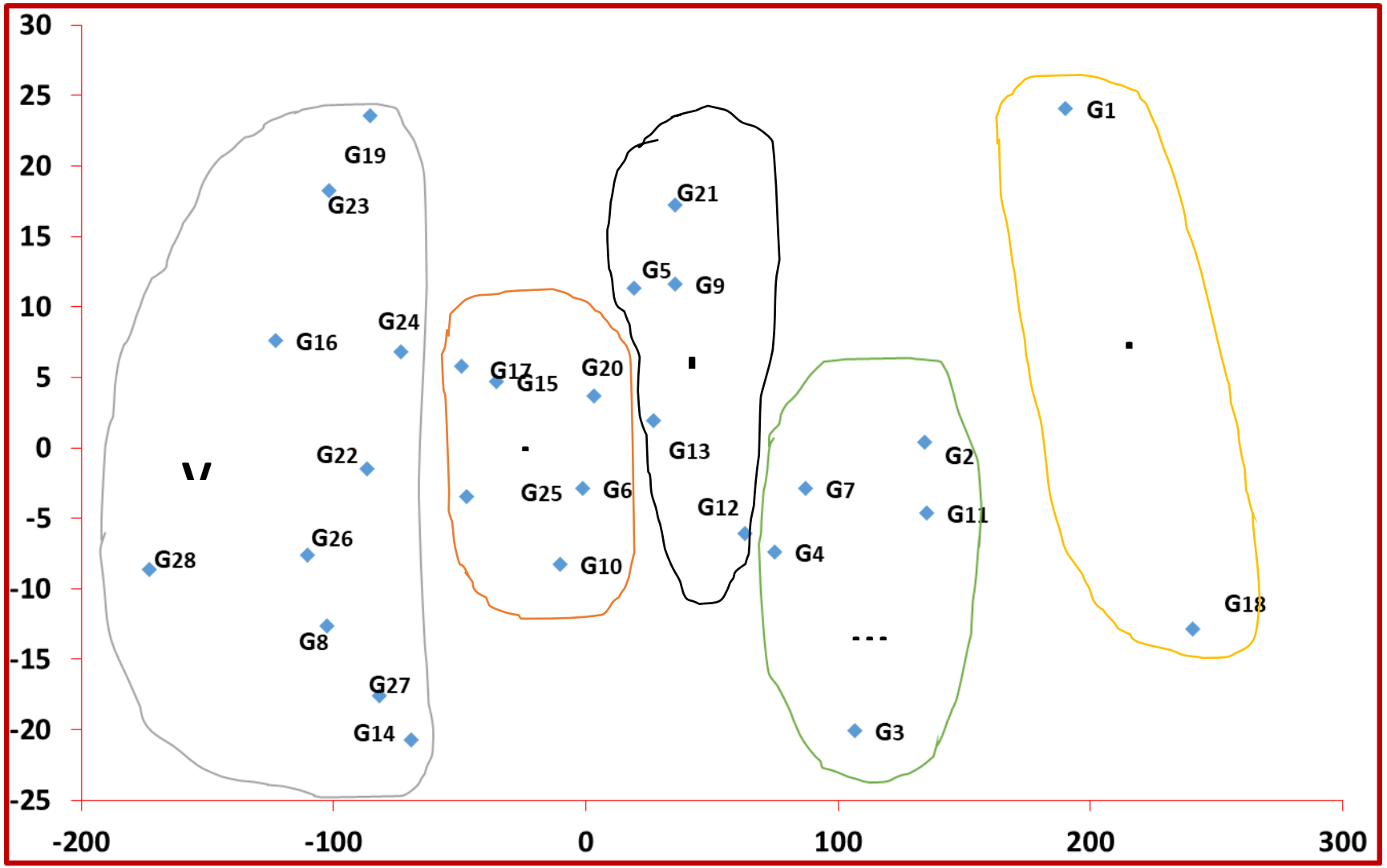


Figure 5. Cluster diagram showing genotypes grouping in different clusters of 28 genotypes of okra

4.6.2 Contribution of different characters to total diversity

The relative contribution of eleven different characters intakes in the evaluation of 28 genotypes towards the expression of genetic divergence is given in Table 11. The percent contribution of component characters ranged from 0.010 to 26.74 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).

Principal components analysis (PCA) results of 11 quantitative traits are presented (Table 11). The PCA analysis results includes the factor scores of each character among the 28 okra accessions, Eigen values, percentage total variance accounted for by eight principal components (PCs). This principal component analysis resulted in eleven principal components (PC1 to PC11) with Eigen values ranged from 0.012 to 2.941. The eleven principal components accounted varied percentage of total variance ranged from 0.1 to 26.74%. Cumulative percent of total variation up to PCA five with eigen value more than unity accounted 80.67%. 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 five components were retained in analysis because eigen values are >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 26.74%, 18.15% and 14.84%, respectively, contributed more to the total of 59.73% 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 and yield percent contribution of 11 characters of 28 genotypes

Principal component axes	Eigen values	Percent variation	Cumulative % of percent variation
I	2.941	26.74	26.74
II	1.996	18.15	44.89
III	1.632	14.84	59.73
IV	1.292	11.75	71.48
V	1.011	9.19	80.67
VI	0.780	7.09	87.76
VII	0.690	6.28	94.04
VIII	0.297	2.70	96.74
IX	0.213	1.94	98.68
X	0.135	1.22	99.9
XI	0.012	0.10	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 13 & 14. Intra cluster average D^2 values ranged from 0.00 to 1.34. It recorded maximum (1.34) in cluster II with six genotypes followed by 1.23 in cluster V with ten genotypes. Inter cluster average D^2 values were higher (20.07) between cluster I and cluster V followed by 14.91 between clusters I and cluster II. The minimum inter cluster value for all the characters were as 5.34 between cluster II and cluster IV. Singh and Jain (2007) also 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 the highest mean values for plant height (137.12 cm), number of fruits per plant (23.00), fruit weight (22.00 g), seeds per fruit (49.17) and fruit yield per plant (508.17) among all the clusters. Apart from observing high cluster mean, low mean values were also envisage for its important in getting early that was recorded in cluster I for the characters viz., days to first flowering (31.33) and days to 50% flowering (38.33). Cluster II had none of highest mean values but lowest value for fruit weight (16.09 g) and seed per fruit (38.78). Cluster III had shown the high mean values days to first flowering (33.80). Among all the clusters, the lowest mean values for germination% (72.40) and primary branches per plant (2.17) was recorded in cluster III. Cluster IV had shown high mean values for germination% (83.67) and days to 50% flowering (39.93). Among all clusters, cluster V had highest mean values for primary branches per plant (2.87) followed by fruit length (13.21 cm). 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 28 genotypes

Cluster	I	II	III	IV	V
I	**0.00**	14.91	7.23	10.97	20.07
II		**1.34**	8.93	5.34	5.84
III			**0.87**	5.43	14.54
IV				**0.73**	10.46
V					**1.23**

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

Sl No.	Cluster	Nearest Cluster with D^2 values	Farthest Cluster with D^2 values
1	I	III (7.23)	V (20.07)
2	II	IV (5.34)	I (14.91)
3	III	IV (5.43)	V (14.54)
4	IV	II (5.34)	I (10.97)
5	V	II (5.84)	I (20.07)

Table 14. Cluster mean for 11 yield and yield related characters in 28 okra genotypes

Characters	I	II	III	IV	V
Germination (%)	75.33	72.50	72.40*	83.67**	74.53
Days to 1st flowering	31.33*	32.83	33.80**	33.20	32.20
Days to 50% flowering	38.33*	38.94	39.73	39.93**	39.10
Plant Height (cm)	137.12**	106.90	113.72	117.83	96.41*
Primary branches (cm)	2.66	2.54	2.17*	2.22	2.87**
No. of fruit's per plant	23.00**	17.00	21.73	20.27	12.07*
Fruit length (cm)	12.43*	12.68	13.17	12.56	13.21**
Fruit diameter (cm)	1.30	1.36	1.36	1.23*	1.40**
Average Fruit weight (gm)	22.00**	16.09*	18.40	16.50	16.30
Seed's per fruit	49.17**	38.78*	40.33	48.53	46.27
Fruit yield per plant (g)	508.17**	271.20	402.20	329.67	194.73*

* Lower value, ** Higher value

4.6.6 Genetic distance

Genetic distance of 28 okra genotypes was measured using Euclidean distance based on 11 traits and the result is presented (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 28 okra genotypes ranged from 0.19 to 4.09 with mean and standard deviation of 1.47 and 0.66, respectively. The most distant genotypes were G1 and G28 (4.09) followed by G1 and G27 (3.32), G1 and G23 (3.60), G1 and G14 (3.37) and G1 and G17 (3.00). The lowest genetic distance was exhibited between G10 and G24 (0.19) followed by G10 and G22 (0.32), G10 and G20 (0.37), G6 and G20 (0.39) and G10 and G25 (0.39). This suggested that the higher chance of improving the crop production through collection, characterization, 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 will 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 collection.

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) 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*. (2014a) 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 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.

Table 15.Genetic Euclidean distances and mean Euclidean distance of 28 genotypes based on 11 traits

Genotypes	Squared Euclidean Distance														
	G1	G2	G3	G4	G5	G6	G7	G8	G9	G10	G11	G12	G13	G14	G15
G2	1.08														
G3	2.83	0.62													
G4	0.88	0.83	1.76												
G5	1.98	1.36	1.83	1.53											
G6	2.14	0.65	0.47	0.81	1.65										
G7	1.84	0.90	1.03	1.48	0.49	1.19									
G8	2.73	2.33	2.86	0.84	2.45	1.62	2.59								
G9	0.92	0.56	1.16	0.59	0.95	0.53	0.78	1.89							
G10	1.33	0.77	1.50	0.44	1.26	0.76	1.44	0.97	0.44						
G11	1.32	0.74	1.41	1.50	1.25	1.63	0.85	2.71	1.08	1.28					
G12	1.49	1.17	2.21	0.90	0.81	1.82	1.32	1.58	1.20	0.77	1.84				
G13	1.57	1.57	2.26	1.35	1.09	1.69	1.21	2.26	0.70	0.88	0.90	1.89			
G14	3.37	1.64	1.73	1.53	1.87	1.36	2.55	1.44	1.88	0.83	2.55	1.12	2.65		
G15	2.04	0.94	1.30	1.41	1.72	1.01	0.99	1.82	0.92	1.01	0.67	2.23	1.01	2.44	
G16	2.79	1.25	1.59	1.62	1.75	1.18	1.64	1.34	1.46	0.92	1.68	1.50	2.28	1.13	0.86
G17	3.00	1.09	0.76	2.09	0.88	0.99	0.55	2.44	1.16	1.39	1.19	1.74	1.70	1.73	0.79
G18	1.27	0.55	1.12	1.52	1.43	1.66	1.19	2.94	1.19	1.19	0.72	1.15	1.61	1.88	1.66
G19	3.09	1.83	1.99	2.56	0.55	2.04	0.78	2.74	1.53	1.69	1.67	1.44	1.64	2.17	1.42
G20	1.57	0.51	1.03	0.61	2.07	0.39	1.88	1.45	0.61	0.37	1.53	1.55	1.58	1.09	1.08
G21	1.51	0.58	1.24	1.40	0.52	1.10	0.52	2.89	0.44	0.93	0.93	1.13	1.02	2.03	1.04
G22	2.16	1.53	2.33	1.11	1.43	1.62	2.00	0.95	1.21	0.32	1.80	0.79	1.21	0.77	1.45
G23	3.60	1.44	0.98	2.06	1.37	0.66	1.62	2.56	1.27	1.43	2.20	2.30	2.15	1.25	1.66
G24	1.66	1.13	1.83	0.61	1.73	0.90	1.92	0.62	0.79	0.19	1.53	1.23	1.11	0.97	0.94
G25	1.59	1.46	2.22	0.68	1.25	1.40	1.45	0.46	0.98	0.39	1.38	0.82	1.00	1.27	1.03
G26	2.46	1.75	2.82	1.30	2.00	1.92	2.42	0.99	1.65	0.60	1.81	1.31	1.79	1.13	1.28
G27	3.32	2.14	2.00	2.02	2.65	1.64	2.90	1.53	1.94	0.97	2.17	2.24	2.09	0.89	1.86
G28	4.09	1.97	2.10	2.66	2.92	1.66	2.46	2.44	1.94	1.41	2.34	2.98	2.47	2.12	0.90

Table 15. Continued..

	G16	G17	G18	G19	G20	G21	G22	G23	G24	G25	G26	G27
G17	0.711											
G18	1.984	1.505										
G19	1.151	0.412	1.870									
G20	1.124	1.614	1.333	2.480								
G21	1.353	0.722	1.123	0.818	1.236							
G22	0.964	1.623	1.569	1.443	1.002	1.461						
G23	1.243	0.741	2.360	1.413	1.216	1.150	1.857					
G24	0.800	1.567	1.614	1.883	0.410	1.464	0.312	1.499				
G25	0.879	1.459	1.586	1.405	1.128	1.503	0.332	2.063	0.302			
G26	0.594	1.853	2.306	1.945	1.255	1.770	0.466	2.212	0.534	0.542		
G27	1.226	1.848	1.926	2.436	1.281	2.623	0.907	1.855	0.756	1.052	1.257	
G28	0.610	1.250	3.073	1.963	1.558	1.833	1.599	1.780	1.387	1.789	1.061	1.787

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 inter relationship 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 program. Considering diversity, variability and all agronomic traits the genotypes G1 and G18 could be selected from cluster I for earliness and high fruit yield (Table 16). G6 and G20 could be selected for less seeds per fruit from cluster II.

Table 16: Finally selected genotypes for important traits

Sl No.	Selection traits	Genotypes	Cluster No.
01	Days to flowering (earliness), number of fruits per plant, fruit yield per plant	G1, G18	I
02	Less seeds per fruit	G6, G20	II

CHAPTER V

SUMMARY AND CONCLUSION

Significant differences were observed among the genotypes for all the traits viz. germination (%), days to first flowering, days to 50% flowering, plant height (cm), primary branches, umber of fruits per plant, fruit length (cm), fruit diameter (cm), fruit weight (g), number of seeds per fruit and fruit yield per plant (g). Lowest days to first flowering were recorded in G1 (29.67) and highest in G23 (36.00). The minimum days to 50% flowering was observed in G13 with 36.00 DAS while in G19 is maximum with 43.00 DAS. The range of plant height was recorded from 79.83 cm (G14) to 152.67 cm (G1). The highest number of primary branches produced by the genotype G27 (6.00) and lowest number in the genotype G21 (1.50).

The genotype G1 (26.33) represented the maximum number of fruits per plant and the minimum was observed by the genotype G22 (10.33). The Maximum fruit length was found in genotype G8 (16.46 cm) and the minimum was observed in the genotype G28 (10.21 cm). The genotype G18 (25.33 g) represented the maximum fruit weight and the minimum was observed by the genotype G28 (10.67 g). The maximum number of seeds per pod was produced by the genotype G19 (58.67) and minimum in the genotype G6 (24.00). Genotype G18 (535.33 g) produced the highest fruit yield per plant and genotype G28 (124.00 g) produced the lowest yield per plant.

GCV ranged from 5.10% to 33.64% while PCV was range between 6.50% and 43.91%. Though, PCV values was greater than GCV. The magnitudinal differences were medium to low in PCV and GCV for germination (10.10 and 9.37), days to first flowering (7.23% and 5.62%), days 50% flowering (6.50% and 5.10%), plant height (14.96% and 14.75%), number of fruits per plant (27.65% and 26.02%) and seeds per fruit (22.16% and 19.32%) 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 (43.91% and 33.64%), fruit length (14.02% and 7.36%), fruit diameter (13.71% and 8.91%), fruit weight (20.89% and 16.25%) and fruit yield per plant (37.51% and 32.48%) suggested a highly significant influence of environment on the expression of these traits.

Heritability in broad sense ranged from 27.58% (fruit length) to 97.32% (plant height) and genetic advance as percent of mean (GAM) ranged from 7.96% for fruit length to 57.94% for

fruit yield per plant. The traits plant height (97.32% and 29.98%), number of fruits per plant (88.55% and 50.44%), fruit weight (60.51% and 26.04%), seeds per fruit (73.02% and 34.00%) and fruit yield per plant (74.99% and 57.94%) 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 germination percentage 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. High h^2_b along with low GA indicates non-additive type of gene action and genotype-environment interaction plays a significant role in the expression of the trait as observed in days to first flowering and days to 50% flowering. 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 fruits per plant had the highest genotypic and phenotypic correlation coefficient. The correlation coefficient showed numbers of fruits per plant serve as most important selection indices of fruit yield. Genotypic correlations were higher in magnitude than phenotypic correlation. Moreover, the traits plant height (0.699 and 0.618), number of fruits per plant (0.879 and 0.796) and fruit weight (0.569 and 0.629) 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 days to 50% flowering (0.007), plant height (0.037), number of fruits per plant (0.756), fruit weight (0.538) 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 days to first flowering (0.2124), plant height (0.5988) via number of fruits per plant. Germination (%) (0.1356) and primary branches per plant (0.1474) had positive indirect effect on fruit yield per plant through fruit weight.

Genetic diversity among 28 genotypes was performed through Principal Component Analysis (PCA), Cluster Analysis using GENSTAT software. The first five components with eigen

value were greater than unity contributed a total of 80.67% variation towards the divergence. As per PCA, D^2 and Cluster Analysis, the genotypes were grouped into five different clusters. Cluster V, II & I composed of ten, six and two genotypes, respectively. Cluster III & IV were consisted of both five genotypes. The highest inter-cluster distance was observed between clusters I and V (20.07) 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 I and III (7.23) .

Conclusion

Results of the present studies indicated significant variation among the genotypes for all the characters studied. Plant height, fruits per plant and fruit weight contributed maximum towards fruit yield improvement. Twenty eight okra genotypes formed five different clusters. Considering genetic variability, diversity and other agronomic performance selection of genotypes G1 and G18 could be selected for earliness and high fruit yield and genotypes G6 and G20 selected for less seeds per fruit for future breeding program. High genotypic distance observed between G1 and G28, G27, G23, G14, G17, respectively. So, divergent genotypes are recommended to use as parents in future hybridization program from more distant cluster I (G1) and cluster V (G28, G27, G23, G14); cluster I (G1) and cluster II (G17).

REFERRENCE

Adekoya, M. A., Ariyo, O. J., Kehinde, O. B. and Adegbite, A. E. (2014). Correlation and path analyses of seed yield in okra (*Abelmoschus esculentus* (L.) Moench) grown under different cropping seasons. *Pertanika J. Tropic. Agric. Sci.***37** (1): 39 – 49.

Adeoluwa,O.O. and Kehinde, O.B. (2013). Genetic variability studies in West African okra (*Abelmoschus caillei*). *Agric. Bio. J. North America.* **2** (10):1326.1335.

Adetuyi, F.O., Osagie, A.U. and Adekunle, A.T. (2008). Effect of postharvest storage techniques on the nutritional properties of Benin indigenous okra [*Abelmoschus esculentus* (L) Moench]. *PakJ. Nutri.***7**: 652657.

Afifi, A.A. and Clark, V. (1990). Computer aided multivariate analysis. Van Nostrand Reinhold. NewYork, USA, Pp 505.

Ahamed KU, Akter B, Ara N, Hossain MF and Moniruzzaman M. (2015). Heritability, correlation and path coefficient analysis in fifty seven okra genotypes. *Intl. J. Appl. Sci.Biotechno.***3** (1): 127133.

Ahiakpa, J.K. (2012). Characterization of twenty-nine (29) accessions of okra [*Abelmoschus* Spp (L.) Moench] in Ghana. Master of Philosophy, University of Ghana, Ghana.

Ahiakpa, J.K., Kaledzi, P.D., Adi, E.B., Peprah, S. and Dapaah, H.K. (2013). Genetic diversity, correlation and path analyses of okra [*Abelmoschus* spp. (L.) Moench] germplasm collected in Ghana. *Intl J. Development, Sustainability*, **2**(2):1396-1415.

Akanbi, W.B., Togun, A.O., Adediran, J.A. and Ilupeju, E.A.O. (2010). Growth, dry matter and fruit yield components of okra under organic and inorganic sources of nutrients. *American-Eurasian J. Sustain. Agric.***4** (1): 113.

Akbar, M., T., Mahmood, M., Yaqub, M., Anwar, M., Ali, N., and Iqba, L. (2003). Variability, correlation and path coefficient studies in summer mustard (*Brassica juncea* L.). *Asian J. Plant Sci.***2**: 696-698.

Akinyele, B.O. and Osekita, O.S. (2006). Correlation and path coefficient analyses of seed yield attributes in okra [*Abelmoschus esculentus* (L.) Moench]. *African J. Biotechnol*. **5** (14):1330-1336.

Akotkar, P.K., De, D.K. and Pal, A.K. (2010). Genetic variability and diversity in okra (*Abelmoschus esculentus* (L.) Moench). *Electronic. J. Plant. Breed.***4**: 393-398.

Aladele, S.E. (2009). Morphological distinctiveness and metroglyph analysis of fifty accessions of West African okra (*Abelmoschus caillei*) (A. Chev.). *J. Plant Breed. Crop Sci.***1** (7): 273-280.

Alam, A.K.M.A. and Hossain, M.M. (2008). Variability of different growth contributing parameters of some okra (*Abelmoschus esculentus* L.) accessions and their inter relation effects on yield. *J. Agri. Rurl. Devel.* **6** (1 &2): 25-35.

Ali, Y., Atta, B.M., Akhter, J., Monneveux, P., and Lateef, Z. (2008). Genetic variability, association and diversity studies in wheat (*Triticum aesitum* L.) germplasm. *Pakistan J. Botanic*. **40**(5): 2087-2097.

Amoatey, H.M., GYP Klu, Quartey, EK, Doku, HA., Sossah, FL., Segbefia, MM. and Ahiakpa. JK. (2015). Genetic diversity studies in 29 accessions of okra (*Abelmoschus* spp (L.) using 13 quantitative traits. *American J. Experiment. Agric.***5** (3): 217-225.

Anderson, T.W. (1989). An introduction to multivariate statistical analysis. John Wileyand Son, New York. PP 675.

Anwar. F., Umer, R., Zahid, M., Tahira, I. and Tufail, H.S. (2011). Inter-Varietal Variation in the Composition of Okra (*Hibiscus esculentus* L.) Seed Oil. *Pakistan J. Bot.***43** (1): 271-280.

Kumar A. (2009). Studies on genetic divergence in okra (*Abelmoschus esculentus* (L.) Moench) genotypes. Thesis submitted to G.B.P.U.A.T, U. S. Nagar, Uttarakhand. p.162.

Ashraful, A. K., Alam, M., Mokbul, MD. and Hossain, (2006). Variability of different yield contributing parameters and yield of some okra (*Abelmoschus esculentus*) accessions. *J. Agric. Rural Dev.***4** (1&2): 119-127.

Azam, S.M., Farhatullah, A. Nasim, S. Shah and Iqbal, S. (2013). Correlation studies for some agronomic and quality traits in *Brassica napus* L. *Sarhad J. Agric.***29** (4): 547-550.

Bali, S.S., Raj, N., Ahmed, N., Singh, A.K and Narayan, S. (2005). Character association and path coefficient studies in okra (*Abelmoschus esculentus* (L.) Moench). *Envir. Eco.* **23**(3): 542-545.

Bendale, V.W., Atanur, S.S., Bhave, S.Cm, Mehta, J.L. and Pethe, U.B. (2003). Genetic divergence for yield and yield components in okra. *Orissa J. Hortic.* **3** (1): 30-33.

Bharathiveeramani, B., Prakash, M and, S.A. (2012). Variability studies of quantitative characters in Maize (*Zea mays* (L.). *Electronic J. Plant Breed.* **3** (4): 995-997.

Bozokalfa, K.M., Esiyokhulya, D.I. and Kaygisiz, T.A. (2010). Estimates of genetic variability and association studies in quantitative plant traits of Eruca spp. Landraces. *Genetika.* **42** (3): 501 -512.

Broschat, T.K. (1979). Principal component analysis in horticultural research. Horticultural Science. **14**:114-117.

Burton, G.W. and De Vane, E.H. (1953). Estimating heritability in tall fescue (*Fistvea arundiancea*) from replicated clonal material. *Agric. J*. **45**: 284-291.

Chahal, G S and Gosal SS. (2002). Principles and procedures of plant breeding biotechnology and conventional approaches. Narosa Publishing House, New Delhi. pp 604.

Charrierl, A. (1984). Genetic Resources of the Genus *Abelmoschus* Ned (Okra). International Board for Plant Genetic Resources, Rome. pp 61.

Chaukhande Pooja, Chaukhande PB and Dod VN. (2011). Genetic variability in okra. Abstracts of National Symposium on Vegetable Biodiversity, held at JNKVV, Jabalpur, during April 4-5, 2011. pp 30.

Chaurasia, PC., Rajhans, KC. and Yadav, M. (2011). Correlation coefficient and path analysis in okra [*Abelmoschus esculentus* (L.) Moench]. *Indian Hort. J.* **1**: 32-36.

Chhatrola, M.D. and Monpara, B.A. (2005). Correlation and path analysis - their implications in okra [*Abelmoschus esculentus* (L.) Moench] improvement. *National J. Pl. Improv.***7** (2): 127-130.

Das, S., Chattopadhyay, A., Chattopadhyay, SB., Dutta, S. and Hazra P. (2012). Genetic parameters and path analysis of yield and its components in okra at different sowing dates in the gangetic plains of eastern India. *African J. Biotechnol.***11**: 16132-16141.

Dhaduk, L.K., Mehta, D.R. and Patel, K.D. (2004). Genetic diversity in okra. *Orissa. J. Hortic.* **32** (1): 70-72.

Dhall, R.K., Arora, S.K. and Mamta R. (2001). Studies on variability, heritability and genetic advance of generations in okra (*Abelmoschus esculentus* L. Moench). *Haryana J. Hortic. Sci.***30** (1 & 2): 76-78.

Dhall, R.K., Arora, S.K. and Mamta R. (2003). Studies on variability, heritability and genetic advance of advanced generations in okra (*Abelmoschus esculentus* (L.) Moench). *J. Res. Punjab agric. Univ.* **40 (**1): 54-58.

Dhankhar, B.S and Dhankar, S.K. (2002a). Variability studies in okra (*Abelmoschus esculentus* (L.) Monch). *Haryana. J. Hort. Sci.* **31** (1): 82-84.

Dhankhar, B.S and Dhankhar, S.K. (2002b). Genetic variability, correlation and path analysis in okra [*Abelmoschus esculentus* (L.) Moench]. *Veg. Sci.* **29** (1): 63-65.

Duzyaman, E. (2005). Phenotypic diversity within a collection of distinct okra (*Abelmoschus esculentus* L.) cultivars derived from Turkish land races. *Genet. Res. Crop Evo.***52**: 1019-1030.

Duzyaman, E. and Vural, H. (2003). Evaluation of pod characteristics and nutritive value of okra genetic resources. *Acta Horticulture (ISHS).* **598**: 103-110.

Ehab. AA. I., Mohamed.Y. A. and Ali M. M. (2013). Genetic behavior of families selected from some local okra [*Abelmoschus esculentus* (L.) Moench] populations in Egypt. *Plant Breed. Biotechnol.***1** (4): 396-405.

Ehab. AA. I., Mohamed.Y. A. and Ali M. M. (2013). Genetic behavior of families selected from some local okra [*Abelmoschus esculentus* (L.) Moench] populations in Egypt. *Plant Breed. Biotechnol.***1** (4): 396-405.

Falconer, D.S. and Mackay, T.F.C. (1996). An Introduction to quantative genetics. Ed, 4. Printice Hall London. PP 464

Gandhi, H. T., Yadav, M. D. and Navale, P. A. (2002). Character association and path analysis in okra. *J. Maharashtra Agril. Univ.***27** (1): 110-112.

Gandhi, H.T., Yadav, M.D. and Navale, P.A. (2001). Studies on variability in okra (*Abelmoschus esculentus* L. Moench). *J. Maharashtra agric. Univ.***26** (2): 146-148.

Gangashetti PI, Laxman M and Satish A. (2013). Breeding investigations in single and double cross F_4 and F_5 populations of bhendi [*Abelmoschus esculentus* (L.) Moench.]. *Mol. Plant Breed.***6**: 96-106.

Ghai, T.R., D. Arora, S.K. Jindal and P. Singh, (2005). Assessment of genetic divergence based on nutritional quality and agronomic traits in okra (*Abelmoschus esculentus* (L.) Moench.). *J. Genet. Breed.***59**: 1-6.

Ghai, T.R., Singh, M. and Arora, S.K. (2004). Induced variability for economic characters in okra (*Abelmoschus esculentus* (L.) Moench). *J. Res. Punjab agric. Univ.***41** (1): 63-67.

Gondane, S.U. (1989). Studies on phenotypic stability and root knot nematodes reaction in okra. Ph.D Horticulture thesis submitted to G.B.P.U.A & T, Pantnagar, March 1979. 160p.

Hammon, S. and Vanstolen, DH. (1989). Characterization and evaluation of okra. The use of plant genetic Resource. pp. 173-174.

Hazem, A., Obiadalla-Ali, Eldekashy, M.H.Z. and Helaly, A.A. (2013). Combining ability and heterosis studies for yield and its components in some cultivars of okra [*Abelmoschus esculentus* (L.) Moench]. *American-Eurasian J. Agric. Environ. Sci.***13** (2): 162-167.

Hazra P and Basu D. (2000). Genetic variability, correlation and path analysis in okra. *Ann. Agric. Res.***21** (3): 452-453.

Hazra, P. Basu, D. and Sahu, F.K. (2002). Genetic divergence in okra. *Indian J. Hor.***59** (4): 406-410.

Henry, RJ. (2005). Conserving genetic diversity in plants of environment, social or economic importance of. In: Henry, RJ, editor. Plant diversity and evolution. CABI Publishing, Wallingford, UK. Pp 317-325.

Ikram, U.H., Khan, A.A., Azhar, F.M. and Ehsan, U. (2010). Genetic basis of variation for salinity tolerance in okra [*Abelmoschus esculentus* (L.) Moench]. *Pakistan J. Bot.***42**: 1567-1581.

Indurani, C and Veeraragavathatham, D. (2005). Genetic variability, heritability and genetic advance in okra (*Abelmoschus esculentus* (L.) Moench.). *Indian. J. Hort*. **62**(3): 303-305.

IPGRI. (1991). Okra Descriptor list. International Crop Network Series 5. International Board for Plant Genetic Resources (IBPGR), Rome, Italy.

Jagan, K K., Ravinder, K. R., Sujatha, M., Sravanthi, V. and Madhusudhan, V. R. (2013). Studies on genetic variability, heritability and genetic advance in okra [*Abelmoschus esculentus* (L.) Monech]. *IOSR J. Agric. Vet. Sci.* **5** (1): 59-61.

Jaiprakash N, R.P. and Ravindra, M. (2004). Correlation and path analysis in okra [*Abelmoschus esculentus* (L.) Moench]. *Indian J. Hort.* **61** (3): 232-235.

Jindal, S.K., Arora, D. and Ghai, T.R. (2010). Variability studies for yield and its contributing traits in okra. *Electron J. Plant Breed.* **1**: 1495-149.

Johnso, R.W., Robinson, H.F. and Comstock, R.E. (1955). Estimating genetic and environmental variability in soya bean. *Agron. J.***47**: 314-318.

Johnson, H.W., Robinson, H.F. and Comstock, R.E. (1955). Genotypic and phenotypic correlations in soybeans and their implications in selection. *Agron. J.***47**: 477-483.

Kamalpreet, K., Mamta, P., Satinder, K., Dharminder, P. and Neena, C. (2013). Assessment of morphological and molecular diversity among okra [*Abelmoschus esculentus* (L.) Moench.] germplasm. *Academic J.* **12** (21): 3160-3170.

Khanorkar, S.M. and Kathiria, K. B. (2010). Heterobeltiosis, inbreeding depression and heritability study in okra [*Abelmoschus esculentus* (L.) Moench]. *Electronic J. Plant Breed.***1** (4): 731-741.

Krushna, D., Harshal, E.P. and Sudha, P. 2007. Genetic variability studies in Okra [*Abelmoschus esculentus* (L.) Moench]. *Asian J. Hort.***2** (1):201-203.

Kuan, P., T.S.K.K. and Ravisankar, C. (2004). Genetic variability and multivariate analysis in okra [*Abelmoschus esculentus* (L.) Moench]. *Tropic. Agric. Res.***16**: 99-113.

Kumar, N. (2006). Breeding of Horticultural crops. New India Publishing Agency, New Delhi, Pp 173-177.

Kumar, N.S., Suguna, V. And Thangavel, P. (2007). Genetic parameters and degree of dominance for yield and its contributing traits in okra (*Abelmoschus esculentus* (L.) Moench).*Adv. Pl. Sci.* **20** (2): 617-619.

Kumar, R.P., Vashisht, R., Gupta, K., Singh, M. and Kaushal, S. (2011). Characterization of European carrot genotypes through principal component analysis and regression analysis. *Intl. J. Veg. Sci.***17**: 3-12.

Kumar, S., Dagnoko, S., Hauqui, A., Ratnadass, A., Pasternak, D. and Kouame, C. (2010). Okra [*Abelmoschus esculentus* (L) Moench]. In West and Central Africa potential and progress on its improvement. *African J. Agric. Res.* **5**: 350-3598.

Kusvuran, S. (2012). Influence of drought stress on growth, ion accumulation and antioxidative enzymes in okra genotypes. *Intl. J. Agric. Bio.* **14**: 401-406.

Lal, G., Singh, D.K. and Jain, S.K. (2001). Response of okra cultivars to varying sowing dates under Tarai, Foot Hill of Himalayas. *Adv. Hort. forestry*. **8**(1): 129-137.

Legendre, P. and Legendre, L. (1998). Numerical ecology, 2nd English edn. Elsevier, Amsterdam. Pp 853.

Lengsfeld, C., Titgemeyer, F., Faller, G. and Hensel, A. (2004). Glycosylated compounds from okra inhibit adhesion of Helicobacter pylori to human gastric mucosa. *J. Agric. Food Chemistry*. **52**(6): 1495-503.

Magar RG and Madrap I.A. (2009). Genetic variability, correlation and path coefficient analysis in okra [*Abelmochus esculentus* (L.) Monch.]. *J. Plant Sci*. **4**(2):498-501.

Mamta Kumari and Choudhury, D.N. (2006). Genetic divergence in okra [*Abelmuschus esculentus* (L.) Moench]. *Veg. Sci.* **33** (1): 71-72.

Manivannan, M.I., Rajangam, J and Geetharani, P. (2007). Variation studies in okra. *Asian. J. Hort.***2** (2): 188-191.

Maurya, R.P., Bailey, J.A. and Chandler., J.S. (2013). Impact of plant spacing and picking interval on the growth, fruit quality and yield of okra [*Abelmoschus esculentus* (L.) Moench]. *American J. Agric. Forestry*. **1**(4): 48-54

Medagam, T. R., Kadiyala, H.B., Mutyala, G., Konda, C.R., Hameedunnisa. B., Reddivenkatagari, S., Krishna, R. and Jampala, D. B. (2013). Correlation and path coefficient analysis of quantitative characters in okra [*Abelmoschus esculentus* (L.) Moench]. *Songklanakarin J. Sci. Techno.* **35** (3): 243-250.

Mehta, D.R., Dhaduk, L.K. and Patel, K.D. (2006). Genetic variability, correlation and path analysis studies in okra [*Abelmoschus esculentus* (L.) Moench]. *Agri. Sci. Digest.* **26** (1): 15-18.

Mihretu Y, Weyessa G and Adugna D, (2014a). Multivariate analysis among Okra [*Abelmoschus esculentus* (L.) Moench] collection in South Western Ethiopia. *J. Plant Sci.* **9**: 43-50.

Mihretu Y, Weyessa G and Adugna D, (2014b). Variability and association of quantitative characters among okra [*Abelmoschus esculentus* (L.) Moench] collection in South Western Ethiopia. *J. Bio. sci.* **14**: 336-342.

Mishra A, Mishra HN, Senapati N and Tripathy P. (2015). Genetic variability and correlation studies in Okra (*Abelmoschus esculentus* (L.) Monech). *Electronic J. Plant Breed.***6** (3)-866-869.

Mishra, S.N., Dash, S.N. and Mishra, D. 1996. Multivariate analysis of genetic divergence in okra (*Hibiscusesculentus*). *Indian J. Agri. Res.* **26** (1): 40.

Mnzava, NM., Dearing, JA., Guarino L, Chweya, JA. and Koeijer, HD. (1999). Bibliography of the genetic resources of traditional African vegetables. In neglected leafy green vegetable crops in Africa. International Plant Genetic Resources Institute, Rome, Italy, pp 110.

Mohapatra, M.R. Acharyya, P. and Sengupta, S. (2007). Variability and association analysis in okra. *Indian Agric.***51** (1-2):17-26.

Muhammad, A., Muhammad, S.M. and Mushtaq (2001). Comparative study on the performance of some exotic okra. *Intl. J. Agri. Bio.***3** (4): 423-425.

Muhammad, R.S., Muhammad, A., Khurram, Z., Muhammad, M. J., Saeed, A., Qumer, I. and Aamir, N. (2013). Growth, yield and seed production of okra as influenced by different growth regulators. *Pakistan J. Agric. Sci.* **50**(3): 387-392.

Nagre PK, Sawant SN, Wagh AP, Paithankar DH and Joshi PS. (2011). Genetic variability and correlation studies in okra. Abstracts of national symposium on vegetable biodiversity, held at JNKVV, Jabalpur, during April 4-5, 2011. pp 4.

Naser M. S. (2014a). Genetic diversity of okra [*Abelmoschus esculentus* (L.) Monech] landraces from different agro-ecological regions revealed by AFLP analysis. *American-Eurasian J. Agri. Environ. Sci.* **14** (2): 155-160.

Naser, M.S. (2014b). Flow cytometric analysis of nuclear DNA between okra landraces [*Abelmoschus esculentus* (L.) Moench]. *American J. Agric. Bio. Sci.***9** (2): 245-250.

Nimbalkar, C.A., Navale, P.A. and Gandhi, H.T. (2002). Regression approach for selecting high yielding genotypes in okra. *J. Maharashtra agric. Univ.***27** (1): 46-48.

Niranjan R S, and Mishra M N. (2003). Correlation and path coefficient analysis in okra (*Abelmoschus esculentus* L. Moench) *Pro. Hort.***35** (2): 192-195.

Nwangburuka, C.C., Denton, O.A., Kehinde, O.B., Ojo, D. K. and Popoola., A. R. (2012). Genetic variability and heritability in cultivated okra [*Abelmoschus esculentus* (L.) Moench]. *Spanish J. Agric. Res.***10** (1): 123-129.

Nwangburuka, C.C., Kehinde,O.B., Ojo, D.K., Denton O.A., and Popoola A.R. (2011). Morphological classification of genetic diversity in cultivated okra [*Abelmoschus esculentus* (L.) Moench] using principal component analysis (PCA) and single linkage cluster analysis (SLCA). *African J. Biotechnol.***10** (54): 11165-11172.

Obilana, A.T. and Fakorede, M.A.B. (1980). Heritability a Treatise. Institute of Agricultural Research. **1**: 72-82.

Okra, good for our health and digestion, (2008). http://healthypage-info.blogspot.com/ (Accessed at February 16, 2014).

Okra.http://www.soilandhealth.org/01aglibrary/010137veg.roots/010137toc.html. (Accessed at January 12, 2014).

Oppong-Sekyere, D., Akromah,R., Nyamah, E.Y., Brenya E., and Yeboah, S. (2011). Characterization of okra (*Abelmoschus* spp. L.) germplasm based on morphological characters in Ghana. *J. Plant Breed. Crop Sci.***3** (13): 367-378.

Osawaru, M.E., Ogwu, M.C. and Omologbe, J. (2014). Characterization of three okra [*Abelmoschus esculentus* (L.) Monech] accessions using morphology and SDSPAGE for the basis of conservation. *Egyptian Acade. J. Bio. Sci. Hort. Bot.* ISSN 2090-3812 www.eajbs.eg.net. (Access date January 5, 2014).

Pal, A.K. Das, N.D. and De, O.K. (2008). Studies on association of important yield components in okra. *Indian J. Hort.* **65 (**3): 358-361.

Pal, M.K., Singh, B., Singh, S.K. and Singh, D. (2010). Character association of edible fruit yield and other characters in okra (*Abelmoschus esculentus* (L.) Moench). *Environ. Eco.***28** (1): 472-475.

Panse, V.G. (1957). Genetics of quantitative character in relation to plant breeding. *Indian J. Genet.***17** (3):17-28.

Parbhat, K. and Mamta, P. (2012). Genetic diversity and its relationship with heterosis in okra. *Vegetable Sci.* **39** (2): 140-143.

Patel R, Sengupta SK and Verma A. (2014). Studies on Genetic parameters in Okra [*Abelmoschus esculentus* (L.)]. *Trends in Biosci.* **7** (14): 1808-1811.

Patel, K.D. Dhaduk, L.K. Mehta, D.R. and Pandya, H.M. (2006). A multivariate analysis of okra genotypes. *Agril. Sci. Digest.* **26** (1): 45-47.

Patro, T.S.K. and Ravisankar, C. (2004). Genetic variability and multivariate analysis in okra [*Abelmoschus esculentus* (L.) Moench]. *Tropical Agric. Res.***16**: 99-113.

Phathizwe, M. and Ekpo, O. (2011). Effects of seed size on seedling vigor of okra [*Abelmoschus esculentus* (L.) Monech] in Swaziland. *Advances in Environ. Bio.* **5** (1):180-187.

Pradip, K., Akotkar, D.K. De and Pal, A.K. (2010). Genetic variability and diversity in okra [*Abelmoschus esculentus* (L).Moench]. *Electronic J. Plant Breed.* **1**(4): 393-398.

Prakash, K., Pitchaimuthu, M., and Ravishankar, K.V. (2011). Assessment of genetic relatedness among okra genotypes [*Abelmoschus esculentus* (L) Moench] using rapd markers. *Electronic J. Plant Breed.* **2**(1): 80-86.

Rajendra, P. M., Jamar, A., Bailey, J. St. and Chandler, A. (2013). Impact of plant spacing and picking interval on the growth, fruit quality and yield of ok [*Abelmoschus esculentus* (L.) Moench]. *American J. Agric. Forestry.* **1** (4): 48-54.

Raju, C., and Shanthakumar,. (2008). Studies on variability and character association in selfed and biparental progenies in bhendi [*Abelmoschus esculentus* (L.) Moench]. Master of thesis, University of Dharwad, India.

Ramanjinappa V, Patil MG, Narayanaswamy P, Ashok Hugar and Arunkumar KH. (2011). Genetic variability, correlation and path analysis in Okra [*Abelmoschus esculentus* (L.) Monch]. *Environ. Eco.* **29** (2A): 778-782.

Rao, C.R. (1952). Advanced Statistical Methods in Biometric Research. Ed. II. New York. John Willey and Sons., pp. 50-55.

Ravindra, M., Jaiprakashnarayan, R.P. and Madalageri, M.B. (2004). Studies on genetic variability for fruit and yield parameters in okra [*Abelmoschus esculentus* (L.) Moench]. *Karnataka J. Hort.* **1**(1): 1-5.

Reddy T.M., Haribhau, K., Ganesh, M., Chandrasekhar R.K., and Begum, H. (2012). Genetic divergence analysis of indigenous and exotic collections of Okra [*Abelmoschus esculentus* (L.) Moench]. *J. Agric. Techno.* **8** (2): 611-623.

Ren, J., Ferson, J., Kresovich, R.LS. and Lamboy, WF. (1995). Identities and relationships among Chinese vegetable brassicas as determined by Random Amplified Polymorphic DNA Markers. **120**(3): 548-555.

Robinson, H. F., Comstock, R.E. and Harvey, P.H. (1955). Estimates of heritability and the degree of dominance in maize. Agron. J. **41**: 353-359.

Saifullah M, and Rabbani MG. (2009). Evaluation and characterization of okra (*Abelmoschus esculentus* L. Moench.) genotypes. *SAARC J. Agric.***7** (1): 91-98.

Saitwal, Y.S., Solanke, S.P., Kalalbandi, B.M. and Mhaske, M.G. (2011). Correlation and path analysis in okra [*Abelmoschus esculentus* (L.) Moench]. *Intl. J. Agri. Sci.* **7** (1): 171-173.

Salesh, K. J., Deepak, A. and Ghai, T R. (2010). Variability studies for yield and its contributing traits in okra. *Electronic J. Plant Breed.* **1**(6): 14951499.

Sankara, R. K. and Pinaki, A. (2012). Performance of okra [*Abelmoschus esculentus* (L.) Moench] cultivars under summer and rainy environments. *Intl. J. Advan. Life Sci.***2**: 17-26.

Santos, B.M., Dittmar, P.J., Olson, S.M., Webb, S.E., and Zhang, S. (2012). Okra Production in Florida. University of Florida IFAS extension. pp 163-171.

Saryam DK, Mittra SK, Mehta AK, Prajapati S and Kadwey S. (2015). Correlation and path co-efficient analysis of quantitative traits in okra [*Abelmoschus esculentus* (l.)Moench]. *Supplement on Genet. Plant Breed.* **10**(2): 735-739.

SAS Institute. (2004). SAS /STAT Guide for personal computers, version 9.0 editions. SAS Institute Inc. Cary, NC, USA

Senapati N. Mishra HN, Beura SK, Dash SK, Prasad G, Patnaik A. (2011). Genetic analysis in Okra hybrids. *Environ. Eco.* **29** (3A): 1240-1244.

Sharma AK and Prasad K. (2015). Genetic divergence, correlation and path coefficient analysis in okra. *Indian J. Agric. Res.* **49** (1): 77-82.

Sharma, J.R. (1998). Statistical and Biometrical Techniques in Plant Breeding. New Age International (P) Limited Publishers, New Delhi. Pp 432.

Shekhavat, A.K.S., Singh, B., Yadav, J.R. and Srivastava, J.P (2005). Character association in okra [*Abelmoschus esculentus* (L.) Moench]. *Plant Archives.***5** (1): 289-291.

Shujaat, A., Azhar, H. S., Rehmani, G., Habib, A., Hasnian, N. and Sikandar, K. S. (2014). Morpho-agronomic characterization of Okra [*Abelmoschus esculentus* (L.) Moench]. *World Appl. Sci. J.* **31**(3): 336-340.

Sibsankar. D., Arup, C., Sankhendu, B. C., Subrata, D. and Pranab, H. (2012). Genetic parameters and path analysis of yield and its components in okra at different sowing dates in the gangetic plains of eastern India. *African J. Biotechnol.* **11**(95): 16132-16141.

Simon S.Y., Musa, I. and Nangere, M.G. (2013a). Correlation and path coefficient analyses of seed yield and yield components in okra [*Abelmoschus esculentus* (L) Moench]. *Intl. J. Advanced Res.* **1**(3): 45-51.

Simon, S. Y.,Gashua, I. B. and Musa, I. (2013b). Genetic variability and trait correlation studies in okra [*Abelmoschus esculentus* (L.) Moench]. *Agric. Bio. J. North America.* **4** (5):532-538.

Singh DK and Jain SK. (2012). Performance of okra hybrids for quantitative attributes. *Pantnagar J. Res.* **10** (1): 66-70.

Singh RK. (1986). Comparison of selection indices on selection experiments in rye. *H.A.U. J. Res.***2**: 145-149.

Singh SP and Singh JP. (2006). Variability, heritability and scope of improvement for yield components in okra [*Abelmoschus esculentus* (L.) Moench]. *Intl. J. Plant Sci.* **1** (2): 154-155.

Singh, A.K., Ahmed, N., Raj Narayan and Narayan, S. (2007). Genetic divergence studies in okra under temperate conditions. *Haryana J. Hort. Sci.* **36** (3& 4): 348-351

Singh, B., Pal, A.K., and Sanjay S (2006). Genetic variability and correlation analysis in okra [*Abelmoschus esculentus* (L.) Moench.]. *Indian J. Hort.* **63**(3): 281-285.

Singh, B.D. (1990). Plant Breeding. pp: 702. Kalyani Publishers, New Delhi, India.

Singh, N. (1993). Genetic studies in okra (*Abelmoschus esculentus* L. Moench.). A M. Sc. thesis, Punjab Agril. Univ., Ludhiana, India. P. 78.

Singh, N. S., Arora, K., Ghai, T. R. and Dhillon, T. S. (1996). Combining ability studies in okra (*Abelmoschus esculentus* L. Moench.). *Punjab Veg. Grower.* **31**: 6-9.

Singh, R.K.,and Chaudhary,B.D. (1985). Biometrical methods in quantative analysis. Kalayani Publishers New Delhi. pp 318.

Singh, SP. and Singh, HN. (1979). Genetic divergence in okra [*Abelmoschus esculentus* (L.) Moench]. *Indian J. Hort.***51** (1): 166-170.

Singh,K.B., Geletu, B. and Malhorta, R.S. (1990). Associatition of some characters with seed yield in chick pea collection. *Euphytica*. **49**: 83-88.

Singh,K.B., Geletu, B. and Malhorta, R.S. (1990). Associatition of some characters with seed yield in chick pea collection. *Euphytica*. **49**: 83-88.

Sivasubramaniah, S. and Meron, M., (1973). Heterosis and in breeding depression in rice. *Madras Agric. J.***60**: 1139-1144.

Sneath, P.H.A., and Sokal, R.R. (1973). Numerical Taxonomy: the principles and practice of numerical classification. Fransisco USA W.F Freeman, Pp 573.

Snowder, G. D., Cushman, R. A and Echternkamp, S.E. (2005). Heritability estimate for bilateral ovulation in Heifers. *American Soc. Animal Sci*.**83** (2): 39-42.

Somashekhar Guddadamath Mohan kumar HD and Salimath PM. (2011). Genetic analysis of segregating populations for yield in okra [*Abelmoschus esculentus* (L) Moench]. *Karnataka J. Agric. Sci.***24** (2): 114-117.

Sorapong, B. (2012). Okra [*Abelmoschus esculentus* (L.) Moench] as a valuable vegetable of the world. *Ratar. Povrt.***49**: 105-112.

Sreenivas G, Arya K, and Sheeba R. (2015). Character association and path analysis for yield and yield components in okra [*Abelmoschus esculentus* (L.) Moench]. *Inl. J. Sci. Res*. **4** (1): 141-148.

Subrata. S., Hazra, P and Chattopadhyay, A. (2004). Genetic variability, correlation and path analysis in Okra [*Abelmoschus esculentus* (L.) Moench]. *Hort. J.* **17**(1): 59-66.

Sudip. C., Bhardwaj, Ml., Ramesh, K., Dharminder, K., Sandeep, K., Nidhish, G., Balbir D. and Subhash, S. (2014). Estimation of parameters of variability for different quantitative traits in Okra, [*Abelmoschus esculentus* (L) Moench]. *Intl. J. Farm Sci.* **4**(3): 33-41.

Swati, B., Reena, N., Meenakshi, R. and Jain, P. K. (2014). Genetic variability in Okra [*Abelmoschus esculentus* (L.). Moench]. *An Intl. Quarterly J. Environ. Sci*.**6**: 153-156.

Tattanakorn, M. and Prabhat, K. (2004). Base line survey export okra production in Thailand. Inter-country program for vegetable IPM in South & SE Asia Phase II and Food & Agriculture Organization of the United Nations.

Temesgen A., (2007). Genetic variability and association among seed yield and yield related traits in kabuli chickpea (*Cicer arietinum* L.) Genotypes. Master of Thesis, Haramaya University, Haramaya.

Temesgen Bedassa, Mebeaselassie Andargie and Million Eshete, (2013). Genetic divergence analysis of garden cress (*Lepidium sativum* L.). *Intl. J. Biodiver. Conser.* **5**(11): 770-774.

Thirupathi, RM., Hari, BK., Ganesh, M, Chandrasekhar, R.K., Begum, H., Purushothama RB. and Narshimulu, G. (2012). Genetic variability analysis for the selection of elite genotypes based on pod yield and quality from the germplasm of Okra [*Abelmoschus esculentus* (L.) Moench]. *J. Agric. Technol.* **8**: 639-655.

Tiwari, B. (2001). Performance of okra [*Abelmoschus esculentus* (L). Moench] hybrids in Tarai conditions of U.P during rainy season. M.Sc. Ag. Thesis submitted to G.B.P.U.A & T, Pantnagar, pp: 77.

Torkpo,S.K, Offei, S. K., Danquah, E. Y. and Blay, E.T. (2006). Esterase, total protein and seed storage diversity in Okra (*Abelmoschus esculentus* L Moench). *West African J. Appl. Eco.* **9**: 7-18.

Tripathi, K.K., Govila, O.P.Ranjini W., and Vibha A. (2011). Biology of okra [*Abelmoschus esculentus* (L). (Moench]. Serious of Crop Specific Biology Document. Ministry of environment and forests government of India and department of biotechnology ministry of science and technology government of India. Pp 22.

Vavilov, N.I. (1951). The origin, variation immunity and breeding of cultivated plants. *Chronica Botanica*, Pp.433-434

Voss, R. and Bell, M. (2007). Okra .World Vegetables, 2nd ed. Aspen Publications. Pp 843.

Wankhade, R.V., Kale, P.B., and Dod, V.N. (1995). Genetics of earliness, yield and fruit characters in okra. *PKV Res. J.* **19**(2):117-120.

WARC (Werer Agricultural Research Center), (2007). Annual climate record at Werer Agricultural Research Center. Annual report, Werer Agro Meteorologies Research Section, Werer.

Weerasekar, D. (2006). Genetic analysis of yield and quality parameters in okra [*Abelmoschus esculentus* (L) Moench]. Master of Thesis, University of, Dharwad, India.

William, J.L. (1999). Okra a versatile vegetable crop. *Hort. Technol.* **9**(2): 179-184.

Yadav, J.R., Singh, B., Gaurav M, Sanjeev K., and Sunil K (2007). Correlation coefficient analysis in okra [*Abelmoschus esculentus* (L.) Moench]. *Plant Archives.* **7**(1): 307-308.

Yadav, S.K. and Dhankhar, B.S. (2001). Correlation studies between various field parameters and seed quality traits in okra cv. Varsha Uphar. *Seed Res.* **29**(1): 84-88.

APPENDICES

Appendix I: Analysis of variance for yield and yield contributing traits of 28 Okra genotypes

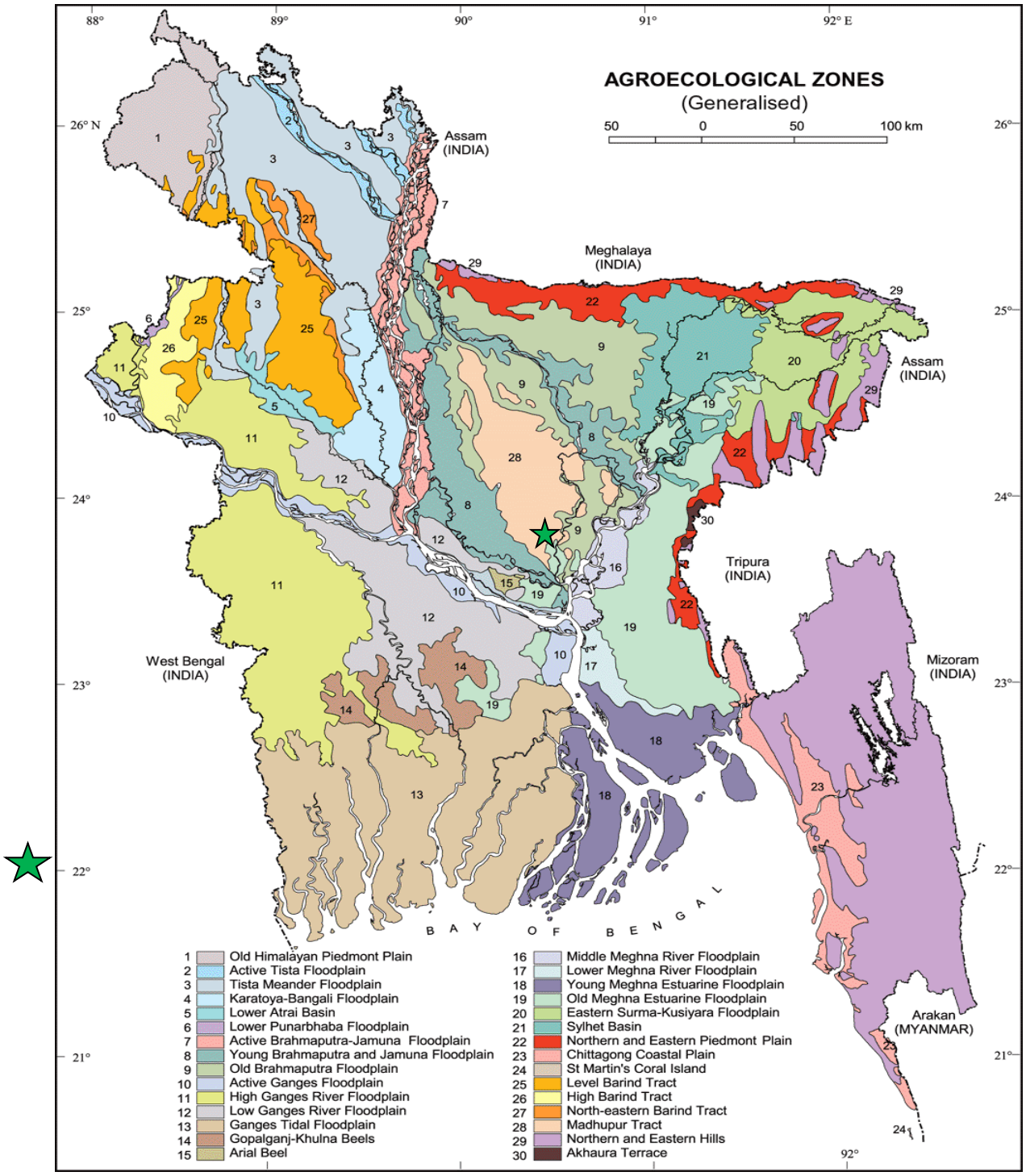
Sources of variation	Mean sum squares											
	df	G (%)	D50%F	DFF	PH	PB	NFP	FL	FD	AFW	SPF	FYP
Replication	2	17.7619	13.5833**	8.3690*	8.5558	0.0595	7.5833	0.0780	0.0758*	1.3465	506.1786**	114.1900
Genotypes	27	157.8607**	14.5445**	12.3792**	775.6125**	2.7076**	61.9224**	5.0863**	0.0628**	28.1022**	245.7831**	30,528.7591**
Error	54	8.1570	2.4969	2.2086	7.0511	0.5144	2.5586	2.3742	0.0197	5.0206	26.9563	3,054.3480

** indicates significant at 0.01 probability level
G (%): Germination (%), DFF: Days to 1st flowering, D50%F: Days to 50% flowering, PH: Plant height (cm), PB: Primary branches, NFP: No. of fruit's per plant, FL: Fruit length (cm), FD: Fruit diameter (cm), AFW: Average Fruit weight (gm), SPF: Seed's per fruit and FYP: Fruit yield per plant (g)

Appendix II. Principal component score I and II

	PCA 1	PCA 2
1	190.23	24.06
2	134.36	0.43
3	106.46	-20.04
4	74.95	-7.38
5	19.18	11.35
6	-1.23	-2.87
7	86.92	-2.87
8	-102.77	-12.60
9	35.34	11.63
10	-10.38	-8.24
11	135.20	-4.65
12	62.94	-6.07
13	27.01	1.90
14	-69.36	-20.74
15	-35.62	4.70
16	-123.11	7.61
17	-49.42	5.80
18	240.66	-12.88
19	-85.61	23.53
20	3.10	3.71
21	35.31	17.20
22	-86.79	-1.46
23	-101.88	18.25
24	-73.26	6.84
25	-47.38	-3.46
26	-110.18	-7.64
27	-81.80	-17.55
28	-172.88	-8.60

Appendix III. Map showing the experimental site under the study



Appendix IV: Morphological, physical and chemical characteristics of initial soil (0-15 cm depth) of the experimental site

A. Physical composition of the soil

Soil separates	%	Methods employed
Sand	36.90	Hydrometer method (Day, 1965)
Silt	26.40	Do
Clay	36.66	Do
Texture class	Clay loam	Do

B. Chemical composition of the soil

Sl. No.	Soil characteristics	Analytical data	Methods employed
1	Organic carbon (%)	0.82	Walkley, 1947
2	Total N (kg/ha)	1790.00	Bremner and Mulvaney, 1982
3	Total S (ppm)	225.00	Bardsley and Lanester, 1965
4	Total P (ppm)	840.00	Olsen and Sommers, 1982
5	Available N (kg/ha)	54.00	Bremner, 1965
6	Available P (kg/ha)	69.00	Olsen and Dean, 1965
7	Exchangeable K (kg/ha)	89.50	Pratt, 1965
8	Available S (ppm)	16.00	Hunter, 1984
9	pH (1:2.5 soil to water)	5.55	Jackson, 1958
10	CEC	11.23	Chapman, 1965

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

Appendix V: Monthly average record of air temperature, rainfall, relative humidity, sunshine hours of the experimental site during study period from March 2017 to July 2017.

Month	Air temperature(◦c)		Relative humidity (%)	Rainfall (mm) total	Sunshine (hr)
	Maximum	Minimum			
Mar, 2017	35	21	74	88	8.3
April, 2017	34	23	76	200	7.5
May, 2017	35	24	79	580	4.0
June, 2017	32	25	80	553	3.0
July, 2017	33	26	83	317	4.0

Source: Bangladesh Meteorological Department (Climate & Weather Division) Agargaon, Dhaka-1212