COMBINING ABILITY AND STABILITY ANALYSIS IN OKRA (*Abelmoschus esculentus* (L.) Moench)

A PhD DISSERTATION

BY

PALLAB KANTA DASH

Registration No. 1405210

DEPARTMENT OF GENETICS AND PLANT BREEDING
HAJEE MOHAMMAD DANESH SCIENCE AND TECHNOLOGY
UNIVERSITY DINAJPUR-5200

JANUARY, 2022

COMBINING ABILITY AND STABILITY ANALYSIS IN OKRA (*Abelmoschus esculentus* (L.) Moench)

Thesis submitted to the
Hajee Mohammad Danesh Science and Technology University, Dinajpur
in partial fulfillment of the requirements for the

Degree of

DOCTOR OF PHILOSOPHY

IN

GENETICS AND PLANT BREEDING

BY

PALLAB KANTA DASH

Registration No. 1405210

DEPARTMENT OF GENETICS AND PLANT BREEDING
HAJEE MOHAMMAD DANESH SCIENCE AND TECHNOLOGY UNIVERSITY DINAJPUR-5200

JANUARY, 2022

COMBINING ABILITY AND STABILITY ANALYSIS IN OKRA (*Abelmoschus esculentus* (L.) Moench)

Thesis submitted to the
Hajee Mohammad Danesh Science and Technology University, Dinajpur
in partial fulfillment of the requirements for the

Degree of

DOCTOR OF PHILOSOPHY IN
GENETICS AND PLANT BREEDING
BY
PALLAB KANTA DASH
Registration No. 1405210

Approved as to style and contents by

Prof. Dr. Bhabendra Kumar Biswas
Supervisor

Prof. Dr. Md. Hasanuzzaman
Member, Supervisory Committee

Prof. Dr. Md. Hasanuzzaman
Chairman, Examination Committee

DEPARTMENT OF GENETICS AND PLANT BREEDING
HAJEE MOHAMMAD DANESH SCIENCE AND TECHNOLOGY
UNIVERSITY DINAJPUR-5200
JANUARY, 2022

DEDICATED

TO

METAL AGRO LIMITED

A research oriented seed company

কৌলিতত্ত্ব ও উদ্ভিদ প্রজনন বিভাগ
হাজী মোহাম্মদ দানেশ বিজ্ঞান ও প্রযুক্তি বিশ্ববিদ্যালয়, দিনাজপুর
DEPARTMENT OF GENETICS AND PLANT BREEDING
Hajee Mohammad Danesh Science and TechnologyUniversity, Dinajpur

---

Date: -----------------

Certification

This is to certify that the thesis entitled **“Combining ability and stability analysis in okra (*Abelmoschus esculentus* (L.) Moench)”** a study on okra, prepared by the examinee, bearing Registration No. 1405210, Session 2014-15, Department of Genetics and Plant Breeding, Hajee Mohammad Danesh Science and Technology University, Dinajpur, for the award of the degree of Doctor of Philosophy in Genetics and Plant Breeding, is a record of original research work carried out by him under my supervision. The work is original and unique one and to the best of my knowledge, no part of the thesis has been produced elsewhere for any degree.

(Professor Dr. Bhabendra Kumar Biswas)
Supevisor
Department of Genetics and Plant Breeding
Hajee Mohammad Danesh Science and Technology
University, Dinajpur, Bangladesh

Phone : + 880-531-65429 Extension 144, Fax : +880-531-61311,
(Attention : Chairman, Dept. of Genetics and Plant Breeding)

DECLARATION

This dissertation entitled “**Combining ability and stability analysis in okra (*Abelmoschus esculentus* (L.) Moench)”** submitted to the Hajee Mohammad Danesh Science and Technology University (HSTU), Dinajpur, Bangladesh for the degree of Doctor of Philosophy is entirely own research work which outlined and carried out by me. The dissertation or its part in any form has not been submitted anywhere else for obtaining any degree nor does it contain results of any collaborative study except where otherwise stated.

The Author
Department of Genetics and Plant Breeding
Hajee Mohammad Danesh Science and Technology
University, Dinajpur, Bangladesh

JANUARY, 2022
HSTU, Dinajpur
Bangladesh

ACKNOWLEDGEMENTS

My first thanks go to Almighty God, the reason being that this (completing research and submitting dissertation) is possible only when circumstances beyond human control line up with the human's plan. All those circumstances such as being alive, being healthy, having peace. I believe, is under his control, therefore, I really want to thank God, the uncaused causer, the unmoved mover and the ultimate reality.

Secondly I wish to express my deepest gratitude and soulful respect to my supervisor, **Professor Dr. Bhabendra Kumar Biswas***, Department of Genetics and Plant Breeding, HSTU, Dinajpur, Bangladesh, for his valuable guidance, advice, constructive suggestions, constant encouragement, fruitful criticism, endless patience and untiring supervision throughout the entire period of this research work as well as in preparing this dissertation.*

I feel a great pleasure in getting this proud privilege offering my sincerest and devoted thanks to my co supervisor **Professor Dr. Md. Hasanuzzaman***, Department of Genetics and Plant Breeding, HSTU, Dinajpur, Bangladesh for his continued guidance, support, encouragement and invaluable suggestions through the research period and very much critical review of the manuscript.*

I am very grateful of getting this privilege in offering my sincere and devoted thanks to **Professor Dr. Md. Abul Kalam Azad***, Department of Genetics and Plant Breeding, HSTU, Dinajpur, Bangladesh for his worthy suggestion, ever willing help and unbiased attitude throughout the course of this investigation.*

It is a great pleasure to express the immense indebtedness and generosity of gratitude to **Professor Dr. Arifuzzaman,** *Chairman, Department of Genetics and Plant Breeding, HSTU, Dinajpur, Bangladesh for his moral encouragement and enthusiastic support during the course of the study. Also indebted to* **M. Waliur Rahman***, Assistant professor and* **Md. Tajul Islam***, Sr. Lab. Tech. and others staff of Genetic and Plant Breeding department, HSTU for their generous help.*

I am highly thankful to **Eng. Sadid Jamil***, Managing Director of Metal Agro Limited and* **KID***.* **Afzal Husain** *Sr. General Manager, Metal Agro Limited for their great permission*

to study Ph.D research program with encouragement and granted leave for this study and preparation of dissertation or manuscript.

I am also highly indebted to all my staff of R and D Farm, Metal Agro Limited, Nagar chanti, Kawapukur, Debigonj, Panchagarh for experimental space with timely crop management out of a lot of research experiments of other vegetables crops.

My sincere appreciation goes to ***Dr. Harun Or Rashid****, Senior Scientific Officer, Bangladesh Agriculture Research Institute (BARI) for his generous help in analysis of experimental data, good suggestion and improvement of the manuscript.*

Though thank is a taboo in friendship, my conscience does not permit to refrain myself from expressing my heartfelt feeling towards my beloved friends ***Abdul Hannan Masum, Md. Shohidul Alam Jahangir, Md. Tofael Ahmed, Dr. Soriful Islam, Dr. Md. Sha Newaz Talukder*** *who gave direct and indirect sympathetic touch for completion of my research work and their jolly company made my life richer.*

My vocabulary fails to get words to express deep sense of gratitude and indebtedness to my parents, my father ***Abani Kanta Dash****, my mother* ***Aseema Rani Dash****, my wife* ***Vaswaty Rani Ringky*** *and my two kids* ***Argho*** *and* ***Rai****, my younger brother* ***Dr. Happy Kumar Dash*** *and his family and my elder sister* ***Anjana Dash Mita*** *and her family for their everlasting love, constant encouragement, prayer support and sacrifice, without which this dream could not have become a reality. They are there every step of the way; they hold my hand throughout the long journey, they are truly the wind beneath my wings. I also wish to express my deepest gratitude and respect to my family members for their everlasting love and support.*

Lastly the presentation that follows is the work assisted by many seen and unseen hands and minds, I am grateful to all of them.

The Author

Combining ability and stability analysis in Okra (*Abelmoschus esculentus* (L.) Moench)

ABSTRACT

The experiments were conducted at Research and Development Farm under Metal Agro Limited, Nagarchanti, Debigonj, Panchagarh during the period from August, 2014 to March, 2017 on okra (*Abelmoschus esculentus* (L.) Moench). The investigation began with fifty genotypes for preliminary evaluation and identification of fruit yield contributing characters. After biometrical analyses for means, correlations and cause and effect, fruit yield per plant, four characters viz. plant height at 100 days, fruit length (cm), fruit weight (g) and number of fruits per plant, appeared as the most effective characters to increase fruit yield per plant but among the characters, fruit length showed considerable heritability (h^2_b=53.30%), therefore, except this character, other three characters might improve through only selection breeding. The fifty genotypes were grouped into six clusters by D^2 statistics and the genotypes collected from different sources were included in the same cluster or in different clusters, suggested migration of okra genotypes were depended upon humans settled in different regions of the world. Seven parents were selected on the basis of mean values and positive and significant GCAs and then twenty one experimental hybrids were produced from these in half-diallel fashion. Out of seven parents, P3, P5 and P6 accessions showed positive and significant GCAs for fruit yield per plant. Moreover, these three accessions were separately distributed in three different clusters, and these accessions found to be excellent general combiners for the development of okra hybrids. From the set of twenty-one experimental hybrids, thirteen hybrids exhibited positive and significant SCAs for fruit yield per plant but on the basis of mean performances and positive and significant SCAs. Three combinations such as P3 * P7, P2 * P4 and P5 * P6 were outstanding for increasing fruit yield in okra. The Vr-Wr graphs on thirteen characters were constructed to reveal additive, dominant, over dominant, epistatic and complementary gene interactions. No non-allelic gene interaction was observed for fruit yield per plant. Heterosis was estimated over better parent, mid parent and two check varieties, Check-1 (Green Finger) and Check-2 (BARI Darosh-1) for thirteen characters. Fruit yield per plant in three crosses showed highly significant heterosis over two check varieties. Response and stability of eight hybrids were evaluated through Eberhart and Russel model. The experimental hybrids were evaluated in four different environments viz.E1=kharif 1of 2015, E2=Kharif 1 of 2016. E3=Kharif 2 of 2016 and E4= Kharif 1 of 2017. The environmental indices revealed that E1=Kharif 1 of 2015 was the most favorable environment and E3=Kharif 2 of 2016 was the worst environment for the evaluating hybrids. The phenotypic index of the hybrid showed that, P6 (1203) * P7 (1205) with fruit yield 540.72 g/plant followed by the P5 (1189) * P7 (1205) with 469.08 g/plant and P5 (1189) * P6 (1203) with 448.18 g/plant exhibited outstanding in performance across the four Kharif seasons in between 2015 to 2017. However, the stability parameters (bi and s^2di) of these three hybrids were also reasonable. Therefore, these three hybrids may be advanced with a view to release new okra hybrid varieties. Furthermore, it is suggested that Kharif 1 (March–June) is the suitable season for cultivation of okra in our country.

CONTENTS

CONTENTS (Contd.)

CONTENTS (Contd.)

CONTENTS (Contd.)

CONTENTS (Contd.)

CONTENTS (Contd.)

LIST OF TABLES

LIST OF TABLES (Contd.)

LIST OF TABLES (Contd.)

LIST OF FIGURES

LIST OF APPENDICES

ABBREVIARIONS AND SYMBOLS

Abbreviation/Symbol	Elaborative
ANOVA	Analysis of variance
AVRDC	Asian Vegetables Research and Development Centre
BAU	Bangladesh Agricultural University
BARI	Bangladesh Agricultural Research Institute
BBS	Bangladesh Bureau of Statistics
CD	Critical difference
CV	Co-effecient of variation
d.f	Degree of freedom
et.al.	Et alu = Other people
FAO	Food and Agriculture Organization
HSTU	Hajee Mohammad Danesh Science and Technology University
i.e.	id est (That is)
σ^2A	Additive variance
σ^2D	Dominance variance
σ^2e	Error variance
σ^2g	Genotypic variance
σ^2ph	Phenotypic variance
h^2b	Heritability in broad sense
Ha	Hectare
g	Gram
GA	Genetic advance
GCA	General combining ability
Kg	Kilogram
LTSL	Lal Teer Seed Limited
LSD	Least significant difference
MOA	Ministry of Agriculture
MAL	Metal Agro Limited
MP	Mid – parent
NSB	National Seed Board
PCV	Phenotypic co-efficient of variation

Abbreviation/Symbol	**Elaborative**
pH	Negative logarithm of hydrogen ion (H+) concentration
TSP	Triple super phosphate
RCB	Randomized complete block
R and D	Research and Development
rp	Phenotypic correlation
rg	Genotypic correlation
SCA	Specific combining ability
SE	standard error
Viz.	namely

CHAPTER I

INTRODUCTION

Okra (*Abelmoschus esculentus* L. (Moench) is an economically important vegetable crop grown in tropical and sub-tropical areas of the world. This vegetable is suitable for cultivation as a garden crop as well as on large commercial farms. It is grown at commercial scales in Bangladesh, India, Turkey, Iran, Western Africa, Yugosalvia, Afganistan, Pakistan, Burma, Japan, Malayasia, Brazil, Ghana, Ethiopia, Cyprus and the Southern United States. In Bangladesh, about 54,103 metric tons produced from 2,864 hectares of land in 2018-2019 (BBS 2019). There is no actual statistics of okra seed requirement and demand. But it assumed that okra seed will be needed about 4 folds higher of present supply. About 15 MT of Okra seed might be needed per year in Bangladesh. The annual requirement of vegetables in Bangladesh is about 11.0 million tons, which is about 5 times higher than the present production. So to meet up the deficit condition, we should rapidly increase our vegetable production as well as quality seed. Quality seeds have been identified as major constraints for low production of vegetables in Bangladesh. The major problems of low yields of different vegetables in Bangladesh are climatic change, a biotic stresses and low level of quality seed use. The important consideration is now to plan for development of varieties that would be high productive and suits the present changing climate/ environment factors.

Okra provides an important source of vitamins, calcium, potassium and other mineral matters which are often lacking in the diet in developing countries (IBPGR, 1990). The composition of edible portion of okra in hundred gram of the fruit contains about energy 35.0 k-cal, 89.6 g moisture, 6.4 g carbohydrates, 1.9 g protein,0.2 g fat, 1.2 g fiber, 0.7 g minerals, 56.0 mg phosphorus, 6.9 mg sodium, 30.0 mg sulphur, 66.0 mg calcium, 0.35mg iron,103.0 mg potassium, 53.0 mg magnesium, 0.19 mg copper, 0.01 mg riboflavin, 0.07 mg thamine, 0.06 bmg nicotinic acid, 13.10 mg vitamin c and 8.0 mg oxalic acid. Source: (Gopalon *et al.*, 2007). So it is obviously contributing to improve nutritional status of the people, particularly in vulnerable groups of people.

Okra (*Abelmoschus esculentus L.* (Moench) 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 though it was originated from Africa but it 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 okra (*Abelmoschus esculentus L.* (Moench) - some scientists argue that one putative ancestor (*A. tuberculatus*) was 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 suggested that the area of domestication was in Ethiopia or North Egypt, but no definite proof was available (Sorapong, 2012). Its origin by hybridization with *A. manihot* is difficult to accept even if its presence, mentioned in the flora of West Africa (Hutchinson and Dalziel, 1958) was not recently confirmed in this area and herbarium samples are lacking.

Okra was previously included in the genus *Hibiscus*, section *Abelmoschus* in the family Malvaceae in the genus *Hibiscus*. Later, it was designated to *Abelmoschus,* which is distinguished from the genus *Hibiscus* (Sorapong, 2012). 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 (Tripathi*et al.*, 2011). Latin bi-nomial names for okra are *Abelmoschus esculentus* and *Hibiscus esculentus* (Kumar *et al*. 2010) and it is commonly known as Bhindi in India, Dharos in Bangladesh, Krajiabkheaw in Thailand, Okra, Ochro, Okoro, Quimgombo, Quingumbo, Gombo, kopi, Arab, Kacang Bendi and Bhindi in South East Asia. However, in Middle East it is known as Bamia, Bamya, or Bamieh and Gumbo in Southern USA and Lady's Finger in England (Ndunguru and Rajabu 2004). On the other hand, in Portuguese and Angola, okra is known as Quiabo, and as Quimbombo in Cuba Gombocommun Gombo, Gumbo in France, Mbamia and Mbinda in Sweden, and in Japan. Lastly it is also found in Taiwan where it is called Qui Kui (Siemonsma and Kouame, 2000).

There are significant variations in the chromosome numbers and ploidy levels of different species in the genus *Abelmoschus.* The lowest number reported is 2n=56 for *A.*

angulosus (Ford, 1938) whereas the highest chromosome number reported are close to 200 for *A. manihot* var. *Caillei* (Singh and Bhatnagar, 1975; Siemonsma, 1982a, 1982b). The chromosome number (2n) of *A. esculentus L.* (Moench) has been variably reported by different authors. The most frequently observed somatic chromosome number however is 2n=130, although Datta and Naug (1968) suggested that the numbers 2n=72,108,120,132 and 144 are in regular series of polyploids with n=12. The existing taxonomical classifications at the species level in the genus *Abelmoschus* are unsatisfactory. Detailed cytogenetical observations on Asian material of okra and related species are likely to provide more examples of the existence of amphidiploids in the genus (Siemonsma, 1982a,Tripathi *et al.*, 2011).

Climatic change is a big issue in vegetable production. The resulting perturbations of the climatic and eco system have been named climatic change. A significant change in climate on a global scale will impact agriculture and consequently affect the world's food supply. More erratic rainfall patterns and unpredictable high temperature spells will consequently reduce crop productivity. Vegetables are generally sensitive to environmental extremes, and thus high temperature and limited soil moisture are the major causes of low yields in the tropics and will be further magnified by climate change. Moreover, increasing temperatures droughts, flooding and salinity will be major limiting factors in sustaining and increasing okra productivity. Okra requires a long warm and humid growing period. It can be successfully grown in hot humid areas. It is sensitive to frost and extremely low temperature. For normal growth and development, a temperature between 24^{o}C and 28^{o}C is preferred. At 24^{o}C the first flower bud may appear in the third leaf axil whole at 28^{o}C it may appear in sixth leaf axil. This higher position is not necessarily accompanied with a delay in time because at higher temperatures the plants grow faster and the higher position is reached earlier. For faster plant growth still higher temperature helps though it delays the fruiting. But at higher temperatures beyond 40^{o}-42^{o}C flowers may desiccate and drop, causing yield losses. For seed germination optimum soil moisture and a temperature between 25^{o}C and 35^{o}C is needed with the fastest germination observed at 35^{o}C.Beyond this range the germination will be delayed and weak seeds may not even germinate. Strong attempt should be taken to develop hybrid varieties of vegetables by public and private sector. Incentive supports and concessions to be provided to private sector to expand their activities in order to achieve increased quality hybrid seed production. hybrid is the progenies of a cross between genetically dissimilar parent's i.e "hybrid seeds are the first filial generation of two distant and distinct parental lines of the same species" and the process of development of hybrid is called hybridization. Hybridization is the most important method of crop improvement. The crop improvement may be done successfully by introduction, selection and hybridization for specific traits, especially increasing productivity, biotic and a biotic stress resistance, nutritional quality enhancement and improvement of their desirable horticultural traits. Some general impact of hybrid variety 20-100% higher yield, more uniform fruits, generally day neutral and year round cultivable, early and quick harvestable, may be drought and heat tolerant and comparatively tolerance to pest and diseases.

The use of hybrid vegetable seed is very small in Bangladesh. At present only 1.4% hybrid seed is available out of the total requirement whereas the use of other countries like Japan 98%, China 61%, India 9% and Europe 42% meet up hybrid seeds demands. Although okra is a common and popular vegetable in Bangladesh but quality variety i.e. widely adaptable and high yielding varieties are not sufficient. There are some companies and government organizations are engaged in organized research and development work in Bangladesh namely Lal Teer (former Eeast West) seed, BARI, ACI seed, Metal seed, Supreme seed, BRAC seed, Getco seed, A.R. Maliks seed etc. They are all doing research to develop hybrid okra. Lal Teer has only one of their own okra hybrids named Green Finger. Metal seed is conducting research on okra to develop high yielding and widely adaptive hybrid variety. Okra is said to be very useful against genitor urinary disorders, Spermatorrhoea and chronic dysentery (Nadkarni, 1927). Its medicinal value has also been reported in curing ulcers and relief from hemorrhoids (Adams, 1975). Nutritionist has recommended the 200g of vegetables are to be consumed per day a healthy by an adult person. Rural consumption of leafy and non-leafy vegetables has remained more or less the same over the past two decades after increasing over the preceding 30 years. Fruit consumption has declined in rural areas after more than doubling in the 1970s. With an average national per capita consumption of 23 g of leafy vegetables, 89 g of non-leafy vegetables and 14 g of fruit, the average Bangladeshi eats a total of 126 g of fruit and vegetables daily. This is far below the minimum daily consumption of 400 g of vegetables and fruit recommended by FAO and the World Health Organization (WHO) (Fresh Plaza, 2020).

Crop improvement depends on the magnitude of genetic variability present in the base population. The expected improvement in yield components primarily depends on the nature and magnitude of heritable portion of total variation. Selection based on a single character may not always be effective. On the other hand, it is very cumbersome process for a breeder to consider a large number of component characters simultaneously in selection procedure. The presence of genetic variability is of utmost importance for any breeding program and due to this reason, plant breeders have emphasized the evaluation of germplasm for the improvement of crop yield as well as for utilization in further breeding programs. Absolute variability in different characters cannot be the decisive factor in deciding which character is showing the highest degree of variability. Furthermore, relative values of phenotypic and genotypic coefficients of variation give a reliable idea about the magnitude of variability present in a population. In this way, it is indispensable to split the overall variation into genetic and non-genetic components and to standardize this by obtaining the coefficients of phenotypic and genotypic variability.

The worth of germplasm collection depends on the number of accessions contained and their diversity, which are imperative for a reasonable utilization of plant genetic resources (Olaoye *et al.,* 2009; Ade-Oluwa and Kehinde, 2011). Genetic diversity is the variability among different genotypes of a species (Bello *et al.,* 2012ab). Genetic diversity plays a major role in crop improvement for identification of distinctive accessions vital for the curators of gene banks (Bello *et al.,* 2011; Osekita and Akinyele, 2008). In any diversity studies, morphological characterization is being recommended as the first step to be taken before in–depth molecular and biochemical analyses are employed (Akash *et al.,* 2013). The success of any progress in a breeding programme however, is dependent not only on the magnitude of genetic variability present in that population, but also on the extent to which its desirable characters are heritable (Olawuyi *et al.,* 2015, Bello *et al.,* 2014ab). The variability available in a population can be partitioned into heritable and non-heritable components with aid of genetic parameters, such as, genotypic coefficient of variation, heritability and genetic advance, which also serve as a basis for selection (Seth *et al.,* 2016). Selection methods and the expected genetic response to selection in crops are determined by the magnitude of heritability estimate of the character for which selection is to be made. Cluster analysis is also a powerful tool to measure genetic divergence among genotypes in any crop. As okra production exhibits a major economy role of a nation, selection of high yielding edible fruit cultivars is very important. Correlation and Path Analysis are considered to be important and efficient tools useful for getting information regarding association of various characters. This is beneficial for plant breeder in developing high yielding cultivar by determining the component traits on which selection can be based for improvement of yield (Rynjah *et al.*, 2020).

Correlation coefficient measures the relationship between two or more series of variable. The genotypic correlation coefficient provides a measure of genotypic association between different characters, while phenotypic correlation includes both genotypic as well as environmental influences. In fact, the component characters influence the yield of economically important characters, such as grain in serials, lint yield in cotton, cane yield in sugarcane etc. Actually there may not be genes for yield *per se*, but it is a result of actions and interactions of the genes, which govern the inheritance of component characters (Grafius, 1959) and opined that the yield improvement through component traits. The degree of influence of one variable on the other can be determined most accurately and precisely by path coefficient analysis (Wright, 1921) which helps in partitioning the correlation coefficient into direct and indirect effects (Dewey and Lu, 1959). This method is helpful to breeders as it determines which character shows close association with yield and contributes indirectly through the other yield components.

For sorting out the total correlation into direct and indirect effects path coefficient analysis helps and is useful for choosing the most useful traits to be incorporated for yield improvement through selection. The study of correlation between plant characters is of great importance to a plant breeder as it provides a measure of the degree of association between yield and other yield attributes. The path coefficient analysis is partitioned the correlation in direct and indirect effects and thus may be useful in choosing the characters that have direct and indirect effects on yield. Hence, study of correlations and path coefficient analysis of yield would be of help in selection of yield component traits in the genetic improvement of quantitative traits, which are positively correlated (Balai *et al.*, 2014). In complex inherited traits, such information reveals the possibility of simultaneous improvement of different attributes and also helps in increasing the efficiency of selection.

Genetic analysis provides a guide line for the assessment of relative breeding potential of the parents or identifies best combiners in crops (Khattak *et al.*, 2004; Weerasingh *et al.*, 2004; Devi *et al.,* 2005), which could be utilized either to exploit heterosis in F_1 or to accumulate fixable genes to evolve variety. The information about the relative contribution of components of variation viz., additive and non-additive, is essential for effective crop improvement program. In order to apply an optimum breeding strategy for targeted quantitative traits, a genetic analysis of those traits needs to be performed (Nistor *et al.,* 2005). Diallel analysis of self and cross pollinated populations is used to study the genetic control of quantitative traits (Jinks and Hayman, 1953; Hayman, 1954; 1958) and to assess general and specific combining abilities (Griffing, 1956). The success of a breeding program depends on the variability of the initial material. Combining ability analysis of single crosses generated from crossing elite and diverse genotypes from the germplasm of okra has been made by several researchers (Kumar and Thania, 2007). Diallel mating design has been used extensively by several researchers to measure general and specific combining ability in okra (Bendale *et al.,* 2004; Jindal and Ghai, 2005; Dahake and Bangar, 2006; Bhalekar *et al.,* 2006; Jindal *et al.,* 2009; Singh *et al.,* 2009; Wammanda *et al.,* 2010). In literature, both additive and non-additive genetic systems, controlling pod yield and yield-relating traits in okra, have been reported (Jindal *et al.,* 2009; Singh *et al.,* 2009; Wammanda *et al.,* 2010). However, the major part of genetic variation for yield and its components was conditioned due to higher magnitude of non-additive genetic effects (Jindal *et al.,* 2009; Wammanda *et al.,* 2010).

Combining ability of the parents is becoming important in plant breeding, especially in hybrid production. It is useful in connection with the testing and compare the performance of the lines in hybrid combinations. Information on the general and specific combining abilities will be helpful in the analysis and interpretation of the genetic basis of important traits. GCA and SCA provide a guideline for the nature of gene action involved in the expression of economic traits. The genetic information obtained from this method is considerable use for selecting parental lines and their crosses to develop and release new high yielding genotypes (El-Sherbeny *et al.* 2005) found that the magnitudes of additive genetic variance (σ^2 A) were larger than those of non-additive ones (σ ^{2}D) for most okra economic traits. On the other hand, Solankey and Singh (2010) stated that non-additive genetic variance was higher than the additive one for days to flowering, plant height, number of branches, number of pods per plant and pod yield per plant. However, Singh *et al.* (2011) indicated that both additive and non-additive gene action involved in the inheritance of days to flowering, number of pods per plants and pod yield per plant. Combining ability analysis provides clues to the usefulness of individuals to be employed as the parents in the hybridization programme as well as simultaneously to screen the hybrids. Besides, it also ascertains the magnitude and nature of quantitative genetic variation which could be of great use to plant breeders for deciding efficient and effective breeding programme. Study of gene action involved is very crucial for choosing of the best parents and crosses for okra yield improvement and has been reported by many researchers (Reddy *et al.,* 2012; Adiger *et al.,* 2013).

Heritability is the portion of genotypic variance to phenotypic variance, which indicates the relative success of selection. It is useful in selection of elite genotype from diverse genetic population. Heritability is that portion of variation transmitted from parent to offspring. Higher the heritable variation greater will be the possibility in fixing the characters by selection. Hence, studies on heritability are of more important to be analyzed, whether the observed variation for a trait is heritable or not. Planning and execution of a breeding program for the improvement of quantitative attributes depends, to a great extent, upon the genetic magnitude of genetic variability. The genotypic and phenotypic coefficient variation are helpful in exploring the nature of variability in the breeding population whereas, the estimate of heritability provides index of transmissibility of characters. Co-efficient of variation is useful in the assessment of genetic variability for the particular character. Heritability denotes the proportion of phenotypic variation due to genotypes thus help the breeders to select the elite variety for a character. Genetic advance denotes the improvement in the mean genotypic values of selected families over base population and thus helps the breeder to select the progenies in the earlier generation itself (Singh *et al.*, 2006).

Pod yield and several yield-contributing characters' lack stability due to strong environmental influence, suggesting the need for breeding for specific environment (Ariyo, 1990). Improvement of complex characters such as pod yield may be accomplished through the component approach of breeding. This method in general assumes strong associations of yield with a number of characters making up yield and simpler inheritance for these component characters. It is known that phenotypic expression of quantitative traits is highly influenced by environmental fluctuations (Allard and Bradshaw, 1964). In multi-environment trails genotype x environment interactions is often exist (Kang, 1998). If there is no interaction, there is no need to conduct yield trails over different locations/environments, as trial may be conducted at only one location and providing universal results (Gauch and Zobel, 1996). Such an ideal situation does not exist in reality. Genotype x environment interaction is expected in plant breeding experiments that involve cultivars of diverse genetic background and diverse test sites (Kang *et al.,* 2006). Genotype x environment interaction study is important to breeders to develop not only improved but also stable varieties, suitable for a particular location or multi-location. The goal of any plant breeding programme is to develop cultivars with high yielding potential with stable performance over a wide range of environments (Olayiwola and Ariyo, 2013). Performance of various okra genotypes keeps varying in varying environmental conditions. Thus, it is imperative to study the performance of a crop in more than one environment to identify genotypes, which give high stability for various yield related traits over a wide range of environment (Jindal *et al.,* 2008). The phenomenon of genotype x environment interaction is a common problem in plant breeding program and has long been a challenge to plant breeder. A variety developed by a plant breeder is usually grown at different locations for many years under different conditions. Assessing any genotype without including its interaction is incomplete and thus limits the accuracy of yield estimates. It is usually preferable to estimate yield stability and reliability values with reference to all GE interaction effects (Ezekiel *et al.,* 2011).

The efficiency and success of hybrid okra breeding depends on the contribution of heterotic effects from the superior inbred lines. The superior cross combination may be exploited as commercial single cross. Usually, the hybrid development programme in okra involves development of inbred lines, evaluation of inbred lines, crossing of selected inbreeds and production of hybrids.

The work was undertaken to fulfill the following objectives.

1. To characterization and screening of okra genotypes.
2. To find out the relationship between yield and yield contributing characters of okra genotypes.
3. To study on combining ability, heritability and heterosis.
4. To search out the best stable hybrids.

CHAPTER 2

REVIEW OF LITERATURE

Okra (*Abelmoschus esculentus* L. (Moench) is one of the important vegetable crops grown in tropical and sub-tropical areas of the world. Many researchers around the world have performed different works on different aspects for the improvement of this crop. A brief review of literature pertaining to the objectives of the present study “Combining ability and stability analysis in okra (*Abelmoschus esculentus* L.)” is presented under the following heads.

2.1 Varibility and diversity in okra

Raval *et al.* (2018) experimented on two parents; female VRO-6 and male AOL-09-02, its F1 and F2 population of okra. The material was evaluated in non-replicated trial as segregating F2 generation is involved. Observations were recorded on twelve characters showing considerable variability. PCV was higher than the respective GCV for all the traits. The high magnitude of PCV and GCV was observed for number of branches/plant at final harvest followed by fruit yield/plant, internodal length, number of fruits per plant and plant height at final harvest. High genetic advance coupled with high heritability was observed for most of the characters. It indicated that additive gene action was more important for these characters.

Kumar *et al.* (2019) evaluated sixty-eight okra accessions for genetic variability, heritability, and genetic advance in okra at Horticulture Research Centre, SVP University of Agriculture and Technology, Meerut (U.P.) during the year 2014-15 and 2015-16. Genetic variability analysis on sixty-eight genotypes of okra (pooled data analysis) revealed high magnitude of genetic variability for the traist viz., pod yield and plant height under study. High magnitude of genotypic coefficient of variation (>20%) for number of pod yield and plant height indicated high degree of genetic variability offering great scope for selection of these characters. The genotypes under study showed moderate heritability (30-60%) showed the environmental influence. High heritability coupled with high genetic advance for the traits like plant height and pod fruit yield per plant indicated the involvement of additive gene action and more chances of fixing by selection to improve such traits. The genotypes viz., B-02, KS-442 are noticed with great potential and can be utilized for improvement of okra germplasm.

Singh *et al*. (2020) investigated on okra during summer season of 2018 in Tarai region of Uttarakhand. The experimental material utilized for this study consisted of 59 genotypes including 15 parents (11 lines, 4 testers) and 44 crosses of okra. The analysis of variance showed that significant genetic differences were present among genotypes for all the characters studied. This suggested that there was adequate amount of genetic variability among the experimental material and hence, a greater scope for the improvement of concerned characters through selection. The values of PCV were higher than that of GCV for all the thirteen characters indicating influence of environmental effects in the expression of these characters. Moderate to high GCV together with moderate to high heritability and genetic advance as per cent of mean was reported for majority of the characters under study except days to 50% flowering and fruit length, which indicated predominant additive gene action. Thus these traits have ample scope for the improvement of concerned traits through selection.

Alake (2020) examined okra [*Abelmoschus esculentus* (L.) Moench] landraces found in Nigeria as sources of genetic variation offering potential to improve agro-morpho-nutritional traits and broaden the gene pool. Objectives of this investigation were to: (1) assess variability of agro-morpho-nutritional traits in okra landraces sourced from five agroecological zones in Nigeria, and (2) estimate divergence among the germplasm. The landraces were evaluated in field experiments over a period of 2 years at the research farm of the Federal University of Agriculture, Abeokuta, Nigeria. Principal component analysis, cluster analysis, and Mahalanobis D2D2 statistics were employed to study the diversity pattern. Differences existed for all evaluated traits among landraces. Genotypes NGB00378b, NGB00297, NGB00347, NGB00293, and NGB00350 combined high seed mineral concentrations with high yield potential. A genotype × year interaction was present, as reflected by relatively low broad-sense heritability (<30%) and genetic advance (GA) (<10%) for pod yield and pod width (PDW), which limits potential for improvement. Heterosis breeding could be effectively used to improve K and Mg, as these traits expressed high variation and broad-sense heritability coupled with moderate GA. Using D^2 divergence analysis, landraces were separated into seven distinct clusters, with no phylo–agroecological pattern of diversity. Based on the present study, selection for a trait in 1 year may not provide the same benefit in other years due to year-to-year fluctuations in environmental conditions, evaluation in more than 1 year is required.

Gerrano (2017) studied on okra to assess the genetic variability and heritability estimates using micronutrient content such as iron, zinc and manganese in the immature green fruits of okra plant for future use in the okra breeding programme to increase nutritional value. The experiment was conducted at the Roodeplaat research farm of the Agricultural Research Council in a randomized complete block design replicated three times. The analysis of variance showed highly significant differences for all of three micronutrients recorded. This indicated that there was high level of genetic differences among the genotypes studied. Phenotypic and genetic coefficient of variations, broad-sense heritability (repeatability) and genetic advance were also estimated for iron, zinc and manganese, which could be exploited in selecting suitable and potential okra parents when breeding for high micronutrient contents. The phenotypic coefficient of variation ranged from 23.04% in Zn to 75.48% in Fe. Furthermore, the highest values for the genetic coefficient of variation were found in Fe. High heritability estimates were observed in all mineral elements Fe (99.86%), Mn (99.72%) and Zn (96.32%) evaluated indicating potential genetic gain as percentage of mean for Fe (155.38), Mn (69.20) and Zn (45.79), respectively when breeding for these micronutrient traits. The present study revealed the genetic potential of the genotypes studied and their importance for use in the quality-breeding programme aimed towards addressing malnutrition in South Africa.

AdeOluwa and Kehinde (2011) evaluated a collection of 35 accessions of West African Okra (*Abelmoschus* caillei) for variability in 20 morphological and agronomic traits (qualitative and quantitative traits). Genotypic and phenotypic variances, genotypic (GCV) and phenotypic coefficients of variation (PCV), heritability, genetic advance of the characters were calculated. The accessions demonstrated wide variability for all characters evaluated. Variation was expressed in all qualitative traits studies except in leaf and petal colour. Phenotypic variances were generally higher than their respective genotypic variances thus revealing the role of environmental factors. High PCV and High GCV were observed for pod fruit yield per plant and peduncle length, respectively. Very low heritability estimate was observed for number of ridges per fruit (7.1%). Moderately high heritability estimate (78.99%) was observed for peduncle length; moderately high PCV and GCV 35.71% and 31.74%, respectively but low genetic advance of 1.99%.

Temam *et al*. (2020) conducted a study with the objective of assess the genetic divergence and estimate the genetic variability components in okra genotypes collected from regional state. A total of 36 genotypes were evaluated of which 33okra genotypes were collected from different areas of Benishangul Gumuz Regional State, 3(three) checks, of 2 introduced and 1(one) released were evaluated for 27 quantitative traits at MARC in year 2018/19 using simple lattice design (6x6). The results from analysis of variance revealed that the presence of significant variation for all quantitative traits except 3 traits. Moreover, the variation of genotypes for fruit yields per hectare ranged from 9.44 to 32.88ton/ha^{-1} with mean 19.59ton/ha^{-1} for genotypes 29620 and 29618, respectively. Most of genotypes had high mean performance as compared to checks for majority of traits. The genotypic (GCV) and phenotypic (PCV) coefficient of variation showed within range of 6.3 to 54.19% and 9.19 to 55.51%, respectively. Heritability in broad sense (H^2) and genetic advance as percent of mean (GAM) had ranged from 43.46 to 97.34% and 9.16 to 109.14%, respectively. The variability components (GCV, PCV, H2 and GAM) were high for all traits except few traits like days to 90% maturity, hundred seed weight low in PCV and GCV. Number of ridge and hundred seed weight showed moderate H^2 whereas days to 90% maturity, number of ridge and percentage of mucilage content had moderate GAM and low for hundred seed weight. The result observed in this study was the presence of a wide genetic variation among genotypes collected from Benishangul Gumuz Regional State.

Ibrahim *et al*. (2013) studied to investigate the genetic behavior of some biological and economical traits of 14 okra populations collected from Dakahlia Governorate, which underwent two cycles of inbreeding with selection. Selection of individual plants based on earliness, high number of pods, and minimum neck/pod ratio was carried out in all generations. The results showed that the means and ranges of all studied traits for all families became smaller in the S_2 generation than those in the S_0 generation. Highly significant variations were observed among populations for all the studied traits. The mean performance clearly indicated the agronomic superiority of some families over the others. Family 9 followed by family 12 showed the earliest flowering plants and the highest yield per plant. Phenotypic variances were higher than the corresponding genotypic variances indicating predominance of environmental effects on the expression of these characters. The magnitude of phenotypic and genotypic coefficients of variation varied from one trait to another. High broad-sense heritability coupled with high genetic advance as percent of mean were shown by the different traits, especially, plant height, number of branches per plant, number of pods per plant, pod length, neck/pod ratio and plant yield. This implicates that these traits were under the control of additive genetic effects, and could be effectively improved through selection. Plant yield had positive and highly significant correlation at genotypic and phenotypic level with number of pods per plant, plant height and neck/pod ratio.

Ashraf *et al.* (2020) conducted an experiment at the experimental farm, Department of Horticulture, Bangabandhu Sheikh Mujibur Rahman Agricultural University, Gazipur with an aim to study the genetic variability of selected okra genotypes. The study was laid out in Complete Randomized Block Design from March 2008 to July 2008. The studied characters were studied to find out the genetic variability, heritability and genetic advance, and correlation coefficient. The genotypes varied significantly ($p< 0.01$) for all of the characters studied. The phenotypic and genotypic variance was the highest for plant height (252.54 and 422.78) followed by fruits per plant (6.33 and 7.19) and yield (6.06 and 7.17). The estimate of heritability in broad sense ranged from 28.60% for fruit weight to 87.96% for fruits per plant. The heritability estimate in broad sense was high (>60%) for branches per plant (63.58%), picking duration (70.04%), days to first fruit harvest (71.46%), fruits per plant (87.96%) and fruit yield (84.55%). The genetic advance (in % of mean) ranged between 5.00% for days to first flowering to 52.08% for yield (t/ha). The highest (≥20%) genetic advance was observed for branches per plant, days to first fruit harvest, fruits per plant and yield (t/ha). The high degree of genotypic and phenotypic coefficients of variation were recorded in number of primary branches per plant (26.10% and 20.81%), fruits per plant (26.26% and 24.63%) and fruit yield (29.90% and 27.49%), respectively. This experiment aimed to evaluate the okra genotypes for genetic variability analysis with a view to providing information onthe selection of high yielding.

Vinithra *et al*. (2019) conducted an experiment to estimate genetic parameters *viz.*, genotypic coefficient variation (GCV), phenotypic coefficient variation (PCV), heritability and genetic advance (GA) along with correlation and path coefficient analysis, from data collected from fifty-eight genotypes. High GCV and PCV were observed for fruit yield per plant, number of node to first fruiting and fruit girth. High heritability coupled with high GA was observed for almost all the characters of interest. These traits could well be improved by resorting to simple selection. The Fruit yield per plant evinced positive significant phenotypic and genotypic association with plant height and average fruit weight. Path coefficient analysis revealed that number of fruits per plant and average fruit weight exerted maximum positive direct effects which were equal to genetic correlation coefficient towards fruit yield per plant. Hence, number fruits per plant and average fruit weight may be good indicator traits for fruit yield improvement in okra breeding.

Mohammed *et al*. (2020) evaluated 36 okra genotypes for 29 agro morphological and biochemical traits at the Melkassa Agricultural Research Center (Ethiopia) during the 2018 main rainy season, using a 6 x 6 simple lattice design. Analysis of variance showed significant differences among genotypes for all the studied traits, except number of epicalyx and fruit diameter. Genotypic coefficients of variation and phenotypic coefficient of variation were high for number of branches, internode length, fresh fruit weight, number of mature pods, fruit yield per plant, fruit yield per hectare, seed yield per plant, seed yield per hectare and seed protein content. Heritability values ranged between 33.63 and 99.81%, while the Genetic Advance as percentage of Mean ranged between 4.29 and 95.45%. High broad sense heritability was coupled with high GAM for plant height, branch, inter nod length, fruit length, panicle length, fresh fruit weight, number of fruit per plant, number of mature pods, seed yield per plant, seed yield per hectare, fibre and protein content. In conclusion, this study showed the presence of genetic variation among genotypes for fruit yield, seed yield and nutritional content, indicating the potential success of developing okra varieties for high fruit yielding and good nutritional content.

Verma *et al.* (2018) evaluated fifty genotypes of okra collected from NBPGR, New Delhi and IIVR, Varanasi during kharif 2016-17 to study the variability, heritability and genetic advance for different morphological and agronomic traits. The analysis of variance revealed significant differences among the genotypes for all the characters studied. The characters like number of branches per plant, fruit yield per plant, width of fruit, number of first fruiting node and length of internode showed high GCV and PCV estimates. The closeness of these parameters indicated the less influence of environment in the expression of characters. High heritability coupled with high genetic advance expressed as percent of mean were observed for yield per plant, width of fruit, number of first fruiting node, number of fruits per plant, length of internode and length of first fruiting node indicating that they are governed by additive genes and could be effectively improved through selection.

Sharma *et al*. (2016) grown the experiment comprising 30 okra (*Abelmoschus esculentus)* genotypes and analysed for yield and its attributing traits at the Department of Vegetable science, Kumarganj, Faizabad during Zaid (2011) period. All the characters studied showed a wide range of variation. The variability for yield among the accessions evaluated was also remarkable. The magnitude phenotypic coefficient of variation was higher than genotypic coeffi-cient of variation for all traits. Both phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were high for plant height (11.10 and 10.60, respectively). Fruit weight exhibited low value of GCV (2.31) and PCV (4.74) and likely to show less response under selection. High heritability (91.3) with high genetic advance (26.74) was recorded for plant height, whereas, ridges per fruit had high heritability (97.0) with moderate genetic advance (18.45). This study aimed to evaluate okra genotypes for variability with a view to providing information on the development of high yielding genotypes to meet the growing food demand of the populace.

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).

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 the 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.

Shamloul and Moghazy (2017) experimented on okra and found that the mean squares of the genotypes were highly significant except plant height (cm) and pod length (cm). General combining ability (GCA) was highly significant for all traits. Therefore, additive genetic variance was more important in the inheritance of these traits. The values of GCA were higher than those of specific combining ability (SCA) for plant height (cm), number of nodes to first flower and pod diameter (cm) indicating that additive genetic variance was more important for these traits. The values of SCA were larger than those of GCA for other tested traits indicating the importance of non-additive effects. The magnitudes of GCA and SCA values were close for the pod diameter, thus illustrating the importance of both values for this trait. The crosses $P_1 \times P_2$ and $P_4 \times P_2$ were promising and showed highly significant estimates of SCA effects. Genetic variances including dominance (σ^2_D) were positive and highly significant for most traits except for pod length. The reciprocal variances were smaller than the additive genetic variances for average pod weight and number of seeds pod^{-1}. The results showed that the reciprocal effect (σ^2_{rec}) or maternal effect was present and should not be neglected. The heritability in broad sense was larger than the corresponding values in narrow sense for all traits. In general, the F_1 hybrid $P_2 \times P_3$ and $P_2 \times P_4$ gave desirable value for early yield trait where the mean number of nodes of first flower was -38.51 and 31.03 g for Average weight of pod plant^{-1}, respectively. However, the F_1 hybrids $P_1 \times P_2$ gave the highest values of hybrid vigor with a mean of 57.1 for number of pods plant^{-1}, 32.14 kg for weight of pods plot^{-1} and 38.59 for number of seeds pod^{-1}. Whereas, the F_1 hybrids $P_1 \times P_2$ and $P_2 \times P_3$ were outstanding for most traits. This result indicated that choice of parents is an important factor. These hybrids can be utilized in breeding programs to produce improved okra lines and new cultivars.

Alake (2020) evaluated on okra in field experiments over a period of 2 years at the research farm of the Federal University of Agriculture, Abeokuta, Nigeria. Principal component analysis, cluster analysis, and Mahalanobis D^2 statistics were employed to study the diversity pattern. Differences existed for all evaluated traits among landraces. Genotypes NGB00378b, NGB00297, NGB00347, NGB00293, and NGB00350 combined high seed mineral concentrations with high yield potential. A genotype × year interaction was present, as reflected by relatively low broad-sense heritability (<30%) and genetic advance (GA) (<10%) for pod yield and pod width (PDW), which limits potential for improvement. Heterosis breeding could be effectively used to improve K and Mg, as these traits expressed high variation and broad-sense heritability coupled with moderate GA. Using D^2 divergence analysis, landraces were separated into seven distinct clusters, with no phylo–agroecological pattern of diversity. Based on the present study, selection for a trait in 1 year may not provide the same benefit in other years due to year-to-year fluctuations in environmental conditions, evaluation in more than 1 year is required.

Massucato *et al.* (2020) worked on okra and estimated genetic parameters for the quantitative traits and the accessions were grouped by Ward's method, using the Gower's and Jaccard's distance measures, respectively, for the morph agronomic and molecular data. Polymorphisms were observed for all qualitative traits, while the quantitative traits were significant by deviance analysis. The genetic parameters confirmed the existence of variability among accessions, and high accuracy and heritability indices were found for the traits related to fruit and plant height. Ward's grouping showed no relationship between the clusters formed with the morphoagronomic and molecular data and the geographical origin of the accessions. No association between morphoagronomic descriptors and AFLP markers was observed. The lack of correlation suggests that both approaches of characterization are important to understand and differentiate the okra accessions.

Amoatey *et al.* (2015) evaluated twenty-nine (29) local and exotic lines (accessions), of okra (*Abelmoschus spp* L.) for variation in phenotypic traits. The accessions exhibited significant variation in all quantitative traits studied. Block coefficients of variation were extremely low, implying that results obtained are reliable and repeatable over replications. Cluster analysis based on Canberra, Furthest Neighbour Similarity Matrix grouped the accessions into two major clusters and subsequently into four sub-clusters, with no duplications, based on the characters studied. Seven pairs of quantitative traits were positive and significantly correlated ($P \leq 0.05$) while three were highly significantly associated ($P \leq 0.01$). The highest correlation ($r = 0.95$) was between number of days to 50% flowering (NDFl) and number of days to 50% fruiting (NDFr).

Prakash *et al.* (2017) estimated genetic diversity among sixty-three okra genotypes using Mahalanobis D^2 statistic. The genotypes were grouped into nine clusters. The maximum number of genotypes was found in cluster I (36) followed by cluster III (15) and Cluster II (6). Remaining all were solitary clusters with single genotype. The characters viz total phenols (21.35 %), number of leaves at 90 DAS (12.08 %), fruit length (11.73 %) and plant height at 90 DAS (10.60%) contributed more towards genetic divergence. Cluster III with fifteen genotypes showed the maximum intra cluster distance ($D^2 = 130.13$)

followed by cluster II (D^2 = 82.57) with six genotypes and Cluster I (D^2 = 66.10) with thirty-six genotypes. The maximum intercluster distance was observed between cluster VI and cluster VI. Hence, genotypes belonging to these clusters may be utilized for hybridization programme to get better recombinants.

Chandramouli *et al*. (2015) assessed a total of 30 okra genotypes (including two check cultivars) for genetic divergence using Mahanalobis D^2 statistic. Based on the distance values, the population was grouped in to six clusters. Cluster I had the maximum number of genotypes (14) followed by cluster III (7), cluster II and V (3), cluster IV (2) and cluster VI (1). The clustering pattern indicated that there was no association between geographical distribution of genotypes and genetic divergence. The intra-cluster distance was maximum in cluster IV (29.91), while inter-cluster distance was the maximum between cluster V and VII (294.67) followed by IV and VI (223.75), thus being a good source for attempting hybridization. The characters namely YVMV infestation, leaf area and fruit yield plant^{-1} contributed the maximum towards genetic divergence therefore, selection of divergent parents based on these characters is recommended for getting good hybrids or desirable segregates in okra. For vegetative character cluster V and VI recorded significantly higher plant height and leaf area, respectively. Regarding fruit character cluster V recorded significantly maximum number of fruits plant^{-1} and VI recorded significantly higher fruit yield plot^{-1}. With a due consideration on superior performance in respect of certain characters in different clusters, the desirable parents were listed out. The trait fruit yield plant^{-1} was found to be improved by opting for inter-cluster crosses between V and VI, IV and VI, III and VI, II and VI, IV and V, II and V as well as I and V.

Ahiakpa *et al*. (2017) experimented on ten quantitative agromorpho-economic traits, six inter-simple sequence repeat (ISSR) primers, and three sequenced regions to study intra-specific genetic diversity among twenty-eight accessions of West African and Asian okra (*Abelmoschus* spp L.) collected from eight geographical regions of Ghana. Pod fruit yield per plant was analysed as dependent variable in relation to other agromorpho-economic traits, showing the correlation and contribution of each trait to crop yield. 50% germination and flowering were the most significant traits followed by plant height and average seeds per plant. Principal coordinate analysis defined three sets of traits, while Agglomerative Hierarchical Clustering (AHC) defined three clusters of the germplasms. ISSR detected very low level of polymorphism among the accessions. Testing the correlation between molecular data and morphological traits using Mantel test showed a significant positive correlation (r-value = 0.71, 0.90) with 50% flowering, fruiting and number of leaves per plant. Eclectic variation between Indiana and the rest of the accessions for both agromorpho-economic traits and molecular markers affirms its potential usefulness as a source of diverse genes for future breeding programmes. Sequencing of regions from all accessions, suggests that they are identical with a common ancestry. Outcomes of this study is timely for an ongoing okra hybridisation programme in Ghana.

Demelie *et al*. (2015) initiated this study with the objectives determining genetic distance of okra collections from different regions of Ethiopian and generated information about genetic diversity of Ethiopian okra collections to other country okra varieties. The field experiment was conducted at Werer Agricultural Research Center in 2014 using 23 local okra collections obtained from Ethiopian Biodiversity Institute and two exotic varieties obtained from Melkassa Agricultural Research Center using in simple lattice design with five incomplete blocks. Data were recorded from 25 quantitative and 10 qualitative traits. Principal component analysis showed eight principal components (PC1 to PC8) with eigen values ranged from 1.0 to 9.07 and with total contribution of 81.3% variation. Genetic distances were estimated using both quantative and qualitative traits. Genetic distance dissimilarity ranged from 3.89 to 18.24 with mean of 9.57. The two introduced varieties exhibited highest genetic distances than local collections. Exotic varieties were grouped in one cluster while the local collections were distributed in nine clusters. This study revealed the presence of genetic diversity among local okra collections and between local okra collections and introduced varieties that can be exploited for future breeding program. Since agro-morphology traits are highly influenced by environment, it is necessary to conduct agro-morphology traits along with a molecular study to determine the genetic diversity within Ethiopian okra collections and between other countries okra varieties.

Reddy *et al*. (2012) experimented on genetic diversity among 100 genotypes of okra (*Abelmoschus esculentus* (L.) Moench) for all the seventeen quantitative characters which pertaining to the growth, earliness and yield. Hundred genotypes were grouped into 11 distinct clusters depending upon the similarities of their D^2 values following Tocher's method. The clustering pattern of germplasm usually did not follow the geographical distribution. Appreciable diversity within and between 11 clusters was observed. The character's fruit length, internodal length and number of marketable fruits per plant were the potent factors in differentiating the germplasm of okra under study. The use of diverse genotypes from the clusters with high intercluster distance (cluster VI and X, VI and IX and VII and XI) in hybridization is expected to result in high heterosis and throw desirable transgressive segregants. The genotypes of six solitary clusters IV (IC043279-A), IC033350 (cluster VI), IC90210 (cluster VII), IC26375 (cluster IX), IC018530 (cluster X) and IC043751-B (cluster XI) being divergent from others may also serve as potential parents for breeding programmes.

Mohammed *et al.* (2020) carried out field experiment at National Cereals Research Institute (NCRI), Badeggi research field, Niger State, to reveal the variability among some okra accessions. Thirty-one accessions of okra were collected from farmer's field and two (LD-88 and Nhae-47) collected from the department of crop production, Federal University of Technology Minna. The accessions were planted in Randomized Complete Block Design (RCBD) with three replications in a plot size of 2m x 1.5m. The experiment was carried out during dry and raining (2014/2015) season. Data were collected on twenty agro-morpholocal traits. Results of the principal component analysis (Table 1 and Table 2) of the combined seasons for the traits studied showed that the first five principal components accounts for 77.2 % and 89.0 % of the total variations in the population. Single Linkage Cluster Analysis (SLCA) display the accessions in accordance to their similarities level through the aid of dendrogram. SLCA of the combined season showed two major cluster groups that were linked at 65.7% level of similarity. Accessions that showed variability and clustered in different group may be useful for improvement of okra.

Pandey *et al.* (2016) studied genetic divergence of 24 okra genotypes using Mahalanobis D^2 statistics revealed that considerable genetic diversity was found among genotypes in okra. Twenty-four diverse genotypes were grouped into five clusters with the highest of 9 genotypes in the cluster III, 4 in the cluster I, Cluster II and Cluster V and 3 in cluster IV. Intra and inter cluster D^2 values ranged from 4.663 to 22.662 and 11.375 to 76.245, respectively. It showed that inter cluster distance was higher than the intra cluster distance indicating wide genetic diversity among the genotypes of different groups. Cluster means for different traits indicated considerable differences between the clusters. Cluster II and IV had in general medium mean performance for most of the characters. Maximum cluster means for Fruit yield per plant was observed in cluster IV (329.649) followed by cluster II (241.906). Primary branches per plant (42.03%) contributed the maximum contribution towards total divergence, while the minimum contribution was reflected by days to 50% flowering (0.36%) and plant height (0.72%).

Koh (2016) grew thirty-six okra germplasms and evaluated for yield and yield related traits at the Department of Plant Breeding and Genetics, Vellayani, Trivandrum, Kerala. The germplasms studied possessed sufficient variability for all the traits. High genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were noticed for almost all characters and narrow difference between GCV and PCV suggest that environmental influence is minimal for the traits studied. High estimates of heritability coupled with high to moderate genetic advance as percent over mean was recorded for all the characters considered. Yield had positive and significant association with number of fruits per plant, fruit weight, fruit girth and number of primary branches indicating that selection based on these characters may improve yield. Principal component analysis indicated that first three principal components contributed for sixty percent total variation among ten characters describing accessions. The cluster analysis revealed that hybridization of cluster I with cluster IV would be beneficial to develop promising varieties under diverse climatic conditions in India.

2.2 Correlation amonng yield contributing traits

Duggi *et al.* (2013) carried out an experiment and found the fruit yield per plant showed strong genotypic correlation with number of fruits per plant, fruit weight and fruit girth. Significant negative correlation of yield with days to 50% flowering was noticed. Plant height and crop duration showed positive significant genotypic correlation among themselves. It is noteworthy that the present study suggested highly significant negative correlation between number of fruits per plant and fruit weight both at genotypic and phenotypic levels, whereas number of fruits per plant had positive genotypic correlation with fruit girth. The number of fruits per plant and fruit girth besides being positively associated with yield, showed positive genotypic correlation between them. These two characters had high heritability too. Hence it would be worthwhile to give due consideration to these characters in selection programs aimed at yield improvement in okra. Highly significant positive correlation between per cent fruit infestation and larval count of shoot and fruit borer in 25 fruits suggested that fruit damage criteria may be employed for the evaluation of shoot and fruit borer resistance in okra.

Ashraf *et al.* (2020) worked on okra and found that different genotypes varied significantly regarding all the studied characters. The fruits per plant and fruit weight of different genotypes had a high degree of significant positive association with fruit yield and a high positive direct effect indicated that these characters had a major contribution towards the fruit yield of the genotypes. The days to first flowering and days to first fruit harvest showed a significant positive correlation with picking duration both genotypic and phenotypic levels. The Picking duration showed a highly significant positive genotypic correlation with fruit diameter and fruit length. At the final harvest plant height showed a highly significant positive genotypic correlation with fruit length and fruit weight at the genotypic level. The fruit length showed a highly significant positive genotypic correlation with fruit weight and fruit diameter and genotypic level. The fruits per plant showed a highly significant positive genotypic and phenotypic correlation with fruit yield. A significant positive genotypic correlation with fruit yield was shown by fruit weight. The fruits per plant (0.979) and fruit weight (0.554) also showed a high positive direct effect on fruit yield.

Walling *et al.* (2020) evaluated twenty-eight genotypes of okra under foothill conditions of Nagaland under School of Agricultural Sciences and Rural Development, Nagaland University in Randomized Block design with three replications. Analysis of variance revealed significant variation for all the genotypes under study. Highest phenotypic and genotypic coefficient of variation was observed in cumulative leaf area, fruit yield per plant and protein content indicating the existence of wide range of genetic variability in the germplasms for these traits. High heritability coupled with high genetic advance as percentage of mean was observed for traits like plant height, size of leaf, number of leaves per plant and fruit yield per plant which suggested that they can be improved through direct selection. The correlation studies indicated that fruit yield per plant showed highly significant positive genotypic correlation coefficients with leaf area index, size of leaf, number of leaves, number of fruits per plant, weight of fruit, fruit length, number of ridges per fruit, number of seeds per fruit and fruit diameter signifying the importance of these traits in selection for yield and are identified as yield attributing characters on which selection can be relied upon for the genetic improvement of yield. Based on the mean performance of the twenty-eight genotypes of okra, it can be concluded that three genotypes IIVRO-608-8-1, IIVRO-770 and Arka Anamika were the best performing genotypes.

Rynjah *et al.* (2020) worked on correlation and path coefficient analysis studies in thirty-six okra genotypes for fourteen traits *viz.*, days to first flowering, days to 50 per cent flowering, plant height, number of branches per plant, internodal length, fruit length, fruit girth, fruit weight, number of fruits per plant, total phenols, peroxidase activity, polyphenol oxidase activity, per cent disease infection and yield per plant. The study revealed that fruit yield per plant was positively correlated with fruit girth, fruit length, number of fruits per plant, plant height and fruit weight at genotypic level of correlation. Whereas the characters, per cent disease incidence, days to fifty per cent flowering, internodal length and days to first flowering were found to have negative correlation with single plant yield at genotypic level. The high positive direct effect on yield plant was contributed by fruit girth followed by plant height, fruit weight, fruit length and number of branches per plant. Hence, improvement in yield will be efficient if selection is based on fruit girth, fruit length, number of fruits per plant, plant height and fruit weight and short flowering period.

Gogineni *et al.* (2015) evaluated on correlation and path analysis in ten different okra hybrids for fruit yield and its component traits. The correlation analysis indicated that fruit yield was significantly associated with fruit length, fruit girth, fruit weight, number of fruits per plant, plant height and duration at both genotypic and phenotypic level, indicating mutual association of these traits. Path coefficient analysis revealed 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.

Chandramouli *et al.* (2019) carried out an experimented on correlation and path coefficient analysis among 30 okra genotypes (including two checks) which revealed that the magnitude of genotypic correlation coefficients was higher than phenotypic correlation coefficients, for the quantitative traits that were studied. The most important economic trait, fruit yield plant^{-1} exhibited positive and significant correlation with plant height, number of primary branches plant^{-1}, number of nodes on main stem, intermodal length, number of fruits plant^{-1}, fruit length, fruit girth, number of pickings and picking duration at both phenotypic and genotypic levels indicating the importance of these traits in selection for yield. Path coefficient analysis was performed taking the fruit yield plant^{-}

^{1} as dependent variable. It was revealed from the results that intermodal length, fruit length, days to first picking, petiole length, picking duration, node at which first flower appeared, fruit girth, number of pickings and number of nodes on main stem exerted a high positive direct effect on fruit yield plant^{-1}. The high direct effect of these traits appeared to be the main factors for their strong association with fruit yield plant^{-1}. The magnitude of direct effects by these traits is indicative of the effectiveness of direct selection based on such traits.

Jaiprakashnarayan and Ravindra (2004) experimented on correlation and path analysis study in 69 okra genotypes using growth, earliness and yield traits. The results indicated the inverse relationship between growth and earliness characters but strong association between growth and yield characters. Total fruit yield per plant was positively and significantly correlated with number of fruits per plant, average fruit weight, number of nodes on main stem, fruit length, plant height at 60 and 100 days after sowing (DAS) and number of leaves on 45 and 100, whereas, total fruit yield per plant had negative and significant association with number of locules per fruit, number of nodes at first flowering and first fruiting. Path analysis revealed that average fruit weight, number of nodes on main stem 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 is suggested for getting yield improvement.

Abd-allah (2015) conducted two field experiments during 2013 and 2014 summer seasons at Sabahia Horticulture Research Station, Alexandria, Egypt. Plant materials of this study were consisted of five genotypes of okra. The present study was directed to estimate the direct and indirect effects of some characters related to fruit and seed production in some okra varieties and lines, originated from a breeding program at Sabaheia Horticultural Research Station. Concerning fruit yield, the results indicated that the direct effect of number of branches/plant was strongly positive (1.222). So, it may indicate a true relationship, and a direct selection through this trait may be effective in improving yield in okra. Nevertheless, correlation coefficient between total number edible pods/plant and edible pod yield was positive and the direct effect of this trait was negative, it seemed that indirect effect appeared to be the cause of correlation. Regarding seed yield, the genotypic correlation between of number of seed/pod and seed yield (0.983) seemed to be close to the estimated value of its direct effect, so, it may indicate a true relationship and direct selection through this trait may be effective for improving seed yield of okra. However, the correlation coefficient between number of branches/ plant and number of mature pods/plant with seed yield was positive (0.790 and 0.718, in order) and the direct effect of these factors were either negative or negligible, it seems that indirect effect appeared to be the cause of correlation. Hence, these traits may be used simultaneously with the other characters.

Shuirkar *et al*. (2018) experimented on okra and found that plant height recorded positive and significant correlation with length of internode (0.2871), days to 50% flowering (0.1882), fresh fruit weight (0.3387). A high significant and negative association of this trait was observed with length of internode (-0.1673), first fruiting node (-0.3138), days to first fruit length (-0.1665). Length of internode was recorded positive and significant correlation with days to 50% flowering (0.4420), days to first picking (0.1753) and highly significant to fresh weight (0.5021). Days to 50% flowering expressed a significant and positive association with first fruiting node (0.2019), days to first flowering (0.2132), days to first picking (0.3118), fruit length (0.1943) and fresh fruit weight (0.2525). Days to first flowering was recorded highly significant and positively correlated with days to first picking (0.2854**). Days to first picking was recorded highly significant and positively correlated with number of fruits per plant (0.3274**). Length of fruit was observed highly significant and positive correlation coefficient with fresh fruit weight (0.3107). Fresh fruit weight was observed positive correlation with fruit yield per plant (0.5633). Number of fruits per plant was observed positive correlation with fresh fruit weight (0.0393).

Aminu *et al*. (2016) conducted on field irrigation experiments to assess the varietal performance and correlation of pod yield and yield attributes under irrigation at the Teaching and Research Farm, University of Maiduguri, Nigeria, during the 2015 and 2016 dry seasons. The results revealed that the most outstanding for fresh pod fruit yield per plant were okra cultivar Kwadag Y'ar gagure Salkade, and Kwadam, in descending order, with yield ranging from 580.38 to 622.67 g, while the Composite cultivar had the lowest value of pod yield of 428.62 g over the two years. The greatest average values for the number of pods per plant and the number of primary branches per plant were observed for Salkade and Y'ar gagure, respectively.the highest fresh pod length and fresh pod diameter were also exhibited for Salkade and Kwadag. The genotypic coefficient of variation was higher than the phenotypic variation for the entire yield-contributing characters. Days to 50% flowering were positive and highly significant differences associated with plant height, number of pods per plant, and fresh weight per pod could be observed. Path coefficient analysis showed that the number of pods per plant exhibited positive and direct influence on the pod yield across the studied years. Indirect influence of other yield components through this character also contributed mainly towards pod yield. Therefore, days to 50% flowering, plant height, pod length, number of pods per plant, pod diameter, number of primary branches per plant, and fresh weight per pod could be taken into consideration for the selection and development of high pod-yielding varieties in okra.

Raval *et al.* (2019) conducted an experiment on okra and found that correlation coefficient and path analysis using parents (female VRO - 6 and male AOL - 09 – 02), their F_1 and F_2 generations. Observations were recorded on thirteen yield and its contributing characters. Among them, fruit yield per plant exhibited positive and highly significant correlation with number of fruits per plant, plant height at final harvest, fruit weight, number of branches/plant, fruit girth, number of seeds/fruit, internodal length, and 100 seed weight. Path coefficient analysis revealed that number of fruits per plant, fruit weight, days to first picking, internodal length, 100 seed weight and fruit length recorded positive direct effect on fruit yield/plant.

Narkhade *et al.* (2015) evaluated on fifty-seven lines of okra including ten different genotypes along with forty-five hybrids and two standard checks in Randomized Block Design with two replications in Kharif 2011. Correlation and Path analysis were carried out to study character association and contribution for days to 50 per cent flowering, Plant height at harvest, number of branches per plant, number of nodes per plant, days to first picking, number of fruits per plant, average length of fruit, average weight of fruit, fruit yield per plant (g), yield per plot (kg), yield per hectare (qt) and reaction to yellow vein mosaic for identification of appropriate selection indices. Genotypic and phenotypic correlation revealed that at both level fruit yield was positively associated with number of fruits, number of nodes per plant, fruit length and fruit weight. Correlation and Path analysis revealed that characters days to first picking, plant height at harvest, number of nodes per plant and number of fruits per plant not only had positive significant association with fruit yield per plant but also had high positive direct effects on marketable fruit yield per plant and are regarded as the main determinants of yield per plant. If selection is based on these characters, then improvement in yield will be efficient.

Kerure *et al*. (2017) experimented on okra and showed yield per plant showed positive association with stem girth, number of branches per plant, plant height, first fruit producing node, fruit length, fruit diameter, average fruit weight, number of fruits per plant, number of seeds per fruit and 100 seed weight while, negative association with days to 50% flowering, number of locules per fruit and days to 80% maturity. The number of fruits per plant had the maximum direct effect on Fruit yield per plant followed by average fruit weight. Number of branches per plant, plant height and first fruit producing node contributed to yield per plant indirectly via stem girth, average fruit weight, and number of fruits per plant. Hence, number of fruits and average fruit weight are identified as key traits for developing high fruit yielding genotypes of okra for future breeding programme.

Thulasiram *et al*. (2017) experimented on thirty genotypes of okra and found that fruit yield per plant was significantly associated with plant height, number of leaves per plant, number of lobes per leaves, number of primary branches per plant, number of nodes per plant and number of fruits per plant. Thus there is an ample scope for improving character through direct selection. Based on positive direct effects of different yield components on yield, it would be rewarding to give emphases on the number of primary branches per plant, number of nodes per plant, number of leaves per plant, leaf area, diameter of fruit and node at which fruit appears, number of lobes per leaves, plant height, internodal length, number of fruits per plant and weight of fruit, however for positive indirect effect number of nodes per plant, plant height, node at which first fruit appears, length of fruit, weight of fruit, number of fruits per plant, chlorophyll content of leaves and incidence of YVMV while formulating selection indices for improvement of yield in okra.

Patil *et al*. (2016) carried out on correlation and path analysis utilizing 40 genotypes of okra during summer season 2015 and findings revealed that plant height exhibited positive and significant correlation with most of yield and yield contributing characters which indicated that these traits might be improved through direct selection. The path analysis study indicates that number of fruits per plant, number of branches per plant, number of nodes/plant exhibited the maximum direct effect on yield per plant. It suggested that these attributes have strong influence on fruit yield. Hence, plant height, number of branches/plant, number of nodes/plant were the determiners of fruit yield per plant and require more attention in okra improvement programme while selecting okra genotypes.

Sanganamoni *et al.* (2017) studied on the character association and path analysis in fifty-two genotypes of okra were studied for 10 important characters. The character association studies revealed that the yield per plant had significant and positive association with number of leaves at 90 days after sowing (DAS) at both genotypic and phenotypic levels whereas number of branches per plant (90 DAS) at only genotypic level. It was significantly and negatively associated with internodal length (45 and 90 DAS) and days to first harvest. Presence of lower difference between the correlation coefficients at genotypic and phenotypic levels for various traits in the present findings indicates the lesser influence of the environment in the expression of these traits and presence of strong inherent association among the traits. Path analysis studies revealed significant positive association at genotypic level among the traits viz number of leaves per plant (90 DAS) and number of branches per plant (45 DAS) and exhibited perfect association with direct effect on yield per plant. These traits can be viewed for direct selection for improvement in the total yield per plant.

2.3 Path coefficient analysis of different characters on yield of okra genotypes

Ashraf *et al.* (2020) conducted an experiment at the experimental farm, Department of Horticulture, Bangabandhu Sheikh Mujibur Rahman Agricultural University, Gazipur from March 2008 to July 2008 to study the correlation and path analysis in the selected okra genotypes. The experiment was carried out in Randomized Complete Block Design with thee replications. The results indicated that different genotypes varied significantly regarding all the studied characters. The Fruits per plant and fruit weight of different genotypes had a high degree of significant positive association with fruit yield and a high positive direct effect indicated that these characters had a major contribution towards the fruit yield of the genotypes. The days to first flowering and days to first fruit harvest showed a significant positive correlation with picking duration both genotypic and phenotypic levels. The Picking duration showed a highly significant positive genotypic correlation with fruit diameter and fruit length. At the final harvest plant height showed a highly significant positive genotypic correlation with fruit length and fruit weight at the genotypic level. The fruit length showed a highly significant positive genotypic correlation with fruit weight and fruit diameter and genotypic level. The fruits per plant showed a highly significant positive genotypic and phenotypic correlation with fruit yield. A significant positive genotypic correlation with fruit yield was shown by fruit weight. The fruits per plant (0.979) and fruit weight (0.554) also showed a high positive direct effect on fruit yield.

Rynjah *et al*. (2020) studied on correlation and path coefficient analysis in thirty-six okra genotypes for fourteen traits viz., days to first flowering, days to 50 per cent flowering, plant height, number of branches per plant, internodal length, fruit length, fruit girth, fruit weight, number of fruits per plant, total phenols, peroxidase activity, polyphenol oxidase activity, per cent disease infection and yield per plant. The study revealed that fruit yield per plant was positively correlated with fruit girth, fruit length, number of fruits per plant, plant height and fruit weight at genotypic level of correlation. Whereas the characters, per cent disease incidence, days to fifty per cent flowering, internodal length and days to first flowering were found to have negative correlation with single plant yield at genotypic level. The high positive direct effect on yield plant was contributed by fruit girth followed by plant height, fruit weight, fruit length and number of branches per plant. Hence, improvement in yield will be efficient if selection is based on fruit girth, fruit length, number of fruits per plant, plant height and fruit weight and short flowering period.

Gogineni *et al.* (2015) carried out correlation and path analysis in ten different okra hybrids for fruit yield and its component traits. The correlation analysis indicated that fruit yield was significantly associated with fruit length, fruit girth, fruit weight, number of fruits per plant, plant height and duration at both genotypic and phenotypic level, indicating mutual association of these traits. Path coefficient analysis revealed 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.

Chandramouli *et al*. (2019) investigated correlation and path coefficient analysis among 30 okra genotypes (including two checks) which revealed that the magnitude of genotypic correlation coefficients was higher than phenotypic correlation coefficients, for the quantitative traits that were studied. The most important economic trait, fruit yield plant^{-1} exhibited positive and significant correlation with plant height, number of primary branches plant^{-1}, number of nodes on main stem, intermodal length, number of fruits plant^{-1}, fruit length, fruit girth, number of pickings and picking duration at both phenotypic and genotypic levels indicating the importance of these traits in selection for yield. Path coefficient analysis was performed taking the fruit yield plant^{-1} as dependent variable. It was revealed from the results that intermodal length, fruit length, days to first picking, petiole length, picking duration, node at which first flower appeared, fruit girth, number of pickings and number of nodes on main stem exerted a high positive direct effect on fruit yield plant^{-1}. The high direct effect of these traits appeared to be the main factors for their strong association with fruit yield plant^{-1}. The magnitude of direct effects by these traits is indicative of the effectiveness of direct selection based on such traits.

Abd-allah (2015) conducted two field experiments during 2013 and 2014 summer seasons at Sabahia Horticulture Research Station, Alexandria, Egypt. Plant materials of this study were consisted of five genotypes of okra. The present study was directed to estimate the direct and indirect effects of some characters related to fruit and seed production in some okra varieties and lines, originated from a breeding program at Sabaheia Horticultural Research Station. Concerning fruit yield, the results indicated that the direct effect of number of branches/plant was strongly positive (1.222). So, it may indicate a true relationship, and a direct selection through this trait may be effective in improving yield in okra. Nevertheless, correlation coefficient between total number edible pods/plant and edible pod yield was positive and the direct effect of this trait was negative, it seemed that indirect effect appeared to be the cause of correlation. Regarding seed yield, the genotypic correlation between of number of seed/pod and seed yield (0.983) seemed to be close to the estimated value of its direct effect, so, it may indicate a true relationship and direct selection through this trait may be effective for improving seed yield of okra. However, the correlation coefficient between number of branches/ plant and number of mature pods/plant with seed yield was positive (0.790 and 0.718, in order) and the direct effect of these factors were either negative or negligible, it seems that indirect effect appeared to be the cause of correlation. Hence, these traits may be used simultaneously with the other characters.

Shuirkar *et al.* (2018) experimented on okra and plant height was recorded positive and significant correlation with length of internode (0.2871), days to 50% flowering (0.1882), fresh fruit weight (0.3387). A high significant and negative association of this trait was observed with length of internode (-0.1673), first fruiting node (-0.3138), days to first fruit length (-0.1665). Length of internode was recorded positive and significant correlation with days to 50% flowering (0.4420), days to first picking (0.1753) and highly significant to fresh weight (0.5021). Days to 50% flowering expressed a significant and positive association with first fruiting node (0.2019), days to first flowering (0.2132), days to first picking (0.3118), fruit length (0.1943) and fresh fruit weight (0.2525). Days to first flowering was recorded highly significant and positively correlated with days to first picking (0.2854**). Days to first picking was recorded highly significant and positively correlated with number of fruits per plant (0.3274**). Length of fruit was observed highly significant and positive correlation coefficient with fresh fruit weight (0.3107). Fresh fruit weight was observed positive correlation with fruit yield per plant (0.5633). Number of fruits per plant was observed positive correlation with fresh fruit weight (0.0393).

Raval *et al.* (2019) studied correlation coefficient and path analysis using parents (female VRO - 6 and male AOL - 09 – 02), their F1 and F2 generations. Observations were recorded on thirteen yield and its contributing characters. Among them, fruit yield per plant exhibited positive and highly significant correlation with number of fruits per plant, plant height at final harvest, fruit weight, number of branches/plant, fruit girth, number of seeds/fruit, internodal length, and 100 seed weight. Path coefficient analysis revealed that number of fruits per plant, fruit weight, days to first picking, internodal length, 100 seed weight and fruit length recorded positive direct effect on fruit yield/plant.

Narkhade *et al.* (2015) evaluated fifty-seven lines of okra including ten different genotypes along with forty-five hybrids and two standard checks in Randomized Block Design with two replications in Kharif 2011. Correlation and Path analysis were carried out to study character association and contribution for days to 50 per cent flowering, Plant height at harvest, number of branches per plant, number of nodes per plant, days to first picking, number of fruits per plant, average length of fruit, average weight of fruit, fruit yield per plant (g), yield per plot (kg), yield per hectare (qt) and reaction to yellow vein mosaic for identification of appropriate selection indices. Genotypic and phenotypic correlation revealed that at both level fruit yield was positively associated with number of fruits, number of nodes per plant, fruit length and fruit weight. Correlation and Path analysis revealed that characters days to first picking, plant height at harvest, number of nodes per plant and number of fruits per plant not only had positive significant association with fruit yield per plant but also had high positive direct effects on marketable fruit yield per plant and are regarded as the main determinants of yield per plant. If selection is based on these characters, then improvement in yield will be efficient.

Thulasiram *et al*. (2017) utilized thirty genotypes belonging to okra (*Abelmoschus* esculentus), to work out the correlation and path coefficient. The genotypic and phenotypic correlation indicated that fruit yield per plant was significantly associated with plant height, number of leaves per plant, number of lobes per leaves, number of primary branches per plant, number of nodes per plant and number of fruits per plant. Thus there is an ample scope for improving character through direct selection. Based on positive direct effects of different yield components on yield, it would be rewarding to give emphases on the number of primary branches per plant, number of nodes per plant, number of leaves per plant, leaf area, diameter of fruit and node at which fruit appears, number of lobes per leaves, plant height, internodal length, number of fruits per plant and weight of fruit, however for positive indirect effect number of nodes per plant, plant height, node at which first fruit appears, length of fruit, weight of fruit, number of fruits per plant, chlorophyll content of leaves and incidence of YVMV while formulating selection indices for improvement of yield in okra.

Kerure *et al.* (2017) estimated genetic parameters such as genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability and genetic advance (GA) along with correlations and path coefficients from data collected on 52 okra genotypes collected from the IIHR, Bengaluru, India. Analysis of variance indicated significant differences among the genotypes for different morphological characters. High GCV and PCV were observed for yield per plant, no. of fruits per plant, no. of seeds per fruit, whereas moderate GCV and PCV was observed for average fruit weight. High heritability coupled with high GAM were observed for almost all the characters studied, except days to 50% flowering and days to 80% maturity shows low heritability with low GAM. The yield per plant, plant height and number of seeds per fruit showed high genetic advance that helped in effective and reliable selection through these characters for crop improvement. Yield per plant showed positive association with stem girth, number of branches per plant, plant height, first fruit producing node, fruit length, fruit diameter, average fruit weight, number of fruits per plant, number of seeds per fruit and 100 seed weight while, negative association with days to 50% flowering, number of locules per fruit and days to 80% maturity. The number of fruits per plant had maximum direct effect on yield per plant followed by average fruit weight. Number of branches per plant, plant height and first fruit producing node contributed to yield per plant indirectly via stem girth, average fruit weight, and number of fruits per plant. Hence, number of fruits and average fruit weight are identified as key traits for developing high fruit yielding genotypes of okra for future breeding programme

Patil *et al*. (2016) carried out correlation and path analysis utilizing 40 genotypes of okra during summer season 2015 and findings revealed that plant height exhibited positive and significant correlation with most of yield and yield contributing characters which indicated that these traits might be improved through direct selection. The path analysis study indicates that number of fruits per plant, number of branches per plant, number of nodes/plant exhibited maximum direct effect on yield per plant. It suggests that these attributes have strong influence on fruit yield. Hence, plant height, number of branches/plant, number of nodes/plant is the determiners of fruit yield per plant and require more attention in okra improvement programme while selecting okra genotypes.

Sanganamoni *et al*. (2017) studied the character association and path analysis in fifty-two genotypes of okra for 10 important characters. The character association studies revealed that the yield per plant had significant and positive association with number of leaves at 90 days after sowing (DAS) at both genotypic and phenotypic levels whereas number of branches per plant (90 DAS) at only genotypic level. It was significantly and negatively associated with internodal length (45 and 90 DAS) and days to first harvest. Presence of lower difference between the correlation coefficients at genotypic and phenotypic levels for various traits in the present findings indicates the lesser influence of the environment in the expression of these traits and presence of strong inherent association among the traits. Path analysis studies revealed significant positive association at genotypic level among the traits viz number of leaves per plant (90 DAS) and number of branches per plant (45 DAS) and exhibited perfect association with direct effect on yield per plant. These traits can be viewed for direct selection for improvement in the total yield per plant.

2.4 Combining ability and gene action in okra

Jinks (1954) explained gca as the result of additive effect and sca of nonallelic interaction effects. Griffing (1956) presented statistical concept of general and specific combining ability. The general combining ability involve additive x additive interaction; whereas, specific combining ability measures dominance, dominance x dominance and additive x dominance interactions. Griffing (1956) described two models; each with four methods, for working out the general and specific combining ability estimates in a set of diallel crosses and showed the relationship of diallel crossing methods to Fisher's method of covariance between relatives as expressed in terms of additive and non-additive genetic variance.

Prakash *et al.* (2002) in their study on line x tester analysis using 7 lines and 3 testers for estimating combining ability for yield and yield components (days to flowering, first fruiting node, height of first fruiting, stem hairiness, plant height, number of branches, number of nodes, fruit weight, fruit length, fruit girth, and number of fruits per plant) was studied in 21 F_1 hybrids developed from 7 okra cultivars, revealed that the estimates of general and specific combining ability and their ratio indicated the predominance of non-additive gene action for all traits. Four out of 10 parents are found best general combiners for fruit yield per plant, as well as two out of 21 hybrids which exhibited favorable SCA effects for the majority of the characters, can be exploited in breeding for improved yield.

In a study, Involving 6x6 diallel crosses of okra *(Abelmoschus esculentus (*L) Moench) Liou. -Minli (2002) reported that Days to flowering, number of fruits per plant, yield, fruit diameter and fruit weight was controlled by additive and non-additive genes. The reciprocal effects were significant for days to flowering, number of fruits per plant, fruit length and fruit weight.

While studying a 8 x 8 half-diallel analysis was performed by using okra genotypes of India, West-African USA and Turkish origins Duzyaman *et.al.* (2005) revealed that general or Specific combining abilities in Yield of promising crosses were obtained particularly in combinations among genotypes of different eco-geographic origin. The possibilities of selecting the parental material for further breeding work and a combination breeding based on additive gene effects are discussed.

As reported by Nichal *et.al.* (2000), combining ability for days to first flowering, plant height number of primary branches on main stem, number of fruiting nodes on main stem, number of fruits per plant, average fruit weight, fruit length, and fruit yield per plant were highly significant except average fruit weight, indicating the importance of additive and non-additive and non-additive genetic components of variation. However, the mean squares due to gca were greater, suggesting the greater role of additive variance in the inheritance of all characters. Ramesh *et al.* (1998) in their study on line and tester analysis reported that 8 out of 18 crosses exhibited significant positive sca effects for pod fruit yield per plant and most of crosses exhibiting sca effects had at least one parent with good gca.

Wammanda *et al.* (2010) developed 36 F_1's from nine parents by half diallel in okra The non-additive gene effect found prominent as the GCA and SeA variances ratio was less than unity for days to 50% flowering and internode distance. Parents Mothol-AE 2, Mothol-AE 3, Gerio-AE 1 and Mothol-AE 1 showed good general combining ability effects for plant height and internodal length. The estimates of sea effect identified that the crosses Mothol-AE 2 x Mothol-AE 3, MothoI-AE 1 x Mothol-AE 3, Mothol-AE 2 x Gerio-AE 1 and Mothol-AE 2 x Mothol-AE 1 were good specific combiners for fruit yield per plant and number offruits per plant.

Raghuvanshi *et al.* (2011) performed combining ability analysis for yield and its components by lines x testers crosses using six lines and four testers. They found that parents VRO 6, HRB 9-2 and VRO 5 were the best general combiners for fruit yield, first flowering node, internodal length, number of primary branches, number of fruits per plant, single fruit weight, fruit length and fruit diameter. The study revealed that the cross combination VRO 6 x Arka Anamika exhibited the highest sea effect followed by HRB 9-2 x P 7, VRO 6 x Arka Abhay, Pusa Kranti x rrVR J J, HRB 92 x Arka Abhay, VRO 5 x IIVR 11 and HRB 55 x Arka Abhay for yield per plant.

Prakash *et al.* (2012) accomplished full diallel analysis involving nine genotypes of okra to study the combining ability for fruit yield and its component characters. The result revealed that the parent Hissar Unnat exhibited good general combining ability for number of branches per plant, number of fruits per plant, fruit weight and fruit yield per plant. The hybrid Kamini x Bakra manifested the maximum sea effect for yield per plant followed by PB 7 x P 7, P 7 x Kamini, Hissar Unnat x PB 7, P 7 x PB 266, P 7 x Hissar Unnat and Kamini x PB 266.

Reddy *et al.* (2012) evaluated 45 hybrids derived from 10 nearly homozygous germplasm lines using half diallel. Analysis of variance for combining ability revealed that the variances due to GCA and SCA were highly significant for number of branches per plant, internodal length, days to 50% flowering, first flowering node first fruiting node, fruit length, fruit width, fruit weight and number of fruits per plant. Significance of GCA and SCA variances implied that both additive and non-additive components of heritable variance were responsible for variation observed. However, the ratio of GCA variance to SCA variance was lower than unity for fruit weight (0.927), fruit length (0.481), plant height (0.413), days to 50% flowering (0.413), first flowering node (0.366), first fruiting node (0.366), internodal length (0.315), yield per plant (0.289) and number of fruits per plant (0.059) suggested the predominance of the non-additive gene action. The parent’s IC 45732, IC 981 an Ie 89976 were good general combiners for fruit yield per plant. The crosse Rc 29119-B x Rc 99716, IC 27826-A x Ie 111443 and IC 89976 x IC 111443 were superior specific combiners for yield per plant.

Ashwani *et al.* (2013) carried out combining ability analysis using five lines and three testers at Vegetable Research Farm, BHU, Varanasi during summer and *kharif* seasons of the year 2009. Based on gca effects across nine characters, Arka Abhay, VRO 6, Hisar Unnat and Punjab Padmini were identified as promising parents for improving number of fruits per plant, fruit girth and days to 50% flowering. The high yielding crosses Arka Abhay x Parbhani Kranti, Hisar Unnat x Punjab Padmini, VRO 6 x Parbhani Kranti and VRO 6 x Arka Anamika depicted significant and positive sea effects for fruit yield.

Two Egyptian and four exotic parental genotypes of okra were self-pollinated for one generation and crossed in half diallel manner to study combining ability for earliness, vegetative and yield components traits by Hazem *et al.* (2013). The general combining ability and specific combining ability mean squares were highly significant for fruit yield per plant, number of fruits per plant, fruit length, fruit girth and plant height. Pusa Sawani was the excellent general combiners for all studied traits except average fruit weight per plant. The results revealed that the cross combination Escandarany x Clemson Spineless, which resulted from crossing between poor x poor general combiner parents, showed desirable negative and significant sea effect for earliness. The Balady x Pusa Sawani showed desirable sea effects for all studied traits except number of branches per plant.

Kumar *et al.* (2013) crossed eight elite diverse lines of okra in half diallel fashion and evaluated these hybrids along with parents. The results revealed that the parents KS 404, KS 7218, VRO 54 and BO 2 were good general combiners for days to 50% flowering; Parbhani Kranti, KS 404 and KS 7109 for plant height; KS 7109. VRO 54 and BO 2 for number of branches per plant; Parbhani Kranti for fruit length; Parbhani Kranti and KS 7109 for fruit diameter and KS 404 and Parbhani Kranti for number of fruit per plant. Siinificant and positive sca effect for YIeld per plant found in 12 cross combinations, the crosses Parbhani Kranti x KS 404 Parbhani Kranti P 7, KS 404 130 2 and K 7218 x VRO 54 manife ted good sca effect for yield per plant. Cross combination KS 404 x BO 2 showed good x poor gca while, K 7218 x VRO 54 involved poor x poor parents of gca combination.

Kishor *et al*. (2013) carried out an experimented on a Line x Tester analysis with five lines and three testers, to estimate the combining ability for ten characters. The result revealed that parents and crosses significantly differed for gca and sca effects, respectively. Combining ability analysis showed higher magnitude of SCA variance for all the characters except days to first flowering and fruit girth indicating preponderance of non-additive gene action.Among the lines, L 5 (Holavanalli Local), L (Thirumala Local) and among the testers, T (Mallapalli 2 3 Local) were identified as good parents. Among the hybrids cross combination L x 5 T (Holavanalli Local x Mallapalli Local) and L x T (Thirumala Local x Punjab 3 21 Phalgani) were found to be best specific crosses for yield per plant.

Pithiya *et al*. (2020) undertook an experiment to study the combining ability for yield and its attributing traits in okra. Information on the magnitude of combining ability was obtained for yield per plant and its related components following line x tester mating design involving 11 diverse varieties/strains (6 lines and 5 testers). The 11 parents and their 30 resultant F_1s were sown in a Randomized Block Design with three replications. Combining ability analysis revealed that the magnitudes of non-additive variance were higher for yield per plant and its contributing traits indicating the predominant role of non-additive gene action (except plant height in which additive gene action was there in the inheritance of that particular trait) in the inheritance of the traits. Among females; GO-2 (8.08) and JOL-2K-19 (6.62), while among males; EC-169513 (9.78) were good general combiners for yield per plant and related traits. The hybrid JOL-2K-19 x AOL-13-73 (31.32) showed high sca effects for yield per plant along with desirable sca effects for a number of branches per plant, numbers of fruits per plant and numbers of nodes per plant.

Yadav *et al.* (2020) estimated combining ability analysis from a Line × Tester crossing programme proposed by Kempthorne in 1957. Total 24 crosses were evaluated from 12 lines and 2 testers. Experiment was conducted at research field of Rama University, Kanpur during year 2019-20 with an aim to evaluate okra hybrids for yield and its attributing traits. Various morphological parameters viz., days to 50% flowering, plant height(cm), number of branches/plant, length of fruit per plant(cm), diameter of fruit (cm), number of seeds per fruit, number of fruits per plant and edible yield per plant (g) were recorded. Analysis of variance revealed that parents and hybrids differed significantly for most of the traits under study. The gca and sca effects were significantly different for majority of the traits. Estimates of gca effect revealed that Parbhani Kranti, K.S-325 and Pusa Sawni are good general combiners for fruit yield, number of fruits per plant and no. of branches per plant etc. The estimation of sca effects reveled that the cross combition Prabhani kranti x A.B – 1, KS 325 x A. B 2, B. O 2 x A. B 2 and K.S-312 x A.B-2 etc. were observed the most promising for fruit yield per plant, fruit length, number of fruits per plant and plant length etc. Thus the parents showing high gca can be utilised in hybridization programme for production of promising recombinants, while the crosses showing high sca for specific characters can be directly used for hybrid development.

Hamada *et al.* (2015) investigated to study combining ability and nature of gene action for some economic traits of okra (*Abelmoschus esculentus* L. MOENCH), using four different parental genotypes that were crossed in a complete diallel design. Mean squares of genotypes were significant for all studied traits, providing evidence for presence of considerable amount of genetic variation among studied genotypes. The general combining ability (GCA) and specific combining ability (SCA) mean squares were highly significant for all studied traits expect days to first flowering which was significant only for GCA. This indicated that both GCA and SCA were important in the inheritance of these traits. Significant reciprocal effect mean squares were found for Fruit Length, Fruit Diameter, Fruit weight and Total yield per plant, indicating that these traits were controlled by extra-nuclear factors as well as nuclear factors. Significant SCA effects in desirable direction were observed for most crosses in some studied traits. Good performance of the obtained crosses may be attributed to additive × dominance or dominance × dominance epistatic interactions. This suggested that the important role of non-additive gene action in the inheritance of the studied traits. The estimations of general combining ability variance (σ^2_{gi}) and specific combining ability variance (σ^2_{si}) of the parental varieties for all studied traits indicated that the developed varieties used in this study are of great importance to improving most studied traits. Estimates of genetic parameters and heritability for all studied traits verified the predominance of non-additive gene action in the inheritance of these traits. As well as, indicated that the studied traits except days to first flowering were not only controlled by nuclear genetic factors, but also the cytoplasmic genetic factors play an important role in the inheritance of these traits. Therefore, the genetic material of this study could be used for hybridization to produce promising crosses with improved economic traits in okra.

Hadiya *et al*. (2018) experimented to study the combining ability for yield and its contributing traits in okra. The experimental material consisted of seven parents and 21 F_1s produced from diallel mating design excluding reciprocal crosses in randomized block design for fourteen characters. The mean squares due to *gca, sca* effects were significant for fruit yield and yield contributing traits studied. None of the parents identified as good general combiner for yield per plant but the parents AOL-10-22, VRO-6, HRB-55 and AOL-12-59 were identified as average general combiners for fruit yield per plant and can be exploited well in further breeding programme. The estimates of *sca* effects revealed that the cross combinations AOL-10-22 × GAO-5, AOL-10-22 × VRO-6, JDNOL-11-01 × Arka Anamika and HRB-55 × AOL-12-59 were observed most promising for fruit yield and some of its related traits could be used as heterotic hybrids.

Kumar and Reddy (2016) evaluated six inbred lines (RNOYR-14, RNOYR-15, RNOYR-16, RNOYR-17, RNOYR-18 and RNOYR-24) along with their fifteen half-diallel crosses in a randomized block design with three replications during summer 2013 at Vegetable Research Station, Rajendranagar, Hyderabad, India to determine the nature of gene action and combining ability for pod yield and its component characters of okra (*Abelmoschus esculentus* (L.) Moench). Combining ability analysis revealed that both general combining ability (gca) and specific combining ability (sca) variances were highly significant for majority of the agro-economic traits indicating the importance of both additive and non-additive gene actions. The ratio of gca variance (σ^2gca) to sca variance (σ^2sca) of less than unity (<1) indicating the preponderance of non-additive gene action involved in the inheritance of all the traits under study. Inbred line RNOYR-16 was the best general combiner, while cross combinations RNOYR- 14×RNOYR-17, RNOYR-16×RNOYR-17 and RNOYR-17×RNOYR-18 were the high specific combiners for total and marketable yield.

Padadalli *et al.* (2019) developed thirty-three hybrids by crossing seven lines and three testers in L X T fashion for twenty-six parameters for productivity and quality traits. The variance due to parents vs. hybrids was also significant for all traits except plant height at 45 DAS, internodal length 45 DAS, days to first flowering, fruit diameter and seed yield per plant. The lines L7, L1 and L3 may be utilized as parent stocks for breeding for, growth parameters, earliness, yield and quality traits etc., among the hybrids L3 x T2, L7 X T2, L3 x T3, L1 x T3 and L7 x T2 showed specific combiner for almost characters as per results due to its an F_5 generation which attain homozygosity so, selection is effective for quality traits of fruits. The information presented here about quality traits of okra showed the potential nutritional importance of okra and it has role in improved nutrition.

Sapavadiya *et al.* (2019) estimated combining ability effects for different traits in a line x tester crossing programme comprising 32 crosses produced by crossing 8 lines and 4 testers. The GCA and SCA mean squares were significant for all the traits under study except number of nodes per plant. The ratio of GCA and SCA variances indicated the preponderance of non-additive gene effect for inheritance of all the traits. Genotypes JOL-09-05, JOL-09-07, Pusa Swani and AOL-09-02 showed good general combining ability for fruit yield appear to be worthy for exploitation of segregation and varietal development. The estimates of SCA effects revealed that the cross combinations JOL-0-05 x AOL-09.02, JOL-09-07 x JOL-2K-19 and JF-55 x AOL-08-05 were observed the most promising for fruit yield and some related traits.

Joshi *et al.* (2019) conducted a study to estimate the magnitude of combining ability and gene action on eighteen hybrids generated by crossing six lines with three testers. The results revealed that seven hybrids showed significant negative value for days to 50 percent flowering. Among the hybrids, the maximum positive sca effect was recorded by the hybrid L5 ×T2 followed by L6 ×T1 The predominance of non-additive gene action was found in days to 50 percent flowering, number of branches per plant, internodal length, fruit girth, fruit weight, number of seeds per fruit, hundred seed weight and fruit yield.

Punia and Garg (2019) experimented and grew nine parents (6 lines and 3 testers) and their 18 F_{1S} in a randomized block design (RBD) with three replications. One check variety, Komal 10 was also used as standard check. Crosses among the nine genotypes were made in line x tester mating design at Horticulture Nursery in university campus, SKRAU, Bikaner during *Zaid* 2014. The estimates of SCA variance were high than GCA variance for all characters except number of fruits per plant. The proportion of variance due to σ^2GCA/σ^2SCA was found to be less than unity for all the characters except number of fruits per plant showing thereby preponderance of non-additive effects. The line Kashi Kranti was identified as the best general combiner for most of the characters viz., days to 50% flowering, days to maturity, plant height, number of branches per plant, number of fruits per plant, fruit length and fruit weight. Another line Kashi Pragati also emerged as good combiner for six characters viz., plant height, number of fruits per plant, fruit length, fruit weight, biological yield and fruit yield per plant. The testers which emerged as good general combiner for yield and its contributing metric characters was Arka Anamika. The cross No. 315 x Hisar Unnat was identified as the best specific combiner for most of the characters viz., plant height, number of branches per plant, fruit length, fruit weight, biological yield and fruit yield per plant.

Yogendra *et al*. (2018) selected okra parents and hybrids tolerant to enation leaf curl virus (ELCV) disease based on estimates of combining ability and heterobeltiosis in the Gangetic plains of West Bengal, the most productive okra growing zones in eastern India. Eight diverse lines were crossed in diallel fashion without reciprocals to obtain 28 F1s. Additive genetic control of ELCV disease severity suggested use of pure line selection in the advanced generations from the highly heterotic crosses could be the best possible method to improvement of this trait. Two parents 285-1-3A-1-17-1 and VRO-178 with good general combining ability effects for tolerance to ELCV disease can now be used in future breeding programme. Partial- to over-dominance reactions for the inheritance of studied traits were recorded. We could able to isolate two outstanding hybrids 285-1-5-1-16-23 × VRO-178 and 285-1-3-1-15-2-1 × VRO-178 based on fruit yield and ELCV disease tolerance under field and epiphytotic conditions, and they could be commercially exploited after critical evaluations. Our study also suggests that either the identified donor parents will be used to develop backcross populations or exploiting promising hybrids in segregating populations for generating new inbred lines with much higher levels of tolerance to ELCV disease in okra.

Wakode *et al*. (2016) experimented to study the combining ability for yield and its attributing traits in okra. The experimental material consisted of seven parents and 42

F1s produced from diallel mating design including reciprocals. Analysis of variance for combining ability was carried out for eleven characters. The mean squares due to gca, sca and reciprocal effects were significant for all the characters, indicating substantial genetic variations for all the characters studied. The genotypes VRO-6, Pusa A-4 and Arka Anamika were identified as good general combiners for most of the characters including fruit yield per plant and can be exploited well in future breeding programme. Similarly, Ajeet Dhanlaxmi 2-4-2 sel x VRO-6, Pusa A-4 x VRO-6 and VRO-6 x Arka Anamika were the good specific combinations and could be used as a heterotic hybrid. For traits viz., nodal position for fruit, days to first flowering, first picking and number of branches additive gene action was observed for governing these traits. However, for other traits σ^2 D was greater than σ^2 A indicating the non-additive gene action for the expression of those traits.

Hadiya *et al.* (2018) undertook an experiment to study the combining ability for yield and its contributing traits in okra. The experimental material consisted of seven parents and 21 F_1s produced from diallel mating design excluding reciprocal crosses in randomized block design for fourteen characters. The mean squares due to gca, sca effects were significant for fruit yield and yield contributing traits studied. None of the parents identified as good general combiner for yield per plant but the parents AOL-10-22, VRO-6, HRB-55 and AOL-12-59 were identified as average general combiners for fruit yield per plant and can be exploited well in further breeding programme. The estimates of sca effects revealed that the cross combinations AOL-10-22 × GAO-5, AOL-10-22 × VRO-6, JDNOL-11-01 × Arka Anamika and HRB-55 × AOL-12-59 were observed most the promising for fruit yield and some of its related traits could be used as heterotic hybrids.

Shwetha *et al.* (2018) studied eight parental lines of okra and their 28 F_1 hybrids obtained from half diallel to identify the good general and specific combiners for yield and quality parameters. Both general a combining ability (GCA) and specific combining ability (SCA) variances were highly significant for all the characters indicating the importance of both additive and nonadditive gene actions. The parents KO1608 and KO1606 were identified as good general combiners for number of fruits per plant, yield per plant, yield per plot and yield per hectare. The parent KO1608 was good general combiner for fruit weight and number of ridges on fruit surface and the parent KO1606 was identified as good general combiner for average fruit weight. The crosses KO1601 x

KO1605 and KO1603 x KO1606 were identified as good specific combiners for average fruit weight, yield per plant, yield per plot and yield per hectare. The maximum sca effects were observed in the crosses KO1601 x KO1604 and KO1606 x KO1607 for number of fruits per plant and fruit length respectively. The cross KO1602 x KO1605 exhibited highest sca effects for fruit diameter and number of seeds per fruit.

Kayande *et al*. (2018) undertook the experiment to study the combining ability for yield and its contributing traits in okra. The experimental material consisted of eleven parents and 28 F_1s produced from line x tester mating design in randomised block design for eleven characters. The mean squares due to gca, sca effects were significant for pod yield and yield contributing traits studied. The parents 38HU, MTPH, 14-11-5, 11-14, PF and 11-6 were identified as good general combiners for most of the characters including fruit yield per plant and can be exploited well in further breeding programme. The estimates of sca effects revealed that the cross combinations 11-1 x 14-11-5, 38HU X 11-14, MPTH X AKOV-107, MPTH X 93M and NO-3 X 11-6 were observed most promising for fruit yield and some of its related traits could be used as heterotic hybrids

Annapurna and Singh (2018) carried out an experiment during rainy season of 2017 and summer season of 2018 where twenty diverse genotypes of okra were crossed in line x tester mating design in RBD with 17 lines and three testers to estimate the general combining ability (GCA), specific combing ability (SCA) and gene action. The lines like Arka Abhay, VRO-5, VRO - 6, JBS -2 and testers like Pusa Sawani proved to be the good general combiner and VRO – 6 x Pusa Sawani was the good specific combiner for most of the yield and yield attributing traits during both the seasons.

2.5 Estimation of heterosis of different characters in okra

The term heterosis is now widely used, which refers to the phenomena in which the F_1 hybrid obtained by crossing the two genetically dissimilar homozygous individuals, shows increased or decreased vigour over the parental values. Shull (1908) referred this phenomenon as the stimulus of heterozygosis. The expression of heterosis may be due to factors such as heterozygosity, allelic interaction such as dominance or over-dominance, nonallelic interaction or epistasis and maternal interactions. The degree of heterosis depends upon the number of heterozygous alleles. Higher the number of heterozygous alleles, more is the heterosis expected (East and Hayes, 1912). The term heterobeltiosis was coined by Fonseka and Patterson (1968), which refers to the increased or decreased vigour of F_1 over its better parent. Hybrids offer opportunities for improvement in productivity, earliness, uniformity, quality and wider adaptability and for rapid deployment of dominance genes for resistance to diseases and pests (Riggs. 1988).

Devi *et al.* (2020) crossed six diverse cultivated genotypes in half diallel fashion to study the extent of heterosis, mode of gene action, combining ability effects, and dominance effects of 14 yield component traits including disease severity of ELCV. Predominance of nonadditive gene action occurred in the control for all characters studied except for percent disease index of ELCV which was conditioned by both additive and nonadditive gene action. Partial, to overdominance, effects were involved in inheritance of fruit yield and most of horticultural traits studied. Two parents ‘2014/OKYV RES-5′ and ‘2014/OKYV RES-10′ were identified as most promising donors for future breeding. Heterosis for yield per plant was manifested through node at first flowering, plant height, fruit length, number of fruit per plant, nodes on the main stem, and seed per fruit. Two promising hybrids ‘2014/OKYV RES-5 × 2014/OKYV RES-10′ and ‘2014/OKYV RES-5 × BCO-1′ were identified based on average values, heterosis manifested, and relevance of specific combining ability effects, and these hybrids could be commercialized in okra growing zones in the tropics after critical testing.

Jagan *et al.* (2018) under took an investigation with the objective of identifying the high yielding parents and F_1 hybrids through Line X Tester mating design to estimate the heterosis. The experiment was conducted by raising four lines and fifteen testers as parents and their 60 F_1 hybrids during kharif 2009 and spring summer 2010. The heterosis recorded for fruit and its thirteen component characters. The F_1 hybrids, Arka Anamika x IC-331217, Arka Abhay x IC-331217, Arka Anamika x IC-326893, Arka Anamika x IC-443670, Arka Abhay x IC-332454 and Arka Abhay x IC-433675 recorded high degree of standered heterosis for yield and its contributing characters. High estimates of heterosis obtain in hybrid combinations revealed considerable genetic divergence among the parental lines.

Kumar *et al.* (2017) conducted a study at Vegetable Research Farm, Department of Horticulture, Institute of Agriculture Sciences, Banaras Hindu University, Varanasi during Spring-Summer and Rainy season of 2012 and 2013 using 12 diverse parental lines of okra and their 66 F_1 hybrids (through diallel cross-excluding reciprocals) with the objective to measure the extent of heterosis over better parent and standard commercial check varieties for the purpose of judging the extent up to which heterosis can be exploited in commercial okra breeding. The extent of heterosis for five best crosses over better parent and check (48.32 % to 82.42 % and 7.13 % to 35.66 %, respectively) for yield per hectare suggested the great scope of realizing higher yield in okra through heterosis breeding. Other economic traits also recorded moderate to high level of heterosis over the better parents. The cross combination IC -282280×EC – 329380 showed high heterosis over better parent and standard check for pod yield (82.42 % and 35.66 %) and number of pods per plant (62.82 % and 48.54 %) respectively. This particular cross combination eventually resulted the height magnitude of heterobeltiosis and standard heterosis for the most of the desirable growth parameters as well as yield attributing characters which may be taken for further breeding programme.

Maciel *et al*. (2017) conducted an experiment where two different methods of hybridization were used: traditional manual hybridization with complete emasculation followed by hand pollination (artificial) and, an experimental methodology, performing manual hybridization with incomplete emasculation followed by entomophilous natural pollination between two inbred lines (UFU-QB-040D and UFU-QB-107G). These inbred lines were obtained from three selection cycles. Three hybrid types were obtained from the two hybridization methods: F_1 THM (UFU-QB-040D x UFU-QB-107G), F_1 IHM (UFU-QB-107G x UFU-QB-040D) and F_1 IHM (UFU-QB-040D x UFU-QB-107G). The resulting hybrid seeds and their parents were evaluated via an experiment set up in a randomized block design with four repetitions. We evaluated fruit production per plant, fruits per plant, number of branchess per plant, superiority of hybrids relative to parents (h) and heterosis (%). At the end of the cycle, morphological characterizations were done of the leaves (pubescence, length and width) and fruit (length, diameter and shape). Heterosis resulting from the incomplete emasculation followed by natural insect pollination was similar to that from the traditional hybrid method, being a viable alternative for the production of hybrid okra seeds without losses in heterosis.

Shamloul and Moghazy (2017) experimented on okra and found that the mean squares of the genotypes were highly significant except plant height (cm) and pod length (cm). General combining ability (GCA) was highly significant for all traits. Therefore, additive genetic variance was more important in the inheritance of these traits. The values of GCA were higher than those of specific combining ability (SCA) for plant height (cm), number of nodes to first flower and pod diameter (cm) indicating that additive genetic variance was more important for these traits. The values of SCA were larger than those of GCA for other tested traits indicating the importance of non-additive effects. The magnitudes of GCA and SCA values were close for the pod diameter, thus illustrating the importance of both values for this trait. The crosses $P_1 \times P_2$ and $P_4 \times P_2$ were promising and showed highly significant estimates of SCA effects. Genetic variances including dominance (σ^2_D) were positive and highly significant for most traits except for pod length. The reciprocal variances were smaller than the additive genetic variances for average pod weight and number of seeds pod^{-1}. The results showed that the reciprocal effect (σ^2_{rec}) or maternal effect was present and should not be neglected. The heritability in broad sense was larger than the corresponding values in narrow sense for all traits. In general, the F_1 hybrid $P_2 \times P_3$ and $P_2 \times P_4$ gave desirable value for early yield trait where the mean number of nodes of first flower was -38.51 and 31.03 g for Average weight of pod plant^{-1}, respectively. However, the F_1 hybrids $P_1 \times P_2$ gave the highest values of hybrid vigor with a mean of 57.1 for number of pods plant^{-1}, 32.14 kg for weight of pods plot^{-1} and 38.59 for number of seeds pod^{-1}. Whereas, the F_1 hybrids $P_1 \times P_2$ and $P_2 \times P_3$ were outstanding for most traits. This result indicated that choice of parents is an important factor. These hybrids can be utilized in breeding programs to produce improved okra lines and new cultivars.

Kishor *et al.* (2013) conducted an experiment at the Department of Plant Breeding and Genetics, College of Agriculture, Vellayani during 2011-2012 to identify potential parents and superior crosses for yield and yield related traits in okra. Fifteen hybrids (F_1s) were developed by crossing five lines and three testers in Line×Tester mating design. Fifteen hybrids along with eight parents were used to estimate the heterosis for ten yield and yield attributing characters. The result indicated that significant standard heterosis for fruit yield per plant was observed in Holavanalli Local×Mallapalli Local, Thirumala Local×Kattakada Local, Kunnapuzha Local×Punjab Phalgani, Thirumala Local×Punjab Phalgani and Thirumala Local×Mallapalli Local. The magnitude of heterobeltiosis for fruit yield per plant was significantly superior in Holavanalli Local×Mallapalli Local and Thirumala Local×Kattakada Local. These two crosses also exhibited significant heterosis for days to first flowering, number of primary branches, number of fruits per plant, fruit weight, fruit length and fruit girth. Among the fifteen hybrids, Holavanalli Local×Mallapalli Local and Thirumala Local×Kattakada Local cross combinations found promising for fruit yield and other traits. Hence, these hybrids need to be tested on larger scale for their commercial values.

Sapavadiya *et al*. (2019) studied on a set of 45 genotypes including 8 females, 4 males, their 32 resultant hybrids and one commercial check variety (GJOH-3) during *khrif* 2016 at the Instructional Farm, Junagadh Agricultural University, Junagadh to study the magnitude of heterosis using line x tester analysis for ten characters. Significant differences were observed among the parents and hybrids indicating considerable genetic variation among these genotypes. Significant standard heterosis and high per se performance with regards to yield per plant were recorded by the crosses *viz.*, JOL-11-12 x AOL-03-02, KS -404 x JOL--2K-19, Pusa Sawani x AOL-03-01 and Pusa Sawani x AOL-08-05.

Eswaran and Kumar (2013) compared fifteen hyids of diallel origin and 60 three–way cross hyids of triallel origin for their heterotic potential. Eight single cross hyids and 60 three–way cross hyids showed significant positive relative heterosis for fruit yield per plant. Six single cross hyids and 53 three–way cross hyids exhibited significant positive better parent heterosis for fruit yield per plant. However, the magnitude of heterobeltiosis was higher with three way cross combinations. The three–way cross combinations which recorded higher better parent heterosis had the higher heterobeltiotic single cross combinations as grandparents.

Devi *et al*. (2017) conducted an experiment to estimate the magnitude of heterosis for fruit yield and yield-contributing characters in okra [*Abelmoschus esculentus* (L.) Moench]. Eight genetically diversed parents namely, Hisar Naveen, Pusa Makhmali, Kashi Pragati, Hisar Unnat, Pusa A-4, No. 315, Varsha Uphar and Kashi Kranti were crossed in a diallel fashion (excluding reciprocals) to develop 28 F_1s. These crosses along with their parents were evaluated in a randomized block design with three replications during *kharif* 2014 and *zaid* 2015 at Swami Keshwanand Rajasthan Agricultural University, Bikaner. Significance of mean squares due to genotypes revealed the presence of considerable genetic variability among them for all yield and yield-attributing characters except days taken to 50% flowering and days to first harvesting. Negatively heterotic crosses like Kashi Pragati × Varsha Uphar for days to 50% flowering (−6.62%) and Varsha Uphar × Kashi Kranti for first flowering nodes (−6.98%), respectively, were important to exploit heterosis for earliness in okra. An appreciable heterosis was observed over better parent (28.90%) and mid parent (29.02%)

for marketable fruit yield per plant which showed good scope of heterosis breeding in okra. The most heterotic crosses for marketable fruit yield per plant and most of the other yield-contributing characters were found in Kashi Pragati × Varsha Uphar, No. 315 × Varsha Uphar, Kashi Pragati × Pusa A-4 and Hisar Naveen × Varsha Uphar. These crosses were considered promising for their use for yield improvement in okra.

Kerure *et al*. (2019) studied on heterosis for commercial exploitation of F_1 hybrids in okra (*Abelmoschus esculentus* (L.) Moench). 45 F1s were developed by crossing 10 elite lines of okra in half diallel fashion during summer 2016. All 45 F1s along with their 10 parents and one standard control (Nunhems hybrid Shakti) were evaluated in a randomized complete block design with three replicates during late kharif (July to October) 2016 at ICAR- Krishi Vigyan Kendra, Babbur Farm, Hiriyur, Chitradurga, Karnataka, India, for heterosis of yield and its components of okra. Significance of mean squares due to genotypes revealed the presence of considerable genetic variability among the material studied for almost all yield and yield attributes. The overall maximum positive significant heterosis for total fruit yield per plant was observed in cross IIHR-875 x IIHR-478 (112.89%) over relative heterosis, (83.78%) over heterobeltiosis and (168.55%) over standard heterosis. Negatively heterotic crosses like IIHR-562 x IIHR-444 for days to 50% flowering (-8.70%) and IIHR-567 x IIHR-107 for fruiting nodes (-9.03%) respectively, are important to exploit heterosis for earliness in okra. Out of 45 F1s, 44 F1s crosses exhibit significant standard heterosis in any given direction for total fruit yield per plant except cross IIHR-604 x IIHR-107 (-0.13%). The F1 hybrid IIHR-875 x IIHR-478 with high yield potential has the potential for commercial cultivation after further evaluation for late kharif season of Karnataka.

Kumar (2019) investigated seven genotypes and their 21 F_1 crosses obtained from half diallel mating design to estimate the magnitude of heterosis for yield and its parameters. The extent of heterosis ranged for all the characters under study. Desirable heterosis for days to 1st flowering was observed in Annika X Rajini over both mid parent and better parent while the cross EC359637 X Arka Anamika significant desirable heterosis over standard check. For average fruit weight, the maximum magnitude of heterosis was obtained in cross EC359637 X Arka Anamika over average parent, Annika X IC014026 over better parent and Annika X EC359637 over better parent. The maximum desirable heterosis for fruit yield per plant was observed in EC359637 X IC014026 over mid parent, better parent and standard check followed EC359637 X IC013664 and EC359637

X EC305768. Higher magnitude of heterosis observed in crosses revealed presence of significant genetic diversity among the genotypes.

Amiteye *et al.* (2019) studied on okra and found the expression of heterosis for key quantitative agro-morphologic traits by 27 F_1 offspring obtained from intraspecific and 24 F1 offspring from inter-specific hybridization among ten parental accessions. The performances of their F1 offspring were evaluated against the respective parents for expression of heterosis for key quantitative traits including days to 50% germination, days to 50% flowering, plant height, fresh fruit weight, length of pod and number of seeds per pod. It was observed that. the cross, T3 X T1 came out with the highest BPH for days to 50% germination while the crosses AG X T4, AG X YL and T2 X T3, respectively recorded highest BPH for (days to 50% flowering and number of branches per plant), (length of pod and Fresh fruit weight) and (Plant height and number of seeds per pod).

Ramya and Senthil (2010) evaluated 42 F_I's developed in a diallel mating of seven parents including reciprocals and reported the highest standard heterosis in Pusa A 4 x Punjab Padmini (55.95%) followed by Punjab Padmini x Pusa A 4 (53.59%), Punjab Padmini x Varsh Uphar (51.38%) and Parbhani Kranti x Punjab Padmini (46.99%) for yield per plant in okra.

Mistry (2012) analyzed heterosis and inbreeding depression by six generation mean for pod fruit yield per plant and yield contributing traits in six inter varietals crosses of okra. The results revealed that all the three crosses exhibited significant heterosis over mid parent and better parents for yield and yield contributing characters followed by significant inbreeding depression, indicating the predominance role of dominance type of gene action.

Wammanda *et al.* (2010) developed 36 F_1's from nine parents by half diallel in okra They observed that heterosis for fruit yield per plant was the greatest in crosses where the high yielding parent such as Mothol- AE2, Mothol- AE3, Mothol- AE 1 and Gerio- AEt were involved. Thus, the hybrid, Mothol- AE2 x Mothol- AE3 had the highest heterotic effect of 23.8% over the higher parent, followed by Mothol- AEI x Mothol- AE3, Mothol- AE5 x Gerio- AEl, Mothol- AE2 x Gerio- AEI, Mothol- AE2 x Motho1- AEI and Mothol- AEI x Gerio- AEI for yield per plant. Likewise, seven crosses expressed positive heterosis for number of fruits per plant. The highest heterosis were expressed by Mothol-

AEI x Gerio- AEI (17.23%) followed by Pella- AEI x Gerio- AEI (11.8%), Mothol- AE5 x Mothol- AEI (9.96%), MothoJ- AE5 x MothoI-AE3 (8.69%), PelIa- AE2 x Mothol- AE3 (7.24%) and Mothol- AE5 x Pella- AE2 (6.98%) for number of fruits per plant.

SoIankey *et al.* (2013) conducted the trial in okra during summer and rainy seasons of years 2006 to 2008 at the Institute of Agricultural Sciences, BHU, Varanasi. They recorded appreciable heterosis over better parents for various horticultural traits and quality traits over both the seasons. The highest better parent and standard heterosis for number of fruits per plant observed in IIVR 198 x Parbhani Kranti (67.27 and 12.25%, respectively) during rainy season. However, the maximum heterobeltiosis manifested by EC 305612 x Pusa Sawani (26.10%) in summer season. It was confounded that the rainy seasons was more yield productive seasons than summer.

Medagam *et al.* (2013) selected ten elites, optimally divergent and nearly homozygous lines of okra from the germplasm and crossed in all possible combinations excluding reciprocals to produced 45 hybrids and tested during *kharif* at the Vegetable Research Station, Hyderabad. Heterosis over mid parent, better parent and standard check were studied for seventeen quantitative characters pertaining to fruit yield and its associated characters. For total yield per plant, the crosses as a whole manifested 7.17 and -15.22% average relative and standard heterosis, respectively. For marketable yield per plant, the crosses as a group manifested 6.77 and -22.64% average relative and standard heterosis, respectively. The hybrid P_5 (IC 45732) X P_7 (IC 89976) exhibited good performance and found heterotic for pod yield.

Ashwani *et al.* (2013) conducted experiment at Vegetable Research Farm, BHU, Varanasi using five lines and three testers by making 15 cross combinations. They found significant and negative heterosis for days to first flowering over mid parent ranged from -4.88% (Hisar Unnat x Parbhani Kranti) to -26.67 % (Arka Abhay x Arka Anamika). Likewise, the range of standard and significant heterosis for plant height varied from 4.49% (VRO 5 x Parbhani Kranti) to 36.18% (Hisar Unnat x Punjab Padmini). Out of 15 crosses, eleven crosses exhibit significant and positive standard heterosis for the number of primary branches and thirteen crosses represent highly significant and negative standard heterosis for days to 50% flowering. Out of 15 crosses, 13 crosses showed highly significant and positive standard heterosis for total number of fruits per plant. The hybrids Arka Abhay x Punjab Padmini (27.15) % exhibited the highest standard heterosis followed by VRO 6 x Parbhani ranti (25.32%) and Arka Abhay x Punjab Padmini (23.40%) for number of fruits per plant.

2.6 Genotype x environment interactions in okra

Sanket *et al*. (2018) tested fifty-five okra genotypes (ten lines, four testers, forty hybrids and one check) okra accessions for stability in three different environments between 2014-15 using Additive main effect and multiplicative interaction (AMMI) and Genotype main effect and Genotype by Environment (GGE) models. The experiment was laid out in a Randomized Complete Block Design (RCBD) with three replications. The mean squares due to genotypes were highly significant for all the traits when tested against pooled error and pooled deviation which indicated the presence of considerable genetic variability in the materials. Highly significant differences were also observed amongst environments for all the traits when tested against pooled error and pooled deviation which indicated the presence of considerable environmental differences for all the traits. The genotypes x environment interactions were significant for all the traits except fruit length when tested against pooled error. Both AMMI and GGE biplots identified most stable, high yielding genotypes that were overall best in performance in relation to yield and stability. Result of stability estimates of 55 genotypes revealed that none of the genotype was stable for all the traits studied. Further, IC – 045796 x GAO – 5 and VIO 47672 x GAO – 5 were the most stable hybrids in terms of fruit yield and its components. For the trait, yield per plant Environment E3 (winter season) was found to be the most unfavourable while Environment E2 (rainy season) was the most favourable environment.

Olayiwola and Ariyo (2015) evaluated inter-character relationships of agronomic traits on genotypes of okra [*Abelmoschus esculentus* (L). Moench] over three environments in Nigeria to compare the stability of relationships and determine traits to be targeted in development of an efficient selection index for okra yield improvement. Data were recorded on seed yield, pod yield, 100-seed weight, pod length, pod width, number of leaves and branches, stem diameter, plant height, and days to flowering. Components of variance and covariance were utilized to calculate environmental, genotypic, and phenotypic correlations among seed yield and other traits. Plant height, stem diameter, and pod yield had significant genotypic and phenotypic correlations among themselves and also had genotypic and phenotypic correlations with seed yield over environments.

These traits could be utilized to develop a selection index to be applied across locations to increase seed yield in okra.

Namita *et al.* (2014) studied the phenotypic stability of 53 genotypes of okra (30 varieties and 23 hyids) grown over three environments for growth and yield characters. Variance due to genotypes and environments was highly significant for these characters. The large variation in regression values indicated large differences in genotype response to different environments. G x E interaction was significant for plant height, intermodal length, number of fruits per plant, total fruit yield per plant and yield per plot. The genotype Arka Abhay was found promising and stable for plant height, internodal length. The hyids KAOH09 and KAOH08 were found highest yielder and also stable for total yield per plant. The F_1 hybrids had greater stability for yield across the environments compared to open pollinated varieties. Stability of the crosses was attributed to the stability of parents. Stability for yield is attributed to stability for component traits.

Sharma *et al.* (2019) studied on Bhindi, which were grown in a Randomized Block Design (RBD) with three replications under six environments (three different dates of sowing in Spring-summer and Kharif). The observations were recorded on five randomly selected plants for characters viz., plant height (cm). no. of branches per plant, days to first flowering, days to first harvest, number of fruits per plant, fruit length (cm), fruit diameter (cm), fruit weight (g), fruit yield per plant(kg) and fruit yield per plot(kg). Since many of the plant economically important characters are quantitatively inherited and highly influenced by the environmental condition. Phenotypic variation results from complex of three variables viz., genetic, environmental, and genotype X environment (GXE) interaction, hence, the stability of the genotypes in the predictable and unpredictable environments is an important factor for realizing the maximum yield. Since, precise information was not available on stability of promising genotypes in Bhindi that can be relied upon. Therefore, the present investigation was done on estimation of stability parameters of the genotypes for different traits in Bhindi to find out the performance of different genotypes, nature and magnitude of variability present under different dates of sowing in different crop seasons (Spring-Summer and Kharif) and to observe the stability of performance of various promising genotypes under different environments in both the seasons. The results thus indicated that genotypes HRB-9-2, Pb-57, HOE-202, D-1-87-5, Pusa Sawani, 71-14, KS-312 and D-1-87-16 had higher potentialities over environments for producing high yield. The genotypes HRB-9-

2, Pb57, HOE-202, D-1-87-5 and Pusa Sawani had average response and are highly stable for fruit yield per plant. These genotypes are likely to perform well in all the environments of both the seasons (Spring-Summer and Kharif season). Thus genotypes as identified in the present study can further be exploited for higher yield and also in breeding for superior and stable genotypes of Bhindi.

Vekariya *et al*. (2019) investigated on 72 genotypes (11 lines, five testers and their resultant 55 hybrids along with a commercial hybrid check 'OH-102') of okra were sown at three different locations at Navsari Agricultural University, Navsari (Gujarat) in Kharif 2018 to obtain the information on stability parameters for yield per plant and its component traits. The stability analysis exhibited significant differences among genotypes (G), environments (E), while genotype x environment interaction was reported non-significant for all traits (except seeds per plant) when tested against pooled deviation indicated that genotypes responded consistently over the environments. Mean square due to genotype x environment interaction (linear) effect was non-significant for all traits (except seeds per plant) indicated that performance of genotypes remained similar for their linear regression on environmental index and significant for seeds per plant indicated that prediction of performance across the environments against these characters would be highly effective. Among locations, Achhalia (E2) was found to be the most favourable for fruit yield and other related traits. Stability analysis for seeds per fruit, revealed that four hybrids viz., AOL-12-52 X Arka Anamika, AOL-12-144 X Parbhani Kranti, AOL-14-32 X Parbhani Kranti and AOL-14-32 X Arka Abhay manifested below average stability, indicated that hybrids specifically adapted to favorable (good) environments while hybrid AOL-12-52 X GJO-3 manifested above average stability, indicated that this hybrid specifically adapted to unfavorable (poor) environments.

Alake (2018) assessed genotype × environment (G × E) interactions for pod yield and pod number in a set of 25 West African okra genotypes that were cultivated in four successive years (otherwise called environments) through field trials, arranged in a randomized complete block design, with three replicates. Significant G × E interactions in measured traits were detected, suggesting that selection for stable genotypes, with respect to these traits must be environmental specific. Consequently, additive main effects and multiplicative interaction model was applied to dissect G × E interactions. For pod yield, the highest percentage (38.4%) of the treatment sum of square was attributable to genotypes followed by G × E interactions (36.0%) and environment

(25.6%), indicating predominance of genotypic variation for this trait. Conversely, prevalence of G × E interactions was observed for pod number.

Patil *et al*. (2017) worked on 37 genotypes of okra and found that the stability analysis exhibited significant differences among genotypes (G), environments (E) and G x E interaction for all characters except variance due to environment and G x E for ascorbic acid content indicating variable response of different genotypes for various traits under varied agro-climatic conditions. The significance of G x E (linear) and pooled deviation for yield per plant and its most of the related traits suggested importance of both linear and non-linear components in building up total G x E interaction. Among the environ ment studied, E2 was found to be mo st favourable wh ereas E 3 most un favourable The parent JOL-09-8 was found to be average stable for yield per plant and its attributes. Among the hybrids, eight were identified as stable over environments for yield per plant and the best three among them were JOL-09-7 x JOL-09-8, JOL-09-7 x AOL-09-17 and JOL-09-7 x AOL-09-2.

Akinyele and Osekita (2011) grown sixty lines of NH47-4 variety of okra (*Abelmoschus esculentus*), obtained from the National Institute of Horticultural Research and Training (NIHORT), Ibadan, Nigeria, in two different locations (Akure and Ilara-Mokin, Ondo State, Nigeria) under rain-fed conditions using the Randomised Complete Block Design (RCBD) with four replicates. The plants' genotypic coefficients of variation and correlations were analysed for eleven quantitative traits, namely days to flowering, days to maturity, number of branches per plant, number of pods per plant, height at flowering, final height, pod length, pod width, number of seeds per pod, weight of 100 seeds and seed yield. The number of branches per plant, number of pods per plant and seed yield showed high genotypic coefficient of variation. Plant height at flowering, final plant height and number of seeds per pod showed positive direct genotypic effect on the number of branches per plant. Number of pods per plant and number of seeds per pod showed very high direct genotypic effect on seed yield. For a reliable selection index, number of pods per plant was a prime character. This was closely followed by height at flowering and then number of seeds per pod. Therefore, greater attention should be given to these traits in variety development.

Prakash *et al.* (2017) was tested the phenotypic stability of sixteen genotypes of okra for growth and yield components by growing them in three different environments. The results revealed significant difference among the genotypes all the traits studied except for plant height at 90 days after sowing and number of fruits per plant. Significant difference among the environments was observed for almost all the characters except for plant height at 90 days after sowing (DAS), number of fruits per plant. GxE interaction was significant for plant height at 45 days after sowing and total yield per plant. The genotypes L5, L8, L9 and L15 were found stable and predictable with high mean value for yield per plant as indicated by regression coefficient approaching unity and non-significant deviation from regression and were stable across different environments.

Considerable work on G x E interaction has been done in cereals and other field crops. However, in case of okra only few references are available. These references are reviewed in the ensuing pages. Rao (1978) from his study of G x E interaction in okra for two seasons found that increasing the number of locations for testing was more beneficial rather then increasing the years of testing because the variance component G. E was highly significant suggesting the presence of considerable degree of first order interaction. Evaluating the performance of six bhindi varieties, viz., Vaishali vadu, Long Green, Pusa Sawani, Pusa Selection 6-2, Pusa Selection 2-2 and Pusa seletion 1-1 for four years, Korla and Rastogi (1979) recorded data for marketable fruit yield (kg) on ten randomly selected plants and observed significant differences among the varieties, V x E and V x E (linear). The deviation from regression was non-significant.

Allard and Bradshaw (1964) coined the term predictable and unpredictable environments; the former includes permanent features of the environment, such as climate, soil type and day length in addition to what are called controllable variables (perkins and Jinks, 1971) like levels of fertilizer applications, sowing dates, sowing density and methods of harvesting etc., while the latter embodies weather fluctuations, such as differences between seasons in terms of the amount and distribution of rainfall and the prevailing temperatures.

CHAPTER III

MATERIALS AND METHODS

Fifty okra inbred lines were developed from the base population generated in the field laboratory which was homozygous through selfing and sib mating methods. Among them seven lines were selected through diversity analysis. The study of correlation and path analysis were done for these inbreds. The half diallel fashion was used to incorporate of the selected inbred lines for the production of F_1 hybrids to assess their combining ability, heterosis, heritability for yield and yield contributing characters of okra. The whole experiments were undertaken and observed at the Research and Development farm of Metal Agro limited at Nagarchanti, Kawapukur, Debigonj, Panchagarh. Six cropping seasons were kept under field level operations during the period of 2014-2017. The location of the experiment site was about 400 km north from the capital city Dhaka. This section described the general aspects of materials and methods, treatments, methods of raising the crops, cultivation, data collection and statistical analysis. The experiments were carried out sequentially.

3.1 Experimental site, soil and climate

The experiments were conducted at Research and Development Farm of Metal Agro Limited, at Nagarchanti, Debigonj, Panchagarh (the location of site 26.11858 ^{0}N, 88.759299 ^{0}E and it is 150 feet or 46 m high from the sea level), from the period of August, 2014 to March 2017.

In present study fifty genetically diversed genotypes of okra were evaluated to find out seven genotypes based on their morphological traits and have to cross among them with half diallel fashion to obtain 21 hybrid progeny.

The present research work was conducted at the experimental field laboratory of the Research and Development farm (RandD) of Metal Agro Limited, Nagarchanti, kawapukur, Debigonj, Panchagarh. This area belongs to the AEZ under Old Himalayan Piedmont Plain (01).

Location and extent: Parts of Panchagarh, Thakurgaon, and Dinajpur districts and has 4008 square km area.

Sub region: (a) Northern, (b) North-central and (c) Southern.

Land type: 58% high land, 34% medium high land, 7% medium low land and 7% homestead and water.

Dominant soil textural class: Soil is mainly loamy and sandy.

Main general soil types: Non calcareous alluvium, non-calcareous grey flood plain soils, non-calcareous brown flood plain soils, non-calcareous dark grey flood plain soils, and black terai soils.

Major agricultural limitation: (a) Land tenure system- big land lords own much of the land. (b) Predominant soils are rapidly permeable (c) Flash flood in depressions (d) Low winter temperature (e) Shortage of surface water (f) Low soil fertility especially in black terai soils.

The experimental plot was prepared by ploughing with rotovetor tractor. The weeds and other unwanted plant materials were removed from the field during the land preparation. A randomized complete block design was used in the experiment with three replications. Seeds were sown on March, 2015 and one seedling/hill was kept for the evaluation. Plant to plant and row to row distance were maintained at 70 cm X 70 cm, respectively. Thus each accession had two rows and each row contained five plants. The following recommended doses of fertilizer were used (a) Urea 50 kg/ha, (b) Triple Super Phosphate (TSP) 170 kg/ha, (c) Muriate of Potash (MP) 50 Kg/ha, Zypsum 100 Kg/ha Zinc and Boron 12Kg/ha respectively. During the final land preparation, one third of the Urea, MP and whole amount of TSP, Zypsum and Zinc (Separately) and Boron was applied in the experimental field. Rest two third of the urea and MP were applied in two splits, one at 20 days after sowing and other were 20 days after 1st top dress. 3rd top dress used this experiment as it was required. Weeding was done two times manually with nirani. Irrigation was done whenever necessary. The crop was sprayed with Ripcord, Dithen M 45, Indofil, Admire and Malation 60 EC to prevent infestation of insect, disease and vector of virus.

The following data are being collected as per synopsis. The data are as follows-

Serial No.	Characters	Serial No.	Character
1	Plant height (cm)	8	Fruit diameter (cm)
2	Number of leaves/ plant	9	Number of ridges per fruit
3	Days to 1st flowering.	10	Number of fruits per plant
4	Days to 50% flowering	11	Fruit weight (g)
5	Node of 1st flower	12.	Number of seeds per fruit
6	Days to 1st edible fruit harvest	13	100- seed weight (g)
7	Fruit length (cm)	14	Fruit yield per plant (g)

Among them most of the characters were collected such as plant height and no of leafs per plant: The plant height was taken from five randomly selected plants of each accession. The length of the main culm (cm) from the ground level to the tip was measured and the average was taken into four times 25 days after sowing, 50, 75 and 100 days respectively and the leaf number was collected on the same days. 1st and 50% flowering: Recorded as days from sowing to flowering when 10% of plants of each accession were flowered and when 50% respectively.

3.2 Experiments

The study aimed at selection of parental lines for diallel crossing, path analysis, analysis of combining ability, heterosis, variability and nature of gene action controlling yield and yield contributing characters and assessment of relationship between them in okra. Accordingly, following four experiments were set up:

Experiment I: Characterization and screening of okra genotypes

Experiment II: Selection of important yield contributing characters of okra

Experiment III: Study of combining ability in okra

Experiment IV: Stability analysis of the experimental hybrids

The elementary breeding materials for the present research work consist of fifty okra genotypes collected from different sources of home and abroad, such as BARI, Bangladesh, Lal Teer Seed Limited, Bangladesh and many Indian companies. The materials with their status are listed in **Table. 3.1.**

Experiment-wise materials and detailed methods are mentioned below-

3.2.1 Experiment – I: Characterization and screening of okra genotypes

3.2.1.1 Materials

Initially fifty okra genotypes (Table 3.1) were taken for preliminary evaluation and selection on yield and yield related characters. These genotypes were selfed for several generations to attained homozygosity. The selfing and sib (K-2,2014 August-September in our weather condition) mating program was accomplished by Metal Agro limited prior to commence the study to maintain the parental lines and to avoid inbreeding depression.

3.2.1.2 Methods

The fifty different genotypes of okra were sown in Research and Development Farm of Metal Agro Limited, Nagarchanti, Kawapukur, Debigonj, Panchagarh. Six cropping seasons were kept under field level operations during the period of 2014-2017. The experiment was conducted by RCBD with three replications.

The seeds were sown direct seeding method on the raised bed which was 5X1.2 m^2 in size for each genotype. The row to row and plant to plant distance was 70 cm X 50 cm, respectively. Cowdung was used 6 tons per acre and fertilizer Urea, TSP, MP, Gypsum, Zinc Sulphate, Borax and Carbofuran were used as basal dose 20,70,20,40,5,5 and 8 kg per acre respectively in the time of land preparation. Urea 30+20 +20 kg and MP 20+20+20 kg per acre were used for 1st, 2nd and 3rd top dress after 15-20 days’ interval due to plant growth condition.

Table 3.1: Description of 50 Inbred lines of Okra

SL. NO.	Acc. No.	Genotype	Description	Status	Remarks
1	1163	G1	Bari Dherosh-1, Metal Agro limited	F_{13}	Homozygous
2	1164	G2	OK-1442, Uni Agro, India	F_{11}	Homozygous
3	1165	G3	8 Ridge, Production field	S_{11}	Homozygous
4	1166	G4	OK-1442, Uni Agro, India	S_9	Homozygous
5	1167	G5	Anamika, Metal Agro Limited	S_4	Homozygous
6	1168	G6	OK-1442, Uni Agro, India	S_9	Homozygous
7	1169	G7	R and D, Test F1, Debigonj, Panchagarh	F_7	Homozygous
8	1170	G8	OK-1442, Uni Agro, India	F_{12}	Homozygous
9	1171	G9	OK-1442, Uni Agro, India	F_{12}	Homozygous
10	1172	G10	OK-1442, Uni Agro, India	F_{11}	Homozygous
11	1173	G11	DEB-401, Debgiri Agro	F_{12}	Homozygous
12	1174	G12	Local,Red Color	S_3	Homozygous
13	1175	G13	R and D, Test F1, Debigonj, Panchagarh	F_8	Homozygous
14	1176	G14	R and D, Test F1, Debigonj, Panchagarh	F_8	Homozygous
15	1177	G15	OK-1442, Uni Agro, India	S_8	Homozygous
16	1178	G16	Niribili, Zillion Seed, Jamalpur	F_{12}	Homozygous
17	1179	G17	Komol, Namdhari Maliks Seed	F_{11}	Homozygous
18	1180	G18	JK Haritha, Metal Agro Limited	F_{13}	Homozygous
19	1181	G19	JK Haritha, Metal Agro Limited	F_{13}	Homozygous
20	1182	G20	Bari Dherosh-1, Gagipur.	S_6	Homzygous
21	1183	G21	Niribili, Zillion Seed, Jamalpur	F_{11}	Homozygous
22	1184	G22	Shobus Bhendi, Local	S_{11}	Homozygous
23	1185	G23	Green Finger, Lal Teer Seed.	S_{10}	Homozygous
24	1186	G24	JkOH-635, JK Seeds, India	F_{11}	Homozygous
25	1187	G25	JkOH-635, JK Seeds, India	F_{11}	Homozygous
26	1188	G26	JK Haritha, Metal Agro Limited	F_{13}	Homozygous
27	1189	G27	Okra No-10, Metal Agro Limited	F_{13}	Homozygous
28	1190	G28	OK-1442, Uni Agro, India	S_9	Homozygous
29	1191	G29	ANU, Joy kishan, United seeds	S_6	Homozygous

30	1192	G30	Bari Dherosh, OK-001, Metal Agro Limited	S_4	Homozygous
31	1193	G31	Anamika, Metal Agro Limited	S_4	Homozygous
32	1194	G32	Aapurba, Zillion Seeds, Zamalpur	F_{12}	Homozygous
33	1195	G33	JK Haritha, Metal Agro Limited	F_{13}	Homozygous
34	1196	G34	JKOH-045, JK Seeds, India	F_{12}	Homozygous
35	1197	G35	JKOH-045, JK Seeds, India	F_{12}	Homozygous
36	1198	G36	OK-1442, Uni Agro, India	S_9	Homozygous
37	1199	G37	Komol, Namdhari Maliks Seed	F_9	Homozygous
38	1200	G38	Local,Rangpur	S_3	Homozygous
39	1201	G39	Tender-5, Metal Agro Limited	F_{12}	Homozygous
40	1202	G40	Tender-5, Metal Agro Limited	F_{12}	Homozygous
41	1203	G41	Aleya, Mollika Seed	F_{10}	Homozygous
42	1204	G42	Anamika, Metal Agro Limited	S_3	Homozygous
43	1205	G43	Okra, P-31 Proline Seed, India	F_{10}	Homozygous
44	1206	G44	Benoy, Maliks Seed	F_{10}	Homozygous
45	1207	G45	VIRAJ, Durga Seed, India	F_{10}	Homozygous
46	1208	G46	Aapurba, Zillion Seeds, Zamalpur	F_{10}	Homozygous
47	1209	G47	Robin, Namdhari Maliks Seed	F_9	Homozygous
48	1210	G48	US-7003, Hyderabad, India	F_9	Homozygous
49	1211	G49	Okra, P-31 Proline Seed, India	F_9	Homozygous
50	1212	G50	JKOH-6166, JK Seeds	F_{10}	Homozygous

3.2.1.3 Data Collection

3.2.1.3.1. Plant height

The height of ten sample plants was recorded in cm from the base of the plant to the tip of the plant after final harvest and their mean value were taken for analysis of this character. Plant height was recorded 25, 50, 75 and 100 days after transplanting to observe the growth rate of the plant.

3.2.1.3.2. Number of leaves

Number of leaves counted from the ground level to the tip of the longest stem and mean value was calculated. Number of leaves was recorded 25, 50, 75 and 100 days after transplanting to observe the growth rate of the plant.

3.2.1.3.3. Days to first flowering

This was recorded by counting the number of days taken from sowing to initiation of first flower in each accession number.

3.2.1.3.4. Days to 50% flowering

This was recorded by counting the number of days taken from sowing to the 50% flower in plants in each accession number.

3.2.1.3.5. Number of fruits per plant

This character was recorded by counting the total number of fruits harvested at different pickings in the sample plant till the final marketable harvest.

3.2.1.3.6. Fruit length

The length of 10 fruits randomly selected from selected plants in observational plot of each genotype in each replication were measured and expressed in centimeter from the attachment end to the tip using a venire slide calipers and the mean value was calculated as fruit length.

3.2.1.3.7. Fruit diameter

Ten fruits selected randomly from each plot in a replication for recording of length were also used for noting their girth at the point of maximum thickness which were averaged and expressed in centimeter (cm).

3.2.1.3.8. Fruit weight

Fruits selected for length and girth were also used for recording the Fruit weight. Fruits were weighed individually and were expressed in grams.

3.2.1.3.9. Number of seeds per fruit

Total number of grain is counted from the ten randomly selected fruits of each unit plot and mean of ten fruits are averaged and used as number of seeds /fruit.

3.2.1.3.10. 100 seed weight

After harvesting one hundred clean sun dried grains were randomly counted from each plot and weighted by a digital balance in gram.

3.2.1.4. Analysis of data

The data recorded for various characters were subjected to statistical analysis based on their sample means. Observations of all the characters were analyzed for variability and other genetic parameters related to fruit yield were taken for character association, heritability and genetic advance study.

3.2.1.4.1 Estimation of genotypic and phenotypic variances

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

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

Where,

GMS = Mean square of variety

EMS = Mean square of error

r = Number of replications

The phenotypic variance (σ^2p) can be calculated by adding genotypic variance (σ^2g) with Error variance (σ^2e) as following formula:

$$\text{Phenotypic variance } (\sigma^2 p) = \text{Genotypic variance } (\sigma^2 g) + \text{Error variance } (\sigma^2 e)$$

Where,

Error variance (σ^2e) = Error mean square (EMS)

3.2.1.4.2 Estimation of genotypic and phenotypic coefficients of variation

The genotypic and phenotypic coefficients of variation were calculated according to the formula suggested by Burton (1952).

$$\text{Genotypic coefficient of variation (GCV)} = (\sqrt{\sigma^2 g}) \text{ X } 100/\text{Mean}$$

Where,

$\sigma^2 g$ = Genotypic variance

Mean = Population mean

Similarly,

$$\text{Phenotypic co-efficient of variance (PCV)} = (\sqrt{\sigma^2 p}) \text{ X } 100/\text{Mean}$$

Where,

$\sigma^2 p$ = Phenotypic variance

Mean = Population mean.

3.2.1.4.3 Estimation of heritability

Heritability in broad sense was estimated by the following formula suggested by Johnson *et al.* (1955).

$$\text{Heritability in broad sense } [h^2 \text{ (b)}] \text{ (\%)} = (\sigma^2 g \text{ X } 100)/ \sigma^2 p$$

Where,

$\sigma^2 g$ = Genotypic variance

$\sigma^2 p$ = phenotypic variance

3.2.1.4.4 Estimation of genetic advance

The expected genetic advance and genetic advance in per cent of mean were calculated according to the formula used by Allard (1960) and Comstock and Robinson (1952).

$$\text{Genetic advance (GA)} = h^2{}_{b}.K.\ \sigma^2 p$$

Where,

h^2_b = Heritability in broad sense

k = Selection differential, the value of which is 2.06 at 5% selection intensity.

3.2.1.4.5 Estimation of genetic advance (GA) in percent of mean

Genetic advance in per cent of mean was calculated from the formula given below,

Genetic advance in per cent of mean, GA (%) = (GA X 100)/Mean

Where,

Mean = Population mean

3.2.1.4.6 Genetic divergence analysis

Mahalanobis's (1936) D^2 statistical analysis was used for assessing the genetic divergence among the test entries for a rational choice of potential parent in a multivariate analysis is a potent tool in divulging the divergence among the genotypes based on multiple characters. Genetic divergence was estimated following Mahalanobis (1936) generalized distance (D^2) extended by Tao (1952). Tocher's method (Rao, 1952) was followed for determining the group constellations. Canonical analysis was done according to Rao (1952) to confirm the results of cluster and D^2 analysis. Mean data for each character were subjected to multivariate analysis techniques for Principal component analysis (PCA), Principal coordinate analysis (PCO) Canonical vector analysis (CVA) and Cluster analysis (CLSA) by computer using GENSTST 5.12 software probreeding program. The generalized distance between any populations is given by formula, $D^2=\sum\sum\lambda ijS^{ai}S^{aj}$

Where,

D^2 = Square of generalized distance

λij = Reciprocal of the common dispersal matrix

$S^{ai} = (\mu i\ 1 - \mu i\ 2)$

$S^{aj} = (\mu j\ 1- \mu j\ 2)$

μ = General mean

Since the formula for computation requires inversion of higher order determinant, transformation of the original correlated unstandardized character means (Xs) to standardized uncorellated variation (Ys) was done to simplify the computational procedure. The D^2 values were obtained as the corresponding uncorrelated (Ys) values of any two genotypes (Rao, 1952).

3.2.1.4.6.1 Clustering of D^2 values

All the [n (n-1)]/D^2 values were clustered using Tocher's methods as described by Rao (1952).

3.2.1.4.6.2 Intra cluster distance

The intra cluster distance was calculated by the formula given by Singh and Chaudhary (1985).

$$\text{Square of intra cluster distance} = (\sum Di^2)/n$$

Where,

$\sum Di^2$= the sum of distance between all possible combinations.

n = Number of all possible combinations.

3.2.1.4.6.3 Inter cluster distance

The inter cluster distances were calculated by the formulae described by Singh and Chaudhary (1985).

$$\text{Square of inter cluster distance} = (\sum Di^2)/ninj$$

Where,

$\sum Di^2$= the sum of distance between all possible combinations (ni, nj) of the entries included in the cluster study.

ni = Number of entries in cluster i.

nj = Number of entries in cluster j.

3.2.2 Experiment – II. Selection of important yield contributing characters of okra

3.2.2.1 Estimation of phenotypic and genotypic correlations

Relationships between yield and yield associated traits (fourteen) were studied at genotypic and phenotypic levels. Genotypic and phenotypic correlation coefficients between characters contributing to yield were estimated following the suggested by Miller *et al.*, (1958).

Genotypic correlation,

$$r_{g1.2} = \frac{Cov.g1.2}{\sqrt{Vg1 \times Vg2}}$$

Where,

Cov.$_{g1.2}$= Genotypic covariance between the variables X_1 and X_2

V_{g1} = Genotypic variance of the variable X_1

V_{g2} = Genotypic variance of the variable X_2

Similarly, Phenotypic correlation,

$$r_{ph1.2} = \frac{Cov.ph1.2}{\sqrt{Vph1 \times Vph2}}$$

Where,

Cov.$_{ph1.2}$ = phenotypic covariance between the variable X_1 and X_2

V_{ph1} = phenotypic variance of the variable X_1

V_{ph2} = phenotypic variance of the variable X_2

3.2.2.2 Analysis of path coefficients

The cause and effect relationship between yield and its component characters, were studied through path coefficient analysis. Path coefficient of the traits related to yield was analyzed from the phenotypic and genotypic correlations (section 3.2.5.2) following method of Singh and Chaudhary (1985) and Dabolkar (1992) which was originally developed by Wright (1921). Dewey and Lu (1959) employed this method for the first time in plants to short out the direct and indirect influences of component characters on yield in crested wheatgrass. Assuming twelve component characters as independent (X1, X2 and X12) and yield as the dependent variable (Xs), path coefficient was obtained by solving a set of simultaneous equation of the following forms:

$r_{1s} = P_{1s} + r_{12} P_{2S} + r_{13} P_{3s} + r_{14} P_{4s} + r_{15} P_{5s} + r_{16} p_{6s} + r_{17} P_{7s} + r_{18} P_{8S} + R_{19} P_{9s} + r_{110} P_{10s} + r_{111} P_{11s} + r_{112} P_{12S}$

$r_{12s} = r_{101} P_{1s} + r_{102} P_{2s} + r_{103} P_{3s} + r_{104} P_{4s} + r_{105}P_{5s} + r_{106} P_{6s} + r_{107} P_{7s} + r_{108} P_{8S} + R_{109} P_{9s} +r_{110} P_{10s} + r_{111} P_{11s} + r_{112} P_{12s}$

Where

P_{1s}, P2s....P_{12s} = path coefficients of the variables $X_{1,}$ X_2.........X_{12} on X_s respectively

r_{1s}, r_{2s}.....r_{12s} = correlation coefficients of the variables X_1, X_2 ....X_{12} with X_s respectively

The residual effect (R) i.e. the variation unaccounted for by the component characters, which were not studied, was estimated using the formula as follows:

Residual effect, $R = [1- (r_{1s} P_{1s} + r_{2s} P_{2s} + \text{.........................} + r_{11s} P_{11s} + r_{12s} P_{12s})]^{1/2}$

3.2.3 Experiment – III: Study of combining ability in okra

3.2.3.1 Materials

Seven diversed okra genotype were selected using statistical tools, cluster analysis and variance making. These parents were crossed/hybridized in a diallel mating system excluding the reciprocals in March- April, 2015. In the August-September, 2015, all the seven parents, their 21 F_{1s} were studied.

Table 3.2 Selected okra lines used in cross combination of half diallel analysis

Sl. No.	Designation	Desired Characters / Characters based on selection
P_1	1163	Female initiation mid type, short inter node, more vigorus growth, more prolific, green color fruit, no seed expose, sharp awn, fruit long size
P_2	1171	Female initiation mid type, inter node short type, vigorus growth, more prolific, light green fruit, slightly seed expose, verry smooth awn, medium size fruit
P_3	1176	Female initiation mid type, long inter node, more vigorus growth, prolific, fruit color deep green, no seed expose, very smooth awn, medium size fruit
P_4	1178	Female initiation mid type, long type inter node, more vigorus growth, fruit color green, more prolific, no seed expose, very smooth awn, long size fruit
P_5	1189	Female initiation late type, long type inter node, more vigorus growth, fruit color light green, more prolific, no seed expose, smooth awn, long size fruit
P_6	1203	Female initiation mid type, medium inter node, more vigorus growth, fruit deep green, more prolific, slightly seed expose, smooth awn, long size fruit
P_7	1205	Female initiation mid type, long type inter node, vigorus growth, fruit color green, more prolific, no seed expose, very smooth awn, medium size fruit

Table 3.3 Half diallel crossing scheme to develop 21 hybrids of Okra

	Male parent								
Female parent		P1	P2	P3	P4	P5	P6	P7	
	P1	1x1	1x2	1x3	1x4	1x5	1x6	1x7	
	P2		2x2	2x3	2x4	2x5	2x6	2x7	
	P3			3x3	3x4	3x5	3x6	3x7	
	P4				4x4	4x5	4x6	4x7	
	P5					5x5	5x6	5x7	
	P6						6x6	6x7	
	P7							7x7	

3.2.3.2 Methods

The selected seven parental genotypes were sown in March, 2015.

Making half diallel crosses: Crossing / hybridization was done in 7X7 diallel fashion between the selected diverse parental lines. Thus the crossing combinations were 21 along with 7 parents in this experiment. All the crosses were made following the appropriate plant breeding technique. The mature F_1 fruits along with their respective parents were harvested at maturity stage and evaluated. The extracted seeds were sun dried and preserved in gene bank with optimum humidity and temperature.

In 2015-2016, two seasons, the seeds of seven parents and their 15 F1's were sown in direct seeding method on the raised bed which was 5x1.2 m^2 in size for each genotype. The seeds were sown row to row and plant to plant distance was 70 cm x 50 cm respectively. Cowdung was used 6 tons per acre and fertilizer Urea, TSP, MP, Gypsum, Zinc Sulphate, Borax and Carbofuran were used as basal dose 20,70,20,40,5,5 and 8 kg per acre respectively in the time of land preparation. Urea 30+20 +20 kg and MP 20+20+20 kg per acre were used for 1st, 2nd and 3rd top dress after 15-20 days' interval due to plant growth condition.

3.2.3.3 Data collection

Data were collected on plant height, number of leaf, days to 1st flowering, days to 50% flowering, node of first flower, days to first edible fruit harvest, fruit length, fruit diameter/grith, ridge per fruit, fruit per plant, average fruit weight, number of seeds per fruit, 100-seeds weight, and yield per plant. Ten random samples plants from each plot replication were taken from F_1 along with their parents for data collection.

3.2.3.4 Data analysis

The data collected on yield and yield contributing characters were subjected to different biometrical analysis to determine variances due to combining ability, heterosis, heritability (broad and narrow sense). Combining ability analysis was carried out following method I of model I (fixed effect) of Griffing (1956) using parents and 21 F_1s populations. In combining ability analysis, the total variance was partitioned into variance due to general combining ability (GCA) effect of the parents and variances due to specific combining ability (SCA) effects of the crosses. The combining ability variances were translated into genetic variance (Bulmer, 1980) and then a heritability value was estimated for each of the character.

3.2.3.5 Analysis of combining ability

The data was analyzed for each character following method -I and Model-I (fixed effect) as out lined by Griffing (1956). The model for the combining ability analysis in model I, method I is:

$$Xij = m + gi + gj + Sij + rij + \frac{1}{bc} \sum_k \sum_l eijkl$$

Where,

i, j = 1,2, ...n (number of parents)

k = 1, 2, ...b (number of blocks)

l = 1, 2, ...c (number of observation in each plot)

Xij = Mean of I X jth genotypes over k and l

m = population mean

gi = gca effect of ith parent

gj = gca effect of jth parent

Sij = Crosses between the ith and jth parents, i.e., specific combining ability (sca) effect

rij = Reciprocal crosses between the ith and jth parents, i.e., reciprocal effect

eijkl = Environmental effect associated with the ijkl individual observation

$\frac{1}{bc} \sum_k \sum_l eijkl$ is the Mean error effect.

3.2.3.6 Estimation of heterosis

Heterosis expressed as present of increase of F_1 hybrid over mid parent (average or relative heterosis), better parent (heterobeltiosis) and commercial check (standard heterosis) were computed for each character using the following formulae (Fehr, 1987).

$$\text{Heterosis, H (\%) over mid parent (MP)} = \frac{F_1 - MP}{MP} \text{ X } 100$$

$$\text{Heterosis, H (\%) over better parent (BP)} = \frac{F_1 - BP}{BP} \text{ x } 100$$

$$\text{Heterosis H (\%) over check (CV)} = \frac{F_1 - CV}{CV} \text{ X } 100$$

Where, F_1, MP, BP and CV are the mean of F_1, two parental populations (MP), better parent (BP) and check variety (CV), respectively.

Significant difference of F_1 with MP, BP and CV were tested using ‘t’ test and was calculated by the formula given below:

$$[t] = \frac{F_1 - MP}{SED} \text{ X } 100 \qquad \text{Where, SED} = \sqrt{2EMS/r}$$

$$[t] = \frac{F_1 - BP}{SED} \text{ X } 100 \qquad \text{Where, SED} = \sqrt{2EMS/r}$$

$$[t] = \frac{F_1 - CV}{SED} \text{ X } 100 \qquad \text{Where, SED} = \sqrt{2EMS/r}$$

Where,

SED = Standard error of difference, EMS = Error mean square and r = Replication

SED (standard error of difference) = √ (Variance / Sample size)

3.2.3.7 Estimation of heritability from parent to offspring

Heritability of the characters was estimated in F_1 generations from the combining ability analysis of a diallel cross using fixed model expectations of mean squares for GCA and SCA (Bulmer, 1980).

Table 3.4 Expected MS of combining ability

Sources of variation	**Df**	**Expectation of mean squares**
GCA	p-1	(p-2) vg + Ve
SCA	p(p-1)/2	Vs + Ve
Error	M	Ve

Where,

Vg = Variance due to GCA

Vs = Variance due to SCA

Ve = Environmental variance

p = number of parents

This variance was transplanted into different components of phenotypic variance as:

Additive genetic variance Val = 2 Vg

Total genetic variance Vg = 2 Vg + Vs

Phenotypic variance Vp = 2 Vg + Vs + Ve

Heritability in broad sense (h^2_b) and narrow sense (h^2_b) were estimated as-

h_2b = (Vg / Vp) x 100

h_2b = (Va / Vp) x 100

3.2.4 Expt. IV. Stability analysis of the experimental hybrids

3.2.4.1 Bartlett's test for homogeneity of variances

Bartlett's Test

Purpose: Test for Homogeneity of Variances

Bartlett's test (Snedecor and Cochran, 1989) is used to test if *k* samples have equal variances. Equal variances across samples is called homogeneity of variances. Some statistical tests, for example the analysis of variance, assume that variances are equal across groups or samples. The Bartlett test can be used to verify that assumption.

Bartlett's test is sensitive to departures from normality. That is, if your samples come from non-normal distributions, then Bartlett's test may simply be testing for non-normality.

Definition

The Bartlett test is defined as:

H_0: $\sigma_1^2 = \sigma_2^2 = \ldots = \sigma_k^2$

H_a: $\sigma_i^2 \neq \sigma_j^2$ for at least one pair (i,j).

Test Statistic: The Bartlett test statistic is designed to test for equality of variances across groups against the alternative that variances are unequal for at least two groups.

$$T=(N-k)\ln s2p-\sum ki=1(Ni-1)\ln s2i1+(1/(3(k-1)))((\sum ki=11/(Ni-1))-1/(N-k))$$

In the above, s_i^2 is the variance of the ith group, N is the total sample size, N_i is the sample size of the ith group, k is the number of groups, and s_p^2 is the pooled variance. The pooled variance is a weighted average of the group variances and is defined as:

$$s2p=\sum i=1k(Ni-1)s2i/(N-k)$$

Significance Level: α

Critical Region: The variances are judged to be unequal if,

$$T>\chi 21-\alpha,k-1$$

where $\chi 21-\alpha,k-1$ is the critical value of the chi-square distribution with k - 1 degrees of freedom and a significance level of α.

3.2.4.2 Stability analysis

The stability of yield performance for each advanced line was calculated by regressing the mean yield of individual lines on environmental index and calculating the deviations from regressing the mean yield of individual lines on environmental index as suggested by Eberhart and Russell (1966). Regression coefficient (bi) was considered as an indication of the stability and deviation from regression coefficient (s^2d) as response of the lines to varying environment, while the environment and genotype × environment interactions were partitioned into three components viz., environment (linear), genotype x environment (linear) and deviation from regression (pooled deviation over the genotypes). As described by Eberhart and Russell (1966), the behavior of the lines was assessed by the model

$$Y_{ij} = m + b_i I_j + d_{ij} + \bar{\varepsilon}_{ij},$$

Where,

Y_{ij} = observation of the i-th (i = 1, 2, ..., g) cultivar in the j-th (j = 1, 2, ...n) environment,

m = general mean,

b_i = regression coefficient,

I_j = environmental index obtained by the difference among the mean of each environment and the general mean $(\sum_{j=1}^{n} I_j = 0), \delta_{ij}$ = the regression deviation of the i-th cultivar in the j-th environment and e_{ij} = effect of the mean experimental error.

CHAPTER IV

RESULTS AND DISCUSSION

The experiments were conducted to study characterization, screening, combining ability and stability analysis for yield and yield contributing characters of okra. The findings of the experiments have been presented under the following headings and sub-headings:

4.1 Characterization and screening of okra genotypes

Though okra contributes to a small share in the world market, but is valued at the highest price among other vegetables. The demand for okra is expected to increase because of increasing preference of the consumers due to specific taste and nutritional quality. Nevertheless, traditional okra varieties are low yield potential compared to other okra varieties. The breeding for new okra variety is to be increasingly more competitive as primitive okra cultivars of our country are popular to the growers, traders and cosumers. Besides, the scientists in Bangladesh are continuously working in developing high nutritional, saline tolerance or resistance to particular disease or insect resistance varieties; their innovation to increase yield are compromised with quality, as a threat from losing their competitive advantage in okra production has been realized. Unless new okra varieties with high quality are available for commercial cultivation, it is a challenge to maintain reputation of local cultivars without evolving new varieties Therefore, the experiments were undertaken to improving the okra cultivation scenario and the results are discussed below-

4.1.1 Plant height

Plant height was recorded 25, 50, 75 and 100 days after sowing (DAS) and the minimum and the maximum value showed at 25 days (7.63 to 12.8) and mean 10.90. 50 days (20.73 to 52.07), mean 38.38, 75 days (46.60 to 143.40) mean 95.27 and 100 days (72.87 to 191.67) and mean 137.46, respectively. These ranges were higher than Rajat *et al.* (2018) observation and moderately similar to Reddy *et al.* (2012) (Table 4.1). The phenotypic variance at 25, 50, 75 and 100 days were 2.19, 45.19, 518.42, and 1018.5 and genotypic variance was 1.26, 37.14, 477.12, and 950.06 were found respectively. The analysis of variance, (Table 4.1) revealed highly significant differences among 50 genotypes for 16 quantitative characters in okra. The range of mean value revealed sufficient variation for all the trails under study. For all the characters under study phenotypic variance was higher than the corresponding genotypic variance. The estimates of GCV lower for plant height 25 and 50, and high magnified (>20) lower in for plant height 75 and 100 days. The PCV also lower in 25, 50 days and higher in 75 to 100 days PCV for plant height suggested (13.794%) by Priyanka *et al.* (2018), which indication the PCV was moderate and GCV was low for this character. The estimate of heritability showed 25 days was moderate and rest 50, 75 and 100 days was high. That was 82.18, 92.03, and 93.28 respectively. These results were similar to the plant height (90.00%) of Reddy *et al.* (2012). But disimilar with Priyanka *et al.* (2018) which was 44.100%.

The estimation of genetic advance as per cent of mean in different days 25, 50, 75 and 100 days were 16.18, 29.65, 35.31, and 44.61%, respectively, which were highly similar to plant height (35.22%) as observed by Reddy *et al.* (2012). But moderate genetic advanced as per cent of mean moderate for plant height (12.527%).

Table 4.1: **Estimation of genetic components of 10 yields related characters in okra**

	PH25	**PH50**	**PH75**	**PH100**	**LN25**	**LN50**	**LN75**	**LN100**	**FFI**	**50FI**
Mean	10.90	38.38	95.27	137.46	6.44	18.08	45.71	54.46	41.02	42.49
σ^2_g	1.26	37.14	477.12	950.06	0.06	13.99	151.15	192.39	2.11	2.39
σ^2_p	2.19	45.19	518.42	1018.50	0.18	20.05	184.92	225.73	3.36	3.77
GCV	10.32	15.89	22.93	22.42	3.79	20.69	26.89	25.46	3.53	3.64
PCV	13.58	17.51	23.89	23.21	6.50	24.76	29.75	27.58	4.47	4.57
h^2_b (%)	57.83	82.18	92.03	93.28	34.20	69.78	81.73	85.23	62.77	63.43
GA (5%)	1.76	11.38	43.17	61.32	0.29	6.44	22.90	26.37	2.37	2.54
GAM (%)	16.18	29.65	35.31	44.61	4.58	35.60	50.09	48.42	5.78	5.97
SE (+-)	0.55	1.64	3.71	4.78	0.20	1.42	3.35	3.33	0.64	0.68
F-value	**	**	**	*	**	**	**	**	**	**
CV%	8.82	11.39	13.74	`13.02	10.27	13.61	12.71	10.60	12.73	10.76

Here, PH25= Plant height at 25 days (cm), PH50= Plant height at 50 days (cm), PH75= Plant height at 75 days (cm), PH100= Plant height at 100 days (cm), LN 25= Leaf number at 25 days, LN50= Leaf number at 50 days, LN75= Leaf number at 75 days, LN100= Leaf number at 100 days, FFI= First female flower initiation and 50FI= Days to 50 % flowering

*= Significant at 5% level and **= significant at 1% level of probability

Table 4.1: Estimation of genetic components of 10 yields related characters in okra (cont'd)

Components	**NFF**	**FEFH**	**Fruit length (cm)**	**Fruit diameter (cm)**	**Fruit weight (g)**	**Number of ridge**	**Fruits per plant**	**Seeds per fruit**	**100 seed weight**	**Fruits yield per plant (g)**
Mean	4.69	47.50	13.82	1.99	19.58	5.10	27.69	57.00	7.17	552.83
σ^2_g	0.14	2.41	1.18	0.04	1.27	0.21	34.11	126.96	0.32	14842.91
σ^2_p	0.25	3.47	2.14	0.05	6.61	0.24	41.86	161.90	0.42	19876.31
GCV	7.92	3.27	7.87	3.20	5.76	8.90	21.08	19.76	7.78	22.03
PCV	10.72	3.92	10.58	5.23	13.13	9.70	23.36	22.32	8.80	25.50
h^2_b **(%)**	54.51	69.41	53.30	37.13	89.24	84.25	81.49	78.41	74.15	74.68
GA (5%)	0.56	2.66	1.67	0.08	1.02	0.86	10.86	20.55	0.99	216.88
GAM (%)	12.04	5.61	12.06	4.01	5.21	16.84	39.21	36.06	13.81	39.23
SE (+-)	0.20	0.59	0.56	0.05	1.33	0.11	1.61	3.41	0.19	40.96
F-value	**	**	**	**	*	**	**	**	**	**
CV%	11.23	12.17	15.08	14.16	11.80	3.85	10.05	10.37	14.60	12.83

Here, NFF=Number of female flower, FEFH=First edible fruit harvesting days and 100 SW= 100 Seed weight (g)

*= Significant at 5% level and **= significant at 1% level of probability

4.1.2 Leaves per plant

Present study showed leaves per plant ranged from 5.40 to 7.00, 10.67 to 28.33, 23.80 to 85.13 and 33.80 to 114.20 who's over all mean were 6.44, 18.08, 45.71 and 54.46 respectively by the days 25, 50, 75 and 100 DAS respectively. Dhruv (2015) observed almost similar leaves per plant which were ranged from 5.67 to 6.67, 10.00 to 14.07, and 16.60 to 22.13 with an overall mean performance of 6.08, 12.55 and 19.46 leaves per plant. The maximum 6.67, 14.07, and 22.13 leaves per plant were noted in genotype 2013/OK HYB-7, while the minimum 5.67, 10.00 and 16.60 leaves per plant were exhibited in genotype Pusasawami (SC). Ahamed *et al.* (2015) observed moderate range of variation in number of leaves per plant (28.00-142.50) with the mean of 57.41. The genotype and phenotypic variance ranged from 0.06-0.18, 13.99 to 20.05, 151.15 to 184.92 and 192.39 to 225.73 for 25, 50, 75 and 100 days respectively. Among them leaves per plant at 75 days showed higher phenotypic coefficient of variation. (29.75) which was 45.27 (PCV%) higher than the leaves per plant 60 DAS (10.45%) and leaves per plant 90 DAS (10.23%) exhibited by Dhruv (2015). Genotypic co- efficient of variation was observed in present study were 3.79, 20.69, 26.89 and 25.46 for the 20, 50, 75 and 100 days respectively. Here also the highest genotypic co efficient of variation observed 26.89 in 75 days which was higher than 2.76% at 30 DAS, 4.70% at 60 DAS and leaves per plant at 90 DAS (9. 03%).The genotypic and phenotypic coefficient of variation (GCV and PCV) is the measures of variability among the genotypes under study. The genotypic coefficient of variation (GCV) measuring the range of genetic variability for different plant characteristics helps to compare this variability and phenotypic co efficient of variation (PCV) indicated the interaction effect of environment on this trait. The present investigation revealed the heritability and genetic advance in leaves per plant were 34.20, 69.78, 81.73, 85.23, and 0.29, 6.44, 22.90 and 26.37 in respect to 25, 50, 75 and 100 days, respectively. However low heritability along with low genetic advance as exhibited due to polygenic inheritance was not found under study, which indicated that this character was less influenced by environment demonstrating either these were simply inherited characteristics governed by a few major genes as additive gene effect even if they were under polygenic control and therefore, selection of this characteristics would be more effective for yield improvement.

4.1.3 First flower initiation

The present experiment revealed the range of first flower initiation was 38.33 to 45.67 days and the mean was 41.02 which was similar to Dhruv (2015), the first flower initiation was recorded in genotype 2012/OKHYB-2(35.67 days) while the genotype 2013/OK HYB-7 and 2012/OK HYB-4 was required the maximum (39.33 days) for first flowering. The average days of first flowering were 37.59 and it ranged from 35.67 to 39.33 days. Another observation expresses the range of days to first flower initiation (43.60-53.70) and mean value found 47.60 what was higher than present study. Reddy *et al.* (1985) recorded days to first flowering ranged from 38.23 days to 46.40 days. The maximum days to first flowering was recorded in 46.40 days and the minimum days were taken 38.23. The variation might be due to its varietal make up of short vegetative phase which enhanced its early flowering. Syfullah *et al.* (2018) observed the phenotypic and genotypic variance as 5.60 and 3.39, respectively which were higher than the present investigation. The estimation of phenotypic coefficient of variation was higher than genotypic coefficient of in present study. The phenotypic coefficient of variation was 4.47 where genotypic coefficient of variation was 3.53 this result was higher than the observation of Kumar *et al.* (2019). They exhibited that the phenotypic coefficient of variation was 2.37 and genotypic co efficient of variation 1.53. The heritability and (percent of mean) genetic advanced showed 62.77 and 2.37, respectively which offered less scope of selection because of non-additive genetic effects present here. The observation of Syfullah *et al.* (2018) showed almost similar results on these components which were 60.55 and 2.95, which indicated that these characteristics were highly influenced by environment. demonstration either these were simply inherited characteristics governed by a few major genes or additive gene effect even if they were under polygenic control and therefore selection of these characteristics would be more effect for yield improvement. High heritability coupled with high genetic advanced showed greater proportion of additive genetic variance and consequence a high genetic gain expected from selection (Devi and Mariappan, 2013). The characters having heritability with low genetic advance as per cent of mean appeared to be controlled by non-additive gene action and selection for such characters may not be effective (Singh and Singh, 2006).

4.1.4 Days to 50% flower initiation

Days of 50% flower initiation were range from 40 to 47.67 days. The mean of 50% flowering was 42.49 which were lower than the result of Mehta *et al.* (2006). They found day to 50% flowering ranged from 48 to 52 and with an average of 49.89. Another observation recorded that day to 50% flowering range was 36.00-43.00 and the mean value expressed 39.27, (Syfullah *et al.* 2018) which was lower than present investigation. The phenotypic and genotypic variance showed as 3.77 and 2.39 which expressed that there was some environmental effect. The phenotypic and genotypic variance observed by Syfullah *et al.* (2018) 6.51 and 4.02 which was higher than present experiment. The estimated value of PCV and GCV were 4.57 and 3.64 which were higher than the observation of Mehta *et al.* (2006). The estimation of heritability of days to 50 flowering on the present experiment was 63.43 which indicated high value of heritability. Present investigation showed GA on days to 50% flowering was 2.54 and genetic advance as present of mean was 5.97. The higher genetic advance and GA present of mean were observed by Syfullah *et al.* (2018) was 3.24 and 8.25, respectively

4.1.5 Node of first flowering

The present investigation revealed that the range of first flowering node was 3.73 to 4.40 and the mean value was 4.69. The same character was studied by Sekeyer et al. (2012) which indicated the range were 3.75 to 10.75 respectively.The minimum value was similar but they differed maximum value which was higher than present study. Another study showed the range of node of first flower maximum and minimum value was 6.67 to7.93 and the mean was 7.34 which were higher than present investigation. Patra *et al.* (2018) observed the range for first flowering node was3.50 to 9.10 and the mean value was 5.19. The genotypic and phenotypic variance was observed in the present study were 0.14 and 0.25 which was similar to the observation of Patra *et al.* (2018). The phenotypic and genotypic coefficient of variation observed in the present study was 10.72 and 7.92. The heritability and genetic advance showed under this investigation was 54.51 and 0.56, which showed moderate heritability and low genetic advance. Similar investigation showed Patra *et al.* (2018) where heritability and genetic advance showed 50 and 0.54, respectively and genetic advance as per cent of mean showed 12.04 in present study and 7.29 in that investigation.

4.1.6 First edible fruit harvesting days

The first edible fruit harvesting days was recorded in present experiment ranged from 44.67 to 52.33 with a mean of 47.50 days. The range of first picking or edible harvest showed 38.33 to 60.33 reported by Kumar *et al.* (2015) and mean value was 52.82 which was higher than present study. Another experiment recorded by Priyanka *et al.* (2018) where days to fruit harvest recorded from 51.00 to 59.67, the mean value was 54.632. The genotypic and phenotypic variance was observed in the present study showed 3.47 and 2.41, respectively. The present investigation found genotypic and phenotypic coefficient of variation was 3.27 and 3.92 for days to first edible fruit harvest. The heritability, genetic advance and genetic advance as per cent of mean was recorded on the present experiment were 69.41, 2.66 and 5.61, respectively which refer high heritability, low genetic advance and genetic advance as per cent of mean. The low heritability, genetic advance and genetic advance as percent of mean were recorded by Kumar *et al.* (2019) which was 26.00, 0.56 and 1.31 respectively. The high heritability, genetic advance and genetic advance as per cent of mean founded on the observation of Priyanka *et al.* (2018) which revealed 78.80, 4.05 and 7.414.

4.1.7 Fruit length

The maximum and minimum value and their mean were 16.07 to 11.87 and 13.82 for fruit length. The observation of Kumar *et al.* (2015) recorded for length of the fruit was maximum and minimum ranged from 9.04 to 12.05 and the mean value obtained 10.20 which were lower than the present investigation. Genotypic and phenotypic variance observed in the present study was 1.18 and 2.14. Ahamed *et al.* (2015) recorded both these component was 6.28 and 6.79 respectively which was higher than the present value. The phenotypic and genotypic co efficient of variation observed on this experiment were 7.87 and 10.58, respectively, this result showed there was an effect of environmental coefficient. Ahamed *et al.* (2015) revealed in the GCV and PCV were 13.95 and 14.50 which was higher than the present study. Syfullah*et al.* (2018) showed the result of GCV and PCV in their experiment was 7.36 and 14.02, the genotypic coefficient of variance was almost similar to the present study but phenotypic coefficient of variance was higher than present study revealed. The heritability, genetic advance and genetic advance as per cent of mean reveled the present study were 55.30, 1.67 and 12.06

respectively. Priyanka *et al.* (2018) found higher value of heritability 85.00 and similar genetic advance 1.524 and lower genetic advance as per cent of mean 10.279.

4.1.8 Fruit diameter

The range of diameter of fruit on the present experiment was 1.70 to 2.67 and the mean value revealed 1.99 (appandix-1). The observation of Kumar *et al.* (2015) was the maximum and minimum value of fruit diameter was 1.96 to 1.29 and the mean value showed 1.55 respectively, which was lower than the present finding. Priyanka *et al.* (2018) exhibited the result of fruit diameter (cm) was the maximum and the minimum ranged 1.613 to 1.767 and the mean value obtained 1.695, respectively, which was lower than the present findings. The genotypic and phenotypic variance was found in the present study was 0.00 and 0.01. The genotypic and phenotypic coefficient of variation was found 3.20 and 5.23 for fruit diameter on present study. Redddy *et al.* (2012) exhibited on their experiment the GCV and PCV value was 8.57 and 9.19, respectively. The heritability, genetic advance and genetic advance as per cent of mean were recorded 37.13, 0.08 and 4.01, respectively. Priyanka *et al.* (2018) observed these components as heritability 23.00, genetic advance 0.025 and genetic advance as per cent of mean 1.462 which were lower than the present study.

4.1.9 Fruit weight

The maximum and minimum value for fruit weight per plant was 23.07 and 15.06 and the mean value arise 19.58 for the present study. The observation of average fruit weight by Ahamed *et al.* (2015) showed the range for fruit weight was 18.25 to 25.41 and the mean value revealed 22.77 which were higher than the present study. Another observation showed lower range for fruit weight Priyanka *et al.* (2018) showed in their experiment the range of fruit weight 19.40 to 16.433 and the mean value was 17.502. Syfullah*et al.* (2018) revealed the range of the maximum and the minimum fruit weight 25.33 to 10.67 and the mean value obtained 17.07 which had a wide range of population and the mean value was lower than the present study. The genotypic and phenotypic variance showed 1.27 and 6.61, respectively. They had a large amount of environmental effect. Ahamed *et al.* (2015) observed the genotypic and phenotypic variance was 7.77 and 9.71 which was higher than the present study. The lower genotypic and phenotypic variance reported by Priyanka *et al.* (2018) that was 0.481 and 0.952. The genotypic and phenotypic co efficient of variation was 5.76 and 13.13 respectively. The higher value was observed 16.25 and 20.89 by Syfullah*et al.* (2018) and lower value was 3.963 and 5.576 found by Priyanka *et al.* (2018). The heritability, genetic advance and genetic advance as per cent of mean was observed in the present study were 19.24, 1.02 and 5.21, respectively. Thirupathireddy *et al.* (2012) investigate the same components and revealed 91.0 for heritability, 4.54 for genetic advance and 31.51 for genetic advance as per cent of mean which were higher than the present investigation.

4.1.10 Fruits per plant

The present study showed the number of fruits per plant ranged from 12.67 to 42.33 and the mean value was 27.69. The similar finding was observed by Ahamed *et al.* (2015), where the maximum and minimum fruits per plant were 6.60 to 3.00 and the mean value was 27.76. Almost similar mean observed by Priyanka *et al.* (2018) but disimilar with maximum and minimum value which was 23.24 to 35.797. The lower phenotypic and genotypic variance observed Priyanka *et al.* (2018) which were 17.220 to 6.939. The genotypic and phenotypic coefficient of variation exhibit in present studies was 21.08 and 23.36. The lower GCV and PCV were observed 9.273 and 14.608 by Priyanka *et al.* (2018) and higher genotypic and phenotypic co efficient of variation observed by Ahamed et.*al* (2015) where the value was 46.37 and 46.59, respectively. The heritability, genetic advance and genetic advance as per cent of mean was observed in this trait were 81.49, 10.86 and 39.21 which indicated high heritability, moderate genetic advance and high genetic advance as per cent of mean. Similar observation were noticed by Syfullah *et al.* (2018) where heritability 88.55, genetic advance 8.62 and GAM 50.44. Low heritability GA and GAM were observed as 40.300, 3.445 and 12.126 by Priyanka *et al.* (2018).

4.1.11 Fruit yield per plant

The present investigation revealed the maximum and minimum value for fruit yield per plant was 861.47 to 286.27 and the mean value was 552.83 for this trait. The higher value for this character was observed. Ahamed *et al.* (2015) had the range was from 98.90 to 1650.00 and the mean value was observed 644.63. The lower value (maximum, minimum) was observed by Priyanka *et al.* (2018) which was 500.54 to 314.19 and the mean value obtained 397.71. The genotypic and phenotypic variance was observed in the present study was 14842.91 and 19876.31, respectively. This value was higher than the investigation of Reddy *et al.* (2012) which revealed genotypic and phenotypic value was

2996.92 and 3400.27. Syfullah et *al.* (2018) found their experiment the genotypic and phenotypic variance for fruit yield per plant as 9158.14 and 12212.49 which were also lower than the present investigation. The genotypic and phenotypic coefficient of variation obtained in present study was 22.03 and 25.50, respectively which were more or less similar to the findings of Kumar *et al.* (2015) where genotypic and phenotypic coefficient of variation were obtained 23.71 and 26.25. The heritability, genetic advance and genetic advance as per cent of mean was recorded in the present experiment were 74.68, 216.88 and 39.23, respectively. Similar heritability was observed on Syfullah *et al.* (2018) findings were 74.99 but they differ in genetic advance 170.72 and genetic advance as per cent of mean 57.94.

4.1.12 Seeds per fruit

The present investigation revealed the range 26.40 to 77.43 and the mean value was 57.00. The almost similar result obtained by Ahamed *et al.* (2015) where range was 59.46. Another observation revealed the lower range and mean than the present investigation that was 24.00 to 58.67 and 44.21, respectively. The highest range was observed for seeds per fruit was 79 to 114 and means value was 98.51, respectively, as observed by Yonas *et al.* (2014).

The genotypic and phenotypic variance was observed in the present study were 126.96 and 161.90. The high genotypic and phenotypic variation was observed in the study by Ahamed *et al.* (2015) which was 423.92 and 425.07, respectively. The PCV and GCV value observed in present study was 22.32 and 19.76. The similar result found by Syfullah *et al.* (2018) for phenotypic and genotypic coefficient of variance was 19.32 and 22.61, respectively. The heritability, genetic advance and genetic advance as per cent of mean were recorded in the present study as 78.41, 20.55 and 36.06, respectively. The low heritability, genetic advance and genetic advance as per cent of mean were observed by Kumari *et al.* (2019).

4.1.13 100 seed weight

The present study revealed the 100 seed weight range from 5.88 to 8.62. The mean value was obtained 7.17. The observation by Sekyere *et al.* (2012) showed range on this character was 2.04 to 6.39 and the mean value was 3.40, which was lower than the present studt. Ahamed *et al.* (2015) observed in their experiment where range found 1.25

to 6.90 and mean value exhibit 4.80 which was also lower than the present study. Singh *et al.* (2017) exhibit the findings on this trait where it recorded from 5.20 to 7.50 and the mean value was 6.18 which greater than others but lower than the present study. The genotypic and phenotypic variance observed in the present study was 0.32 and 0.42. Yonas *et al.* (2014) observed in their experiment genotypic and phenotypic variances were 1.28 and 1.94 which was higher than the present study. The genotypic and phenotypic coefficient of variation was recorded in the present investigation was 7.78 and 8.80 which was lower than the finding of Yonas *et al.* (2014). Estimation of heritability, genetic advance and genetic advance as per cent of mean was revealing in the present study as 74.15%, 0.99% and 13.81%, respectively. Ahamed *et al.* (2015) also showed high heritability and genetic advance which was 98.12% and 202.13% which indicated the possibility of important of this character via selection.

Clustering or grouping genotypes:

Quantification of genetic diversity existing within and between groups of germplasm is important and particularly useful in proper choice of patterns for realizing higher heterosis and obtaining useful recombinants. Among the several methods available, Mahalanobis generalized distance estimated by D^2 statistic is a unique tool for discriminating populations considering a set of parameters together rather than inferring from indices based up on morphological similarities, eco-geographical diversity and phylogenetic relationship. In the present study based on D^2 values, 50 okra genotypes were grouped into six different clusters.

Table 4.2 Distribution of 50 lines of Okra in six clusters

Clusters	Number of inbred in cluster	Lines	Accessions
I	16	G6, G11, G12, G14, G15, G17, G18, G21, G22,G33,G35, G36, G40, G47, G48, G49	1168,1173,1174,1176, 1177,1179,1180,1183, 1184,1195,1197,1198, 1202,1209,1210,1211.
II	4	G35, G30, G32, G37	1197,1192,1194,1199.
III	7	G8, G9, G19, G20, G29, G38, G42	1170,1171,1181,1182, 1191,1200,1204.
IV	8	G1, G2, G3, G4, G7, G10, G31, G43	1163,1164,1165,1166, 1169,1172,1193,1203
V	1	G5	1167
VI	14	G13, G16, G23, G24, G26, G27, G28 G34,G39,G41, G44, G45, G46,G50	1175,1178,1185,1186, 1188,1189,1190,1196, 1201,1205,1206,1207, 1208,1212.

Among the six clusters, cluster I contained the largest having 16 genotypes, followed by cluster VI with 14 genotypes, cluster IV with 8 genotypes, cluster III with 7 genotypes, cluster II with 4 genotypes and cluster V having a single genotype. The clustering pattern of genotypes was observed to be random indicating that geographical diversity and genetic divergence were independent. Syfullah *et al.* (2018) observed the clustering pattern of 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 including 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, respectively. Clustering pattern was not influenced by geographical distribution of genotypes. Patro and Ravisankar (2014) are studied cluster analysis and revealed considerable variation among forty-one genotypes of okra which was grouped into eight clusters. Prakash *et al.* (2017) describe 63 okra genotypes which were grouped into nine different clusters. Among them cluster I having 36 genotypes followed by cluster III with 15, cluster II with 6, rest of all cluster IV, V, VI, VII, VIII, IX had solitary single genotype.

The genotypes belonging to different location were included in the same cluster. This result indicated that geographic distribution and genetic divergence did not follow the same trend, which might be due to continuous exchange of genetic materials among the countries of the world. On the other hand, Ranpise *et al.* (2017) described genotypes for the hybridization should be selected from the more distant clusters as changes were more to obtained heterotic combinations as compared to combinations involving genotypes from same cluster.

Table 4.3 Average intra (bold) and inter cluster distances (D^2) for 50 lines of okra

Cluster	I	II	III	IV	V	VI	No of Genotypes
I	**31.62**	350.33	76.60	103.11	239.90	176.08	16
II		**46.08**	274.62	449.76	175.04	176.06	4
III			**28.85**	177.45	175.04	176.06	7
IV				**58.09**	323.25	277.70	8
V					**0.00**	130.19	1
VI						**38.32**	14

The values along the diagonal indicated intra-cluster distances

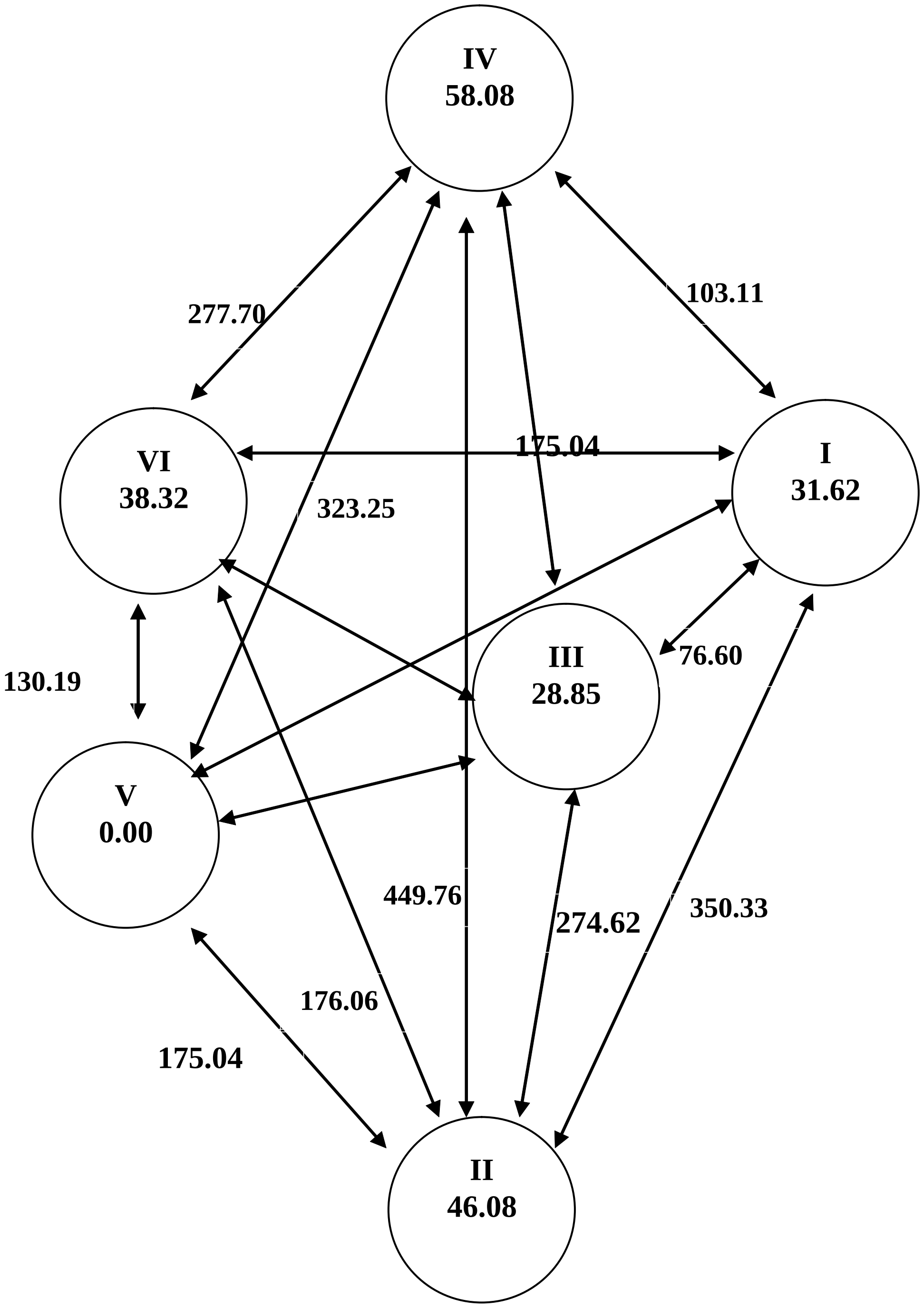

Figure 4.1. The diagram for intra and inter cluster distances of 50 genotypes of okra

The intra cluster distances were calculated from there inter genotypic distances as per Singh and Chowdhury (1985). The averages of intra and inter distance (D^2 values) were presented in Table-4.3. It was noticed that inter group distance were always higher than those intra group distance. The maximum inter cluster distance was observed between cluster II and IV (449.76), followed by I and II (350.33) and between IV and V (323.25). The lowest inter cluster distance was observed between I and III (76.60) followed by I and IV (103.11) and between V and VI (130.19), respectively. The intra cluster divergence vatied from 0.00 to 58.09 which belonging V and IV (58.09) where the number of genotype one and eight respectively. The intra and inter cluster distances have been diagrammatically presented in Fig-4.1. Genotypes among the clusters seperated by high D^2 values could be used in hybridization program for obtaining wide spectrum of variation among the segregates (Rahman 2006 and Bimal 2008).

The performance of mean of different clusters for 20 characters were described in table-4.4. Cluster I was consisting of sixteen genotypes where the lowest mean value was observed in first flowering 4.56, number of ridge per fruit 5.02. Among them cluster mean of fruit data 2.35 was the highest rest of all cluster mean on that character and number of ridge per fruit was the second highest among all six cluster mean on that character. The highest cluster mean was observed in cluster I was fruit yield per plant 477.42 which was the second lowest among all the cluster for this trait. The second highest in cluster I was plant height at 100 days 130.06 and followed by plant height at 75 days 95.14, seeds per fruit 57.22 and number of leaf at 100 days, respectively. These characters were needed for early type of variety development. Cluster II had two genotypes and it observed the highest cluster mean for fruit yield per plant 824.03 which was also height on that trait among all cluster means and followed by plant height at 100 days which was also the highest among all the cluster. The lowest value except the fruit diameter and number of ridge per fruit was node of 1st flowering 5.13 followed by number of leaf at 25 days 6.79 and 100 seed weight 7.26, respectively. The moderate value was observed in cluster II were fruit length 15.75, fruit weight 20.95, 1st flowering 41.75, 50% flowering 43.16, respectively.

Table 4.4 Cluster mean for twenty characters in 50 lines of okra

Characters	Clusters					
	I	II	III	IV	V	VI
Plant height at 25 days	10.56	11.48	11.25	10.05	7.08	11.67
Plant height at 50 days	38.48	41.17	39.98	31.99	20.73	41.60
Plant height at 75 days	95.14	104.93	96.07	69.13	46.60	110.68
Plant height at 100 days	130.06	166.55	134.41	105.94	84.13	160.97
Number of leaf at 25 days	6.26	6.79	6.45	6.33	6.47	6.60
Number of leaf at 50 days	16.73	22.15	17.42	14.27	24.53	20.51
Number of leaf at 75days	41.21	60.19	44.39	37.09	85.13	49.50
Number of leaf at 100 days	47.37	70.93	52.02	48.68	114.20	58.15
First flower initiation (days)	40.60	41.75	41.09	41.63	45.67	40.60
Fifty percent flower initiation day	42.02	43.16	42.48	43.08	47.67	42.14
Node of first female flower (days)	4.56	5.13	4.60	4.61	5.20	4.77
First edible fruits harvesting days	47.08	48.83	47.57	47.71	51.33	47.19
Fruits length (cm)	13.49	15.75	13.65	13.50	13.73	13.94
Fruit diameter(cm)	2.35	1.92	2.00	2.00	1.97	2.01
Fruits weight (g)	18.82	20.95	19.69	19.58	19.33	20.01
Number of ridge per fruits	5.02	5.00	5.00	5.63	5.00	5.00
Number of fruits per plant	24.98	38.07	26.88	19.63	35.43	32.31
Fruits yield per plant	477.42	824.03	553.21	381.53	691.96	649.28
Seeds per fruit	57.22	51.23	65.27	48.35	47.43	59.89
100 seed weight (g)	7.35	7.26	6.91	6.93	5.88	7.33
Genotypes	16	4	7	8	1	14

Cluster III was contained 7 genotypes. It possessed the lowest value in fruit diameter 2.00 followed by ridge per fruit 5.00. Number of leaf at 25 days (6.45) and 100 seed weight (0.91) respectively. The height value of cluster III observed 553. 21 followed by plant height at 100 days (134.41), The moderate value was exhibited first edible fruit harvest (44.39), number of leaf at 100 days (52.02) respectively. Cluster IV had eight genotypes, the lowest value on fruit yield per plant observed in this cluster among all the cluster. Otherwise no remarkable feature was not noticed in this cluster for different characters. The single genotype which was belonging to the cluster V, it observed the lowest value of 100 seed weight (5.88), among all the cluster on that trait. and the highest value of number of leaf at 100 days (114.20) among all the cluster on particular character. Cluster VI consist of 14 genotypes; it was the second highest on the number of genotypes. There was no remarkable feature noticed in this cluster for different characters. None of the genotypes included this cluster which showed the highest or lowest mean values of 20 different yield and yield contributing character of okra yield was the ultimate goal for any crop production. The highest yield was 824.03 in clusters II followed by 691.96 in cluster V and 649.28 in cluster VI. The single fruit weight observed the highest in cluster II 20.95, followed by cluster VI (20.01) and cluster III (19.69) respectively. Number of Seeds per fruit observed highest value (65.27) in cluster III, followed by (59.89) in cluster VI and (57.22) in cluster I accordingly. Syfullah *et al.* (2018) observed a close perusal of these cluster mean for different characters indicated considerable genetic differences among the clusters for all the characters. Ranpise *et al.* (2018) indicated that the variation for the quantitative trait among clusters a substantial variation in cluster mean observed for various characters in okra was also reported by Ghai *et al.* (2009) and Singh and Jain (2012).

Principal component analysis (PCA) results of 20 characters were presented in Table 4.5. The PCA analysis results includes the factor scores of each character among the 50 okra genotypes, eigen value, percentage total variance account for twenty principal components (A to T) with eigen values ranged from 0.0114 to 4.0395 (Table 4.5). The twenty principal components accounted varied percentage of total variance ranged from 0.00 to 91.83%. Cumulative percent of total variation up to PCA three with eigen value

Table 4.5 Eigen values and percentage of variation for corresponding 20 component characters in 50 lines of okra

Principal component axis	Eigen values	Percentage of total variation account for	Cumulative percentages
I	4.0395	91.83	91.83
II	3.3125	5.83	97.66
III	2.8906	1.10	98.76
IV	1.7420	0.79	99.55
V	1.0568	0.25	99.80
VI	0.7962	0.09	99.80
VII	0.7009	0.04	99.84
VIII	0.5958	0.03	99.87
IX	0.5048	0.02	99.89
X	0.4421	0.01	99.99
XI	0.4094	0.01	100
XII	0.3321	0.00	100
XIII	0.2784	0.00	100
XIV	0.2241	0.00	100
XV	0.1609	0.00	100
XVI	0.0906	0.00	100
XVII	0.0718	0.00	100
XVIII	0.0591	0.00	100
XIX	0.0267	0.00	100
XX	0.0114	0.00	100

Table 4.6 Ten highest and ten lowest distances among the lines of okra

Genotypic combinations	**Distances**
A. 10 highest inter genotypic distances	
G4-G32	576.25
G4-G30	543.63
G4-G25	543.43
G31-G32	505.36
G32-G43	495.37
G4-G37	492.60
G2-G32	476.25
G25-G31	472.14
G30-G31	471.81
G3-G32	463.16
B. 10 lowest inter genotypic distances	
G45-G50	5.09
G23-27	5.63
G28-G34	6.17
G48-G49	7.15
G17-G40	7.30
G11-G35	7.36
G7-G47	7.38
G12-G40	7.68
G1-G7	8.43
G15-G40	8.49

Selected: G-1, G-9, G-14, G-16, G-27, G-41, G-43

Table 4.7 Latent vectors for 15 principal component characters in Okra

Characters	Vector 1	Vector 2
Plant height at 25 days (cm)	0.00104	0.02561
Plant height at 50 days (cm)	0.00113	0.02547
Plant height at 75 days (cm)	0.00134	0.00462
Plant height at 100 days (cm)	0.00235	0.02848
Number of leaf at 25 days (cm)	0.00420	0.02004
Number of leaf at 50 days (cm)	-0.00046	0.01044
Number of leaf at 50days (cm)	0.00407	0.03368
Number of leaf at 100 days (cm)	-0.00097	0.00196
1st flower initiations day	0.04227	-0.05191
50% flower initiation day	0.99904	0.01139
Node of first female flower	0.00957	-0.99664
1st edible fruits harvesting days	0.00015	0.01001
Fruits length (cm)	0.00021	0.00193
Fruit diameter (cm)	0.00543	0.00234
Fruits weight (g)	-0.00121	0.00749
Number of ridge per fruits	0.00081	0.00138
Number of fruits per plant	0.00762	0.00043
Fruits yield per plant	0.00238	-0.00042
Seeds per fruit	0.00426	0.00562
100 seed weight (g)	0.08543	0.06732

more than unity accounted 98.76%. Nwangburuka *et al.* (2011) and Mihretu *et al.* (2014a) were in close conformity with the findings, where the principal component axes contributed 64.32%, 78.59% and 83% variation. The first five components were retained in analysis because eigen values are greater than 1. The other factors having eigen value < 1 were ignored (Kumar *et al.* 2011). The first three principal components value of 91.83, 5.83 and 1.10 respectively. Contribution more to the total of 98.76% variation, near about similar result was reported by Amoatey*et al.* (2015) and Akotkar *et al.* (2010). 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 thoise with lower absolute values closer to zero.

4.1.14 Contribution of characters in account of divergence of the genotypes

Contribution of different characters responsible for genetic divergence in the genotypes was presented in the Table 4.7. Vector I observed from PCA expressed that the important character responsible for genetic divergence in the major axis were days to 50% flower initiation (0.99904), 100 seed weight (0.08543), 1st flower initiation days (0.04227), node of first flowering (0.00957). Therefore, considerable emphasis should be given on these characters to increase fruit yield in okra. Other characters had minor contribution in determining genetic divergence. In vector II which was the second axis of differentiation, 100 seed weight (0.06732), number of leaf at 50 days (0.03368), plant height at 100 days (0.02848), number of leaf at 25 days (0.02004), played a major role while rest of all characters contributed less in determining genetic divergence. These characters of plant for both the vectors were positive across two axes indicating the important component of genetic divergence among the characters. Negative values were observed in vector I, number of leaf at 50 days (-0.00046), number of leaf at 100 days (-0.00097) and average fruit weight (-0.99664), days to first flowering (-0.05191) and Fruit yield per plant (-0.00042) respectively.

With respect to the relative predominance of different characters under study it would be apparent from the absolute size of coefficients that days to fifty percent flower initiation (0.99904), 100 seed weight (0.08543) and days to first flower initiation (0.04227) were predominant in the primary axis of differentiation. However, in vector II, 100 seed weight (0.06732), number of leaf at 50 days (0.03368), and plant height at 100 days (0.02848) were predominant.

4.2 Experiment – II: Selection of important yield contributing characters of okra

4.2.1 Correlation studies among different pairs of characters in okra genotypes

Mutual association of characters was often expressed in phenotypic and genotypic data with direction and magnitude of correlation coefficients among yield related traits which were presented in Table (4.8). Plant breeders always look for genetic variation among characters to select the desirable types which were highly correlated among themselves and with yield and the analysis of the relationship among these characters are vital for selection criteria. Magnitude of genotypic coefficients of correlation was higher compared to their corresponding phenotypic coefficient values indicating that there was an inherent association among various traits studies (Table 4.8).

4.2.2 Analysis of correlation

4.2.2.1 Plant height at 100 days

Phenotypic, genotypic and environmental coefficient of correlation revealed that plant height had positive and significant correlated with fruits per plant (rg= 0.4985 **), 100 seed weight (rg= 0.3586*) and fruit yield per plant (rg= 0.5770 **) at both genptypic and phenotypic level. But significant and negative was found in 50% flower initiation (-0.110 **) in phenotypic level and negative relation also revealed with fruit diameter in both genotypic and phenotypic level. Otherwise other characters showed positive correlation with plant height. Syfullah *et al.* (2018) observed plant height positive and significant phenotypic and genotypic correlations with fruit yield (0.699 and 0.618) and number of fruits per plant (0.809 and 0.761), also showed negative correlation with fruit diameter (-0.361* and -0.236), respectively.

Table 4.8 Genotypic (r_g), Phenotypic (r_p) and Environmental correlation (r_e) coefficients among yield and yield related characters in okra

Characters		PH100	50FI	FEFH	Fruit length (cm)	Fruit diameter (cm)	Fruit weight (g)	Fruits per plant	Seeds per fruit	100SW	Yield per plant
PH100	r_g	1	-0.1617	-0.0392	0.2629	-0.0728	0.2526	0.4985**	0.0301	0.3586*	0.5770**
	r_p		-0.1107	-0.0516	0.2034	-0.0237	0.1301	0.4507**	0.0068	0. 31 20*	0.5014**
	r_e		0.0877	-0.1401	0.0838	0.0933	0.0993	0.1442	-0.1574	0.1044	0.1522
50FI	r_g		1	0.9687**	-0.0070	0.1217	0.2426	0.0019	-0.1803	-0.5672**	0.0774
	r_p			0.7997**	0.0390	0.1262	0.1389	0.0217	-0.1218	-0.3687**	0.0989
	r_e			0.4693**	0.1067	0.1399	0.0996	0.0781	0.0192	00.0659	0.1499
FEFH	r_g			1	0.0911	0.1360	0.4055**	0.0576	-0.1943	-0.5414**	0.1942
	r_p				0.1063	0.0408	0.1681	0.0576	-0.1316	-0.3839**	0.1649
	r_e				0.1347	-0.0645	0.0400	0.0602	0.0459	0.0163	0.0899
Fruit length (cm)	r_g				1	-0.0864**	-0.2007	0.5018**	-0.1718	0.0538	0.4666**
	r_p					-0.3633	0.3155*	0.3391*	-0.1108	0.0550	0.4116**
	r_e					0.2442	0.6341**	0.0079	0.0074	0.0604	0.3320**
Fruits diameter (cm)	r_g					1	0.3864**	-0.4023**	-0.0420	-0.1179	-0.2758
	r_p						0.3590*	-0.2023	0.0048	-0.0176	-0.0592
	r_e						0.3590*	0.0564	0.0746	0.1100	0.2162

Fruit weight	r_g						1	-0.0702	-0.3265*	0.0627	0.3275*
	r_p							-0.0331	-0.0864	-0.0136	0.3097*
	r_e							-0.0137	0.0968	-0.0816	0.4104**
Fruits per plant	r_g							1	0.2072	0.0673	0.9226**
	r_p								0.1545	0.0350	0.8582**
	r_e								-0.0557	-0.0792	0.6396**
Seeds per fruit	r_g								1	-0.1789	0.1112
	r_p									-0.2361	0.0917
	r_e									-0.4219**	0.0284
100SW	r_g									1	0.1112
	r_p										0.0917
	r_e										0.0284
Fruit yield per plant	r_g										1

Here, PH100= Plant height at 100 days (cm), 50FI= Days to 50 % flowering, FEFH=First edible fruit harvesting (days) and 100SW=100 Seed weight

** = Significant at 1% level. * = Significant at 5% level. ns = Insignificant

4.2.2.2 50% Flower initiation

This character showed positive and significant correlation in all level viz. genotypic, phenotypic and environmental level with days to first edible fruit harvest which were (rg=0.9687**), (rp=0.7997**) and (re=0.4693**) and negative and significant correlation with 100 seed weight both in genotypic and phenotypic level viz. (rg=-0.5672**), rp=-0.3687**). Beside this negative correlation exhibited with Seeds per fruit in both level and fruit length in genotypic level only and rest of all showed positive correlation with 50% flower initiation. Syfullah *et al.* (2018) recorded negative correlation between day to 505 flowering with fruit yield per plant and average fruit weight which was contradictory to the present study.

4.2.2.3 First edible fruit harvesting

The one and only positive correlation was observed with fruit weight (rg=0.4055**) in genotypic level. Negative and significant correlation showed with 100 seed weight viz. (rg= -0.5414**), (rp= -0.3839**) respectively. Seeds per fruit in both level and fruit diameter in environmental level showed negative correlation with first edible fruit harvest. And rest of all parameters exhibited positive correlation with first edible fruit harvest. Days to first picking / harvest observed positive and significant correlation with fruit yield per plot (rp= 0.416) (Kumar *et al.*, 2015).

4.2.2.4 Fruit length

This character exhibited positive and significant correlation with fruit yield per plant in genotypic, phenotypic and environment level viz. (rg = 0.4666**), (rp = 0.4116**) and (re = 0.3320**), respectively it also showed significant and positive correlation with fruits per plant in genotypic and phenotypic (5%) level. Significant and positive correlation with fruit weight in phenotypic (rp = 0.3155*, 5%) and environmental (re = 0.6341**) level. Negative and significant correlation observed only fruit diameter (rg = -0.0864**), also negative correlation with fruit diameter (rg = -0.3633) and fruit weight in genotypic level (rg = -0.2007), both genotypic and phenotypic level of seeds per fruit viz. (rg = -0.1718), (rp = -0.1108), respectively. Otherwise all characters showed positive correlation with these traits.

4.2.2.5 Fruit diameter

Fruit diameter showed positive and significant correlation with fruit weight viz. (rg = 0.3864**), (rp = 0.3590* 5%) and (re = 0.3590* 5%) showed negative significant result for fruits per plant in genotypic level viz (-0.4023**) negative correlation also observed for seeds per fruit in genotypic level. Hundred seed weight and fruit yield per plant showed negative correlation in both genotypic and phenotypic level. Rest of all showed positive correlation with this trait. Syfullah *et al.* (2015) recorded significantly negative correlated between fruit diameter and seeds per fruit genotypically (-0.571**). But only phenotypically negative correlation and also negative correlation with fruit yield per plant both genotypic and phenotypically.

4.2.2.6 Fruit weight

Significant and positive correlated only observed for fruit yield per plant in three level viz genotypic (rg = 0.3275*), phenotypic (rp = 0.3097*) and environmental (0.4104**), respectively. significant and negative correlation observed only Seeds per fruit in genotypic level (rg = -0.3265*), negative correlation also observed in three levels for fruit per plant, phenotypic level in seeds per fruit and both phenotypic and environmental level in 100 seed weight.

4.2.2.7 Fruits per plant

Significant and positive correlation only observed for fruit yield per plant in genotypic (rg = 0.9226**) phenotypic (rp = 0.8582**) and environmental (re = 0.6396**) level. Negative correlation exhibited Seeds per fruit and 100 seed weight and rest of all component showed possitive correlation with this trait. Dhall *et al.* (2000) observed that total fruit yield per plant positively and significantly correlated with number of fruit per plant. The present study was agreed with the results reported by Niranjan and Mishra (2003) who observed number of fruits per plant was positively and significantly correlated with fruit yield per plant. Singh *et al.* (2007) also observed same results.

4.2.2.8 100 seed weight

Hundred seed weight showed positive correlation with fruit yield per plant but the result not significant in any level of significance. Yonas *et al.* (2014) observed 100 seed weight was positive and highly significant genotypic correlation with fruit yield per plant (r = 0.68).

4.2.2.9 Seeds per fruit

The present study showed all level of positive but not significant result with fruit yield per plant and with 100 seed weight found strongly negative correlation with environment (-0.4219**) but both genotypic and phenotypic correlation obtained negative with seed per fruit. The findings of Yonas *et al.* (2014) observed seeds per fruit was positive and highly significant genotypic (rg = 0.56) and phenotypic (rp = 0.44) correlation with yield per plant.

4.2.3 Path coefficient analysis in Okra genotypes

The mutual relationship of component characters might vary both in magnitude and direction and the simple correlation coefficient may not provide the exact relationship between yield and yield attributes. Therefore, it is necessary to conduct path coefficient analysis which permits a critical examination of specific direct and indirect effects of characters and measure their relative intensity in determining the ultimate goal yield (Syfullah *et al.,* 2018). The path coefficient analysis (Table 4.9) showed that the number of fruits per plant (0.9070) had the highest positive direct effects on fruit yield per plant followed by fruit weight (0.4940) and days to 50% flowering initiation (0.0763) and plant height at 100 days (0.0580) respectively. The fruit length showed the highest direct negative effect on yield (-0.7741), though their association was positive.and followed by fruit diameter (-0.1829), days to first edible fruit harvest (-0.1626), 100 seed weight (-0.1269) under this circumstances, a restricted simutaneous selection model was to be followed i.e. restrictions were to be imposed to nullify the undesirable indirect effects via fruit diameter (0.1987), fruits per plant (0.4551) and plant height at 100 days (0.0152), in order to make use of the direct effect, while indirect effect of fruit length via fruits per plant was high and positive (Mehta *et al.,* 2006). The indirect positive effects of plant height on fruits per plant (0.4522) via fruit weight (0.1248) fruit diameter (0.0133) and days to first edible fruit harvest (0.0064) and negative indirect effect on 50% flower initiation (-0.0455), respectively.

Table 4.9 Path coefficient showing direct (bold value) and indirect effects of yield and yield related characters of okra

	PH100	50FI	FEFH	Fruit length (cm)	Fruit diameter (cm)	Fruit weight (g)	Fruits per plant	Seeds per fruit	100SW	Fruit yield per plant
PH100	**0.0580**	-0.0123	0.0064	-0.0204	0.0133	0.1248	0.4522	0.0006	-0.0455	0.5770**
50FI	-0.0094	**0.0763**	-0.1575	0.0005	-0.0223	0.1198	0.0017	-0.0038	0.0720	0.0774
FEFH	-0.0023	0.0739	**-0.1626**	-0.0071	-0.0249	0.2003	0.4522	-0.0041	0.0687	0.1942
Fruit length (cm)	0.0152	-0.0005	-0.0148	**-0.7741**	0.1987	-0.0991	0.4551	-0.0037	-0.0068	0.4666**
Fruit diameter (cm)	-0.0042	0.0093	-0.0221	0.0841	**-0.1829**	0.1909	-0.3649	-0.0009	0.0150	-0.2758
Fruit weight	0.0146	0.0185	-0.0659	0.0155	-0.0707	**0.4940**	-0.0637	-0.0070	-0.0080	0.3275*
Fruits per plant	0.0289	0.0001	-0.0094	-0.0388	0.0736	-0.0347	**0.9070**	-0.0044	-0.0085	0.9226**
Seeds per fruit	0.0017	-0.0138	0.0316	0.0133	0.0077	-0.1613	0.1879	**-0.0213**	0.0227	0.1112
100SW	0.0208	-0.0433	0.0880	-0.0042	0.0216	0.0310	0.0610	-0.0038	**-0.1269**	0.0442**

PH100= Plant height at 100 days, 50FI= Days to 50% flower initiation, FEFH= Days to First Edible Fruit Harvesting, 100SW= 100 Seed weight (g), and *= significant at 1% and 5% level respectively.

Residual Effect= 0.1320

The present study showed direct and positive effect on days to 50% flower initiation (0.0763), also positive and indirect effect observed with fruit weight (0.1198), 100 seed weight (0.0720) and negative effect recorded for plant height (-0.0094) followed by first edible fruit harvest (-0.1575), fruit diameter (-0.0223) and seeds per fruit (-0.0038) respectively. Days to edible harvest showed negative and direct (-0.1626) effect on fruit yield per plant and indirect negative effect also observed on fruit length (-0.0071), followed by fruit diameter (-0.0249), plant height (-0.0023) and Seeds per fruit (-0.0041) also, and positive indirect effect recorded on days to 50% flowering, (0.0739), fruit weight (0.2003), fruits per plant (0.4522) and 100 seed weight (0.0687), respectively (Table-4.9). Vrundaraval *et al.* (2019) observed days to edible harvest of 1^{st} picking in positive and direct effect (0.01) on yield per fruit, though the correlation coefficient with fruit yield per plant revealed significant negative and all components showed indirect positive effect to fruit yield per plant except number of fruits per plant (-0.19). The fruit diameter also showed direct and negative effect to fruit yield per plant (-0.1829) followed by fruits per plant (-0.3649), first edible fruit harvest (-0.0221), plant height (-0.0042) and positive indirect effect for 50% flowering, fruit length (0.0841), fruit weight (0.1909) and 100 seed weight (0.0150).

4.2.3.1 Fruit weight

The present study revealed that fruit weight had the second highest significant and positive direct effect with fruit yield per plant (0.4940). The positive indirect effect showed viz plant height (0.0146), followed by 50% flowering (0.0185), fruit length (0.0155), respectively and negative indirect effect observed on first edible fruit harvest (-0.0659), fruit diameter (-0.0707), fruits per plant (-0.0637), Seeds per fruit (-0.0070) and 100 seed weight (-0.0080), with fruit yield per plant (Table 4.9).

4.2.3.2 Fruits per plant

The highest direct and positively significant result (0.9070) observed for fruits per plant with fruit yield per plant. The positive indirect effect revealed plant height 100 days (0.0289) followed by 50% flowering, fruit diameter (0.0736) and indirect negative effect found on first edible fruit harvest (-0.0094), fruit length (-0.0388), fruit weight (-0.0347), Seeds per fruit (-0.0044) and 100 seed weight (-0.0085), respectively (Table 4.9).

4.2.3.3 Seeds per fruit

The present study revealed negative direct effect on this character to yield per plant. All characters showed indirect positive effect except 50% flower initiation and fruit weight (-0.1613) to fruit yield per plant (-0.0138) (Table 4.9).

4.2.3.4 100 Seed weight

The observation of 100 seed weight (-0.1269) was direct negative effect on yield per plant. The all characters showed positive in direct effect except 50% flowering (-0.0433), fruit length (-0.0042), and seeds per fruit (-0.0038) respectively, (Table 4.9).

4.3 Experiment III: Study on combining ability in Okra

4.3.1 Combining ability

The diallel analysis helps to obtain information on the genetic systems governing the inheritance of attributes to be improved, and hence may help in predicting the performance in subsequent generations by assessing the potential of different crosses. The diallel cross is defined as all possible crosses among a group of parents. Plant Breeders use diallel analysis as an aid in selection and to investigate genetic properties of parents and their crosses. A diallel analysis can provide useful information regarding the genetic control of a quantitative trait. It provides information on average performance of individual lines in crosses known as general combining ability (GCA). It also gives information about the performance of crosses relative to the average performance of parents involved in the cross known as specific combining ability (SCA). Significant GCA and SCA effects provide information to help determine the efficacy of breeding for improvements in given traits and they can be used to identify lines to serve as parents in a breeding program for trait improvement (Kearsey and Pooni, 1996). In addition, this technique enables the breeder to combine desirable genes that are found in two or more genotypes (Dabholkar,1992). The following parents were used for combining ability in this study: P1 (1163), P2 (1171), P3 (1176), P4 (1178), P5 (1189), P6 (1203), P7 (1205).

4.3.2 Analysis of combining ability

General combining ability is the average performance of a line in hybrid combinations, while SCA is used to designate deviations of certain crosses from expectations based on the average performance of the lines involved (Sprague and Tatum, 1942). Genetically, GCA is primarily associated with genes, which are additive in their effects, whereas SCA is attributed to the non-additive genetic portion of the total genetic effects (Rojas and Sprague, 1952). Additive effects are the predictable portion of the genetic effects and are therefore useful to plant breeders. Diallel cross designs are frequently used in plant breeding research to obtain information on general combining ability (GCA) and specific combining ability (SCA). So, the choice of appropriate parental material for crossing is the first foremost step in the development of new crop cultivars. Knowledge on the effects of general combining ability (GCA) and specific combining ability (SCA) is useful in the selection of parental genotypes. General and specific combining ability (SCA) is useful in the selection of parental genotypes. General and specific combining ability are important indicators of the potential value of inbred lines in hybrid combinations. In combining ability analysis, parents were categorized into (i) good combiners for the highest GCA effects (ii) Poor combiners for the lowest value of GCA effects, (iii) average combiners for those having moderate GCA effects between the highest and the lowest values. Similarly, on the basis of SCA effects, specific combiners (crosses) were also defined into same group for different plant characters.

Table 4.10 Analysis of variance for various characters in okra

Sources of variation	df	PH100	LN100	FFI	50FI	NFF	FEFH	Fruits per plant	Fruit diameter (cm)	Fruit length (cm)	Fruit weight (g)	Seeds per fruit	100SW	Fruit yield per plant
Replications	2	504.14	6.91	0.84	29.78**	0.67	0.56	70.05	0.02	1.57	33.52**	28.17	0.16	71712.50*
Lines	27	14389.26**	977.73**	1227.99	2291.97**	21.34**	1680.22**	675.76**	2.84**	142.37**	212.84**	3532.58**	1680.22**	238425.00**
Parents	6	10376.25**	799.62**	782.60**	1470.55**	15.17**	1061.11**	386.58**	1.79**	80.39**	119.97**	2393.21**	1061.11**	132542.70**
Hybrids	20	16241.96**	1035.71	1395.80**	2603.46**	23.45**	1915.82**	794.25**	3.25**	167.37**	250.60**	3973.50**	1915.82**	281999.30**
Parent *vs* hybrids	1	1413.27*	886.88**	544.08**	990.86**	16.30**	682.71**	41.14	1.03**	14.29**	15.04	1550.23**	682.71**	2232.83
Error	54	287.61	43.50	0.56	2.53	0.26	1.21	38.01	0.036	1.47	5.02	17.12	1.21	20519.02

Here, PH100= Plant height at 100 days (cm), LN100= Leaf number at 100 days, FFI= First flower initiation, 50FI+ 50% flower initiation, NFF=Number of female flower, FEFH= First edible fruit harvesting days

*and ** Significant at 5% and 1% levels, respectively.

Table 4.11 Mean square due to general and specific combining ability for different characters in okra

Sources of variation	**PH100**	**LN100**	**FFI**	**50FI**	**NFF**	**FEFH**	**Fruit per plant**	**Fruit diameter(cm)**	**Fruit length (cm)**	**Fruit weight**	**Seeds per Fruit**	**100SW**	**Yield per Plant**
GCA	1895.79**	120.29	12.20**	9.15**	0.16	10.58**	16.90	0.0042	12673.98	2.48	65.68**	0.05*	12075.13
SCA	443.31**	68.28	2.24*	2.46**	0.12	3.38*	8.03	0.0029	5563.76	2.04	29.41**	0.11**	4560.94
Error	94.09	53.95	1.46	0.74	0.079	1.44	12.42	0.0028	7186.28	1.85	5.58	0.03	6586.75
σ^2gca	200.18	7.37	1.19	0.93	0.009	1.02	0.50	0.0001	609.74	0.07	6.68	0.0029	609.82
σ^2sca	349.21	14.33	1.82	1.72	0.04	1.94	-4.39	0.0001	-1622.52	0.19	23.83	0.08	-2025.80
Potence ratio	0.57	o.51	0.65	0.54	0.22	0.52	-0.11	1.62	-0.37	0.37	0.28	0.03	-0.30

Here, PH100= Plant height at 100 days (cm), LN100= Leaf number at 100 days, FFI= First flower initiation, 50FI+ 50% flower initiation, NFF=Number of female flower, FEFH= First edible fruit harvesting days, 100SW= 100 seed weight

*and ** Significant at 5% and 1% levels, respectively

The analysis of variance for yield and yield contributing characters for combining ability indicates significant differences among genotypes for all the traits (Table.4.10). This indicated that the experimental material under study had sufficient genetic diversity for different traits. Further partitioning of sum of squares due to lines indicated that the differences among parents were significant for all the characters under observation. In case of hybrids, significant difference obtained for all the traits except leaf number 100 days, while mean squares due to parent vs. hybrids were significant in all parameters except fruit per plant, fruit weight and yield per plant. Shwetha *et al.* (2018) observed the variance due to genotypes (crosses and parents) was highly significant (at P=0.01) for all the yield and quality parameters, viz., fruit length, fruit diameter, average fruit weight, number of fruit per plant, total yield per plant, number of seeds per fruit. Parents differed significantly among themselves for all the yield and quality parameters studies except for fruit diameter and average fruit weight. There was highly significant (at P=0.01) difference among the crosses for all the yield and quality parameters studied. Variance due to parents vs. crosses was significant for fruit length, average fruit weight, number of fruits per plant and for all other parameters variance due to parent’s vs crosses was not significant.

Table 4.12 General combining ability effects for different characters in okra

Sl no	Parent	**LN100**	**PH100**	**FFI**	**50FI**	**NFF**	**FEFH**	**Fruit diameter(cm)**	**Fruit length (cm)**	**Fruit weight (g)**	**Fruits per plant**	**Seeds per fruit**	**100SW**	**Fruit yield per plant**
P_1	1163	-3.79	-15.64 **	-1.19**	-1.60**	-0.44**	-1.06**	-0.03*	-0.45**	-0.94*	-2.72*	-0.83	-0.02	-76.56**
P_2	1171	-0.11	-19.20**	-2.48**	-2.46**	-0.18**	-2.13**	-0.04*	-0.31*	-0.75	-0.26	3.25**	-0.02	-13.35
P_3	1176	-1.91	13.23**	0.22	0.36	0.11	-1.06**	-0.01	-0.04	-0.13	-0.47	-4.54**	0.02	16.16
P_4	1178	-1.55	-7.04**	0.15	0.29	0.18*	0.87**	0.01	-0.01	-0.31	0.28	-2.03**	-0.16**	20.91*
P_5	1189	-0.73	11.38**	0.41	0.73**	0.09	0.94**	0.03	0.53**	1.18	1.07**	2.49**	-0.02	22.63**
P_6	1203	4.55*	0.08	1.89**	1.73**	0.10	1.53**	0.02	0.25	0.45	1.62**	0.50	0.11*	32.42**
P_7	1205	3.54	17.19**	1.00**	0.95**	0.15*	0.90**	0.02	0.04	0.51	0.49	1.16	0.09	-2.21
No. of positive significant parents		1	3	2	3	2	4	-	1	-	2	2	1	3
No. of negative significant parents			3	2	2	2	3	2	2	1	1	2	1	1

Here, PH100= Plant height at 100 days (cm), LN100= Leaf number at 100 days, FFI= First flower initiation, 50FI+ 50% flower initiation, NFF=Number of female flower, FEFH= First edible fruit harvesting days, 100SW= 100 seed weight (g). *and ** Significant at 5% and 1% levels, respectively

The estimation of general combining ability (gca) effects of seven parental inbred lines in F_1 generation were presented in Table 4.12. In the present study, parents were classified as good, average and poor combiner based on their gca effects. Parents with desirable and significant GCA effects were considered as good combiners, while parents exhibiting insignificants estimates were classified as average combiners. Therefore, the magnitude and direction of the significant effects of gca for the seven parents provides meaningful breeding program for crop improvement, character wise interpretation of gca effects were given below:

4.3.2.1 Leaf number

For leaf number negative estimates of general combining ability (gca) effects were considered desirable.

4.3.2.2 Plant height

For plant height (Table 4.12) positive and significant gca effect showed in three parents P3 (13.23**), P5 (11.38**) and P7 (17.19**), respectively. Negative and significant effect showed in P1 (-15.64**), P2 (-19.20**) and P4 (-7.04**). Positive and insignificant result showed only in one parent P6 (0.08) M. Amaranath Reddy *et al.* (2013) reported that out of eight parents showed for gca only four parents viz Arkaabhay (10.941**), DBh-37 (10.849**), DBh-39 (6.605**) and DBh-43 (3.118**), respectively significant positive effect and significant negative effect showed two parents viz. ArkaAnamika (-2.070*), DBh-30 (-5.030**) and other two parents showed insignificant negative effect that was DBh-47 (-1.441), and DBh-55(-1.091) respectively for plant height.

4.3.2.3 First flower initiation

For days to first flowering, negative estimates of general combining ability (gca) effects were considered desirable, since there were preferable for earliness of the parents (Table-4.12). The estimates of gca effects range from -2.48 in P2 to 1.73 in P6 P2 (-2.48**) had negative estimates and was the best general combiner for this trait among all the genotypes followed by P1 (-1.19**). Therefore, this parent might be used in the breeding program for developing early flowering i.e. early fruiting varieties. Two parents P6-1203 (1.89**) and P7 (1.00**) had significant positive estimates and therefore they were poor combiners. The rest three P3 (0.22), P4 (0.15) and P5 (0.41) were average combiners as it showed insignificant gca effect for this trait.

4.3.2.4 Days to 50% flowering

Present study revealed negative and significant effect for gca were P1 (-1.60**) and P2 (-2.46**) which will be best combiner out of seven parents. Three parents showed positive and significant result P5 (0.73**), P6 (1.73**) and P7 (0.95**) respectively. Only two parents showed positive insignificant effect P3 (0.36) and P4 (0.29) which were selected as poor combiners for this trait.

4.3.2.5 Node of first flowering

Present study expressed negative and positive significant difference among the parental genotype. The highest negative significant value observed in 1163 (-0.44**) genotype followed by 1171 (-0.18**) which were the most desirable for the highest yield. The positive and significant value observed only in two genotypes i.e. 1178 (0.18*) and 1205 (0.15*), respectively. Another three parental genotypes showed positive non-significant effect. There was no negative non-significant effect among the genotypes.

4.3.2.6 Days to first edible fruit harvest

out of seven parent, only three had revealed negative and significant value for days to first edible fruit harvest. The highest negative and significant effect observed in P2=1171 (-2.13**) followed by P1=1163 (-1.06**) and P3 = 1176 (-1.06**) respectively which indicated as good combiners. The positive and significant effect found in three rest of four parents. The highest positive effect showed in p6 = 1203 (1.53**) followed by P5 = 1189 (0.94**), P7 = 1205 (0.90**) and P4 = 1178 (0.87**) respectively.

4.3.2.7 Fruit diameter

Present investigation showed negative and significant effect only in P1=1163 (-0.03*) and p2=1171 (-0.04*), respectively. The negative non-significant effect observed in 1176 (-0.01) and rest all four parent showed positive and in significant effect for this trait.

4.3.2.8 Fruit length

Present study revealed positive and significant effect only in one parent for this character P5= 1189 (0.53**) and positive insignificant effect showed in P6= 1203 (0.25) and P7 = 1205 (0.04), respectively. The negative and significant effect observed in P1 = 1163 (-0.45**) and P2 = 1171 (-0.31*) and negative significant effect in P3 = 1176 (-0.04) and P4 = 1178 (-0.01), respectively.

4.3.2.9 Fruit weight

Negative and significant effect for gca were observed in P1 (-0.94*) which would be the best combiner out of seven parents. Three parents showed negative and insignificant result P2 (-0.75), P3 (-0.13) and P4 (-0.31), respectively. Other three parents showed positive insignificant effect P5 (1.18), P6 (0.45) and P7 (0.51) which were selected as poor combiners for this trait.

4.3.2.10 Fruits per plant

The range of fruits per plant were obtained from -2.72* to 1.62** in some lines. The highest positive significant effect observed in P6-1203 (1.62**) followed by P5-1189 (1.07**). The positive non-significant effect observed in P4-1178 (0.28) and P7-1205 (0.49) parental lines. The highest negative significant effect observed in P1-1163 (-2.72*). The negative insignificant value found in P2-1171 (-0.26) and P3-1176 (-0.47), respectively.

4.3.2.11 Seeds per fruit

Present study showed a wide range of variation for seeds per fruit. The highest value was 3.25 to lowest value -4.54 respectively. The positive and significant value observed in P2= 1171 (3.25**) and P5=1189 (2.49**) respectively which indicated as good combiner for this trait. Positive and insignificant found in P6=1203(0.50) and P7=1205 (1.16). The negative and significant value found in P3=1176 (-4.54**), P4=1178 (-2.03**) and negative but insignificant value observed in P1=1163 (-0.83).

4.3.2.12 100 Seed weight

Hundred seed weight within 7 parents had the positive and significant value in P6 = 1203(0.11*) and positive insignificant in P7 = 1205 (0.09), P3 = 1176 (0.02) respectively. The negative and significant value was found in P4= 1178 (-0.16**) and negative insignificant same as P1 = 1163 (-0.02), P2 = 1171 (-0.02), P5 = (-0.02), respectively.

4.3.2.13 Fruit yield per plant

Present study showed fruit yield per plant had a wide variation. The highest positive significant effect observed in P6=1203 (32.42**) followed by P5=1189 (22.63**), P4=1178 (20.19*) and positive insignificant found in P3= 1176 (16.16), respectively. The negative significant value was found only in P1=1163 (-76.56**) and negative insignificant observed in P2=1171 (-13.35) and P7= 1205(-2.21) respectively.

Vr-Wr graph:

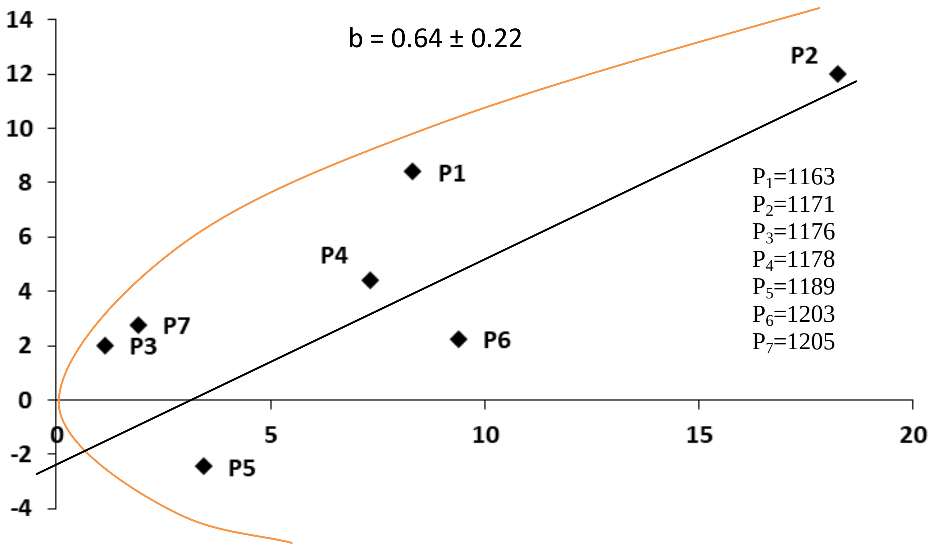

Figure 4.2 Vr-Wr graphs for plant height (cm) at 100 days

Figure-4.2: As parental array points are scattered around the regression line in the Vr-Wr graph that means genetic diversity is present among the parents for the characters. Regression co-efficient is 0.64 (<1) which indicates absence of epistatic interaction or absence of non-allelic interaction to express the characters. Regression line intercept below the origin of Wr line representing some allelic pairs of p5 genotype showed over-dominance. Parents p3 and p7 distributed to the nearest of the origin indicated they had the maximum number of dominant alleles, whereas parents p2 is distributed far away from the origin, i.e it had the maximum number of recessive alleles, besides p1, p4 and p6 were distributed in the middle from the origin which indicated these parents had equal frequency of dominance and recessive alleles or additive gene. The width of the parabola indicated the diversity of genotypes. And the distribution of parental array points was within the parabola.

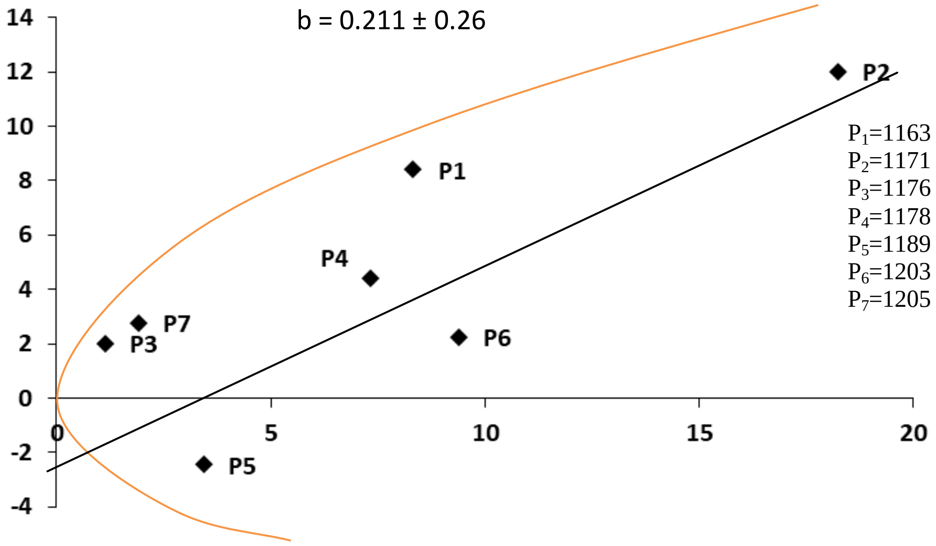

Figure 4.3 Vr-Wr graph for number of leaf at 100 days

From the Vr-Wr graph, as parental array points were scattered around the regression line that meant genetic diversity was present among the parents for the characters. Regression co-efficient was 0.211(<1) which indicated absence of epistatic interaction or absence of non-allelic interaction to express the characters. Regression line intercept below the origin of Wr line representing some allelic pairs of p5 genotype show over-dominance. Parents p3 and p7 distributed to the nearest of the origin indicate they had the maximum number of dominant alleles, whereas parents p2 is distributed far away from the origin, i.e it had maximum number of recessive alleles, besides p1, p4 and p6 were distributed in the middle from the origin which indicated these parents had equal frequency of dominance and recessive alleles or additive gene. The width of the parabola indicated the diversity of genotypes. And the distribution of parental array points is within the parabola.

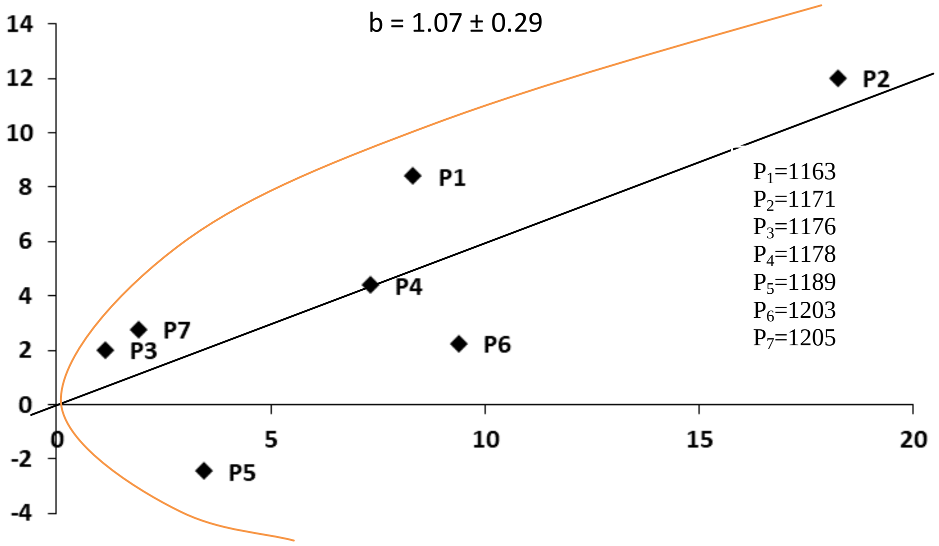

Figure 4.4. Vr-Wr graph for days to first female flower initiation

From the Vr-Wr graph, as parental array points were scattered around the regression line that means genetic diversity was present among the parents for the characters. Regression co-efficient was 1.07(>1) which indicated presence of epistatic interaction or presence of non-allelic interaction to express the characters. Regression line intercept through the origin of Wr line representing complete dominance for days to first female flower initiation. Parents p3 and p7 distributed to the nearest of the origin indicated they had maximum number of dominant alleles, whereas parents p2 is distributed far away from the origin, i.e it had maximum number of recessive alleles, besides p1, p4 and p6 were distributed in the middle from the origin which indicate these parents had equal frequency of dominance and recessive alleles or additive gene. The width of the parabola indicated the diversity of genotypes. And the distribution of parental array points was within the parabola.

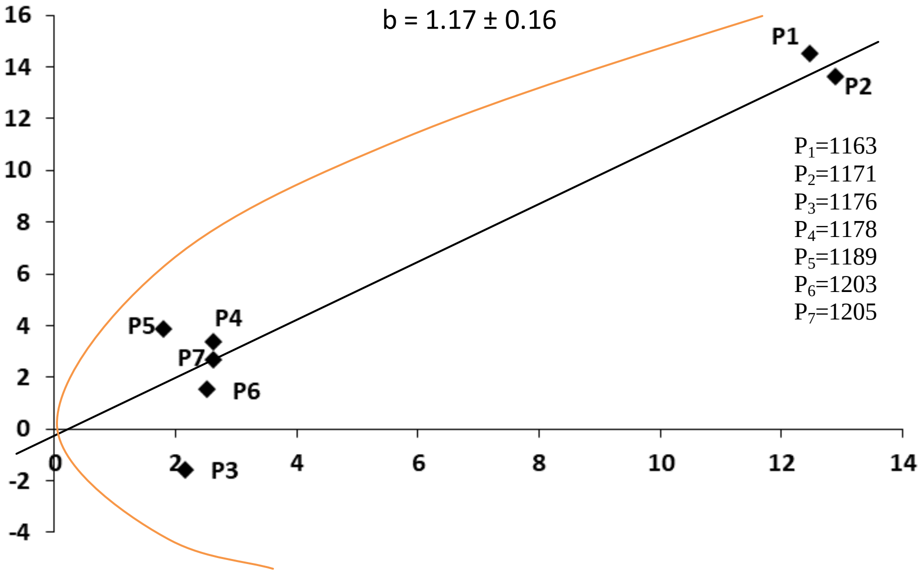

Figure 4.5. Vr-Wr graph for days to 50% flowering initiation

From the Vr-Wr graph, as parental array points were scattered around the regression line that means genetic diversity was present among the parents for the characters. Regression co-efficient was 1.17(>1) which indicated presence of epistatic interaction or presence of non-allelic interaction to express the characters. Regression line intercept below the origin of Wr line representing over-dominancefor days to 50% flowering initiation. Parents p4, p5, p6 and p7 distributed to the nearest of the origin indicate they had maximum number of dominant alleles, whereas parents p1 and p2 were distributed far away from the origin, i.e they had maximum number of recessive alleles. The width of the parabola indicated the diversity of genotypes. And the distribution of parental array points was within the parabola.

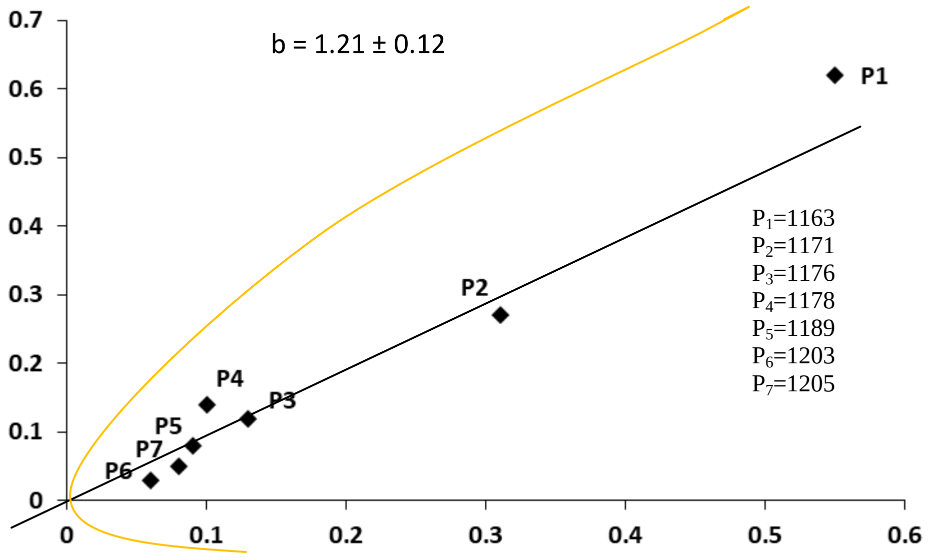

Figure 4.6. Vr-Wr graph for node of first flowering

From the Vr-Wr graph, as parental array points were scattered around the regression line that means genetic diversity was present among the parents for the characters. Regression co-efficient was 1.21(>1) which indicated presence of epistatic interaction or presence of non-allelic interaction to express the characters. Regression line intercept through the origin of Wr line representing complete-dominance for node of first flower. Parents P3, P4, P5, P6 and P7 distributed to the nearest of the origin indicate they had maximum number of dominant alleles, whereas parents P1 was distributed far away from the origin, i.e they had maximum number of recessive alleles. Besides P2 was distributed in the middle from the origin which indicated these parents had equal frequency of dominance and recessive alleles or additive gene. The width of the parabola indicates the diversity of genotypes. And the distribution of parental array points was within the parabola

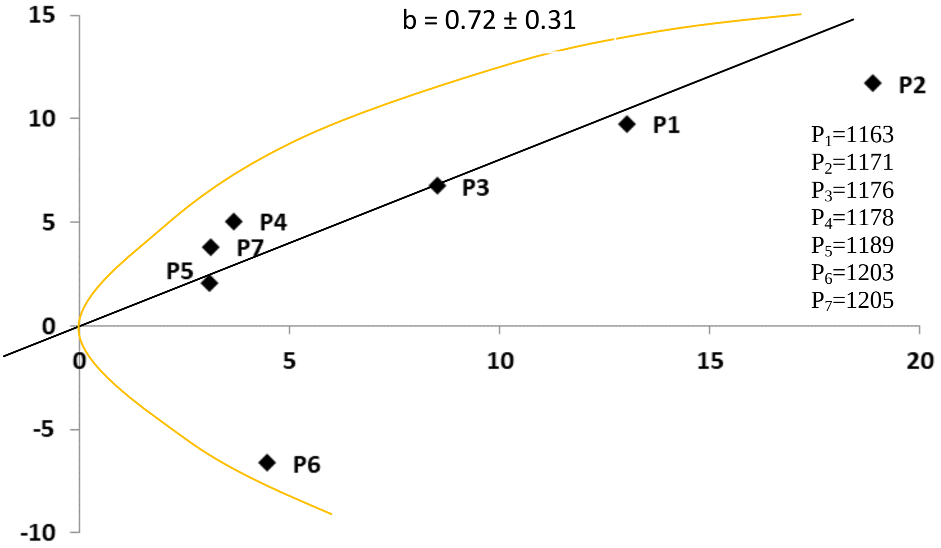

Figure 4.7. Vr-Wr graph for first edible fruit harvesting days

From the Vr-Wr graph, as parental array points were scattered around the regression line that means genetic diversity was present among the parents for the characters. Regression co-efficient is 0.72 (<1) which indicated absence of epistatic interaction or absence of non-allelic interaction to express the characters. Regression line intercept through the origin of Wr line representing complete dominance for first edible fruit harvesting days. Parents p4, p5 and p7 distributed to the nearest of the origin indicated they had maximum number of dominant alleles, whereas parents p1 was distributed far away from the origin, i.e it had maximum number of recessive alleles, besides p3 was distributed in the middle from the origin which indicated this parent had equal frequency of dominance and recessive alleles or additive gene. The width of the parabola indicates the diversity of genotypes. And the distribution of parental array points was within the parabola.

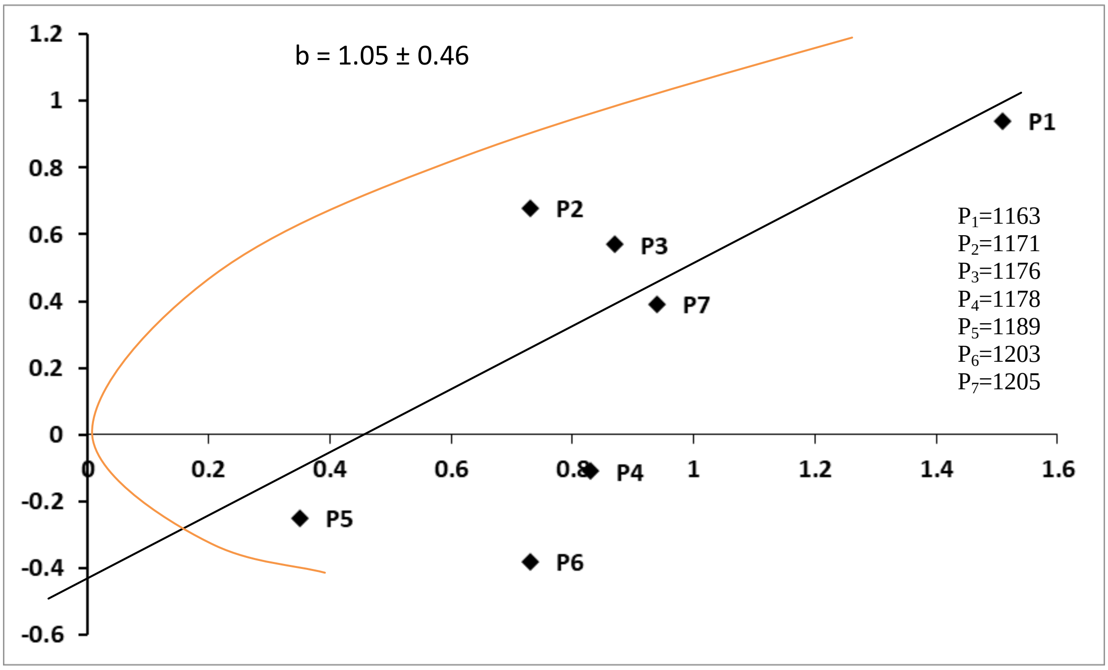

Figure 4.8. Vr-Wr graph for length of fruits

From the Vr-Wr graph, as parental array points were scattered around the regression line that means genetic diversity was present among the parents for the characters. Regression co-efficient is 1.05 (>1) which indicates presence of epistatic interaction or presence of non-allelic interaction to express the characters. Regression line intercept below the origin of Wr line representing over-dominance for length of fruits. Parent's p2, p3 and p7 were distributed in the middle from the origin which indicates this parent had equal frequency of dominance and recessive alleles or additive gene and parentp1 was distributed far away from the origin, i.e it had maximum number of recessive alleles. The width of the parabola indicated the diversity of genotypes. And the distribution of parental array points was within the parabola.

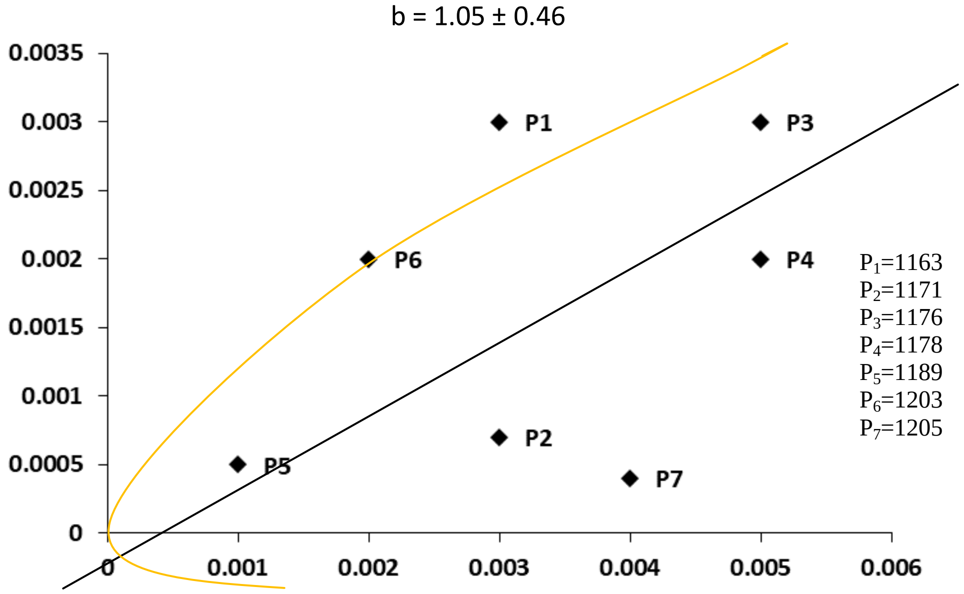

Figure 4.9. Vr-Wr graph for fruit diameter (cm)

From the Vr-Wr graph, as parental array points were scattered around the regression line that means genetic diversity was present among the parents for the characters. Regression co-efficient is 1.05 (>1) which indicated presence of epistatic interaction or presence of non-allelic interaction to express the characters. Regression line intercept below the origin of Wr line representing over-dominance for fruit diameter. Parents p5 distributed to the nearest of the origin indicated it had maximum number of dominant alleles and parents p2 was distributed in the middle from the origin which indicated this parent had equal frequency of dominance and recessive alleles or additive gene and parent p4, p3 were distributed far away from the origin, i.e they had maximum number of recessive alleles. The width of the parabola indicates the diversity of genotypes where p1 was outside the parabola. And the distribution of parental array points was within the parabola.

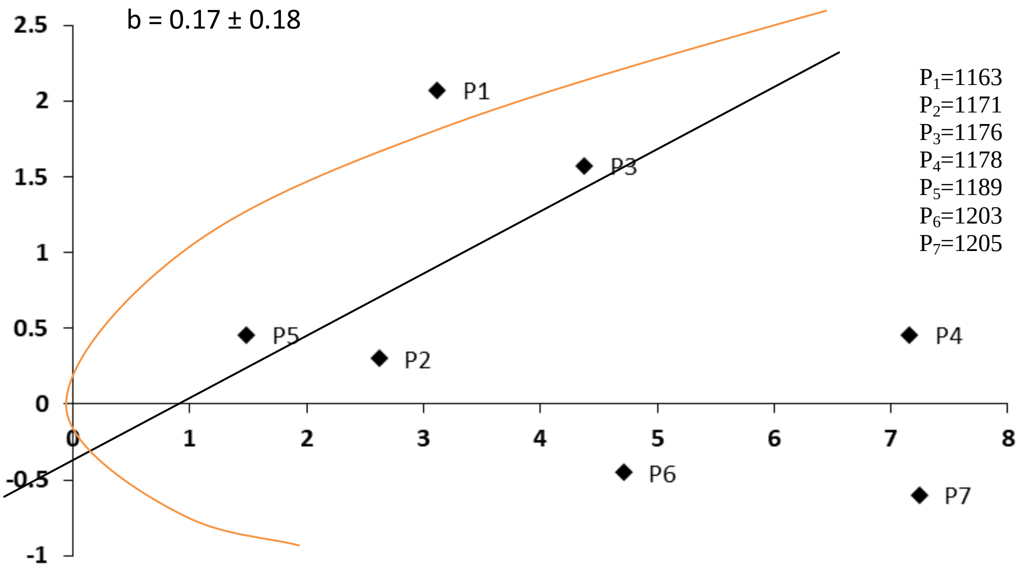

Figure 4.10. Vr-Wr graph for fruit weight (g)

From the Vr-Wr graph, as parental array points were scattered around the regression line that means genetic diversity was present among the parents for the characters. Regression co-efficient is 0.17(<1) which indicated absence of epistatic interaction or absence of non-allelic interaction to express the characters. Regression line intercept below the origin of Wr line over-dominance for fruit weight. Parents p2 and p5 distributed to the nearest of the origin indicate they had maximum number of dominant alleles, whereas parents p7 was distributed far away from the origin, i.e it had maximum number of recessive alleles; besides p1, p3 and p6 were distributed in the middle from the origin which indicated these parents had equal frequency of dominance and recessive alleles or additive gene. The width of the parabola indicates the diversity of genotypes where p1 was outside the parabola. And the distribution of parental array points was within the parabola.

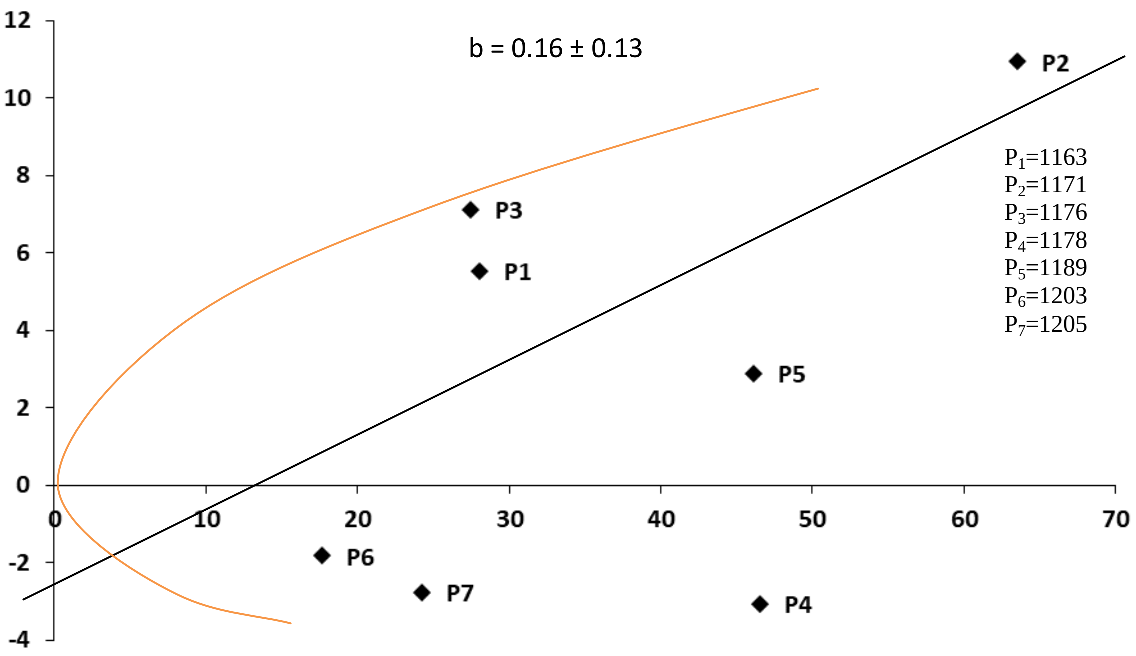

Figure 4.11. Vr-Wr graph for fruits per plant

From the Vr-Wr graph, as parental array points were scattered around the regression line that means genetic diversity was present among the parents for the characters. Regression co-efficient was 0.16 (<1) which indicates absence of epistatic interaction or absence of non-allelic interaction to express the characters. Regression line intercept below the origin of Wr line over-dominance for for fruits per plant. Parents p6 and p7 distributed to the nearest of the origin indicate they had maximum number of dominant alleles, whereas parents p2 was distributed far away from the origin, i.e it had maximum number of recessive alleles; besides p1, p3, p4 and p5 were distributed in the middle from the origin which indicate these parents had equal frequency of dominance and recessive alleles or additive gene. The width of the parabola indicates the diversity of genotypes. And the distribution of parental array points was within the parabola.

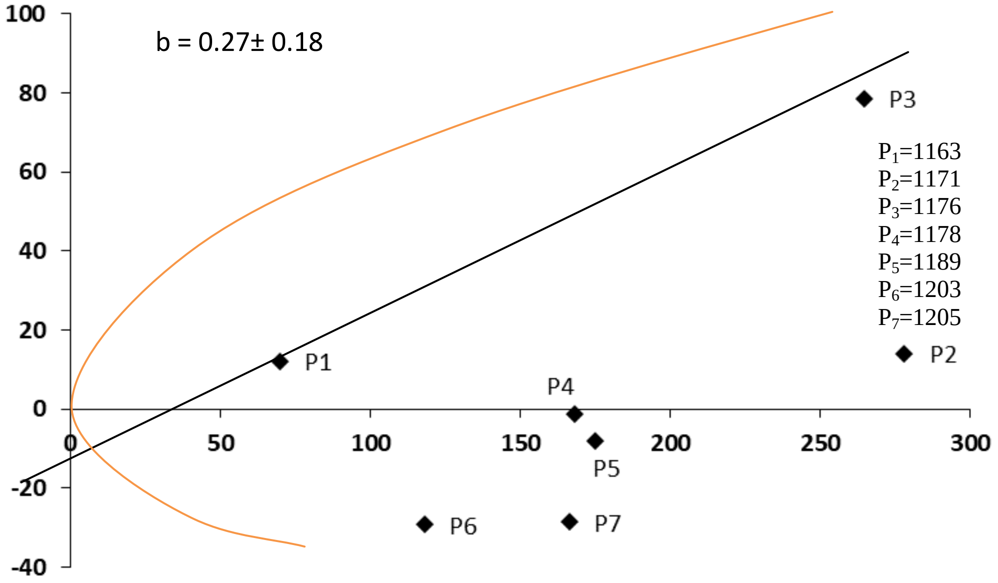

Figure 4.12. Vr-Wr graph for fruit yield per plant

From the Vr-Wr graph, as parental array points were scattered around the regression line that means genetic diversity was present among the parents for the characters. Regression co-efficient is 0.27 (<1) which indicated absence of epistatic interaction or absence of non-allelic interaction to express the characters. Regression line intercept below the origin of Wr line over-dominance for for fruits yield per plant. Parents p1 was distributed to the nearest of the origin indicate it had maximum number of dominant alleles, whereas parents p2 and p3 were distributed far away from the origin, i.e they had maximum number of recessive alleles; besides p2 and p3 were distributed in the middle from the origin which indicate these parents had equal frequency of dominance and recessive alleles or additive gene. The width of the parabola indicates the diversity of genotypes. And the distribution of parental array points was within the parabola.

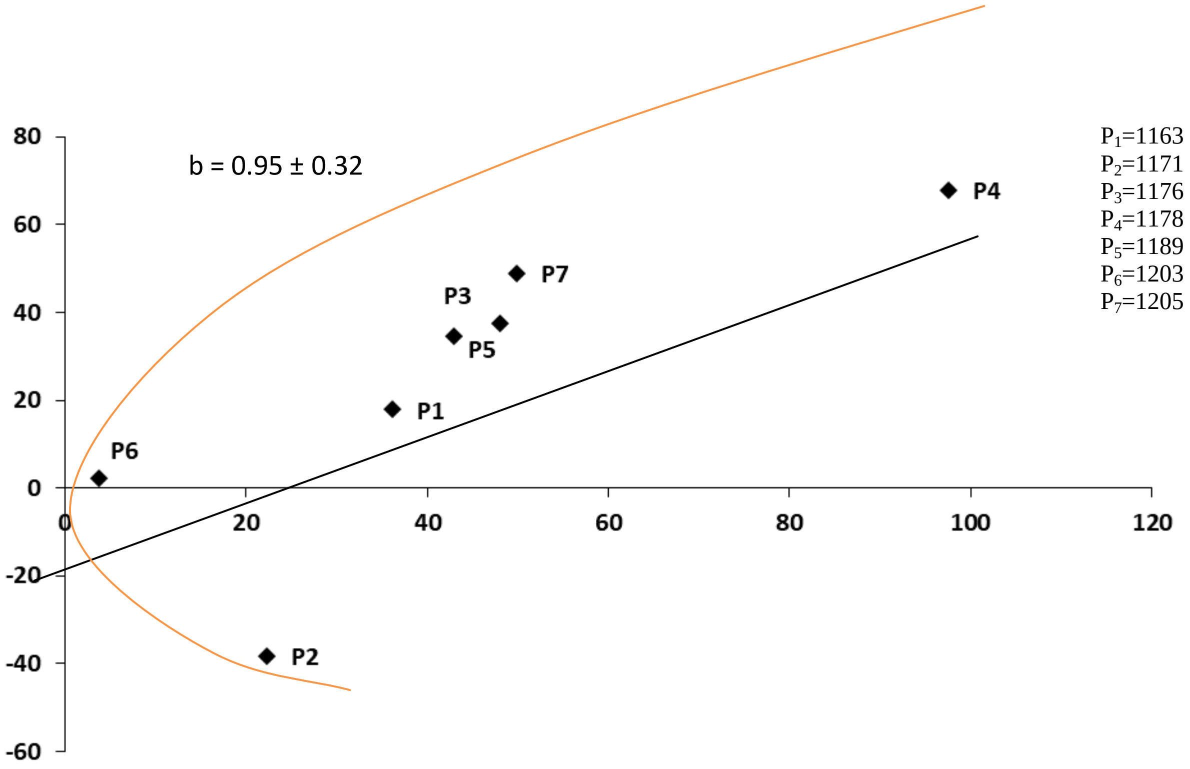

Figure 4.13. Vr-Wr graph for seeds per fruit

From the Vr-Wr graph, as parental array points were scattered around the regression line that meant genetic diversity was present among the parents for the characters. Regression co-efficient was 0.95 (<1) which indicates absence of epistatic interaction or absence of non-allelic interaction to express the characters. Regression line intercept below the origin of Wr line over-dominance for seeds per fruits. Parent p6 was distributed to the nearest of the origin indicate it had maximum number of dominant alleles, whereas parents p4 was distributed far away from the origin, i.e it had the maximum number of recessive alleles; besides p1, p2, p3, p5 and p7 were distributed in the middle from the origin which indicated these parents had equal frequency of dominance and recessive alleles or additive gene. The width of the parabola indicated the diversity of genotypes. And the distribution of parental array points was within the parabola.

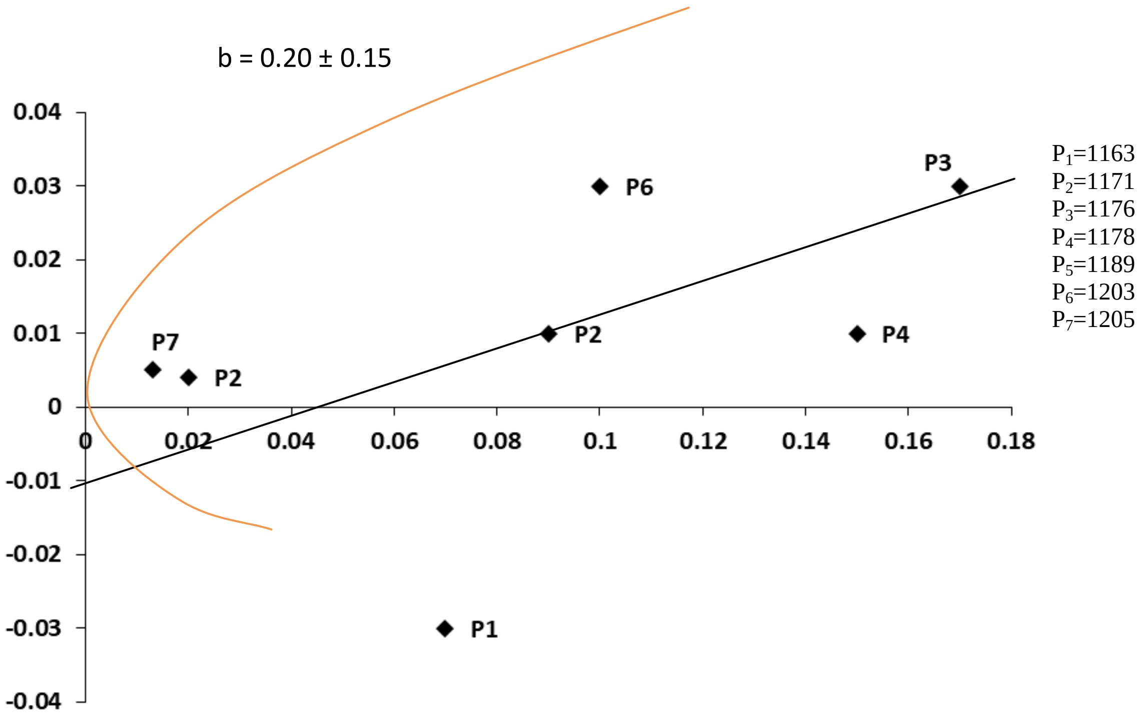

Figure 4.14. Vr-Wr graph for 100 seed weight (g)

From the Vr-Wr graph, as parental array points were scattered around the regression line that meant genetic diversity was present among the parents for the characters. Regression co-efficient was 0.20 (<1) which indicated absence of epistatic interaction or absence of non-allelic interaction to express the characters. Regression line intercept below the origin of Wr line over-dominance for 100 seed weight. Parent p2, p7 were distributed to the nearest of the origin indicated they had maximum number of dominant alleles, whereas parents p3, p4 were distributed far away from the origin, i.e they had maximum number of recessive alleles; besides p1, p2 and p6 were distributed in the middle from the origin which indicated these parents had equal frequency of dominance and recessive alleles or additive gene. The width of the parabola indicates the diversity of genotypes. And the distribution of parental array points was within the parabola.

Table 4.13 Specific combining ability effects for different characters of okra

Sl no	Cross combinations	PH100	LN100	FFI	50FI	NFF	FEFH	Fruit diameter (cm)	Fruit length (cm)	Fruit weight (g)	Fruits per plant	Seeds per fruit	100SW	Fruit yield per plant (g)
1	P1 X P2	-15.53**	-4.03	-0.67	0.80**	0.31**	2.25**	-0.04	0.05	0.28*	-0.97*	4.45**	0.23**	-41.17**
2	P1 X P3	17.11**	-1.90	1.30**	1.98**	0.09	1.51**	0.02	0.38*	1.12**	4.13**	2.99**	0.13	8.92
3	P1 X P4	11.85**	9.34**	0.70	1.06**	0.49**	0.58	0.05*	-0.09	-0.39**	5.99**	4.47**	0.64**	32.91**
4	P1 X P5	9.56**	-4.14	0.78*	0.94**	0.51**	0.18	0.07**	1.58**	1.68**	2.88**	-0.69	-0.20**	116.23**
5	P1 X P6	-18.01**	5.51*	1.30**	1.61**	0.29**	0.9*	0.04	0.86**	1.50**	-1.27**	4.03**	-0.06	-16.77
6	P1 X P7	29.88**	11.52**	3.19**	3.06**	0.52**	4.21**	-0.07**	-0.71**	-1.02**	3.43**	-8.46**	-0.27**	1.61
7	P2 X P3	8.19**	4.43	2.59**	2.83**	0.36**	2.25**	0.08**	0.53**	3.27**	2.25**	3.02**	0.15*	104.11**
8	P2 X P4	1.00	7.67**	-0.001	0.57*	0.09	-0.01	0.05*	-0.09	0.54**	10.41**	10.63**	0.20**	207.87**
9	P2 X P5	47.11**	12.31**	1.74**	1.46**	-0.02	1.25**	0.05**	0.36*	-0.09	10.33**	-6.83**	0.16*	171.73**
10	P2 X P6	31.01**	3.70	3.59**	2.80**	0.63**	4.66**	-0.04*	0.81**	-0.38**	0.58	-2.84**	-0.07	27.95*
11	P2 X P7	-1.57	-12.55**	-1.19**	-0.43	0.19*	-0.38	-0.06**	0.08	-0.21	-0.52	-4.06**	0.22**	-87.23**
12	P3 X P4	7.37*	12.06**	-1.04**	-0.57*	0.001	1.25**	0.05**	0.74**	1.32**	1.97**	0.84	0.19**	53.04**
13	P3 X P5	-8.65**	8.44**	1.04**	0.98**	-0.31**	1.84**	0.02	-0.07	-0.91**	1.96**	-6.05**	0.16*	94.64**
14	P3 X P6	9.25**	2.76	0.44	0.31	0.08	1.58**	0.01	0.66**	-0.80**	3.28**	-1.23	-0.47**	98.84**
15	P3 X P7	1.87	-0.76	-1.89**	-2.24**	0.30**	-0.12	0.06**	1.33**	1.16**	5.71**	7.05**	0.61**	218.74**
16	P4 X P5	-15.44**	-15.71**	-0.89*	-1.94**	-0.57**	-2.42**	-0.06**	-0.26	0.45**	-6.01**	4.30**	0.20**	-104.54**
17	P4 X P6	-30.28**	0.80	-4.04**	-3.61**	-0.45**	-3.01**	-0.05*	-0.57**	3.40**	1.51**	4.38**	-0.26**	86.02**
18	P4 X P7	25.94**	1.62	1.85**	0.83**	-0.23*	0.95*	0.08**	1.25**	4.19**	6.67**	-5.87**	-0.24**	109.65**
19	P5 X P6	21.76**	10.38	0.37	0.28	0.10	1.25**	-0.07**	-0.38*	-0.67**	7.43**	-4.51**	-0.36**	137.26**
20	P5 X P7	-8.21**	0.20	-1.41**	-0.94**	-0.21*	-0.45	0.001	-0.21	-1.77**	2.39**	5.37**	0.12	13.19
21	P6 X P7	-1.18	-4.82	-0.56	0.06	-0.16	-0.71	0.03	0.33	2.51**	-1.16**	0.56	0.13	-38.32
Number of +ve significant cross		11	7	9	12	9	12	8	11	12	15	10	10	13
Number of –ve significant cross		6	2	6	5	5	2	6	4	7	4	7	6	4

Here, PH100= Plant height at 100 days (cm), LN100= Leaf number at 100 days, FFI= First flower initiation, 50FI=50% flower initiation day, NFF=Number of female flower, FEFH= First edible fruit harvesting days, 100SW= 100 seed weight (g). *and ** Significant at 5% and 1% levels, respectively

4.3.3 Specific combining ability (SCA) effects of the crosses

The sca effects signify the role of non-additive gene action in the expression of the characters. It indicates the highly specific combining ability leading to the highest performance of some specific cross combinations that is why it is related to a particular cross. High sca effects may arise not only in crosses involving high combiners but also in those involving low combiners. Thus in practice, some of the low combiners should also be accommodated in hybridization program. The sca effect of 21 crosses in F1 generation for 12 characters studied were presented in table-17. The character wise interpretation of sca effects were given below:

4.3.3.1 Plant height

The effect of sca for plant height obtained in the present study range from OK-17 (P4XP6) = 30.28** to OK-09 (P2XP5) =47.11**. There was a wide range of variation. Among 21 cross combinations 11 crosses showed positive and significant effect and 6 combinations exhibited negative and significant effect which was more desirable, OK-17 (P4XP6) =-30.28**, OK-05(P1XP6) = -18.01**, OK-01(P1XP2) =-15.53** and OK-16 (P4XP5) = -15.44**,respectively. Positive and insignificant observed only two cross combinations and negative insignificant exhibited other two combinations respectively.

4.3.3.2 First flower initiation

Present study revealed that days to first flower initiation ranged from OK-17 (P4XP6) = -4.04** to OK-10 (P2XP6) = 3.59**. The highest negative significant effect observed in P4XP6 combinations (-4.04**) followed by P3XP7 = (-1.89**), P2XP7= (-1.19**), P3XP4= (-1.04**), respectively. From this observation we can identify P3, P4 and P7 as a good combiner for this trait.

4.3.3.3 Days to 50% flowering

Among 21 cross combinations significant positive effect showed in 12 combinations and significant negative effect showed in 5 combinations. The range of SCA effect on this trait was -3.61** for (P4XP6) to 3.06** for (P1XP7). The highest negative significant effect -3.61** for (P4XP6) which was desirable for this trait and followed by -2.24** (P3XP7), -1.94** for (P4XP5), respectively. Negative but insignificant effect showed only one combinations -0.43 (P2XP7) and the rest of three showed positive insignificant effect.

4.3.3.4 Node of 1st flowering

The range of first flowering node was from -0.57** to 0.001. The expected highest value observed for this character in OK-16 (P4XP5) = -0.57** followed by OK-17 (P4XP6) = -0.45**, OK-18 (P4XP7) = -0.23* and OK-20 (P5xP7) = for -0.21*, respectively. From this observation P4 and P7 exist as good combiners.

4.3.3.5 Days to first edible fruit harvest

The present study revealed the range of days to first edible fruit harvest varied from -3.01** to 4.66** among 21 cross combinations. The highest negative significant effect observed in OK-17 (P4 X P6) = -3.01** and followed by OK-16 (P4 X P5) = -2.42** which indicated P4, P5 and P6 were found SCA effect and they were good combiner. Negative insignificant effect showed other five cross combinations, positive and significant effect observed 12 cross combinations and rest two combinations showed positive insignificant effect on this study.

4.3.3.6 Fruit diameter

For fruit diameter, positive and significant effect showed only in 8 cross combinations. The highest positive and significant effect observed in OK-7 (P2 X P3) = 0.08** and OK-18 (P4 X P7) = 0.08**folled by OK-4 (P1 X P5) = 0.07**, OK-15 (P3 X P7) =0.06** and OK-9 (P2 X P5) = 0.05**and OK-12 (P3 X P4) =0.05**, OK-3 (P1 X P4) = 0.05** and OK-8 (P2 X P4) = 0.05** respectively. Positive and insignificant effect observed in 6 combinations and also 6 combinations showed negative and significant effect and only one cross combinations express negative insignificant result.

4.3.3.7 Fruit length

Present investigation revealed the among 21 cross combinations significant and positive effect were showed in 10 combinations. The range value was 1.58** to -0.09. The highest positive and significant effect observed in OK-4 (P1 X P5) =1.58** followed by OK-15 (P3 X P7) = 1.33**, OK-5 (P1 X P6) = 0.86**, OK-10 (P2 X P6) = 0.81** and OK-12 (P3 X P4) = 0.74**, respectively. Negative and significant effect was observed in three cross combinations viz. highest negative significant effect OK-6 (P1 X P7) = -

0.71** followed by OK-16 (P4 X P5) = -0.57** and OK-19 (P5 X P6) = -0.38** respectively. Rest three was positive insignificant and five were negative insignificant.

4.3.3.8 Fruit weight

Among 21 cross combinations positive and significant effect was obtained in 8 cross combinations and negative significant effect was observed in only 2 cross combinations and the rest 7 were negative insignificant and 4 were positive insignificant effect. The highest positive significant effect observed in OK-18 (P4 X P7) = 2.57** followed by OK-04(P1 X P5) = 1.99**, OK-07 (P2 X P3) = 1.85**, OK-15 (P3 X P7) = 1.86** and OK-12 (P3 X P4) = 1.52** respectively. The negative and significant SCA estimates in 2 cross combinations viz. OK-06 (P1 X P7) = -2.93** and OK-19 (P5 X P6) = -1.32** hence they were considered as poor combiner for fruit weight.

4.3.3.9 Fruits per plant

The range for fruits per plant exhibited in the present study was 4.87** to -4.19**. The highest positive and significant effect observed in OK-08 (P2 X P4) = 4.87**, and followed by OK-19 (P5 X P6) = 4.39**, OK-15 (P3 X P7) 3.24** and OK-03 (P1 X P4) =3.02* respectively. Among the 21 cross combinations positive and significant effect was observed only in 4 cross combinations. Negative and significant found 2 cross combinations. Positive and negative insignificant combination was observed in 8+7 crosses, respectively.

4.3.3.10 Seeds per fruit

Present study revealed that most combinations exerted positive and significant effect on this trait. Among 21 cross combinations positive and significant effect was observed in 10 combinations, negative and significant found in 7 combinations and negative and positive insignificant observed in 2 and 2, respectively. The highest positive and significant effect observed in OK-08 (P2 X P4) = 10.63** followed by OK-15 (P3 X P7) = 7.05**, OK-20 (P5XP7) = 5.37**, OK-03 (P1 X P4) = 4.47 and OK-1 (P1 X P2) = 4.45** respectively. The highest negative significant effect found in OK-06 (P1 X P7) = -8.46** followed by OK-09 (P2 X P5) = -6.83**, OK-13 (P3 X P5) = -6.05**, OK-18 (P4 X P7) = -5.87** and OK-19 (P5 X P6) = -4.51** respectively which were indicated as poor specific combiners.

4.3.3.11 100 seed weight

In 100 seed weight, positive and significant effect in 10 cross combinations and negative significant in 6 cross combinations was obsedved. Positive insignificant revealed 3 and negative insignificant observed in 2 cross combinations. The highest positive significant effect was observed in OK-03 (P1 X P4) = 0.64** followed by OK-15 (P3 X P7) = 0.61**, OK-1 (P1 X P2) = 0.23** and OK-11 (P2 X P7) = 0.22**, respectively. The highest negative significant effect was observed in OK-14 (P3 X P6) = -0.47** followed by OK-19 (P5 X P6) = -0.36**, OK-06 (P1 X P7) = -0.27** and OK-17 (P4 X P6) = -0.26** respectively. These crosses showed as a poor specific combiner.

4.3.3.12 Fruit yield per plant

Among 21 cross combinations, present study revealed positive and significant effect in 13 cross combinations. The highest positive significant effect was observed in OK-15 (P3 X P7) =218.74** followed by OK-08 (P2 X P4) =207.87**, OK-18 (P4 X P7) = 122.25**, Ok-09 (P2 x P5) =171.73**, Ok-19 (P5 X P6) =137.26** and Ok-04 (P1 X P5) =116.23** respectively. Negative significant performance was observed only in three cross combinations that were Ok-16 (P4 X P5) = -104.54**, Ok-11 (P2 X P7) = -87.23** and Ok-01 (P1 X P2) = -41.17**. The negative insignificant effect observed in two cross combinations and positive insignificant found in three combinations.

4.3.4 Estimation of heterosis and gene action in okra genotypes

Heterosis may be defined as the amount by which the mean of an F1 family exceeds its better parent. Since the F1 and parental generation means may be specified in terms of genetic parameters, the expected magnitude of heterosis can be similarly specified. Before doing so, however, we must have defined what we mean by the better parent and by the F1 exceeding it. We have so far adopted the convention that P1 corresponds to the parent with the greater mean value and P2 to the parent with the smaller mean value, but for the present purpose, either P1 or P2 may be the better parent according to the character under consideration. for example, heterosis for a character such as yield usually implies that the F1 has a greater yield than its greater yielding parent (F1>P1). On the other hand, heterosis for characters such as earliness or time taken to reach a particular stage in development, usually implies that the F1 has a lower value than its lower parent (F1<P2). Although the reverse will be the case if the same characters are measured in terms of rates of development. A general specification of heterosis must, therefore, be

able to accommodate heterosis both in the positive (F1>P1) and in the negative (F1<P2) directions.

4.3.4.1 Plant height

The present study revealed the value of 21 F1 crosses and heterosis over better parent (BP) and mid parent (MP) and standard two parents (SP) are presented in Table-4.14. The data for the plant height showed that the ranged from P2 (1171) X P (1185) = 94.18** to P4 (1178) X P6 (1203) = -31.81** respectively for average heterosis. P2 (1171) XP5 (1189) =38.19** to P4 (1178) XP6 (1203) = -34.09** for heterobeltiosis and P2 (1171) XP5 (1189) =30.99** to P4 (11780) XP6 (1203) = -41.26** for standard heterosis for check-2 respectively. The positive and significant value observed for average heterosis was in 18 cross combinations which was most deserved for this character and negative significant value observed only one cross combinations. Heterobeltiosis observed in 11 cross combinations positive and significant and negative significant value observed in 3 cross combinations. Standard heterosis observed in check-1, 13 cross combinations positive significant and 6 cross combinations showed negative significant value. For check-2 standard heterosis observed in 11 cross combinations positive significant and 6 parents showed negative significant value, respectively.

4.3.4.2 Leaf number of 100 days

Present study revealed for leave number, the range of parents from 49.67 to 75.47 and with a mean of 59.33 and the range for crossing obtained 53.87 to 87.87 with a mean of 68.48 for this character at 100 days. The positive and significant value observed for number of leaf in 13 cross combinations and there was no significant negative value found in this study. The range value for average parent showed 69.64 to -5.02. The highest positive and significant value observed in P3 (1176) XP4 (1178) =69.64**, followed by P1 (1163) XP4 (1178) =55.47**, P2 (1171) XP4 (1178) =39.64**and P5 (1189) XP6 (1203) =38.81** respectively. The heterobeltiosis observed positive and significant in 7 crosses and negative significant in 7 crosses. The range of heterobeltiosis from 64.81 to -18.99 respectively. The highest positive and significant value observed in P3 (1176) XP4 (1178) =64.81** followed by P1 (1163) X P4 (1178) = 52.91**, P5 (1189) X P6 (1203) = 31.93 and P2 (1171) X P4 (1178) = 31.11** respectively. The negative and significant value observed in P3 (1176) X P7 (1205) = -18.99** followed

Table 4.14 Heterosis over mid parent, better parent, Check1 and Check2 for plant height at hundred days and leaves number at 100 days

Sl no	Cross combinations	Plant height at hundred days (PH100)		Leaves number at 100 days (LN100)					
		MP	BP	Check1	Check2	MP	BP	Check1	Check2
1	P1 (1163) X P2 (1171)	21.30 **	2.50	-38.53**	-40.39**	11.06**	2.67 ns	24.86**	45.17**
2	P1 (1163) XP3 (1176)	28.61 **	0.28	7.50**	4.24	25.38**	23.82**	27.84**	48.63**
3	P1 (1163) X P4 (1178)	14.20 **	-2.97	-16.79**	-19.31**	55.47**	52.91**	63.24**	89.79**
4	P1 (1163) XP5 (1189)	29.78 **	4.70	2.35	-0.75	-2.88 ns	-10.22**	9.19	26.94**
5	P1 (1163) XP6 (1203)	-1.74	-18.81 **	-25.39**	-27.65**	20.70**	6.51ns	43.78**	67.16**
6	P1 (1163) XP7 (1205)	35.68 **	6.68 **	11.74**	8.36**	9.29**	-8.48**	40.00**	62.77**
7	P2 (1171) XP3 (1176)	43.90 **	-0.28	6.90*	3.66	5.53 ns	-3.56 ns	17.30**	36.37**
8	P2 (1171)X P4 (1178)	29.72 **	-3.85	-17.54**	-20.04**	39.64**	31.11**	59.46**	85.39**
9	P2 (1171) X P5 (1189)	94.18 **	38.19 **	35.08**	30.99**	14.78**	14.78**	39.59**	62.29**
10	P2 (1171) X P6 (1203)	70.98 **	23.98 **	13.94**	10.49**	10.27**	4.80 ns	41.49**	64.49**
11	P2 (1171)X P7 (1205)	30.30 **	9.11 **	-4.80	-7.68**	-2.85 ns	-12.81**	33.38**	55.07**
12	P3 (1176) XP4 (1178)	18.10 **	6.29 **	13.94**	10.49**	69.64**	64.81**	75.95**	104.56**
13	P3 (1176)X P5 (1189)	14.07 **	9.04 **	16.89**	13.35**	13.92**	4.11 ns	26.62**	47.21**

14	P3 (1176) X P6 (1203)	22.49 **	13.75 **	21.94**	18.25**	34.52**	17.42**	58.51**	84.29**
15	P3 (1176)X P7 (1205)	20.02 **	18.65 **	27.19**	23.33**	-2.29 ns	-18.99**	23.92**	44.07**
16	P4 (1178) XP5 (1189)	2.51	-3.78 **	-5.95*	-8.80**	8.05**	1.44 ns	23.38**	43.44**
17	P4 (1178) XP6 (1203)	-31.81 **	-34.09 **	-39.43**	-41.26**	4.64 ns	-6.31 ns	26.49**	47.05**
18	P4 (1178) XP7 (1205)	26.13 **	14.69 **	20.14**	16.50**	0.83 ns	-14.40**	30.95**	52.24**
19	P5 (1189) X P6 (1203)	19.79 **	16.21 **	13.59**	10.15**	38.81**	31.93**	78.11*	107.07**
20	P5 (1189) XP7 (1205)	11.80 **	8.06**	13.19**	9.76**	-2.26 ns	-12.28**	34.19**	56.01**
21	P6 (1203) XP7 (1205)	10.39 **	3.63	8.55**	5.26*	-5.02 ns	-10.60**	36.76**	58.99**
Number of +ve significant crosses		18	11	13	11	13	7	**20**	**21**
Number of -ve significant crosses		1	3	6	6	0	7	**0**	**0**
Range		94.18 to -31.81	38.19 to -34.09	35.08 to -39.43	30.99 to -41.26	69.64 to -5.02	64.81 to -18.99	78.11 to 9.19	107.07 to 43.44

*and ** Significant at 5% and 1% levels, respectively

by P4 (1178) X P7 (1205) = -14.40**, P4 (1178) X P7 (1205) = -14.40**, P2 (1171) X P7 (1205) = -12.81**, and P5 (1189) X P7 (1205) = -12.28** respectively. For standard heterosis present study revealed all combinations had positive and significant value except P1 (1163) X P5 (1189) = 9.19 for check-1 and for check-2 there was no negative or insignificant value. The range for check-1 78.11 to 9.19 and for check-2 107.07 to 43.44, respectively.

4.3.4.3 First flower initiation

The mean value obtained for this trait 52.86 for parent and 54.22 for crosses (Appendix-IV and V) . The range value obtained for parent 45.67 to 57.00 and 49.33 to 58.33 for cross combinations respectively. Present study revealed for this trait out of 21 crosses 10 crosses exhibited significant positive heterosis over mid parent and there is no positive significant cross over better parent. The highest desirable heterosis was recorded in the cross P2 (1171) X P6 (1203) = 13.64** followed by P2 (1171) X P3 (1176) = 9.46** and P1 (1163) X P7 (1205) = 9.32** respectively. Out of 21 crosses none of the crosses exhibited significantly positive heterosis over check-1 and check-2 i.e. green finger (F1) and BARI Dharosh-1 (OP).

4.3.4.4 50% flower initiation

Present study exhibited the range for 50% flower initiation was 48.00 to 59.67 for parent and mean value revealed 55.48 (Appendix-IV and V). And for crosses 53.67 to 59.67 and mean value observed 57.38 respectively. The range of average parent better parent and standard heterosis observed from 13.46 to -6.74, 9.52 to -4.55, -5.29 to -14.81 and -6.28 to -15.71 respectively. The number of positive significant crosses for mid parent 14 and better parent 3 whereas negative significant observed in 3 for mid parent, 10 for better parent and 21 for both standard heterosis, check-1 and check-2, respectively.

Table 4.15 Heterosis over mid parent, better parent, check1 and check2 for days to first female flower initiation and days to 50% flower initiation

Sl no	Cross combinations	First female flower initiation (FFI)				Days to 50% flower initiation (50FI)			
		MP	BP	Check1	Check2	MP	BP	Check1	Check2
1	P1 (1163) X P2 (1171)	5.34**	2.78	-13.45**	-15.43**	10.65**	9.52**	-14.81**	-15.71**
2	P1 (1163) X P3 (1176)	6.93**	1.89	-5.26**	-7.43**	9.84**	2.98**	-8.47**	-9.42**
3	P1 (1163) X P4 (1178)	1.59	-6.43**	-6.43**	-8.57**	4.94**	-3.95**	-10.05**	-10.99**
4	P1 (1163) X P5 (1189)	5.57**	0.00	-5.85**	-8.00**	6.54**	-1.72 ns	-9.52**	-10.47**
5	P1 (1163) X P6 (1203)	6.03**	-2.34	-2.34 ns	-4.57**	6.13**	-3.35**	-8.47**	-9.42**
6	P1 (1163) X P7 (1205)	9.32**	1.80	-0.58 ns	-2.86ns	10.84**	1.70 ns	-5.29**	-6.28**
7	P2 (1171) X P3 (1176)	9.46**	1.89	-5.26**	-7.43**	13.46**	5.36**	-6.35**	-7.33**
8	P2 (1171) X P4 (1178)	-0.00	-9.94**	-9.94**	-12.00**	3.43**	-6.21**	-12.17**	-13.09**
9	P2 (1171) X P5 (1189)	7.38**	-0.62	-6.43**	-8.57**	5.03**	-4.02**	-11.64**	-12.57**
10	P2 (1171) X P6 (1203)	13.64**	2.34	2.34 ns	0.00ns	7.74**	-2.79**	-7.94**	-8.90**
11	P2 (1171) X P7 (1205)	6.58**	-2.99	-2.26**	-7.43**	5.00**	-4.55**	-11.11**	-12.04**
12	P3 (1176) X P4 (1178)	-3.64*	-7.02**	-7.02**	-9.14**	-1.45ns	-3.95**	-10.05**	-10.99**
13	P3 (1176) X P5 (1189)	3.75*	3.11	-2.92ns	-5.14**	3.51**	1.72 ns	-6.35**	-7.33**
14	P3 (1176) X P6 (1203)	1.82	-1.75	-1.75	-4.00*	2.59**	-0.56 ns	-5.82**	-6.81**
15	P3 (1176) X P7 (1205)	-2.45	-4.79*	-7.02**	-9.14**	-2.33**	-4.55**	-11.11**	-12.04**
16	P4 (1178) X P5 (1189)	-3.61*	-6.43**	-6.43**	-8.57**	-3.70**	-4.52**	-10.05**	-11.52**

17	P4 (1178) X P6 (1203)	-9.36**	-9.36**	-9.36**	-11.43**	-6.74**	-7.26 **	-12.17**	-13.09**
18	P4 (1178) X P7 (1205)	0.59	-0.58	-0.58 ns	-2.86ns	0.85**	0.56 ns	-5.82**	-6.81**
19	P5 (1189) X P6 (1203)	1.81	-1.17	-1.17 ns	-3.43*	0.85ns	-0.56 ns	-5.82**	-6.81**
20	P5 (1189) X P7 (1205)	-1.83	-3.59	-5.85**	-8.00**	0.85ns	-1.70 ns	-8.47**	-9.42**
21	P6 (1203) X P7 (1205)	-0.59	-1.75	-1.75 ns	-4.00*	-1.14ns	0.00 ns	-5.29**	-6.28**
Number of +ve significant crosses		10				14	3		
Number of -ve significant crosses		3	6	13	17	3	10	21	21
Range		**13.64to -9.36**	**3.115 to-9.94**	**-13.45 to 2.34**	**-15.43 to 0.00**	**13.46 to -6.74**	**9.52 to -4.55**	**-5.29 to -14.81**	**-6.28 to -15.71**

*and ** Significant at 5% and 1% levels, respectively

Table 4.16 Heterosis over mid parent, better parent, check1 and check2 for days to NFF and FEFH

Sl no	Cross combinations	Number of female flower (NFF)				First edible fruit harvesting days (FEFH)			
		MP	BP	Check1	Check2	MP	BP	Check1	Check2
1	P1 (1163) X P2 (1171)	17.65**	11.11**	6.38**	-0.79ns	15.46**	12.96**	-8.96**	-10.29**
2	P1 (1163) X P3 (1176)	11.01**	-0.79ns	7.23**	0.00 ns	12.27**	11.59**	-8.96**	-10.29**
3	P1 (1163) X P4 (1178)	8.04**	-8.07**	11.49**	3.97 ns	3.95**	-4.17**	-8.46**	-9.80**
4	P1 (1163) X P5 (1189)	10.13**	-4.74**	11.06**	3.57 ns	5.17**	-1.61ns	-8.96**	-10.29**
5	P1 (1163) X P6 (1203)	12.66**	0.00ns	9.79**	2.38 ns	10.09**	3.24*	-4.98**	-6.37**
6	P1 (1163) X P7 (1205)	13.48**	0.38ns	11.06**	3.57 ns	11.43**	3.72**	-2.99**	-4.41**
7	P2 (1171) X P3 (1176)	11.06**	4.72*	13.19**	5.56 ns	15.36**	12.20**	-8.46**	-9.80**
8	P2 (1171) X P4 (1178)	1.57ns	-9.12**	10.21**	2.78 ns	3.17**	-6.77**	-10.95**	-12.25**
9	P2 (1171) X P5 (1189)	1.80ns	-7.30**	8.09**	0.79 ns	7.33**	-1.61ns	-8.96**	-10.29**
10	P2 (1171) X P6 (1203)	12.63**	5.43**	15.74**	7.94**	17.06**	7.57**	-1.00ns	-2.45**
11	P2 (1171) X P7 (1205)	12.99**	5.38**	16.60**	8.73**	5.54**	-3.72**	-9.95**	-11.27**
12	P3 (1176) X P4 (1178)	-0.56ns	-5.96**	14.04**	6.35**	4.49**	-3.13*	-7.46**	-8.82**
13	P3 (1176) X P5 (1189)	-3.79*	-7.30**	8.09**	0.79 ns	7.43**	1.08ns	-6.47**	-7.84**
14	P3 (1176) X P6 (1203)	4.69**	3.88**	14.04**	6.35**	9.46**	3.24*	-4.98**	-6.37**
15	P3 (1176) X P7 (1205)	9.73**	8.46**	20.00**	11.90 ns	3.41**	-3.19*	-9.45**	-10.78**
16	P4 (1178) X P5 (1189)	-8.05**	-9.82**	9.36**	1.98 ns	-4.23**	-5.73**	-9.95**	-11.27**
17	P4 (1178) X P6 (1203)	-4.60**	-9.12**	10.21**	2.78 ns	-3.98**	-5.73**	-9.95**	-11.27**

18	P4 (1178) X P7 (1205)	-3.85*	-8.07**	11.49**	3.97 ns	2.11**	1.04ns	-3.48**	-4.90**
19	P5 (1189) X P6 (1203)	3.76*	0.73ns	17.45**	9.52**	6.20**	5.91**	-1.99ns	-3.43**
20	P5 (1189) X P7 (1205)	-2.62ns	-5.11**	10.64**	3.17 ns	-0.00**	-0.53ns	-6.97**	-8.33**
21	P6 (1203) X P7 (1205)	1.93ns	1.54ns	12.34**	4.76*	0.80**	0.00ns	-6.47**	-7.84**
Number of +ve significant crosses		12	6	21	6	17	8	0	0
Number of -ve significant crosses		4	10	0	0	3	7	19	21
Range		17.65 to -8.05	11.11 to -9.82	20.00 to 6.38	1190 to -0.79	17.06 to -0.00	12.96 to -0.53	-10.95 to -2.99	-12.25 to -2.45

*and ** Significant at 5% and 1% levels, respectively

Table 4.17 Heterosis over mid parent, better parent, check-1, check-2 for length and diameter

Fruit length						**Fruit diameter**			
Sl no	**Cross combinations**	MP	BP	Check1	Check2	MP	BP	Check1	Check2
1	P1 (1163) X P2 (1171)	8.32**	6.38**	16.00**	25.76**	1.92ns	1.66ns	3.03ns	4.62ns
2	P1 (1163) X P3 (1176)	13.54**	11.70**	21.37**	31.59**	4.96*	4.17ns	5.05ns	6.67**
3	P1 (1163) X P4 (1178)	4.20ns	-2.41ns	17.49**	27.38**	6.80**	6.18*	7.07**	8.72**
4	P1 (1163) X P5 (1189)	19.06**	8.70**	38.36**	50.00**	4.26ns	0.62ns	9.09**	10.77**
5	P1 (1163) X P6 (1203)	13.90**	6.19**	29.13**	40.00**	1.68ns	-2.45ns	7.07**	8.72**
6	P1 (1163) X P7 (1205)	3.07ns	-0.32ns	12.18**	21.62**	1.70ns	-1.31*	5.72**	7.35**
7	P2 (1171) X P3 (1176)	10.02**	9.83**	19.76**	29.84**	7.38**	-1.26ns	7.74**	9.40**
8	P2 (1171) X P4 (1178)	10.12**	4.93ns	26.33**	36.96**	6.53**	6.31*	7.07**	8.40**
9	P2 (1171) X P5 (1189)	10.50**	2.58ns	30.57**	41.55**	3.37ns	5.65*	8.42**	8.72**
10	P2 (1171) X P6 (1203)	11.92**	6.14**	29.07**	39.94**	-2.39ns	0.00ns	3.03ns	10.09**
11	P2 (1171) X P7 (1205)	8.90**	7.21**	20.66**	30.81**	-1.78ns	-6.13*	2.36ns	4.62ns
12	P3 (1176) X P4 (1178)	15.83**	10.19ns	32.66**	43.82**	9.31**	-4.40ns	8.75**	3.93ns
13	P3 (1176) X P5 (1189)	10.48**	2.39ns	30.33**	41.29**	4.05ns	9.12**	8.08**	10.43**
14	P3 (1176) X P6 (1203)	10.76**	4.86**	27.52**	38.25**	2.42ns	-0.31ns	7.07**	9.74**
15	P3 (1176) X P7 (1205)	17.25**	15.23**	29.67**	40.58**	6.36**	-2.45ns	9.76**	8.72**

16	P4 (1178) X P5 (1189)	5.19**	2.35ns	30.27**	41.23**	0.97ns	2.52ns	5.05ns	11.45**
17	P4 (1178) X P6 (1203)	-8.84**	-9.30**	10.30**	19.58**	1.61ns	-3.11ns	6.40**	6.67**
18	P4 (1178) X P7 (1205)	11.65**	8.01**	30.03**	40.97**	8.14**	4.40ns	11.78**	8.03**
19	P5 (1189) X P6 (1203)	1.89ns	-0.38ns	26.81**	37.48**	-4.01ns	-4.60ns	4.75**	13.50**
20	P5 (1189) X P7 (1205)	0.75ns	-5.09**	20.81**	30.97**	0.94ns	0.31ns	9.43**	6.32**
21	P6 (1203) X P7 (1205)	14.46**	10.19**	34.00**	45.28**	0.93ns	-0.31ns	0.00ns	10.43**
	Number of +ve significant crosses	16	11	21	21	7	4	15	18
	Number of –ve significant crosses	1	2	0	0	0	2	0	0
	Range	19.06 to -8.84	15.23 to -9.30	38.36 to 10.30	50.00 to 19.58	9.31 to -4.01	9.12 to -6.13	11.78 to 0.00	13.50 to 3.93

*and ** Significant at 5% and 1% levels, respectively

4.3.4.5 Node of first flowering (NFF)

Present study revealed the range of first flowering node from 6.67 to 9.50 for parent and 8.33 to 9.40 for crosses respectively (Appendix-IV and V). The mean value observed for parent 8.36 and 8.76 for crosses. The ranges of heterosis for mid parent, better parent and standard heterosis were 17.65** to -8.05**, 11.11**to -9.82** and 20.00** to 6.38** (F1) and 11.90 to -0.79 respectively (Table 4.16). 12 crosses showed positive and significant and 4 parent showed negative significant effect for mid parent where 6 and 10 crosses showed positive and negative significant effect for better parent heterosis. Standard heterosis showed 21 crosses positive significant for check-1 and 6 crosses for check-2 but there was no negative significant effect.

4.3.4.6 Days to first edible fruit harvest

Present experiment showed for this character the range of parental line and crosses were 51.67 to 64.00 and 59.67 to 66.33 respectively. The mean value obtained for parents and crosses were 58.67 and 62.22 respectively (Appendix-IV and V). The significant positive heterosis obtained for mid parent, better parent and standard were 17, 8, and 0 respectively and number of negative significant observed 3, 7, 19 and 21 crosses respectively. The range of heterosis for mid parent, better parent and standard revealed for this character were 17.06 to -0.00, 12.96 to -0.53, -10.95 to -1.00 and -12.25 to -2.45 respectively. The highest positive and significant value recorded for mid parent P2 (1171) X P6 (1203) = 17.06**, followed by P1 (1163) X P2 (1171) = 15.46**, P2 (1171) X P3 (1176) = 15.36** and P1 (1163) X P3 (1176) = 12.27** respectively. The highest positive significant value for better parent P1 (1163) X P2 (1171) = 12.96** followed by P2 (1171) X P3 (1176) = 12.20** and P1 (1163) X P3 (1176) = 11.59** respectively. The standard heterosis for check-1 and check-2 revealed negative significant value in 19 and 21 cross combinations respectively. The range value obtained -10.95** to -2.99** for check-1 in significant level and -12.25** to -2.45** for check-2 respectively (Table 4.16).

4.3.4.7 Fruit length

The investigation revealed the range for length 11.74 to 14.21 for parent and 12.32 to 15.45 for crosses and the mean value obtained for parent 12.84 and 14.00 for crosses respectively (Appendix-IV and V). The heterosis observed for over mid parent, better parent and checks were depicted 16,11,21 and 21 positive significant respectively. The range of heterosis showed over mid parent, better parent, check-1 and check-2 were 19.06 to -8.84, 15.23 to -9.30, 38.36 to 10.30 and 50.00 to 19.58 respectively (Table-4.17).

4.3.4.8 Fruit diameter

Fruit diameter ranged from 1.97 to 2.17. Parent P6 (1203) had highest which was followed by P5 (1189) = 2.15 and lowest value observed in P3 (1176) and P4 (1178) = 1.97 respectively. Among the hybrids, fruit diameter ranged from 2.03 in P2 (1171) X P7 (1178) to 2.21 in P4 (1178) X P7 (1205) (Table-4.17). Total 7 cross combinations showed positive heterosis over mid parent for this trait. It was ranged from 9.31** in P3 (1176) X P4 (1178) to 4.96* in P1 (1163) X P3 (1176). The negative estimate of heterosis varied from -1.78 in P2 (1171) X P7 (1205) to -4.01. P5 (1189) X P6 (1203) over mid parent. For heterobeltiosis, it was ranged from 5.65 in P2 (1171) X P5 (1189) to 9.12 in P3 (1176) X P5 (1189) for positive significant effect and -1.31 in P1 (1163) X P7 (1205) to -6.13 in P2 (1171) X P7 (1205) for negative significant effect for this trait. Most of the crosses showed positive significant heterosis over check-1 commercial variety (Green Finger, F1) and check-2 (BARRI Dharosh – 1 OP) . It was ranged from 11.78 to 0.00 for check-1 and 13.50 to 3.93 for check-2 respectively. The highest positive standard heterosis was 11.78 % in P4 (1178) X P7 (1205) for check-1 and 13.50 in P5 (1189) X P6 (1203) for check-2 respectively.

4.3.4.9 Fruit weight

The mean fruit weight for seven parents varied from 14.99 to 20.13. Parent P5 (1189) was the highest (20.13) fruit bearing parent which was followed by parent P2 (1171) =16.13 and P6 (1203) =15.93 (Appendix-IV and V). Fruit weight ranged from 16.19 to 22.77 for F1 hybrids. The percent of heterosis were ranged from -2.18 to 49.29 over mid parent values. The positive heterosis was varied from 4.93% to 49.29%. The highest positive significant heterosis was exhibited by the cross P4 (1178) X P7 (1205) =49.29** followed by the crosses P4 (1178) X P6 (1203) = 43.95**, P2 (1171) X P3 (1176) = 36.23**, P3 (1176) X P4 (1178) =33.96** and P3 (1176) X P7 (1205) = 27.46** respectively gave good results considering average fruit weight. The positive heterobeltiosis effect was range from -14.57 in P5 (1189) X P7 (1205) to 47.20 in P4

Table 4.18 Heterosis over mid parent, better parent, check-1 and check-2 for weight of fruit and fruit per plant

Fruit weight						**Fruits per plant**			
Sl no	**Cross combinations**	MP	BP	Check1	Check2	MP	BP	Check1	Check2
1	P1 (1163) X P2 (1171)	10.77**	8.14**	18.68**	**30.52****	41.26**	39.13**	29.19**	62.18**
2	P1 (1163) X P3 (1176)	24.12**	22.95**	28.16**	40.95**	60.39**	54.66**	54.66**	94.15**
3	P1 (1163) X P4 (1178)	16.32**	15.95**	22.00**	34.16**	69.73**	61.30**	66.30**	108.77**
4	P1 (1163) X P5 (1189)	14.93**	1.32ns	38.78**	52.62**	50.83**	38.06**	54.35**	93.76**
5	P1 (1163) X P6 (1203)	23.54**	21.34**	31.52**	44.64**	19.73**	0.45ns	37.58**	72.71**
6	P1 (1163) X P7 (1205)	6.54**	5.38ns	10.16**	21.15**	50.38**	37.29**	54.35**	93.76**
7	P2 (1171) X P3 (1176)	36.23**	31.40**	44.22**	58.60**	61.76**	53.73**	53.73**	92.98**
8	P2 (1171) X P4 (1178)	13.86**	11.51**	22.38**	34.59**	101.61**	88.86**	94.72**	144.44**
9	P2 (1171) X P5 (1189)	4.93**	-5.50*	29.43**	42.34**	95.08**	76.11**	96.89**	147.17**
10	P2 (1171) X P6 (1203)	10.19**	6.50**	20.18**	32.17**	35.70**	12.47**	54.04**	93.37**
11	P2 (1171) X P7 (1205)	10.50**	6.74*	17.14**	28.83**	42.02**	27.90**	43.79**	80.51**
12	P3 (1176) X P4 (1178)	33.96**	31.90**	38.78**	52.62**	54.74**	52.41**	57.14**	97.27**
13	P3 (1176) X P5 (1189)	16.12**	1.29ns	38.73**	52.57**	50.74**	42.78**	59.63**	100.39**
14	P3 (1176) X P6 (1203)	15.12**	11.72**	21.09**	33.17**	50.73**	22.90**	68.32**	111.31**
15	P3 (1176) X P7 (1205)	27.46**	27.27**	30.16**	43.14**	42.07**	55.25**	74.53**	119.10**
16	P4 (1178) X P5 (1189)	15.36**	1.99ns	39.68**	53.62**	64.33**	12.22**	25.47**	57.50**

17	P4 (1178) X P6 (1203)	43.95**	41.84**	53.74**	69.62**	16.76**	19.05**	63.04**	104.68**
18	P4 (1178) X P7 (1205)	49.29**	47.20**	54.88**	69.08**	35.83**	61.88**	81.99**	128.46**
19	P5 (1189) X P6 (1203)	4.99**	-5.96*	28.80**	70.32**	68.88**	41.04**	93.17**	142.50**
20	P5 (1189) X P7 (1205)	-2.18ns	-14.57**	28.80**	41.65**	55.31**	46.41**	64.60**	106.63**
21	P6 (1203) X P7 (1205)	33.05**	29.29**	17.01**	28.68**	46.81**	9.98**	50.62**	89.08**
	Number of +ve significant crosses	20	14	21	21	21	20	21	21
	Number of –ve significant crosses	0	3	0	0	0	0	0	0
	Range	49.29 to -2.18	47.20 to -14.57	54.88to 10.16	70.32 to 21.15	101.61 to 19.73	88.86 to 0.45	96.89 to 29.19	147.17 to 57.50

*and ** Significant at 5% and 1% levels, respectively

(1178) X P7 (1205). The highest percent of positive significant heterosis over standard check-1 was found 54.88 and in check-2, 70.32% respectively (Table-4.18).

4.3.4.10 Fruits per plant

The estimation of heterosis indicated the highest (101.61**) positively significant heterosis over mid parent in hybrid P2 (1171) X P4 (1178) followed by P2 (1171) X P5 (1189) =95.08**, P1 (1163) X P4 (1178) = 69.73** and P5 (1189) X P6 (1203) = 68.88** respectively for number of fruits per plant. Considering the heterosis over better parent, the highest positively significant heterobeltiotic effect was found 88.68** in P2 (1171) X P4 (1178), followed by 76.11** in P2 (1171) X P5 (1189), 61.30** in P1 (1163) X P4 (1178) and 61.88** in P4 (1178) X P7 (1205) respectively. The few of the hybrids showed significantly positive heterosis effect over standard check-1 and 2. The highest positive significant heterosis showed by the cross P2 (1171) X P5 (1189) = 96.89** for check-1 and 147.17** for check-2. And the second highest was observed in P2 (1171) X P4 (1178) = 94.72** for check-1 and 144.44** for check-2. Therefore, the crosses P2 (1171) X P4 (1178) and P2 (1171) X P5 (1189) could be considered as the the most promising for this trait among 21 hybrids (Table-4.18).

4.3.4.11 Fruit yield per plant

Fruit yield per plant is a complex character. It depends on so many characters, such as number of fruits per plant, fruit length, fruit diameter, weight per plant, days to first flowering etc. However, most of the crosses showed positive significant heterosis over mid parent values for fruit yield per plant indicating the possibilities of exploiting those crosses for hybrid variety development. The extent of heterosis over mid parent value range from 15.82 in P2 (1171) X P7 (1205) to 110.23% in P3 (1176) X P7 (1205). The significant positive heterosis was also observed 105.54% in the cross P2 (1171) X P3 (1176), 105.38% in P2 (1171) X P4 (1178) and 101.17% in P2 (1171) X P5 (1189) respectively. The range of heterobeltiosis was obtained from 4.52 in P1 (1163) X P6 (1203) to 94.09 in P2 (1171) X P3 (1176) cross combinations. The considerable heterobeltiosis was also observed in P2 (1171) X P4 (1178) = 88.57, P2 (1171) X P5 (1189) = 88.61 and P3 (1176) X P7 (1205) = 76.75, respectively. On the other hand, most of the crosses showed positive significant heterosis over standard check-1 (F1 Green Finger) and check-2 (BARRI Dharosh-1 OP). The highest positive significant standard heterotic effect was found 105.02 in P3 (1176) X P7 (1205) in check-1 and

Table 4.19 Heterosis over mid parent, better parent, check-1, check-2 for Fruit yield per plant and seeds per fruit

Fruit yield per plant						**Seeds per fruit**			
Sl no	**Cross combinations**	MP	BP	Check1	Check2	MP	BP	Check1	Check2
1	P1 (1163) X P2 (1171)	22.69*	20.25ns	11.41ns	92.47**	11.99 **	1.11ns	44.56**	46.13**
2	P1 (1163) X P3 (1176)	53.64**	42.36**	31.89**	127.47**	12.44**	9.23**	25.82**	27.19**
3	P1 (1163) X P4 (1178)	39.98**	30.95**	39.28**	140.64**	25.69**	18.96**	37.03**	38.52**
4	P1 (1163) X P5 (1189)	65.91**	58.56**	61.17**	178.46**	2.44**	-9.99**	36.90**	38.39**
5	P1 (1163) X P6 (1203)	19.59*	4.52ns	29.46**	123.67**	11.03**	2.46ns	39.56**	41.07**
6	P1 (1163) X P7 (1205)	20.10*	8.01ns	25.28**	116.45**	-8.33**	-16.89**	17.72**	19.00**
7	P2 (1171) X P3 (1176)	105.54**	94.09**	72.65**	198.29**	13.81**	0.13ns	43.16**	44.72**
8	P2 (1171) X P4 (1178)	105.38**	88.57**	100.58**	246.53**	30.74**	12.39**	60.70**	62.44**
9	P2 (1171) X P5 (1189)	101.17**	88.61**	91.72**	231.23**	-10.73**	-13.40**	31.71**	33.14**
10	P2 (1171) X P6 (1203)	47.76**	26.94**	57.24**	105.66**	-1.29ns	-3.63**	37.78**	39.28**
11	P2 (1171) X P7 (1205)	15.82ns	2.32ns	18.69ns	190.82**	-1.80ns	-2.26ns	39.75**	41.27**
12	P3 (1176) X P4 (1178)	81.57**	58.25**	68.33**	210.08**	15.41**	12.35**	22.03**	23.35**
13	P3 (1176) X P5 (1189)	98.65**	76.56**	79.47**	216.29**	-8.91**	-21.93**	18.73**	20.03**
14	P3 (1176) X P6 (1203)	80.45**	47.80**	83.07**	254.21**	6.00**	-4.74**	29.75**	31.16**
15	P3 (1176) X P7 (1205)	110.23**	76.75**	105.02**	123.63**	16.24**	2.68**	45.44**	47.02**
16	P4 (1178) X P5 (1189)	24.45**	21.69**	29.44**	123.71**	11.77**	-6.33**	42.47**	44.02**

17	P4 (1178) X P6 (1203)	57.23**	46.12**	81.00**	212.71**	18.08**	3.62**	41.14**	42.67**
18	P4 (1178) X P7 (1205)	60.25**	53.60**	78.17**	207.82**	-1.01ns	14.57**	21.01**	22.33**
19	P5 (1189) X P6 (1203)	72.60**	57.12**	94.63**	236.25**	-4.72**	-9.70**	37.34**	38.84**
20	P5 (1189) X P7 (1205)	41.32**	32.58**	53.79**	165.70**	5.93**	2.29ns	55.57**	57.26**
21	P6 (1203) X P7 (1205)	19.28**	15.48ns	43.05**	147.14**	0.36ns	-1.56ns	39.43**	40.95**
	Number of +ve significant crosses	20	16	19	21	13	7	21	21
	Number of –ve significant crosses	0	0	0	0	4	8	0	0
	Range	110.23 to 15.82	94.09 to 4.52	105.02 to 11.41	254.21 to 92.47	30.74 to -10.73	18.96 to -21.93	60.70 to 17.72	62.44 to 19.00

*and ** Significant at 5% and 1% levels, respectively

followed by 100.58 in P2 (1171) X P4 (1178), 94.63 in P5 (1189) X P6 (1203) respectively. For check-2 highest positive significant standard heterotic effect was found 254.21% in P3 (1176) X P6 (1203) followed by 246.53 in P2 (1171) X P4 (1178) 236.25% in P5 (1189) X P6 (1203) and 231.23% in P2 (1171) X P5 (1189), respectively. These crosses can be utilized in heterosis breeding program for the improvement of fruit yield per plant in okra (Table-4.19).

4.3.4.12 Seeds per fruit

Maximum crosses (13 crosses out of 21) exhibited significant positive heterosis over mid parent values. The highest positive significant heterosis over mid parent was 30.74% in P2 (1171) X P4 (1178) followed by 25.69% in P1 (1163) X P4 (1178), 18.08% in P4 (1178) X P6 (1203) and 16.24% in P3 (1176) X P7 (1205) respectively and the lowest was recorded in -10.73% in P2 (1171) X P5 (1189) followed by P3 (1176) X P5 (1189) = -8.91%, P1 (1163) X P7 (1205) = -8.33% and P5 (1189) X P6 (1203) = -4.72% over mid parent value of okra. Average crosses showed significant positive heterosis over their better parent. The highest significant heterobeltiotic effect was found in P1 (1163) X P4 (1178) = 18.96 followed by P4 (1178) X P7 (1205) = 14.57, P2 (1171) X P4 (1178) = 12.39 and P3 (1176) X P4 (1178) = 12.35 respectively. Considerable positive significant heterobeltiotic effect was found in hybrid combinations. On the other hand, all of the crosses showed (21 crosses out of 21) positive significant heterosis over standard check-1 (F1 green finger) and check-2 (BARRI Dharosh-1 OP). The highest positive significant standard heterotic effect was found 60.70% in P2 (1171) X P4 (1178) followed by 55.57% in P5 (1189) X P7 (1205) and 45.44% in P3 (1176) X P7 (1205) for check-1 and 62.44% in P2 (1171) X P4 (1178), 57.26% in P5 (1189) X P7 (1205) and 47.02% in P3 (1176) X P7 (12050 for check -2, respectively (Table-4.19).

4.3.4.13 100 Seed weight

Present study revealed the range and mean of 100 seed weight in parent 3.90 to 4.40 and 4.15 and in hybrid 4.13 to 5.30 and 4.64 respectively (Appendix-IV and V). Most all of the cross combinations showed positive and significant value in mid parent level. The highest positive significant effect observed in P3 (1176) X P7 (1205) =24.71 followed by P1 (1163) X P4 (1178) = 23.46%, P2 (1171) X P4 (1178) = 23.21% and P2 (1171) X P3 (1176) = 18.85% respectively. For better parent heterobeltiosis range obtained for 21.67 to -4.58 respectively. 15 cross combinations showed positive and significant

Table 4.20 Heterosis over mid parent, better parent, check-1, check-2 for 100 seed weight

100 Seed weight					
Sl no	**Cross combinations**	MP	BP	Check1	Check2
1	P1 (1163) X P2 (1171)	13.82**	11.11**	19.66**	26.13**
2	P1 (1163) X P3 (1176)	12.80**	11.90**	20.51**	27.03**
3	P1 (1163) X P4 (1178)	23.46**	19.05**	28.21**	35.14**
4	P1 (1163) X P5 (1189)	7.75**	5.30**	18.80**	25.23**
5	P1 (1163) X P6 (1203)	18.22**	15.87**	24.79**	31.53**
6	P1 (1163) X P7 (1205)	5.06*	3.05ns	15.38**	21.62**
7	P2 (1171) X P3 (1176)	18.85**	16.94**	23.93**	30.63**
8	P2 (1171) X P4 (1178)	23.21**	21.67**	24.79**	31.53**
9	P2 (1171) X P5 (1189)	9.52**	4.55ns	17.95**	24.32**
10	P2 (1171) X P6 (1203)	14.52**	14.05**	17.95**	24.32**
11	P2 (1171) X P7 (1205)	13.94**	9.16**	22.22**	28.83**
12	P3 (1176) X P4 (1178)	12.86**	9.68**	16.24**	22.52**
13	P3 (1176) X P5 (1189)	8.59**	5.30**	18.80**	25.23**
14	P3 (1176) X P6 (1203)	1.22ns	0.00ns	5.98ns	11.71**
15	P3 (1176) X P7 (1205)	24.71**	21.37**	35.90**	43.24**
16	P4 (1178) X P5 (1189)	8.43**	2.27ns	15.38**	21.62**
17	P4 (1178) X P6 (1203)	8.40**	6.61**	10.26**	16.22**
18	P4 (1178) X P7 (1205)	0.81ns	-4.58ns	6.84**	12.61**
19	P5 (1189) X P6 (1203)	4.35ns	0.00ns	12.82**	18.92**
20	P5 (1189) X P7 (1205)	7.98**	7.58**	21.37**	27.93**
21	P6 (1203) X P7 (1205)	14.29**	9.92**	23.08**	29.73**
	Number of +vesignifiucant crosses	18	15	20	21
	Number of –ve significant crosses	0	0	0	0
	Range	24.71 to 0.81	21.67 to -4.58	35.90 to 5.98	43.24 to 11.71

*and ** Significant at 5% and 1% levels, respectively

heterobeltiosis in this trait. The highest positive significant value observed in P2X P4 = 21.67 followed by P3 X P7 = 21.37, P2 X P3 = 16.94 and P1X P6 =15.87, respectively. Standard heterosis showed most of all positive significant result both of check-1 and check-2 (Table-4.20).

The highest positive significant effect observed in P3 X P7 =35.90 followed by P1 X P4 = 28.21, P1 X P6 =24.79, P2 X P4 = 24.79 and P6 X P7 = 23.08 for check-1 and for check-2 highest positive significant value observed in P3X P7 = 43.24 followed by P1 X P4 = 35.14, P1 X P6 = 31.53, P2X P4=31.53 and P6 X P7= 29.73 respectively for this trait.

4.3.5 Gene Action

The knowledge of genetic architecture of various traits is very essential in the plant breeding program for getting efficient results. Improvement of vegetables crop for both quantitative and qualitative characters depends on the sound knowledge of genetic architecture. Various biometrical approaches have been developed to decipher the genetic architecture and inheritance of different characters related to yield. Generation mean analysis is one such approach that provides information about nature and magnitude of gene actions involved. Generation mean analysis is a simple but useful technique for estimating gene effects for a polygenic trait, its greatest merit lying in the ability to estimate epistatic gene effect such as additive X additive (aa), dominance X dominance (dd) and additive X dominance (ad) effects.

The pooled data estimates of components of genetic variance and their corresponding standard errors for the trait have been presented here, while as the proportion of related genetic parameters along with the estimates of average degree of dominance and heritability in narrow sense are presented below:

Genetic variances are used for working out various genetic parameters. Six components of variance were worked out i.e. additive variance (D), dominance variance (H1), proportion of positive and negative genes in parents (H2), expected environmental components (E), mean of Fr over the array (F) and dominance effect (h2). These estimates were used to generate some genetic ratios, i.e. average degree of dominance (H1/D)1/2, ratio of dominant and recessive genes in the parents [(4DH1)1/2 – F], the number of gene groups (h2/H2) and the proportion of positive and negative genes (H2/4H1).

4.3.5.1 Plant height

Present study revealed positive and significant value for plant height in additive, dominance and proportion of positive and negative gene in parents and dominance effect also. The non-significant effect observed in mean of Fr over the array and expected environment component. These result indicating the involvement of both additive and dominance components in the inheritance of these of these traits. However, the magnitude of dominance components in general was higher than the corresponding additive component. This suggest the greater role of dominance component in the inheritance of these traits.

4.3.5.2 Number of leaf

Present study revealed higher value for additive (D) and dominance (H_1) as 83.58±53.56 and 430.2354±128.95, respectively whereas Ayesha *et al.* (2017) observed their experiment for D value-2.0833* (90 DAS) and H1- 0.565 which was lower than the present study. The ratio of positive and negative genes in parents (H_2) and dominance effect (h2) also observed highly positive and significant for this trait but Ayesha *et al.* (2017) observed less value for positive and negative ratio (0.257) positive non-significant. Positive significant value observed in dominant effect (h^2=1.824*) in their observation. The mean of Fr over the array (F) was observed 132.1901±128.50 which was positive and non-significant, depicted the relative frequency of dominant and recessive alleles in the parents was proportionally equal. The average degree of dominance $(H_1/D)^{1/2}$=2.27 was greater than the unity in this character, indicating over dominance in the expression of the trait and E value showed positive non-significant 3.4931±18.93. The observation $H_2/4H_1$ was 0.21 for this trait which was less than 0.25 revealing asymmetrical distribution of genes in parents with respect to this trait. The value of KD/KR was 2.07 which was greater than unity of the trait, indicating excess of dominant alleles as compared to recessive alleles. The estimate of (h^2/H_2) was 0.69 greater than 0.50 for number of leaf, indicating greater proportion of dominant gene/genes group for this trait. Heritability (ns) was 12% which was low indicated the major role of non-additive gene action in the inheritance of this characters and limited scope of their improvement through straight selection.

Table 4.21 Components of genetic variation for plant height at 100 days, number of leaf at 100 days and first female flower initiation

Components per Ratio	Plant height at 100 days (cm)	Number of leaf at 100 days per plant	Days to first flower initiation
D	1067.68**±267.40	83.58±53.56	19.01**±2.74
H_1	2224.8789**±643.75	430.2354**±128.95	22.7994**±6.60
H_2	1870.5105**±567.23	354.7470**±113.62	15.9868**±5.82
h^2	1879.7509**±380.98	244.1168**±76.31	5.1400±3.91
F	460.2513±641.48	132.1901±128.50	20.1747**±6.58
E	5.1185±94.53	3.4931±18.93	0.6865±0.97
$(H_1/D)^{1/2}$	1.44	2.27	1.10
$H_2/4H_1$	0.21	0.21	0.18
$[(4DH_1)^{1/2}+F)]$ / $[(4DH_1)^{1/2}-F)]$	1.35	2.07	2.88
h^2/H_2	1.00	0.69	0.32
% Heritability (Narrow sense)	50	12	37

*and ** Significant at 5% and 1% levels, respectively.

D= Additive variance, H_1= Dominance variance, H_2= Proportion of positive and negative genes in parents, F= Mean of Fr over the array, E= Expected environmental component, h^2= Dominance effect, $(H_1/D)^{1/2}$= Average degree of dominance, h^2/H_2= The number of gene group, $H_2/4H_1$ = the proportion of positive and negative genes, $[(4DH_1)^{1/2}+ F]/[(4DH_1)^{1/2}- F]$ = KD/KR= Ratio of dominant and recessive gene in the parents.

Table 4.22 Components of genetic variation for days to 50% flowering, number of first female flower and days to first edible fruit harvesting days

Components/ Ratio	Days to 50% flowering	Node of first female flower	First edible fruit harvesting days
D	23.73**±1.51	0.93**±0.05	24.86**±3.40
H_1	22.52**±3.65	0.97**±0.12	36.44**±8.18
H_2	14.51**±3.26	0.57**±0.10	25.06**±7.21
h^2	10.48**±2.16	46**±0.07	36.98**±4.84
F	25.95**±3.64	1.17**±0.12	31.35**±8.15
E	0.38±0.54	0.01±0.02	0.36±1.20
$(H_1/D)^{1/2}$	1.10	1.02	1.21
$H_2/4H_1$	0.18	0.15	0.17
$[(4DH_1)^{1/2}+F)]$ / $[(4DH_1)^{1/2}-F)]$	2.88	1.01	1.01
h^2/H_2	0.32	80.70	1.48
% Heritability (Narrow sense)	42	38	27

*and ** Significant at 5% and 1% levels, respectively.

D= Additive variance, H_1= Dominance variance, H_2= Proportion of positive and negative genes in parents, F= Mean of Fr over the array, E= Expected environmental component, h^2= Dominance effect, $(H^1 /D)^{1/2}$= Average degree of dominance, h^2/H_2= The number of gene group, $H_2/4H_1$ = the proportion of positive and negative genes, $[(4DH_1)^{1/2}+ F]/ [(4DH_1)^{1/2}- F]$ = KD/KR= Ratio of dominant and recessive gene in the parents.

Table 4.23 Components of genetic variation for fruit length, fruit diameter and fruits weight

Components/ Ratio	Fruit length (cm)	Fruit diameter (cm)	Fruit weight (g)
D	0.77**±0.27	0.006**±0.001	3.15**±2.06
H_1	2.99**±0.66	0.01**±0.002	18.32**±4.98
H_2	2.84**±0.58	0.008**±0.002	15.44**±4.39
h^2	3.97**±0.39	0.01**±0.001	27.62**±2.95
F	0.51±0.65	0.008**±0.002	4.18±4.96
E	0.06±0.10	0.001**±0.0004	0.11±0.73
$(H_1/D)^{1/2}$	1.97	1.29	2.41
$H_2/4H_1$	0.24	0.20	0.21
$[(4DH_1)^{1/2}+F)]/ [(4DH_1)^{1/2}-F)]$	1.02	1.12	1.01
h^2/H_2	1.40	1.25	1.79
% Heritability (Narrow sense)	21	16	18

*and ** Significant at 5% and 1% levels, respectively.

D= Additive variance, H_1= Dominance variance, H_2= Proportion of positive and negative genes in parents, F= Mean of Fr over the array, E= Expected environmental component, h^2= Dominance effect, $(H^1/D)^{1/2}$= Average degree of dominance, h^2/H_2= The number of gene group, $H_2/4H_1$ = the proportion of positive and negative genes, $[(4DH_1)^{1/2}+ F]/ [(4DH_1)^{1/2}- F]$ = KD/KR= Ratio of dominant and recessive gene in the parents.

Table 4.24 Components of genetic variation for fruit per plant, Seeds per fruit and 100 seed weight

Components per Ratio	Fruits per plant	Seeds per fruit	100 seed weight (g)
D	10.45±10.92	102.59**±15.89	0.03±0.03
H_1	142.74**±26.284	175.97**±38.12	0.39**±0.08
H_2	136.73**±23.16	139.89**±33.71	0.37**±0.07
h^2	396.11**±15.56	52.52**±22.64	0.72**±0.05
F	10.76±26.19	107.87**±38.12	0.02±0.08
E	1.07±3.86	0.45±5.62	0.007±0.011
$(H_1/D)^{1/2}$	3.70	1.31	3.61
$H_2/4H_1$	0.24	0.20	0.24
$[(4DH_1)^{1/2}+F)]/[(4DH_1)^{1/2}-F)]$	1.01	1.00	1.02
h^2/H_2	2.90	0.38	1.95
% Heritability (Narrow sense)	7	30	12

*and ** Significant at 5% and 1% levels, respectively.

D= Additive variance, H_1= Dominance variance, H_2= Proportion of positive and negative genes in parents, F= Mean of Fr over the array, E= Expected environmental component, h^2= Dominance effect, $(H^1/D)^{1/2}$= Average degree of dominance, h^2/H_2= The number of gene group, $H_2/4H_1$ = the proportion of positive and negative genes, $[(4DH_1)^{1/2}+ F]/[(4DH_1)^{1/2}- F]$ = KD/KR= Ratio of dominant and recessive gene in the parents.

Table 4.25 Components of genetic variation for fruit yield per plant

Components per Ratio	**Fruit yield per plant**
D	2972.63±4683.01
H_1	70445.38**±11274.22
H_2	61172.42**±9934.17
h^2	61172.42**±9934.17
F	4218.64±11234.45
E	735.78±1655.69
$(H_1/D)^{1/2}$	4.87
$H_2/4H_1$	0.22
$[(4DH_1)^{1/2}+F)]/ [(4DH_1)^{1/2}-F)]$	1.01
h^2/H_2	1.00
% Heritability (Narrow sense)	20

*and ** Significant at 5% and 1% levels, respectively.

D= Additive variance, H_1= Dominance variance, H_2= Proportion of positive and negative genes in parents, F= Mean of Fr over the array, E= Expected environmental component, h^2= Dominance effect, $(H^1 /D)^{1/2}$= Average degree of dominance, h^2/H_2= The number of gene group, $H_2/4H_1$ = the proportion of positive and negative genes, $[(4DH_1)^{1/2}+ F]/ [(4DH_1)^{1/2}- F]$ = KD/KR= Ratio of dominant and recessive gene in the parents.

4.3.5.3 Days to first flowering

Present experiment revealed positive and significant value for additive genetic variance component D=19.01**±2.74 and measures of dominance components (H_1 and H_2) were also observed positive and significant value i.e. H_1= 22.7994**±6.60 and H_2=15.9868**±5.82 respectively. These results indicated the improvement of both additive and dominance components in the inheritance of these traits. However, the magnitude of dominance components, in general, was higher than the corresponding additive component. This suggest the greater role of dominance component in the inheritance of these traits.

The knowledge of number of gene groups responsible for a particular character is important for the genetic progress through selection. the ratio of h^2/H_2=0.32 was low (less than 0.50) indicating that a few genes or group of genes generally controlled the inheritance of particular character.

4.3.5.4 Days to 50% flowering

The investigation revealed six components of variance were positive and significant value except environmental components (E), and they were additive variance D=23.73**±1.51, dominance variance (H1) = 22.52±3.65, proportion of positive and negative genes in parents (H_2) = 14.51**±3.26, dominance effect (h^2) = 10.48**±2.16 and mean of Fr over the array (F) = 25.95**±3.04 respectively. Only expected environmental component observed positive non-significant E= 0.38±0.54 value. These results indicated the involvement of both additive and dominance components in the inheritance of these traits. However, the magnitude of dominance components, in general was higher than the corresponding additive component but here additive component was higher than the corresponding dominance component. This suggest the lower effect of dominance component in the inheritance of this trait.

4.3.5.5 Node of first female flower

Present study expressed five component of variance positive and significant effect i.e. additive variance (D) = 0.93**±0.05, dominance variance (H_1) = 0.97**±0.12, proportion of positive and negative genes (H_2) = 0.57**±0.10, dominance effect (h^2) = 46**±0.07 and mean of Fr over the array (F) = 1.17**±0.12, respectively. The magnitude of dominance components in general was higher than the corresponding additive component. This suggested the greater role of dominance component in the inheritance of the trait.

The study also showed the average degree of dominance [$(H_1/D)^{1/2}$=1.02] was almost similar to the unity for this character indicating dominance in the expression of the trait. The estimates of $(H_2/4H_1)$ = 0.25 also similar to 0.25 revealing symmetrical distribution of genes in parents with respect to the trait. the value of KD/KR ratio was similar to unity indicate balance of dominant alleles as compared to recessive alleles and the estimates of (h^2/H_2) = 80.70 was greater than 0.50 for this trait revealing greater proportion of dominant genes/gene groups for these traits and heritability (n.s) found 38% indicating the major role of non-additive gene action in the inheritance.

4.3.5.6 Days to first edible fruit harvest

Present study showed the estimate of additive genetic variance was positive and significant for this character which indicating high transmissibility in the progeny. Therefore, direct selection would be of much use for such character which was in accordance with Indu Rani *et al.* (2002), Vachhani and Shekhat (2008), Senthil Kumar (2011), Mrinmoy *et al.* (2013). The F value found positive significant for days to first edible fruit harvest implying that dominant alleles were preponderance for this trait in the parents. The estimates of components of variation due to dominance (H_1) and proportion of dominance due to positive and negative genes (H_2) showed the importance of non-additive gene effects than additive gene effects in controlling the expression of days to first edible fruit harvest. The magnitude of dominance effect was more compare to the additive component in this character, hence solution may be practiced in the segregating population and also intermating of selection plants in segregating population or recurrent selection may be practiced to improve the yield.

4.3.5.7 Fruit length

Present study revealed positive and significant value in four components out of six. The additive variance (D), dominance variance (H_1), proportion of positive and negative genes in parents (H_2) and dominance effect showed positive significant value. The expected environmental component (E) and mean of Fr over the array (F) showed positive but no significant value for this character.

4.3.5.8 Fruit diameter

Present study observed all positive and significant effect of genetic variation within six components of variance for the character. The equal distribution of positive and negative genes in the parents helps the breeder in selecting a particular desirable trait without losing other traits of interest. In the present study, symmetrical distribution of positive and negative genes in the parental lines was revealed from the character fruit diameter indicating the additive genetic variance could only be justified by either the dominance or the over dominance effects of genes in heterozygous position. The value of KD/KR ratio was greater than unity of the trait indicating excess of dominant alleles as compared that the parents used were carrying more dominant than recessive alleles for the trait. The knowledge of number of gene groups responsible for a particular trait is important for the genetic progress through selection in the present study; the ratio of h^2/H_2 was greater than the unity indicating greater proportion of dominant genes/gene groups for this trait generally controlled the inheritance of a particular character. The estimates of narrow sense heritability were low for fruit diameter. This result indicated the major role of non-additive gene action in the inheritance and limited scope of their improvement through straight selection.

4.3.5.9 Fruit weight

Present investigation revealed positive and significant value in four components out of six for the trait. The additive and dominance both were significant indicating involvement of both additive and dominance components in the inheritance of the trait. Moreover, the magnitude of dominance components, in general, was higher than the corresponding additive components. This result suggested the greater role of dominance components in the inheritance.

4.3.5.10 Fruits per plant

The present experiment revealed three genetic components positive and significant out of six. The dominance variance (H_1), proportion of positive and negative genes in parents (H_2) and dominance effect (h^2) showed positive significant value and the rest of all showed positive insignificant for the trait.

4.3.5.11 Seeds per fruit

Present study revealed position and significant value of all genetic components (D, H_1, H_2, h^2 and F) except expected environmental component (E). The estimate of $H_2/4H_1$ was less than 0.25 revealing asymmetrical distribution of genes in parents with respect to the trait. The value of KD/KR ratio was similar to the unity indicating equal of dominant alleles as compared to recessive alleles. The estimates of (h^2/H_2) were greater than 0.50, indicated greater proportion of dominant genes/gene groups for this trait. The heritability (n.s) estimates was medium (30-55%) indicating the major role of non-additive gene action in the inheritance and limited scope of improvement through straight selection.

4.3.5.12 100 Seed weight

Present investigation revealed positive and significant value of three genetic variances out of six for this trait. The dominance variance (H_1), proportion of positive and negative genes in parent (H_2) and dominance effect (h^2) showed positive and significant value and the rest three observed positive non-significant. The estimates of ($H_2/4H_1$) were near about equal to 0.25, indicating symmetrical distribution of genes in parents. The knowledge of number of gene groups responsible for a particular character is important for the genetic progress through selection. The ratio of h2/H2 was greater than 0.50, indicating greater proportion of dominant genes/gene groups for the trait. The heritability (n.s) estimates for 100-seed weight was low, indicating the major role of non-additive gene action in the inheritance of most of the characters and limited scope of their improvement through straight selection.

4.3.5.13 Fruit yield per plant

Present study estimates of additive genetic variance were positive and significant for component of variation due to dominance (H_1), proportion of positive and negative genes in parents (H_2) and dominance effect (h2) and rest three components showed positive non-significant effect for the trait. The estimated mean degree of dominance $(H_1/D)^{1/2}$ estimate was more than unity indicating over dominance or presence of repulsive phase linkage. The similar results were reported by Vachhani and Shekhat (2008) and Senthil Kumar (2011).

4.4 Stability analysis of the experimental hybrids

The phenotype of an individual is determined by the effects of its genotype and environment surrounding it. The effects of genotype and environment on phenotype may not always independent. The phenotypic response to change in environment is not same for all the genotypes, the consequences of variation in phenotype depend upon environment. Very often breeders encounter situations where the relative rankings of varieties change from location to location and/or from year to year. The interplay in the effect of genetic and non-genetic on development is termed as genotype environment interaction (Comstock and Moll, 1963).

Bartlett's test (Bartlett, 1937) was carried out to assess homogeneity of error variances against four environments. The error variances were not statistically different, suggested the samplings were unbiased and G X E interactions are predictable through Eberhat and Russel model. However, one-way ANOVA on thirteen characters are presented in Appendix 1.The data presented in Appendix 1 revealed that out of thirteen characters only fruit diameter was non-significant against G and G X E interactions. Therefore, the characters under study in general were homogenously distributed among the four environments; hence further statistical tool was applied to estimate the G X E interactions for the experimental okra hybrids.

The stability analysis of variance of mean data (Table-4.26) revealed that the mean square for genotypes were highly significant for all the characters indicating genetic variability among the genotypes for these characters except fruit diameter of the genotypes. Prakash *et al.* (2017) observed non-significant value for plant height (90 DAS) among the genotypes. Similarly, the mean squares due to environment were highly significant for all the characters. This indicated that environments were effective in influencing the performance of the genotypes. Highly significant mean squares due to E+ (G x E) were also observed for all these traits except fruit diameter revealed that genotypes interacted significantly with the environments while testing the significance of mean square due to genotype x environment interaction against pooled error, it was observed that mean square were significant for all the characters except fruit diameter. The mean square due to environment (linear) was significant and highly significant for all the characters when tested against pooled error. The mean squares due to pooled deviation were found to be highly significant for all the traits except fruit diameter. On

Table 4.26 Mean square from analysis of variance for different agronomic character in four environment using Eberhart and Russel, 1966

Source of variation	DF	PH100	LN100	1st flower initiation (days)	50% flower initiation (days)	Nodes of 1st female flower	First edible fruit harvest(days)
Genotypes	7	298.65**	27.88**	8.00**	7.46**	1.10**	11.52**
ENV + GXE	24	791.72**	179.02**	40.20**	48.93**	7.89**	44.34**
ENV (Linear)	1	9418.62**	2628.71**	809.36**	1007.40**	62.21**	809.89**
GXE (Linear)	7	360.79**	46.64**	3.75**	4.33**	1.26**	4.33**
Polled deviation	16	441.06**	83.82**	8.08**	8.53**	7.40**	13.99**
Polled error	56	7.15	7.00	1.55	0.99	0.36	2.38

Table 4.26 Mean square from analysis of variance for different agronomic character in four environment using Eberhart and Russel, 1966 (continued)

Source of variation	DF	Fruit length (cm)	Fruit diameter (cm)	Fruit weight (g)	Fruits per plant	Fruit yield per plant (g)	Seeds per fruit	100 seed weight(g)
Varieties	7	0.65**	0.0087	2.47**	13.78**	9565.21**	20.87**	0.51**
ENV + GXE	24	1.02**	0.0085	4.53**	76.44**	34609.75**	63.89**	2.62**
ENV (Linear)	1	4.19**	0.0474**	5.72**	1201.85**	465832.00**	496.62**	22.73**
GXE (Linear)	7	0.32*	0.0048	3.75**	10.92**	8514.14**	75.37**	1.07**
Polled deviation	16	1.12**	0.0077	4.80**	34.77**	19075.24**	31.82**	2.03**
Polled error	56	0.30	0.0244	0.44	3.09	1284.28	2.10	0.011

comparing relative magnitude of genotype x environment (linear) and pooled deviation from linearity (non-linear). It was found that the linear portion was considerably low for plant height, number of leaf, days to 1st flowering, 50% flowering etc. for all characters except seeds per fruit as evidenced from larger portion of non- linear component over linear component. This indicated importance of both nonlinear and linear portions in determining genotype x environment interaction for these attributes.

4.4.1 Plant height (100 days)

Plant height differed in the genotypes at all the stages of crop growth, difference in plant height among the genotypes is by virtue of their growth habit. At 100 days after sowing the genotuypes G-5, G-8 was found to be stable with respect to plant height as indicated by their high mean values, regression coefficient approaching unity and non-significant deviation from regression (Table-4.27), hence this genotypes are specially adapted to favorable environment.

Table 4.27 Stability parameter for different character in okra

Genotypes	Plant height 100 days		Deviation from regression (S^2di)	Leaf number 100 days		Deviation from regression (S^2di)	1st flower initiation		Deviation from regression (S^2di)
	Mean	Regression coefficient (bi) ± SE of bi		Mean	Regression coefficient (bi) ± SE of bi		Mean	Regression coefficient (bi) ± SE of bi	
P1 (1163)×P7 (1205)	91.83	1.97±0.67	525.58	43.10	1.27 ±0.51	82.09	49.17	0.81± 0.54	28.92
P2 (1171)×P5 (1189)	100.06	0.81 ± 1.08	1395.84	43.57	1.07 ± 0.38	45.49	45.83	0.90 ± 0.23	4.70
P2 (1171)×P6 (1203)	96.13	0.28 ± 0.21	50.75	47.67	1.25 ± 0.73	172.16	46.08	1.24 ± 0.13	1.22*
P3 (1176)×P6 (1203)	112.65	0.39 ± 0.48	278.01*	46.77	1.44 ± 0.37	41.66	46.25	1.14 ± 0.15	1.91*
P3 (1176)×P7 (1205)	117.97	1.17 ± 0.24	68.47	48.57	1.14 ±0.29	25.49	45.33	0.85 ± 0.28	7.23
P5 (1189)×P6 (1203)	104.01	1.43 ± 0.71	588.10	42.54	0.38 ± 0.56	99.48	44.92	1.28 ± 0.26	6.20*
P5 (1189)×P7 (1205)	104.01	0.79 ± 0.62	455.43	45.57	0.50 ± 0.62	122.04	46.33	0.83 ± 0.25	5.66
P6 (1203)×P7 (1205)	108.05	1.14 ± 0.35	147.27	49.52	0.95 ±0.45	63.53	48.00	0.95 ± 0.23	4.71
Mean									
SE m	12.96			5.65			1.76		

Table 4.27 Stability parameter for different character in okra (continued)

Genotypes	50% Flower initiation		Deviation from regression (S^2di)	Node of 1st flowering		Deviation from regression (S^2di)	First edible fruit harvest		Deviation from regression (S^2di)
	Mean	Regression coefficient (bi) ± SE of bi		Mean	Regression coefficient (bi) ± SE of bi		Mean	Regression coefficient (bi) ± SE of bi	
P1 (1163)×P7 (1205)	51.42	0.73 ± 0.48	28.24	8.13	0.44 ±0.88	5.90	57.83	0.64±0.79	62.59
P2 (1171)×P5 (1189)	48.42	0.92 ± 0.17	3.19*	8.15	1.16±1.08	8.95	53.50	0.89±0.33	10.17
P2 (1171)×P6 (1203)	48.33	1.23 ± 0.19	4.39*	7.82	1.43 ±0.99	7.56	53.25	1.19±0.25	5.31*
P3 (1176)×P6 (1203)	48.50	1.15 ± 0.20	4.72*	8.18	1.29 ±0.72	3.95	53.50	1.09±0.24	5.19*
P3 (1176)×P7 (1205)	47.83	0.83 ± 0.29	4.72	9.47	1.27± 0.66	3.28	52.92	0.91±0.34	10.99
P5 (1189)×P6 (1203)	47.67	1.21 ± 0.23	10.12*	8.58	1.27± 0.43	1.28	52.67	1.38 ± 0.34	5.60*
P5 (1189)×P7 (1205)	49.75	0.86 ± 0.19	6.41*	7.93	0.66 ±1.36	14.29	54.75	0.89±0.20	3.48*
P6 (1203)×P7 (1205)	50.58	0.98 ± 0.19	4.26*	8.07	0.48 ±1.30	13.08	0.89	0.89±0.17	2.29*
Mean									
SE m	1.80				1.68		2.31		

Table 4.27 Stability parameter for different character in okra (continued)

Genotypes	Fruit length (cm)		Deviation from regression (S^2di)	Fruit diameter(cm)		Deviation from regression (S^2di)	Fruit weight(g)		Deviation from regression (S^2di)
	Mean	Regression coefficient (bi) ± SE of bi		Mean	Regression coefficient (bi) ± SE of bi		Mean	Regression coefficient (bi) ± SE of bi	
P1 (1163)×P7 (1205)	14.28	0.13 ±1.61	1.26	2.09	-0.06±1.70	0.0089	18.13	-2.66±2.90	5.87
P2 (1171)×P5 (1189)	14.12	0.38 ±1.26	0.73	1.96	2.25±1.23	0.0008	16.67	1.50±2.13	3.10
P2 (1171)×P6 (1203)	14.06	1.18 ±0.68	0.14	2.11	0.02±1.67	0.0085	17.67	0.07±2.80	5.45
P3 (1176)×P6 (1203)	14.48	1.06 ±1.06	0.48	2.07	1.03±0.42	-0.0071	17.22	0.35±3.16	6.10
P3 (1176)×P7 (1205)	13.47	1.8 7±1.47	1.03	2.02	2.10±0.81	-0.0042	17.45	4.84±0.87	0.39*
P5 (1189)×P6 (1203)	13.47	2.26 ±1.08	0.51	2.02	0.46±0.45	-0.0070	16.67	2.22±2.11	3.04
P5 (1189)×P7 (1205)	14.20	0.10 ± 0.81	0.25	2.07	0.60±1.46	0.0045	17.40	-0.81±1.76	2.05
P6 (1203)×P7 (1205)	14.50	0.12 ± 2.73	3.80	2.05	1.61±0.30	-0.0076*	19.05	2.49±3.82	10.31
Mean									
SE m	0.65			0.05			1.35		

Table 4.27 Stability parameter for different character in okra (continued)

Genotypes	Fruits per plant		Deviation from regression (S^2di)	Fruit yield per plant		Deviation from regression (S^2di)	Seeds per fruit		Deviation from regression (S^2di)
	Mean	Regression coefficient (bi) ± SE of bi		Mean	Regression coefficient (bi) ± SE of bi		Mean	Regression coefficient (bi) ± SE of bi	
P1 (1163)×P7 (1205)	24.19	0.62±0.56	46.24	435.06	0.31±0.57	18333.05	62.69	-0.59±0.28	4.06
P2 (1171)×P5 (1189)	22.62	1.34±0.09	0.07**	381.32	1.32±0.17*	1215.42	65.03	0.92±0.51	15.64
P2 (1171)×P6 (1203)	23.10	0.91±0.20	5.56*	424.57	0.79±0.35	6544.64	61.73	0.69±0.95	55.88
P3 (1176)×P6 (1203)	22.99	1.23±0.13	1.45*	395.25	1.11±0.22*	2473.08	65.36	0.14±0.81	40.13
P3 (1176)×P7 (1205)	24.59	1.15±0.22	6.51*	443.81	1.54±0.28*	4220.62	61.39	1.91±0.82	40.79
P5 (1189)×P6 (1203)	26.25	1.10±0.69	70.30	448.18	1.22±0.71	28873.04	61.82	0.64±0.67	27.01
P5 (1189)×P7 (1205)	27.25	1.04±0.52	38.10	469.08	0.86±0.34	6443.47	66.52	3.03±0.51	15.52*
P6 (1203)×P7 (1205)	27.43	0.60±0.82	100.80	540.72	0.86±1.18	81073.91	66.99	1.27±0.90	49.96
Mean									
SE m	3.64			85.25					

Table 4.27 Stability parameter for different character in okra (continued)

Genotypes	100 seed weight		Deviation from regression (S^2di)
	Mean	Regression coefficient (bi) ± SE of bi	
P1 (1163)×P7 (1205)	5.02	0.18±0.98	2.73
P2 (1171)×P5 (1189)	5.56	1.42±0.64	1.17
P2 (1171)×P6 (1203)	5.29	1.75±0.73	1.51
P3 (1176)×P6 (1203)	5.28	1.42±0.73	1.52
P3 (1176)×P7 (1205)	4.52	1.08±0.86	2.10
P5 (1189)×P6 (1203)	4.69	1.44±0.30	0.26*
P5 (1189)×P7 (1205)	5.41	0.51±1.13	3.64
P6 (1203)×P7 (1205)	5.22	0.20±1.08	3.34
Mean			
SE(m)	0.88		

4.4.2 Leaf number (100 Days)

Present investigation showed high mean value for number of leaf at 100 days. The highest mean value observed G-8 followed by G-5 and G-3. But their regression coefficient observed G-8 bi<1 and G-5, G-3 was bi>1 which indicated less sensitive to environmental changes for G-8 and rest two showed highly sensitive to environmental changes. There was no significant value for this trait.

4.4.3 First flower initiation

Stability estimated to assess the stability over the environment is presented in table-2, for days to first flowering, a perusal of the data revealed that nonlinear component was significant for 3 genotypes, indicating larger contribution of non-linear components towards G X E interaction. Among them G-6, G-5 and G-2 were found early flowered and exhibited unit regression along with non-significant value of deviation (except G-6) from regression. Thereby suggesting major role of nonlinear component towards G X E interaction.

4.4.4 50% flower initiation

Present study showed the mean value of G-6 and G-5 is lower which indicate the earliness of the variety and regression coefficient (bi) revealed zero or less than unity which indicated less sensitive to environmental changes. The value of deviation from regression showed all significant except G-1 and G-5. This observation suggesting to stable with respect to yield by this regression technique.

The lowest mean value of present study was G-6 (47.67) followed by G-5(47.83), G-3(48.33), G-2(48.42) and G-4(48.50) which were lower than grand mean (49.06) and their regression coefficient observed almost bi=1 and deviation from regression showed average stability indicating poorly adapted to all environment. The genotype G-1(51.42) followed by G-8(50.58) and G-7(49.75) were higher than grand mean and regression coefficient almost bi=1 and stability average high indicating well adapted to all environments, i.e. average sensitivity to environmental changes. All genotypes except G-1 and G-5 showed significant for deviation from regression.

4.4.5 Node of first flowering

It was observed that G-3 and G-7 genotypes were stable for node at which first flower appears due to non-significant deviation from regression. The mean value of G-5 and G-6 were higher than population mean and regression coefficient were less than unity, deviation from regression showed below average indicated the specially adapted to favorable environments.

4.4.6 Days to first edible fruit harvest

The present study showed the magnitude of mean performance of different genotypes were lower than population mean and their regression coefficient (bi) exhibited unit along with significant value of deviation from regression indicating poorly adapted to all environments. All genotypes except G-1, G-2 and G-5 showed significant deviation from regression (S^2di) respectively for this character. In conclusion a genotype is considered as stable when it possesses high or low mean performance in relation to genotype mean (depending on the characters), non-significance of regression coefficient (bi) and non-significance of deviation from regression (S^2di).

4.4.7 Fruit length

The stability parameters for fruit length revealed that the genotypes G-8, G-4, G-1 and G-7 were specially adapted for this trait over all the favorable environments as they had mean value above the population mean, regression coefficient (bi) lower than unity and non-significant deviation from regression was below average. The genotype G-6, G-5 was lower mean than population mean abd regression coefficient (bi) near to unity and were found to be highly stable over all the environments as they were also associated with non-significant deviation from regression.

4.4.8 Fruit diameter

Present study revealed 4 genotypes namely G-1, G-3, G-4 and G-7 showed average fruit diameters above the population mean, below unity of regression coefficient and stability response below average was indicating specially adapted to favorable environments. And rest of the genotypes revealed low mean value in respect of population mean and regression coefficient bi>1 and deviation from regression showed near about zero indicating poorly adapted to all environments.

4.4.9 Fruit weight

Present study depicted three genotypic mean value like G-1, G-3, and G-8 were above than population mean and their regression coefficient was below than unity and deviation around the regression line was considered as a measure of stability. Genotypes with non-significant deviation (S^2 d) along with high mean performance, average response are considered to be the most stable genotypes. The genotypes G-5 showed below than population mean and regression coefficient was greater than unit value and significant deviation from regression showed near about zero indicating specially adapted to unfavorable environments. Rest of the varieties showed stable and exhibited unit regression coefficient along with non-significant value of deviation from regression.

4.4.10 Fruit per plant

Present study showed that the genotypes G-2, G-3, G-4 and G-5 showed low mean value than the population mean and the regression coefficient near unity, significant deviation from regression. The other genotypes like G-6, G-7 and G-8 possessed higher mean values and regression coefficient greater than unity indicating their instability and suitability to favorable environments, since their deviation from regression were non-significantly different from zero. None of the genotypes possessed wide adaptability for this trait.

4.4.11 Fruit yield per plant

For fruit yield per plant genotype G-5 possessed significant regression coefficient greater than unity and high mean value revealing suitability for favorable environment. G-8 followed by G-7 and G-6 possessed high mean value and regression coefficient near about value indicating well adapted to all environment but their performance cannot have predicted over environments, since their deviations from regressions from regression were non-significantly different from zero. The genotype G-2 possessed significant value for regression coefficient which greater than unity and low means value compared to population mean indicated poorly adapted to all environments.

4.4.12 Seeds per fruit

Present study revealed for this character G-7 showed high mean value than population mean, regression coefficient was greater than unit value and deviation from regression was significantly different from zero indicating specially adapted to unfavorable environments. The genotype G-1, G-3, G-4 and G-6 possessed low mean value than population mean and regression coefficient lower than unit value and deviation from regression were non-significant different from zero indicating they poorly stable or adapted to all environments. The genotype G-2 and G-8 were found stable as they were high mean value and exhibited unit regression coefficient along with non-significant value of deviation from regression. Thereby suggesting major role of nonlinear component towards G X E interaction.

4.4.13 100 Seed weight

Present study expressed for this characters the genotype G-2, G-7, G-3 and G-4 showed high mean value than population mean and regression coefficient near to unit value and deviation from regression non-significantly different from zero indicated that they were stable for good or favorable environments but their performance cannot be predicted over environments since their deviations from regression were different from zero.

Table 4.28 Estimate of environmental index for various characters under different environments

Sl No	Characters	Environmental index			
		E1	E2	E3	E4
1	PH100	-18.36	-12.05	4.43	25.98
2	LN100	12.45	-11.52	-4.94	4.01
3	1st flower initiation(days)	8.65	-3.34	-3.34	-1.96
4	50% flower initiation (days)	9.60	-4.35	-3.31	-1.93
5	Nodes of 1st female flower	0.59	-2.32	0.35	1.37
6	First edible fruit harvest(days)	8.68	-3.52	-2.47	-2.68
7	Fruit length(cm)	0.07	0.55	-0.38	-0.24
8	Fruit diameter(cm)	0.05	-0.00	-0.04	-0.00
9	Fruit weight(gm)	0.70	-0.35	-0.29	-0.06
10	Fruits per plant	10.03	-4.80	-5.13	-0.08
11	Fruit yield per plant(gm)	196.36	-94.67	-103.45	1.76
12	Seeds per fruit	4.31	3.40	-2.84	-4.87
13	100 seed wt(gm)	-0.58	1.35	0.04	-0.81

E1= K2-2015, E2=K1-2016, E3=K2-2016, and E4=K1-2017 respectively.

4.14 Environment index

The information on quantitative genetics has made a major contribution synthesis of more efficient genotypes. Since many of the plant characters which are of economic values are quantitatively inherited and highly influenced by the environmental condition. It is difficult to judge whether observed variation is heritable or due to the influence of environments. Therefore, there is imperative need of partitioning the observed variability through into its heritable and non-heritable components through suitable genetic parameters viz., phenotypic and genetic advance for selection of a few promising genotypes from existing populations. Moreover, phenotypic variation is a complex of three variables viz., generic, environmental and GxE interaction. It is a common practice in traits involving varieties and breeding lines to grow a series of genotypes in a range of different environments. If all the genotypes respond similarly to all the environments, tested their relative performance in other environments may be predicted with some confidence A GXE interaction exists where the relative performance of genotypes changes from environment to environment. The presence of GXE interaction is a major problem in getting reliable estimates of heritability and it makes it difficult to predict with greater accuracy the rate of genetic progress under selection for a given character.

The present study showed (Table 4.28) that the magnitude of performance of different traits including yield was more in E1 than all the environments as compared to the other environments in Table 4.28 presented various plant characters in 21 F1 of okra grown under four environments. From the estimation of environmental index (Table 4.28) it was observed that the character’s plant height and leaf number were favored both in E4, while the character 1st flower and 50% flower initiation both were favored in E2 E3 and E4 and showed delay in E1 environment. Only node of 1st flowering expressed earliness in E2 among them. First edible fruit harvest also showed earliness in all environments except E1. The character fruit length expressed more favored in E1 and E2 but fruit diameter showed less effectiveness in different environmental condition. Fruit weight also showed positive effectiveness for E1 and rest all negative. The observation showed fruits per plant and fruit yield per plant highly favored in E1 and rest all environment showed less effective. Seeds per fruit also favored in E1 and E2 while 100 seed weightfavored for E2 and E3 environment (Sanket *et al.*, 2018; Olayiwola and Ariyo, 2015).

On the basis of above results and discussion, the following suggestions may be forwarded –

1. The fifty genotypes collected from different sources were devided into six clusters by D2 statistics indicated ample genetic diversity among themselves hence there is a wides scope of developing suitable parental lines with a view to evolve high yielding okra hybrids..
2. After evaluation of 21 experimental hybrids along with two check varieties such as Green Finger (F1) and BARI Darosh -1 (OPV) for different quantitative characters revealed three hybrid combination like P2 X P4, P3 X P7 and P5 X P6 outstanding yield potential as compared to two check varieties.
3. Of the two seasons Kharif-1 was more favourable for cultivation of okra.

Therefore, the selected three hybrids may be advanced for further trial to release as new okra hybrid varieties.

CHAPTER V

SUMMARY AND CONCLUSION

Okra is the staple vegetable for most of the world people and it is principally eaten as a green fruit after cooking. Being a major vegetable, except usual cultivation, evaluation on green fruit potential and identification of suitable season have been given less priority. Few landraces are existing and eachlandrace differs in its agro-morphological, physico-chemical and cooking characteristics depending on the genetic background and growing environmental factors. Green fruit yield potential is influenced by the varietal characteristics and consumer preference; differ from one region to another region of our country. To cope with the growing population, urbanization, climate change, food security, nutrient security, and changing food preference, there is a need not only high green fruit yielding varieties but also for succulent soft fiber possessing improved okra varieties. In light of the facts, four experiments were sequentially conducted during July, 2015 to December, 2017. The fifty different genotypes of okra were sown in Research and Development Farm of Metal Agro Limited, Nagarchanti, Kawapukur, Debigonj, Panchagarh. For accomplishing the total investigation. However, experiment wise results and output are described below-

Experiment I: Characterization and screening of okra genotypes

The important character, plant height was recorded 25, 50, 75 and 100 days after sowing (DAS) and exhibited enonmous variation in them. Leaves per plant ranged from 5.40 to 7.00, 10.67 to 28.33, 23.80 to 85.13 and 33.80 to 114.20 who's over all mean were 6.44, 18.08, 45.71 and 54.46 respectively by the days 25, 50, 75 and 100 DAS.First flower initiation was 38.33 to 45.67 days and the mean was 41.02 and the minimum days of 50% flower initiation were 47.67 and 40 days respectively.The range of first flowering node was 3.37 to 4.40 the mean value was 4.69.The First edible fruit harvest was recorded in present experiment range from 52.33 to 44.67 and the mean value 47.50 exhibited.The maximum and minimum value and their mean were 16.07 to 11.87 and 13.82 revealed in the present investigation.The range of diameter of fruit on the present experiment was 1.70 to 2.67 and the mean value revealed 1.99. The maximum and minimum value for fruit weight per plant was 23.07 and 15.06 and the mean value arise 19.58 for the present study. The number of fruits per plant ranged from 12.67 to 42.33 and the mean value was 27.69. The maximum and minimum value for fruit yield per plant was 861.47 to 286.27 and the mean value was 552.83 for this trait. The maximum and minimum value for 100 seed weight was 8.62 to 5.88, respectively.

Among the six clusters, cluster I contained the largest having 16 genotypes, followed by cluster VI with 14 genotypes, cluster IV with 8 genotypes, cluster III with 7 genotypes, cluster II with 4 genotypes and cluster V having single genotype. The clustering pattern of genotypes was observed to be random indicating that geographical diversity and genetic divergence were independent. The cluster I comprised two genotypes, including G1 and G18, cluster II contained six genotypes including 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 the highest ten genotypes namely G8, G14, G16, G19, G22, G23, G24, G26, G28 and G30, respectively.

It was noticed that inter group distance were always higher than those intra group distance. The maximum inter cluster distance was observed between cluster II and IV (449.76), followed by I and II (350.33) and between IV and V (323.25). The lowest inter cluster distance was observed between I and III (76.60) followed by I and IV (103.11) and between V and VI (130.19) respectively. The intra cluster divergence varied from 0.00 to 58.09 which belonging V and IV (58.09) where the number of genotype one and eight. Cluster I was consisting of sixteen genotypes where the lowest mean value was observed in first flowering 4.56. number of ridge per fruit 5.02. among them cluster mean of fruit data 2.35 was the highest rest of all cluster mean on that character and number of ridge per fruit was second highest among all six cluster mean on that character. The highest cluster mean was observed in cluster I was fruit yield per plant 477.42 which was the second lowest among all the cluster for this trait. The second highest in cluster I was plant height at 100 days 130.06 and followed by plant height at 75 days 95.14, Seeds per fruit 57.22 and number of leaf at 100 days respectively. These characters were needed for early type of variety development. Cluster II had two genotypes and it observed highest cluster mean for Fruit yield per plant 824.03 which was also highest on that trait among all cluster means and followed by plant height at 100 days which was also the highest among all the cluster. The lowest value except the fruit diameter and number of ridge per fruit was node of 1st flowering 5.13 followed by number of leaf at 25 days 6.79 and 100 seed weight 7.26 respectively. The moderate value was observed in cluster II were fruit length 15.75, fruit weight 20.95, 1st flowering

41.75, 50% flowering 43.16 respectively. Cluster III was contained 7 genotypes. It possessed the lowest value in fruit diameter 2.00 followed by ridge per fruit 5.00. Number of leaf at 25 days 6.45and 100 seed weight 0.91 respectively. The height value of cluster III observed 553. 21 followed by plant height at 100 days 134.41, The moderate value was exhibited first edible fruit harvest 44.39, number of leaf at 100 days 52.02 respectively. Cluster IV had eight genotypes, the lowest value on fruit yield per plant observed in this cluster among all the cluster. Otherwise no remarkable feature was not noticed in this cluster for different characters. The single genotype which was belonging to the cluster V, it was observed lowest value of 100 seed weight 5.88, among all the cluster on that trait. and highest value of number of leaf at 100 days 114.20 among all the cluster on particular character. Cluster VI consist of 14 genotypes; it was the second highest on the number of genotypes. there was no remarkable feature noticed in this cluster for different characters. None of the genotypes included this cluster which showed the highest or lowest mean values of 20 different yield and yield contributing character of okra yield was the ultimate goal for any crop production. the highest yield was 824.03 in cluster II followed by 691.96 in cluster V and 649.28 in cluster VI. The single fruit weight observed highest in cluster II 20.95, followed by cluster VI 20.01 and cluster III 19.69 respectively. Number of Seeds per fruit observed highest value 65.27 in cluster III, followed by 59.89 in cluster VI and 57.22 in cluster I accordingly. The PCA analysis results includes the factor scores of each character among the 50 okra genotypes, Eigen value, percentage total variance account for twenty principal components (A to T) with Eigen values ranged from 0.0114 to 4.0395. The twenty principal components accounted varied percentage of total variance ranged from 0.00 to 91.83%. Cumulative percent of total variation up to PCA three with Eigen value more than unity accounted 98.76%. Vector I observed from PCA expressed that the important character responsible for genetic divergence in the major axis were days to 50% flower initiation (0.99904), 100 seed weight (0.08543), 1st flower initiation days (0.04227), node of first flowering (0.00957). Therefore, considerable emphasis should be given on these characters to increase fruit yield in okra. Other characters had minor contribution in determining genetic divergence. In vector II which was the second axis of differentiation, 100 seed weight (0.06732), number of leaf at 50 days (0.03368), plant height at 100 days (0.02848), number of leaf at 25 days (0.02004), played a major role while rest of all characters contributed less in determining genetic divergence. These characters of plant for both the vectors were positive across two axes indicating the important component of genetic divergence among the characters. Negative values were observed in vector I, number of leaf at 50 days (-0.00046), number of leaf at 100 days (-0.00097) and average fruit weight (-0.99664), days to first flowering (-0.05191) and Fruit yield per plant (-0.00042) respectively.

Experiment II: Selection of important yield contributing characters of okra

Phenotypic (rp), genotypic (rg) and environmental (re) coefficient of correlation revealed that plant height had positive and significant correlated with fruits per plant (Rg= 0.4985 **), 100 seed weight (rg= 0.3586*) and fruit yield per plant which ws (rg= 0.5770 **). Both genotypic and phenotypic level. But significant and negative was found in 50% flower initiation (-0.110 **) in phenotypic level and negative relation also revealed with fruit diameter in both genotypic and phenotypic level. Otherwise other characters showed positive correlation with plant height. Days to50% flower initiation showed positive and significant correlation in all level viz. genotypic, phenotypic and environmental level with days to First edible fruit harvest which were (rg=0.9687**), (rp=0.7997**) and (re=0.4693**) and negative and significant correlation with 100 seed weight both in genotypic and phenotypic level viz. (rg=-0.5672**), rp=-0.3687**) beside this negative correlation exhibited with seeds per fruit in both level and fruit length in genotypic level only and rest of all showed positive correlation with 50% flower initiation.

Days to first edible fruit harvest exhibited positive correlation with fruit weight (rg=0.4055**) in genotypic level. Negative and significant correlation showed with 100 seed weight viz. (rg= -0.5414**), (rp= -0.3839**) respectively. Seeds per fruit in both level and fruit diameter in environmental level showed negative correlation with first edible fruit harvest. And rest of all parameters exhibited positive correlation with first edible fruit harvest. Fruit length showed positive and significant correlation with fruit yield per plant in genotypic, phenotypic and environment level viz. (rg = 0.4666**), (rp = 0.4116**) and (re = 0.3320**) respectively also showed significant and positive correlation with fruits per plant in genotypic and phenotypic (5%) level. Significant and positive correlation with fruit weight in phenotypic (rp = 0.3155*, 5%) and environmental (re = 0.6341**) level. Negative and significant correlation observed only fruit diameter (rg = -0.0864**), also negative correlation with fruit diameter (rg = -0.3633) and fruit weight in genotypic level (rg = -0.2007), both genotypic and phenotypic level of seeds per fruit viz. (rg = -0.1718), (rp = -0.1108) respectively.Fruit diameter showed positive and significant correlation with fruit weight viz. (rg = 0.3864**), (rp = 0.3590* 5%) and (re = 0.3590* 5%) showed negative significant result for fruits per plant in genotypic level viz (-0.4023**) negative correlation also observed for Seeds per fruit in genotypic level. 100 seed weight and fruit yield per plant showed negative correlation in both genotypic and phenotypic level. Rest of all showed positive correlation with this trait. Significant and positive correlated only observed for fruit yield per plant in three level viz genotypic (rg = 0.3275*), phenotypic (rp = 0.3097*5%) and environmental (0.4104**), respectively. significant and negative correlation observed only Seeds per fruit in genotypic level (rg = -0.3265* 5%), negative correlation also observed in three levels for fruit per plant, phenotypic level in Seeds per fruit and both phenotypic and environmental level in 100 seed weight Significant and positive correlation only observed for fruit yield per plant in genotypic (rg = 0.9226**) phenotypic (rp = 0.8582**) and environmental (re = 0.6396**) level. Negative correlation exhibited Seeds per fruit and 100 seed weight and rest of all component showed possitive correlation with this trait.

100 seed weight showed positive correlation with fruit yield per plant but the result not significant in any level of significance. Seed per fruit showed all level of positive but not significant result with fruit yield per plant and with 100 seed weight found strongly negative correlation with environment (-0.4219**) but both genotypic and phenotypic correlation obtained negative with seed per fruit.

The path coefficient analysis showed that the number of fruits per plant (0.9070) had height positive direct effects on fruit yield per plant followed by fruit weight (0.4940) and days to 50% flowering initiation (0.0763) and plant height at 100 days (0.0580) respectively. The fruit length showed highest direct negative effect on yield (-0.7741), though their association was positive. And followed by fruit diameter (-0.1829), days to First edible fruit harvest (-0.1626), 100 seed weight (-0.1269) under this circumstances, a restricted simultaneous selection model was to be followed i.e. restrictions were to be imposed to nullify the undesirable indirect effects via fruit diameter (0.1987), fruits per plant (0.4551) and plant height at 100 days (0.0152), in order to make use of the direct effect, while indirect effect of fruit length via fruits per plant was high and positive. The indirect positive effects of plant height on fruits per plant (0.4522) via fruit weight (0.1248) fruit diameter (0.0133) and days to First edible fruit harvest (0.0064) and negative indirect effect on 50% flower initiation (-0.0455) respectively.The present study showed direct and positive effect on days to 50% flower initiation (0.0763), also positive and indirect effect observed with fruit weight (0.1198), 100 seed weight (0.0720) and negative effect recorded for plant height (-0.0094) followed by First edible fruit harvest (-0.1575), fruit diameter (-0.0223) and Seeds per fruit (-0.0038) respectively. Days to edible harvest showed negative and direct (-0.1626) effect on fruit yield per plant and indirect negative effect also observed on fruit length (-0.0071), followed by fruit diameter (-0.0249), plant height (-0.0023) and Seeds per fruit (-0.0041) also, and positive indirect effect recorded on days to 50% flowering, (0.0739), fruit weight (0.2003), fruits per plant (0.4522) and 100 seed weight (0.0687) respectively. The fruit diameter also showed direct and negative effect to fruit yield per plant (-0.1829) followed by fruits per plant (-0.3649), first edible fruit harvest (-0.0221), plant height (-0.0042) and positive indirect effect for 50% flowering, fruit length (0.0841), fruit weight (0.1909) and 100 seed weight (0.0150).

Experiment III: Study of combining ability in okra

For leaf number negative estimates of general combining ability (gca) effects were considered desirable. For plant height positive and significant gca effect showed three parents among seven those were P3 (13.23**), P5 (11.38**) and P7 (17.19**) respectively. Negative and significant effect showed P1 (-15.64**), P2 (-19.20**) and P4 (-7.04**). Positive and insignificant result showed only one parent P6 (0.08). For days to first flowering, negative estimates of general combining ability (gca) effects were considered desirable, since there were preferable for earliness of the parents. Because it indicates the general capacity of easy parent to transmit its behavior to progeny in cross combinations with other parents. The estimates of gca effects range from -2.48 in P2 (1171) to 1.73 in P6 (1203) out of this parent's lines, P2 (-2.48**) had negative estimates and was the best general combiner for this trait among all the genotypes followed by P1-1163 (-1.19**). Therefore, this parent might be used in the breeding program for developing early flowering i.e. early fruiting varieties. Two parents P6-1203 (1.89**) and P7 -1205 (1.00**) had significant positive estimates and therefore they were poor combiners. The rest three P3 (0.22), P4-1178 (0.15) and P5-1189 (0.41) were average combiners as it showed insignificant gca effect for this trait. Present study revealed negative and significant effect for gca were P1 (-1.60**) and P2 (-2.46**) which will be best combiner out of seven parents. Three parents showed positive and significant result

P5 (0.73**), P6 (1.73**) and P7 (0.95**) respectively. Only two parents showed positive insignificant effect P3 (0.36) and P4 (0.29) which were selected as poor combiners for this trait. Present study expressed for this character negative and positive significant difference among the parental genotype. The highest negative significant value observed in 1163 (-0.44**) genotype followed by 1171 (-0.18**) which were most desirable for highest yield. The positive and significant value observed only two genotypes i.e. 1178 (0.18*) and 1205 (0.15*0 respectively. Another three parental genotypes showed positive non-significant effect. There was no negative non-significant effect among the genotypes. Present investigation revealed negative and significant value only three parents out of seven. The highest negative and significant effect observed in parent-P_2,(-2.13**) followed by P_1 (-106**) and P_3 (-1.06**) respectively which were indicated as good combiners. The positive and significant effect found rest of four parents. The highest positive effect showed in p6 (1.53**) followed by P5(0.94**), P7(0.90**) and P4 (0.87**) respectively. Present investigation showed negative and significant effect only P_1 (-0.03*) and P_2 (-0.04*) respectively. The negative non-significant effect observed in P_3 (-0.01) and rest all four parent showed positive and in significant effect for this trait. Present study revealed positive and significant effect only one parent for this character P5 (0.53**) and positive insignificant effect showed in P6 (0.25) and P7 (0.04) respectively. The negative and significant effect observed in P1(-0.45**) and P2(-0.31*) and negative in significant effect in P3 (-0.04) and P4(-0.01) respectively. Present study revealed the result of fruits per plant within seven parental lines positive and negative significant effect. The range value obtained from -2.72* to 1.62** respectively. The highest positive significant effect observed in P6 (1.62**) followed by P5 (1.07**) respectively. The positive non-significant effect observed in P4 (0.28) and P7 (0.49) parental lines. The highest negative significant effect observed in P1 (-2.72*). The negative insignificant value found in P2(-0.26) and P3 (-0.47) respectively.

Present study showed a wide range of variation for seeds per fruit. The highest value was 3.25 to lowest value -4.54 respectively. The positive and significant value observed in P2 (3.25**) and P5 (2.49**) respectively which indicated as good combiner for this trait. Positive and insignificant found in P6 (0.50) and P7 (1.16). The negative and significant value found in P3 (-4.54**), P4 (-2.03**) and negative but insignificant value observed in P1(-0.83) respectively. Present investigation revealed 100 seed weight within 7 parents, the positive and significant value found in P6 (0.11*) and positive insignificant in P7 (0.09), P3 (0.02) respectively. The negative and significant value found in P4 (-0.16**) and negative insignificant same as P1 (-0.02), P2 (-0.02), P5 (-0.02) respectively. Present study showed fruit yield per plant was a wide of values. The highest positive significant effect observed in P6 (32.42**) followed by P5 (22.63**), P4 (20.19*) and positive insignificant found in P3 (16.16) respectively. The negative significant value found in P1 (-76.56**) only and negative insignificant observed in P2 (-13.35) and P7 (-2.21), respectively.

From the Vr-Wr graph, as parental array points are scattered around the regression line that means genetic diversity is present among the parents for the characters. Regression co-efficient is 0.27 (<1) which indicates absence of epistatic interaction or absence of non-allelic interaction to express the characters. Regression line intercept below the origin of Wr line over-dominance for for fruits yield per plant. Parents p1 is distributed to the nearest of the origin indicate it has maximum number of dominant alleles, whereas parents p2and p3 are distributed far away from the origin, i.e they have maximum number of recessive alleles; besides p2 and p3 are distributed in the middle from the origin which indicate these parents have equal frequency of dominance and recessive alleles or additive gene. The width of the parabola indicates the diversity of genotypes. And the distribution of parental array points is within the parabola.

Fruit yield per plant in 21 cross combinations present study revealed positive and significant effect in 13 cross combinations. The highest positive significant effect observed on ok-15 (P3 X P7) =218.74** followed by ok-08 (P2 X P4) =207.87**, ok-18 (P4 X P7) = 122.25**, Ok-09 (P2 x P5) =171.73**, Ok-19 (P5 X P6) =137.26** and Ok-04 (P1 X P5) =116.23** respectively. Negative significant observed only three cross combinations that was Ok-16 (P4 X P5) = -104.54**, Ok-11 (P2 X P7) = -87.23** and Ok-01 (P1 X P2) = -41.17**. The negative insignificant effect observed in two cross combinations and positive insignificant found in three combinations. Fruit yield per plant is a complex character. It depends on so many characters, such as number of fruits per plant, fruit length, fruit diameter, weight per plant, days to first flowering etc. However, most of the crosses showed positive significant heterosis over mid parent values for fruit yield per plant indicating the possibilities of exploiting those crosses for hybrid variety development. The extent of heterosis over mid parent value range from 15.82 in P2 X P7 to 110.23% in P3 X P7. The significant positive heterosis was also observed 105.54% in the cross P2 X P3, 105.38% in P2 X P4 and 101.17% in P2 X P5, respectively. The range of heterobeltiosis was obtained from 4.52 in P1X P6 to 94.09 in P2 X P3 cross combinations. The considerable heterobeltiosis was also observed in P2 X P4= 88.57, P2 X P5 = 88.61 and P3 X P7 = 76.75 respectively. On the other hand, most of the crosses showed positive significant heterosis over standard check-1 (F1 Green Finger) and check-2 (BARRI Dharosh-1 OP). The highest positive significant standard heterotic effect was found 105.02 in P3XP7 in check-1 and followed by 100.58 in P2 XP4, 94.63 in P5 X P6, respectively. For check-2 highest positive significant standard heterotic effect was found 254.21% in P3 X P6 followed by 246.53 in P2 X P4 236.25% in P5 X P6 and 231.23% in P2 X P5 respectively. These crosses can be utilized in heterosis breeding program for the improvement of fruit yield per plant in okra. Present study estimates of additive genetic variance were positive and significant for component of variation due to dominance (H_1), proportion of positive and negative genes in parents (H_2) and dominance effect (h^2) and rest three components showed positive non-significant effect for the trait. The estimated mean degree of dominance $(H_1/D)^{1/2}$ estimate was more than unity indicating over dominance or presence of repulsive phase linkage.

Experiment IV: Stability analysis of the experimental hybrids

For fruit yield per plant genotype G-5 possessed significant regression coefficient greater than unity and high mean value revealing suitability for favorable environment. G-8 followed by G-7 and G-6 possessed high mean value and regression coefficient near about value indicating well adapted to all environment but their performance cannot have predicted over environments, since their deviations from regressions from regression were non-significantly different from zero. The genotype G-2 possessed significant value for regression coefficient which greater than unity and low means value compared to population mean indicated poorly adapted to all environments. The present study showed that the magnitude of performance of different traits including yield was more in E1 than all the environments as compared to the other environments. in Table 4.28 presented various plant characters in 21 F1 of okra grown under four environments. From the estimation of environmental index (Table 4.28) it was observed that the character's plant height and leaf number were favored both in E4, while the character 1st flower and 50% flower initiation both were favored in E2 E3 and E4 and showed delay in E1 environment. Only node of 1st flowering expressed earliness in E2 among them. First edible fruit harvest also showed earliness in all environments except E1. The character fruit length expressed more favored in E1 and E2 but fruit diameter showed less effectiveness in different environmental condition. Fruit weight also showed positive effectiveness for E1 and rest all negative. The observation showed fruits per plant and fruit yield per plant highly favored in E1 and rest all environments showed less effective. Seeds per fruit also favored in E1 and E2 while100 seed weight favored for E2 and E3 environment.

REFERENCES

Abd-allah, S. (2015). Path coefficient analysis for some character on fruit and seed yield of okra. *Journal of Horticulture*, 2(2): 140-144.

Adams, C. F. (1975). *Nutritive value of American foods in common units* (No. 456). Agricultural Research Service, US Department of Agriculture.

AdeOluwa, O. O. and Kehinde, O. B. (2011). Genetic variability studies in West African okra (*Abelmoschus* caillei). *Agriculture and Biology Journal of North America*, 2(10): 1326-1335.

Adiger, S., Shanthakumar, G. and Salimath, P. M. (2013). Selection of parents based on combining ability studies in okra [*Abelmoschus esculentus* (L.) Moench]. Karnataka Journal of Agricultural Science, 26(1): 6-9.

Ahamed, K. U., Akter, B., Ara, N., Hossain, M. F. and Moniruzzaman, M. (2015). Heritability, correlation and path coefficient analysis in fifty-seven okra genotypes. *International Journal of Applied Sciences and Biotechnology*, 3(1): 127-133.

Ahiakpa, J. K., Magdy, M., Werner, O., Amoatey, H. M., Yeboah, M. A., Appiah, A. S. and Ros, R. M. (2017). Intra-specific variation in West African and Asian germplasm of okra (*Abelmoschus* spp L.). *Annals of Agricultural Sciences*, 62(2): 131-138.

Akash, M. W., Shiyab, S. M. and Saleh, M. I. (2013). Yield and AFLP analyses of interlandrace variability in okra (*Abelmoschus esculentus* L.). Life Sci. J. 10(2): 2771-2779.

Akinyele, B. O. and Osekita, O. S. (2011). Genotype environment interaction in NH47-4 variety of okra *Abelmoschus esculentus* (Linn.) Moench. *International Journal of Genetics and Molecular Biology*, 3(4): 55-59.

Akotkar, P. K., De, D. K. and Pal, A. K. (2010). Genetic variability and diversity in okra (*Abelmoschus esculentus* L. Moench). *Electronic Journal of Plant Breeding*, 1(4): 393-398.

Alake, C. O. (2018). Genotype × environment interaction effects on pod yield and pod number in West African Okra. *Archives of Agronomy and Soil Science*, 64(11): 1503-1517.

Alake, C. O. (2020). Genetic variability and diversity in okra landraces using agro-morphological traits and seed elemental minerals. *International Journal of Vegetable Science*, *26*(2), 127-149.

Allard, R. W. (1960). Principles of Plant Breeding John Wiley. *New York*.

Allard, R. W. and Bradshaw, A. D. (1964). Implications of genotypes environment interactions in applied plant breeding. *Crop Science*. 4: 503-508.

Aminu, D., Bello, O. B., Gambo, B. A., Azeez, A. H., Agbolade, O. J., Iliyasu, A. and Abdulhamid, U. A. (2016). Varietal performance and correlation of okra pod yield and yield components. *Acta Universitatis Sapientiae, Agriculture and Environment*, 8(1): 112-125.

Amiteye, S., Amitaaba, T., Akama, C. and Amoatey, H. M. (2019). Estimates of heterosis in F1 hybrid progeny of Okra (*Abelmoschus* spp. (L.) Moench), International journal of pure and applied Bioscience. 7(6): 1-8.

Amoatey, H. M., Klu, G. Y. P., Quartey, E. K., Sossah, F. L., Segbefia, M. M. and Ahiakpa, J. K. (2015). Genetic diversity studies in 29 accessions of okra (*Abelmoschus spp* L.) using 13 quantitative traits. *Journal of Experimental Agriculture International*, 217-225.

Annapurna, A. and Singh, S. P. (2018). Analysis of combining ability status and nature of gene action among hybrids for yield and quality traits in Okra [*Abelmoschus esculentus* (L.) Moench], International journal of pure and applied Bioscience. 6(2): 1547-1553.

Ariyo, O. J. (1990). Effectiveness and relative discriminatory abilities of techniques measuring genotype x environment interaction and stability in okra [*Abelmoschus esculentus* (L.) Moench]. *Euphytica*, 47(2): 99-105.

Ashraf, A. H., Rahman, M. M., Hossain, M. M. and Sarker, U. (2020). Study of correlation and path analysis in the selected Okra genotypes. *Asian Research Journal of Agriculture*, 1-11.

Ashwani, K., Baranwal, D. K., Aparna, J. and Srivastava, K. (2013). Combining Ability and Heterosis for yield and its contributing characters in okra (*Abelmoschus esculentus* (L.) Moench). *Madras. Agric. J*, 100(1-3): 30-35.

Ayesha, R., Satish, D., Hadimani, H. P. and Siddappa, R. (2017). Nature of gene action in okra (*Abelmoschus esculentus* (L.) Moench), through diallel analysis. *Int. J. Curr. Microbiol. App. Sci.* 6(10): 256-260.

Balai, T. C., Maurya, I. B., Shankar, V. and Narendra, K. (2014). Correlation and path analysis in genotypes of okra [*Abelmoschus esculentus* (L.) Moench]. *The Bioscan.* 9(2): 799-802.

Bartlett, M. S. (1937). Properties of sufficiency and statistical tests. Proceedings of the Royal Statistical Society: Series A, 160: 268–282.

BBS. (2017). Yearbook of Agricultural Statistics-2017. Bangladesh Bureau of Statistics, Statistics and Information Division (SID), Ministry of Planning, Government of Peoples' Republic of Bangladesh, Dhaka. 256-257 pp.

BBS. (2018). Yearbook of Agricultural Statistics-2018. Bangladesh Bureau of Statistics, Statistics and Information Division (SID), Ministry of Planning, Government of People s' Republic of Bangladesh, Dhaka. 252-253 pp.

BBS. (2019). Yearbook of Agricultural Statistics-2019. Bangladesh Bureau of Statistics, Statistics and Information Division (SID), Ministry of Planning, Government of People s' Republic of Bangladesh, Dhaka. 285-286 pp.

Bello, O. B., Abdulmaliq, S. Y., Ige, S., Mahamood, J., Oluleye, F., Azeez, M. A. and Afolabi, M. S. (2012a). Evaluation of early and late/intermediate maize varieties for grain yield potential and adaptation to a southern guinea savanna agro-ecology of Nigeria. *International Journal of Plant Research*, 2(2): 14-21.

Bello, O. B., Afolabi, M. S., Ige, S. A., Abdulmaliq, S. Y., Azeez, M. A. and Mahmood, J. (2012b). Nitrogen use efficiency and grain yield in a diallelic cross of maize populations. *International Journal of Plant Research.* 2(3), 94-102.

Bello, O. B., Afolabi, M. S., Ige, S. A., Abdulmaliq, S. Y., Azeez, M. A. and Mahmood, J. (2011). Yield response of diallelic crossed maize (*Zea mays* L.) genotypes to varying nitrogen regimes in Nigeria. *Journal of Bio-Science.* 19: 43-52.

Bello, O. B., Olawuyi, O. J., Ige, S. A., Mahamood, J., Afolabi, M. S., Azeez, M. A. and Abdulmaliq, S. Y. (2014a). Agro-nutritional variations of quality protein maize (*Zea mays* L.) in Nigeria. *Journal of Agricultural Sciences (Belgrade)*, 59(2): 101-116.

Bello, O. M., Olawuyi, O. J., Abdulmaliq, S. Y., Ige, S., Mahamood, J., Azeez, M. A. and Afolabi, M. S. (2014b). Yield performance and adaptation of early and intermediate drought-tolerant maize genotypes in Guinea Savanna of Nigeria. *Sarhad Journal of Agriculture*, 30(1): 53-66.

Bendale, V. W., Madav, R. R., Bhave, S. G. and Pethe, U. B. (2004). Heterosis and combining ability of Okra (*Abelmoschus esculentus* (L.) Moench) cultivars. *Journal of Soils and Crops.* 14: 269-272.

Bhalekar, S. G., Desai, U. T., Mote, P. U. and Pawar, B. G. (2006). Combining ability studies in okra. *Journal of Maharashtra Agricultural Universities*, 31(2): 182-184.

Bhatt, J. P. (2011). Diallel analysis for fruit yield, its components and quality traits in okra [*Abelmoschus esculentus* (L.) Moench]. Unpublished M.Sc. (Agri.) thesis submitted to Anand Agricultural University, Anand.

Bimal, C. K. (2008). *Morpho-Biochemical Diversity and Heterosis in Bitter gourd (Momordica charantia L.)* (Doctoral dissertation, Ph. D Dissertation. Dept. of Hort. BSMRAU, Salna, Gazipur. Bangladesh).

Bulmer, M. G. (1980). *The mathematical theory of quantitative genetics*. Clarendon Press.

Burton, G. W. (1952). Quantitative inheritance in grasses. *Pro VI Int Grassl Cong*, 1952: 277-283.

Chahal, G. S. and Gosal, S. S. (2002). *Principles and procedures of plant breeding: Biotechnological and conventional approaches*. Alpha Science Int'l Ltd.

Chandramouli, B., Dorajee Rao, A. V. D., Shrihari, D. and Paratpara Rao, M. (2015). Desirable cross combinations based on cluster analysis among okra (*Abelmoschus esculentus* Linn.) genotypes. In *III international symposium on underutilized plant species 1241* (pp. 231-238).

Chandramouli, B., Paratpara Rao, M., Shrihari, D. and Dorajee Rao, A. V. D. (2019). Correlation and path co-efficient analysis in Okra (*Abelmoschus esculentus* Linn.) genotypes. Acta Hortic. 1241: 221-230.

Comstock, K. and Robinson, P. R. (1952). Estimation of genetic advance. Ind. J. Hill. 6(2): 171– 174.

Comstock, R. E. and Moll, R. H. (1963). *Genotype environment interactions. Statistical genetics and plant breeding* (No. REP-1173. CIMMYT.).

Dabholkar, A. R. (1992). Elements of Biometrical Genetics. Concept Publishing Company, New Delhi, India.

Dahake, K. D. and Bangar, N. D. (2006). Combining ability analysis in Okra. Journal of Maharashtra Agricultural Universities. 31: 39-41.

Datta, P. C. and Naug, A. (1968). A few strains of *Abelmoschus esculentus* (L.) Moench their karyological in relation to phylogeny and organ development. *Beitr. Biol. Pflanzen*, 45: 113-126.

Demelie, M., Mohamed, W. and Gebre, E. (2015). Genetic diversity of ethiopian Okra collections through multivariate analysis at Werer, Rift Valley of Ethiopia. *The International Journal of Science and Technoledge*, 3(8): 186.

Devi, A. P., Bhattacharjee, T., Banerjee, S., Maurya, P. K., Chatterjee, S. and Chattopadhyay, A. (2020). Heterotic expression of okra hybrids for tolerance to enation leaf curl virus. *International Journal of Vegetable Science*, 26(2): 163-189.

Devi, E. S., Singh, N. B., Devi, A. B., Singh, N. G. and Laishram, G. M. (2005). Gene action for fruit yield and its components in tomato (*Lycopersicon esculentum* Mill.) Indian Journal of Genetics and Plant Breeding. 65: 221-222.

Devi, N. D. and Mariappan, S. (2013). Genetic variability, heritability and genetic advance for yield and its components snake gourd (*Trichosanthes anguina* L.). African J. Agric. Res., 26: 3857-3859.

Devi, S., Choudhary, B. R. and Verma, I. M. (2017). Combining ability analysis for yield and yield contributing characters in okra [*Abelmoschus esculentus* (L.) Moench]. *The Bioscan*, 12(3): 1593-1596.

Dewey, D. R. and Lu, K. (1959). A Correlation and path-coefficient analysis of components of crested wheatgrass seed production 1. *Agronomy Journal*, 51(9): 515-518.

Dhall, R. K., Arora, S. K. and Rani, M. (2000). Correlation and path analysis in advanced generations of Okra [*Abelmoschus esculentus* (L.) Moench.]. *Indian Journal of Horticulture*, 57(4): 342-346.

Dhruv, P. S. (2015). Thesis, Study on Genetic variability, Correlation and Path Analysis in Okra (*Abelmoschus esculentus* (L.) moench). Jawaharlal Nehru Krishi Vishwa Vidyalaya. Jabalpur, Madha pradesh, India. PP. 36

Duggi, S., Magadum, S. K., Srinivasraghavan, A. and Oommen, S. K. (2013). Correlation analysis in Okra (*Abelmoschus esculentus* (L.) moench). *Bioinfolet-A Quarterly Journal of Life Sciences*, 10(2b): 632-636.

Düzyaman, E. (2005). Phenotypic diversity within a collection of distinct okra (*Abelmoschus* esculentus) cultivars derived from Turkish land races. *Genetic Resources and Crop Evolution*, 52(8): 1019-1030.

Duzyaman, E. and Vural, H. (2002). A study on heterosis in yield among okra genotypes from different eco-geographic origin. *Ege Universitesi Ziraat Fakultesi Dergisi*, 39: 9-16.

East, E. M. and Hayes, H. K. (1912). Heterozygosis in evolution and in plant breeding. US Department Agric. *Bulletin.* 243.

Eberhart, S.A. and Russell, W.L. (1966). Stability parameters for comparing varieties . Crop Science. 6: 36-40.

El-Sherbeny, G. A. R., Obiadalla-Ali, H. A. and El-Gendy, S. E. A. (2005). Estimates of genetic parameters using line by tester analysis for some economic traits in Okra (*Abelmoschus esculentus* L.) under different nitrogen levels. *Assuit Journal Agriculture Science*, 36(5): 121-134.

Eswaran, R. and Kumar, S. T. (2013). Studies on the heterotic potential of single and three-way cross hybrids of okra (*Abelmoschus esculentus* (L.) Moench. *Paripex-Indian Journal of Research (PIJR)*, 2: 1-3.

Ezekiel, S. A., Ariyo, O. J. and Kehinde, O. B. (2011). Stability assessment of some West African okra (*Abelmoschus caillei*) genotypes in Nigerian Genebank. Journal of Life Sciences. 5: 906-912.

Fehr, W. R. (1987). Heterosis. *Principles of cultivar development; Theory and techniques*, 1.

Fonseca, S. and Patterson, F. L. (1968). Hybrid Vigor in a Seven Parent Diallel Cross in Common Winter Wheat (*Triticum aestivum* L.) 1. *Crop Science*, 8(1): 85-88.

Ford, C. E. (1938). A contribution to a cytogenetical survey of the Malvaceae. *Genetica*, 20(5-6): 431-452.

Fresh Plaza. (2020). Bangladesh: Vegetable production rises by 32% in five years.

Gauch, H. G. and Zobel, R. W. (1996). AMMI analysis of yield trials. In M.S. Kang and H.G. Gauch, Jr. (eds.), Genotypeby-environment interaction, pp. 85-122. CRC Press, Boca Raton, FL.

Gerrano, A. S. (2017). Preliminary study on variability and heritability estimates of micronutrient composition in the immature fruits of okra (*Abelmoschus esculentus*) genotypes in South Africa. *Cogent Food and Agriculture,* 3(1): 1408253.

Ghai, T. R., Jindal, S. K. and Deepak, A. (2009). Genotype x environment interactions for fruit traits in Okra (*Abelmoschus esculentus* L. Moench). *Crop Improvement.* 36(2): 72-79.

Gogineni, S., Arya, K., Issac, S. R. and Kuriakose, J. M. (2015). Character association and path analysis for yield and yield components in okra (*Abelmoschus esculentus* (L.) Moench). *International Journal of Scientific Research*, 4(6): 141-143.

Gopalan, C., Sastri, B. R., Balasubramanian, S. C., Rao, B. S. N., Deosthale, Y. G. and Pant, K. C. (2007). Nutritive value of Indian foods. Hyderabat: National Institute of Nutrition, Indian Council of Medical Research.

Grafius, J. E. (1959). Heterosis in Barley. *Journal of Agronomy.*, 51: 515-518

Griffing, B. R. U. C. E. (1956). Concept of general and specific combining ability in relation to diallel crossing systems. *Australian journal of biological sciences,* 9(4): 463-493.

Hadiya, D. N., Mali, S. C., Gamit, A. M. and Sangani, J. L. (2018). Combining ability studies in okra [*Abelmoschus esculentus* (L.) Moench]. *Journal of Pharmacognosy and Phytochemistry,* 7(5): 2525-2528.

Hamada, M., El-Aziz, A. and Zaater, M. (2015). Nature of gene action for some economic traits and combining ability in several geneotypes of okra. *Journal of Agricultural Chemistry and Biotechnology*, 6(3): 53-63.

Hayman, B. I. (1954). The theory and analysis of diallel crosses. Genetics. 39: 789-809.

Hayman, B. I. (1958). The theory and analysis of diallel crosses II. Genetics. 43: 63-65.

Hazem, A. O. A., Eldekashy, M. H. Z. and Helaly, A. A. (2013). Combining ability and heterosis studies for yield and its components in okra [*Abelmoschus esculentus (*L.) Moench]. *American-Eurasian Journal of Agricultural and Environmental Sciences.* 13(2): 162-167.

Hazra, P. and Basu, D. (2000). Genetic variability, correlation and path analysis in okra. *Annals of Agricultural Research*, 21(3): 452-453.

Hutchinson, J. and Dalziel, J. M. (1958). Flora of West Tropical Africa. *Flora of West Tropical Africa. The British West African Colonies, British Cameroons, the French and Portuguese Colonies south of the Tropic of Cancer to Lake Chad, and Fernando Po., 1*(Part II).

IBPGR. (1990): Report of international workshop on Okra genetic resources. National Bureau for plant genetic Resources (NBPGR), New Delhi, India

Ibrahim, E. A. A., Abed, M. Y. and Moghazy, A. M. (2013). Genetic behavior of families selected from some local okra (*Abelmoschus esculentus* L. Moench) populations in Egypt. *Plant Breeding and Biotechnology*, 1(4): 396-405.

Jagan, K., Reddy, R. K., Sujatha, M., Sravanthi, V. and Reddy, M. S. (2018). Heterosis for yield and yield components in okra (*Abelmoschus esculentus* L.). *Journal of Pharmacy and Biological Sciences*, 7: 69-70.

Jaiprakashnarayan, R. P. (2003). Studies on genetic variance and heterosis in okra. *M.Sc.(Agri.) Thesis*, University of Agricultural Sciences, Dharwad.

Jaiprakashnarayan, R. P. and Ravindra, M. (2004). Correlation and path analysis in okra [*Abelmoschus esculentus* (L.) Moench]. *Indian Journal of Horticulture*, 61(3): 232-235.

Jindal, S. K. and Ghai, T. R. (2005). Diallel analysis for yield and its components in okra. *Vegetable Science*, 32(1): 30-32.

Jindal, S. K., Arora, D. and Ghai, T. R. (2008). Stability analysis for earliness in okra (*Abelmoschus esculentus* (L.) Moench), Research Journal of Punjab Agriculture University. 45(3 and 4): 148 – 155.

Jindal, S. K., Arora, D. and Ghai, T. R. (2009). Heterobeltiosis and combining ability for earliness in okra [*Abelmoschus esculentus* (L.) Moench]. *Crop Improvement,* 36(2): 59-66.

Jinks, J. L. (1954). The analysis of continuous variation in a diallel cross of Nicotiana rustica varieties. *Genetics*, 39(6): 767.

Jinks, J. L. and Hayman, B. I. (1953). The analysis of diallel crosses. Maize Genetics Cooperative News Letter. 27: 48-54.

Johnson, H. W., Robinson, H. F. and Comstock, R. E. (1955). Estimates of genetic and environmental variability in soybeans . *Agronomy Journal*, 47(7): 314-318.

Joshi, J. L., Jayalakshmi, G., Rajan, R. E. B. and Muralidharan, A. (2019). Studies on gene action and combining ability for earliness, fruit yield and yield contributing characters in Bhendi (*Abelmoschus esculentus* L. Moench). *Plant Archives*, 19(2): 2964-2966.

Kang, M. S. (1998). Using genotype-byenvironment interaction for crop cultivar development. *Advance Agronomy.* 62: 199-252.

Kang, M. S., Aggarwal, V. D. and Chirwa, R. M. (2006). Adaptability and stability of bean cultivars as determined via yield stability statistic and GGE biplot analysis. *Journal of Crop Improvement.* 15(1): 97-120.

Kayande, N. V., Kumbhalkar, H. B. and Shinde, S. (2018). Selection of parents based on combining ability studies in Okra (*Abelmoschus esculentus* L. Moench). International Journal of Current Microbiology and Applied Sciences. Special Issue-6: 1935-1940.

Kearsey, M. J. and Pooni, H. S. (1996). The genetic analysis of quantitative traits. Champman and Hall, London.

Kerure, P. and Pitchaimuthu, M. (2019). Evaluation for heterosis in okra [*Abelmoschus esculentus* (L.) Moench]. *Electronic Journal of Plant Breeding,* 10(1): 256-263.

Kerure, P., Pitchaimuthu, M. and Hosamani, A. (2017). Studies on variability, correlation and path analysis of traits contributing to fruit yield and its components in okra (*Abelmoschus esculentus* L. Moench). *Electronic Journal of Plant Breeding*, 8(1): 134-141.

Khattak, G. S. S., Ashraf, M. and Zamir, R. (2004). Gene action for synchrony in pod maturity and indeterminate growth habit in mungbean (*Vigna radiata* (L.) Wilczek). Pakistan Journal of Botany. 36: 589-594.

Kishor, D. S., Arya, K., Duggi, S., Magadum, S., Raghavendra, N. R., Venkateshwaralu, C. and Reddy, P. S. (2013). Studies on heterosis for yield and yield contributing traits in okra (*Abelmoschus esculentus* (L.) Moench). *Molecular Plant Breeding*, *4*.

Kishor, D. S., Duggi, S., Arya, K. and Magadum, S. (2013). Combining ability studies in okra (*Abelmoschus esculentus* (L.) Moench). *Bioinfolet-A Quarterly Journal of Life Sciences*, 10(2a): 490-494.

Koh, H. J. (2016). Genotypic Variation among Okra (*Abelmoschus esculentus* (L.) Moench) Germplasms in South India.

Korla, B. N. and Rastogi, K. B. (1979). A note on phenotypic stability for fruit yield in Bhindi. The *Punjab Horticultural Journal*. 19: 182-83.

Kumar, A. M. I. T., Verma, R. B., Solankey, S. S. and Adarsh, A. N. U. P. A. M. (2015). Evaluation of okra (*Abelmoschus esculentus*) genotypes for yield and yellow vein mosaic disease. *Indian Phytological society*. 68(2): 201-206.

Kumar, A., Baranwal, D. K., Aparna, J. and Srivastava, K. (2013). Combining ability and heterosis for yield and its contributing characters in Okra (*Abelmoschus esculantus* (L.) Moench). *Journal of Madras Agriculture.*, 100(1-3): 30-35.

Kumar, A., Kumar, M., Sharma, V. R., Singh, M. K., Singh, B. and Chand, P. (2019). Genetic variability, heritability and genetic advance studies in genotypes of Okra [(*Abelmoschus esculentus* (L.) Moench]. *Journal of Pharmacognosy and Phytochemistry*, 8(1): 1285-1290.

Kumar, M., Yadav, A. K., Yadav, R. K., Singh, H. C., Yadav, S. and Yadav, P. K. (2013). Genetic analysis of yield and its components in okra (*Abelmoschus esculentus* (L) Moench). *Vegetable Science*, 40(2): 198-200.

Kumar, N. S. and Anandan, A. (2006). Combining ability and heterosis for fruit yield characters in Okra (*Abelmoschus esculentus* L. Moench). *International Journal of Plant Science*, 1(1): 88-91.

Kumar, N. S., Saravanan, K., Sabesan, T. and Ganesan, J. (2005). Genetics of yield components in Okra (*Abelmoschus esculentus* (L.) Moench). Indian Journal of Agricultural Research. 39: 150- 153.

Kumar, N., Saravaiya, S. N., Patel, A. I. and Nazaneen, N. S. (2015). Heterosis studies in Okra *[Abelmoschus esculentus* (L.) Moench*]. Trends Bioscience*, 8(1): 236-241.

Kumar, N.S. (2011). Genetic analysis of diallel cross for fruit yield and its component traits in okra (*Abelmoschus esculentus* (L.) Moench), plant archives, 1(2): 719-721.

Kumar, R., Yadav, J. R., Tripathi, P. and Tiwari, S. K. (2005). Evaluating genotypes for combining ability through diallel analysis in okra. *Indian Journal of Horticulture,* 62: 88-89.

Kumar, S. and Pathania, N. K. (2011). Combining ability and gene action studies in okra. *Journal of Research,* 48(1and2): 43-47.

Kumar, S. and Reddy, M. T. (2016). Combining ability of inbred lines and half-diallel crosses for economic trait in okra [*Abelmoschus esculentus* (L.) Moench]. *Jordan Journal of Agricultural sciences,* 12(2): 479-498.

Kumar, S. and Thania, N. K. (2007). Heterosis and combining ability studies for shoot and fruit borer infestation *(Earias* spp.) in okra *(Abelmoschus esculentus* (L.) Moench). The Asian Journal of Horticulture. 2: 126-130.

Kumar, S. and Yadav, Y. C. (2009). Correlation coefficient and path analysis studies in okra [*Abelmoschus esculentus* (L.) Moench]. *Annals of Horticulture*, *2*(2): 166-170.

Kumar, S. C. S. (2019). Exploitation of heterosis for yield and yield attributes in okra [*Abelmoschus esculentus* (L.) Moench]. *IJCS*, 7(4): 853-857.

Kumar, S. N. (2011). Genetic analysis of diallel cross for fruit yield and its component traits in okra [*Abelmoschus esculentus* (L.) Moench]. *Plant Archives,* 1(2): 719-721.

Kumar, S. P., Sriram, P. and Karuppiah, P. (2006). Studies on combining ability in okra *[Abelmoschus esculentus* (L.) Moench*]. Indian Journal of Horticulture*, 63: 182-184.

Kumar, S. P., Sriram, P. and Karuppiah, P. (2006). Studies on combining ability in okra (*Abelmoschus esculentus* (L.) Moench). Indian Journal of Horticulture. 63:182-184.

Kumar, S., Dagnoko, S., Haougui, A., Ratnadass, A., Pasternak, N. and Kouame, C. (2010). Okra (*Abelmoschus* spp.) in West and Central Africa: Potential and progress on its improvement. *African Journal of Agricultural Research*, *5*(25): 3590-3598.

Kumar, S., Singh, A. K., Yadav, H. and Verma, A. (2017). Heterosis study in Okra [*Abelmoschus esculentus* (L.) Moench] genotypes for pod yield attributes. *Journal of Applied and Natural Science*, *9*(2): 774-779.

Kumari, A., Singh, V. K., Kumari, M. and Kumar, A. (2019). Genetic variability, correlation and path coefficient analysis for yield and quality traits in Okra [*Abelmoschus esculentus* (L.) Moench]. *International Journal Current Microbiology and Applied Sciences.*, *8*(6): 918-926.

Liou-Minli, Guo-Jiewei, Wu-Shutu, Liou-Ml, Guo, J. W. and Wu, S. T. (2002). Combining ability analysis of yield components in okra. *Journal of Agriculture and Forestry,* 51: 1-9.

Maciel, G. M., Luz, J. M., Campos, S. F., Finzi, R. R. and Azevedo, B. N. (2017). Heterosis in okra hybrids obtained by hybridization of two methods: Traditional and experimental. *Horticultura Brasileira,* 35(1): 119-123.

Mahalanobis, P. C. (1936). On the generalized distance in statistics. *National Institute of Science of India.* 2: 49-55.

Massucato, L. R., Nakamura, K. K., Ruas, P. M., Zeffa, D. M., Silva, D. J. H. D. and Gonçalves, L. S. A. (2020). Genetic diversity among Brazilian okra landraces detected by morphoagronomic and molecular descriptors. *Acta Scientiarum. Agronomy*, 42.

Medagam, T. R., Kadiyala, H., Mutyala, G. and Hameedunnisa, B. (2013). Heterosis for yield and yield components in okra [*Abelmoschus esculentus* (L.) Moench]. *Chilean Journal of Agricultural Research.*, 72(3): 316-325.

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

Mehta, N., Asati, B. S. and Mamidwar, S. R. (2007). Heterosis and gene action in okra. *Bangladesh Journal of Agricultural Research*, 32(3): 421-432.

Mihretu, Y., Weyessa, G. and Adugna, D. (2014). Variability and association of quantitative characters among okra (*Abelmoschus esculentus* (L.) Moench) collection in south western Ethiopia. *Journal of Biological Sciences*, 14(5): 336-342.

Miller, P. A., Williams Jr, J. C., Robinson, H. F. and Comstock, R. E. (1958). Estimates of genotypic and environmental variances and covariances in upland cotton and their implications in selection 1. *Agronomy Journal*, *50*(3): 126-131.

Mishra, A. Mishra, H. N., Senapati, N. and Tripathy, P. (2015). Genetic variability and correlation studies in okra [*Abelmoschus esculentus* (L.) Moench]. *Electronic Journal of Plant Breeding*, 6(3): 866-869.

Mistry, P. M. (2012). Heterosis, heterobeltiosis and inbreeding depression in okra [*Abelmoschus esculentus* (L). moench]. *Agricultural Science Digest-A Research Journal*, *32*(4): 332-335.

Mohammed, A. K., Oladiran, J. A., Gana, A. S. and Bashir, M. (2020). Variability studies among some okra (*Abelmoschus esculentus* L. Moench.) accessions from Niger State, Nigeria.

Mrinmoy, D., Asif, M., Venkatesha, K. T. and Kumar, V. (2013). Nature of gene action in okra through diallel analysis. *Asian Journal of Biological Science,* 8(1): 145-146.

Nadkarni, K. M. (1927). Indian meterica media Nadkarni and Co., Bombay.

Namita, R., Dr Mulge, R. and Arunkumar, K. (2014). Stability Assesment in Okra *Abelmoschus esculantu* L. Moench Paripex. Indian Journal of Research, 3(6): 98-100.

Narkhade, G. W., Deshmukh, S. B. and Mahajan, R. C. (2015). Correlation coefficient and path analysis studies in Okra (*Abelomoschus esculentus* L Moench). *Ecology, Environment and Conservation paper,* 21: 285-88.

Ndunguru, J. and Rajabu, A. C. (2004). Effect of okra mosaic virus disease on the above-ground morphological yield components of okra in Tanzania. *Scientia Horticulturae*, 99(3-4): 225-235.

Nichal, S. S., Datke, S. B., Deshmukh, D. T., Patil, N. P. and Ujjainkar, V. V. (2000). Diallel analysis for combining ability studies in okra (*Abelmoschus esculentus* (L.) Moench). *Annals of plant Physiology*, 14(2): 120-124.

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

Nistor, T., Sturzu, R., Nistor, G., Mirlogeanu, S. and Anghel, J. (2005). Genetic control of the agronomically useful genetic traits in cotton. *Romanian Agricultural Research* 22: 27-32.

Nwangburuka, C. C. and Denton, O. (2011). Genotype x environment interaction and seed yield stability in cultivated okra using the additive main effect and multiplicative interaction (AMMI) and genotype and genotype x environment interaction (GGE). *Archives of Applied Science Research*, *3*(4): 193-205.

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 Journal of Agricultural Research*, 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 Journal of Biotechnology*, 10(54): 11165-11172.

Olaoye, G., Bello, O. B., Olayiwola, L. S. and Abubakar, A. Y. (2009). Analyses of moisture deficit grain yield loss in drought tolerant maize (*Zea mays* L.) germplasm accessions and its relationship with field performance. *African Journal of Biotechnology*. 8(14): 3229-3238.

Olawuyi, O. J., Bello, O. B., Ntube, C. V. and Akanmu, A. O. (2015). Progress from selection of some maize cultivars' response to drought in the derived savanna of Nigeria. *AGRIVITA J. Agric. Sci.* 37(1): 8-17.

Olayiwola, M. O. and Ariyo, O. J. (2013). Relative discriminatory ability of GGE biplot and YSi in the analysis of genotype x Environment interaction in okra (*Abelmoschus esculentus* (L.) Moench). *International Journal of Plant Breeding. and Genetics.* 7(3): 146-158.

Olayiwola, M. O., and Ariyo, O. J. (2015). Inter-character relationships of okra traits as affected by environment. *International Journal of Vegetable Science*, 21(3): 249-263.

Osekita, O. S. and Akinyele, B. O. (2008). Genetic analysis of quantitative traits in ten cultivars of Okra-*Abelmoschus esculentus* (Linn.) Moench. *Asian J. Plant Sci*, 7(5): 510-513.

Padadalli, S., Satish, D., Babu, A. G., Chittapur, R., Prabhuling, G., and Peerjade, D. (2019). Studies on combining ability in okra [*Abelmoschus esculentus* (L.) Moench] through Line X Tester analysis for productivity and quality traits. *Journal of Pharmacognosy and Phytochemistry*, 8(4): 639-643.

Pandey, A. K., Sharma, P. K. and Yadav, G. C. (2016). Genetic divergence analysis of Okra (*Abelmoschus esculentus* L. Moench). *Indian Horticulture Journal*, 6(2): 168-170.

Patil, B. T., Rode, V. R., Bhalekar, M. N. and Shinde, K. G. (2016). Correlation and path analysis studies in okra (*Abelmoschus esculentus* L. Moench). *Vegetable Science*, 43(2): 226-229.

Patil, S. S., Desai, D. T., Patil, P. P. and Patel, S. R. (2017). Genotype x environment interaction for fruit yield and component characters in okra [*Abelmoschus esculentus* (L.) Moench]. *Electronic Journal of Plant Breeding*, *8*(3): 787-791.

Patra, N. R., Nayak, N. J. and Baisakh, B. (2018). Evaluation of elite genotypes for YVMV resistance in Okra (*Abelmoschus esculentus* (L.) Moench). *Int. J. Curr. Microbiol. App. Sci*, 7(12): 594-608.

Patro, T. S. K. and Ravisankar, C. (2004). Genetic variability and multivariate analysis in okra (*Abelmoschus esculentus* (L.) Moench). Tropical Agriculture Research. 16: 99 – 113.

Patro, T. S. K. and Ravisankar, C. (2014). Genetic variability and multivariate analysis in okra [*Abelmoschus esculentus* (L.) Moench]. *Tropical Agricultural Research*, 16: 99-113.

Perkins, J. M. and Jinks, J. L. (1971). Specificity of the interaction of genotypes with contrasting environments. *Heredity*, 26(3): 463-474.

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

Pithiya, D. J., Jethava, A. S., Zinzala, S. N. and Vachhani, J. H. (2020). Study on combining ability in okra [*Abelmoschus esculentus* (L.) Moench. *IJCS*, 8(1): 676-679.

Prakash, M., Alloli, T. B., Satish, D., Mansur, C. P., Raghavendra, S. and Hadimani, H. P. (2017). Genetic diversity analysis in Okra (*Abelmoschus esculentus* (L.) Moench) Genotypes for Productivity and Quality Traits. *International Journal of Current Microbiology and Applied Sciences.*, 6(10): 2951-2956.

Prakash, M., Kumar, B. S., Padmavathi, S. and Sathyanarayanan, G. (2012). Studies on combining ability and heterosis through full diallel analysis in bhendi [*Abelmoschus esculentus* (L.) Moench]. *Crop Research*, 43(1to3): 81-84.

Prakash, M., Kumar, M. S., Saravanan, K., Kannan, K. and Ganesan, J. (2002). Line x tester analysis in okra. *Annals of Agricultural Research*. 23: 233-237.

Priyanka, D. V., Reddy, M. T., Begum, H., Sunil, N. and Jayaprada, M. (2018). Studies on genetic variability, heritability and genetic advance in genotypes of okra [*Abelmoschus esculentus* (L.) moench]. *International Journal of Current Microbiology and Applied Sciences*, *7*(5): 401-411.

Punia, M. and Garg, D. K. (2019). General and specific combining ability effects and variances for fruit yield and its contributing traits in Okra (*Abelmoschus esculentus* (L.) Moench). *International Journal of Chemical Studies.* 7(1): 1824-1830.

Raghuvanshi, M., Singh, T. B., Singh, A. P., Singh, U., Singh, V. P. and Singh, B. (2011). Combining ability analysis in Okra [*Abelmoschus Esculantus* (L.) Moench]. *Vegetable Science*, 38(1): 26-29.

Rahman, S. M. H. E. (2006). *Genetic diversity, combining ability and interrelationships among yield components in Sweet Gourd (Cucurbita moschata)*, Ph.D Dissertation. Dept. of Hort. BAU, Mymensingh, Bangladesh).

Rajat, S., Poonam, K., Rishu, S. and Sahare, H. A. (2018). Correlation studies in okra (*Abelmoschus esculentus* L. Moench) genotypes. *Plant Archives*, 18(2): 1871-1874.

Ramesh, P., Syamal, M. M., Singh, A. K. and Pathak, R. (1998). Line X tester analysis for combining ability in okra (*Abelmoschus sculentus* L. Monch). *Recent Horticulture*, 4: 127-132.

Ramya, K., and Kumar, N. S. (2010). Heterosis and combining ability for fruit yield in okra (*Abelmoschus esculenths* (L.) Moench). *Crop Improvement*, 37(1): 41-45.

Rani, C. I., Veeraragavathatham, D. and Muthuvel, I. (2002). Combining ability analysis in certain okra hybrids (*Abelmoschus esculentus* (L.) Moench) and parents. *Madras Agricultural Journal*, 89(10-12): 608-612.

Ranpise, P. S., Joshi, V. R. and Patil, B. T. (2018). Diversity studies in okra (*Abelmoschus esculentus* L. Moench.). *Journal of Pharmacognosy and Phytochemistry*, 7(1): 1412-1414.

Rao, C. R. (1952). Advanced statistical methods in biometric research. *New York*, 351-382.

Rao, T. S. (1978). Genotype x environment interactions in okra (*Abelmoschus esculentus* (L.) Moench) [India]. *Madras Agricultural Journal*. 85(12): 775-778.

Raval, V. A. I., Patel, J. M., Vashi, C. B. and Chaudhari, B. N. (2019). Correlation and path analysis studies in okra (*Abelmoschus esculentus* (L.) Moench). *International Journal of Chemical Studies*, 7(1): 1230-1233.

Raval, V., Patel, A. I., Rathod, S., Sumita, Z. and Chaudhari, B. N. (2018). Genetic variability, heritability and genetic advance studies in okra (*Abelmoschus esculentus* (L.) Moench). *International Journal of Chemical Studies*, 6(3): 3319-3321.

Reddy, K. R., Singh, R. P. and Rai, A. K. (1985). Variability and association analysis in okra. *Madras Agric. J*, 72(8): 478-480.

Reddy, M. A., Sridevi, O., Salimath, P. M. and Nadaf, H. L. (2013). Combining ability for yield and yield components through diallel analysis in Okra [*Abelmoschus esculentus* (L.) Moench]. *IOSR Journal of Agriculture and Veterinary Science*, 5(2): 01-06.

Reddy, M. T. (2010). Genetic diversity, heterosis, combining ability and stability in okra (*Abelmoschus esculentus* (L.) Moench). PhD Thesis. Acharya N.G. Ranga Agricultural University, Rajendranagar, Hyderabad, India.

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]. *Journal of Agricultural Technology,* 8(2): 611-623.

Ren, J., McFerson, J., Kresovich, R. L. S. and Lamboy, W. F. (1995). Identities and Relationships among Chinese Vegetable Brassicas as Determined by Random Amplified Polymorphic DNA Markers. 120(3): 548-555.

Rewale, V. S., Bendale, V. W., Bhave, S. G., Madav, R. R. and Jadhav, B. B. (2003). Heterosis for yields and yield components in okras. *Journal of Maharashtra Agricultural Universities (India)*. 28(3): 247-249.

Riggs, T. J. (1988). Breeding F1 hybrid varieties. *Journal of Horticultural Sciences,* 63: 362-369.

Rojas, B. A. and Sprague, O. F. (1952). A Comparison of Variance Components in Corn Yield Trials: III. General and Specific Combining Ability and Their Interaction with Locations and Years 1. *Agronomy Journal*, 44(9): 462-466.

Rynjah, S., Arumugam, T., Ganesan, K. N. and Kamalkumaran, A. (2020). Correlation and path coefficient analysis studies in okra (*Abelmoschus esculentus* (L.) Moench). *Journal of Pharmacognosy and Phytochemistry*, 9(3): 1423-1427.

Sanganamoni, M., Patil, H. B. and Ajjappalavara, P. S. (2017). Correlation and path coefficient studies on growth earliness and yield parameters in okra, *Abelmoschus esculentus* (L) Moench. *International Journal of Farm Sciences*, 7(4): 81-86.

Sanket, J., More, K. N., Chaudhari, G. B., and Chawla, S. L. (2018). Genotype x environment interaction and stability analysis for earliness, seed yield and fruit yield in Okra using the additive main effect and multiplicative interaction

(AMMI). *International Journal of Current Microbiology and Applied Sciences*. 7(03): 373-383.

Sapavadiya, S. B., Kachhadia, V. H., Savaliya, J. J., Sapovadiya, M. H. and Singh, S. V. (2019). Heterosis studies in okra (*Abelmoschus esculentus* (L.) Moench). *The Pharma Innovation Journal,* 8(6): 408-411.

Sekyere, D. O., Akromah, R., Nyamah, E. Y., Brenya, E. and Yeboah, S. (2012). Evaluation of some okra (*Abelmoschus esculentus* (L.) Moench) germplasm in Ghana. African Journal of Plant Science. 6(5): 166-178.

Seth, T., Chattopadhyay, A., Chatterjee, S., Dutta, S. and Singh, B. (2016). Selecting parental lines among cultivated and wild species of okra for hybridization aiming at YVMV disease resistance. *Journal of Agricultural Sciences and Technology*. 18: 751–762.

Shamloul, G. M. and Moghazy, A. M. (2017). Heterosis and nature of gene action in okra (*Abelmoschus esculentus* (L.) Moench). *Acta horticulturae*.

Sharma, P. K., Mishra, D. P. and Pandey, A. (2016). Genetic variability studies for yield and its contributing traits in okra [*Abelmoschus esculentus* (L.) Moench]. *Journal of Applied and Natural Science, 8*(3): 1634-1637.

Sharma, R. K., Singh, R. S., Kumar, A., Singh, A. K. and Choudhary, S. K. (2019). Genotype X environment interaction and stability parameters of genotypes for different traits in Bhindi [*Abelmoschus esculentus* (L.) Moench]. *International Journal of Current Microbiology and Applied Sciences*, *8*(6): 3300-3310.

Sharma, V., Singh, P. K., Bhakar, S. R., Yadav, K. K., Lakhawat, S. S., Sharma, V. and Yadav, S. (2019). Integration of soil moisture sensor based automated drip irrigation system for okra crop. *Ind. J. Pure App. Biosci*, *7*(4): 277-282.

Shuirkar, G., Naidu, A. K., Pandey, B. R., Mehta, A. K., Dwivedi, S. K., and Sharma, H. L. (2018). Correlation coefficient analysis in okra. *The Pharma Innovation Journal*, *7*(6): 644-647.

Shull, G. H. (1908). What is heterosis? *Genetica*, 33, 430-446.

Shwetha, A., Mulge, R., Evoor, S., Kantharaju, V. and Masuti, D. A. (2018). Diallel analysis for combining ability studies in Okra [*Abelmoschus esculentus* (L.)

Moench] for yield and quality parameters. *International Journal of Current Microbiology and Applied Sciences*, *7*(9): 2114-2121.

Siemonsma, I. S. (1982a). La culture du gombo (*Abolmoschus* ssp) legume fruit. Thesis Univ Wageningen, the Netherlands.

Siemonsma, I. S. and Kouama, C. (2000). *Abolmoschus esculentus* (L.) Moench. Wageningen Agricultural University, Wageningen, Netherlands.

Siemonsma, J. S. (1982). La culture du gombo (*Abelmoschus* spp.), légume-fruit tropical (avec référence spéciale à la Côte d'Ivoire).

Siemonsma, J. S. (1982b). West African okra: Morphological and cytological indications for the existence of a natural amphiploid of *Abelmoschus esculentus* (L.) Moench and A. Manihot (L.) Medikus. *Euphytica*, 31(1): 241-52.

Singh, A. K., Ahmed, N., Narayan, R. and Chatoo, M. A. (2007). Genetic variability, correlations and path coefficient analysis in okra under Kashmir conditions. *Indian Journal of Horticulture*, 64(4): 472-474.

Singh, A. K., Singh, D. K., Singh, N. K., Kushwaha, M. L. and Maurya, S. K. (2020). Genetic analysis in okra under tarai region of Uttarakhand. *IJCS*, 8(1): 2767-2770.

Singh, B., Pal, A. K. and Singh, S. (2006). Genetic variability, correlation and path analysis in okra (*Abelmoschus esculentus* (L.) Moench). Indian Journal of Horticulture. 63(3): 281- 285.

Singh, B., Singh, S. K. and Singh, K. V. (2011). Study on combining ability in okra (*Abelmoschus esculentus* L. Moench). Indian Journal of Horticulture, 67: 154-159.

Singh, D. K. and Jain, S. K. (2012). Performance of okra hybrids for quantitative attributes. *Pantnagar Journal of Research*, 10(1): 66-70.

Singh, D. P. (2015). *Studies on Genetic Variability, Correlation and Path Analysis in Okra (Abelmoschus esculentus (L.) Moench)* (Doctoral dissertation, JNKVV).

Singh, D. R., Singh, P. K., Syamal, M. M. and Gautam, S. S. (2009). Studies on combining ability in okra. Indian Journal of Horticulture. 66: 277-280.

Singh, H. B. and Bhatnagar, A. (1975). Chromosome number in an okra from Ghana. *Indian Journal of Genetics and Plant Breeding,* 36: 26-27.

Singh, N., Singh, D. K., Sati, U. C., Rawat, M. and Pandey, P. (2017). Genetic analysis studies in okra [*Abelmoschus esculentus* (L.) Moench]. *International Journal of Pure Applied Biosciences*, *5*(4): 361-367.

Singh, R. V. and Chaudhary, B. D. (1985). Biometrical methods in quantitative genetic analysis in bread wheat. Indian Journal of Genetics. 52: 369–375.

Snedecor, G. W. and Cochran, W. G. (1989). Statistical Methods, Eighth Edition, Iowa State University Press.

Solankey, S. S. and Singh, A. K. (2010). Studies on combining ability in okra [*Abelmoschus esculentus* (L.) Moench]. Asian Journal of Horticulture, 5(1): 49-53.

Solankey, S. S., Singh, A. K. and Singh, R. K. (2013). Genetic expression of heterosis for yield and quality traits during different growing seasons in okra (*Abelmoschus* esculentus). *Indian J. Agric. Sci*, 83(8): 17-21.

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

Sprague, G. F. and Tatum, L. A. (1942). General vs. specific combining ability in single crosses of corn 1. *Agronomy Journal*, 34(10): 923-932.

Syfullah, K., Sani, M. N. H., Nasif, S. O., Parvin, S., Rony, M. M. H., Islam, M. S. and Hossain, M. S. (2018). Genetic Variability, Heritability, Character Association and Morphological Diversity in Okra (*Abelmoschus esculentus* L. Moench).

Syfullah, K., Sani, M. N. H., Nasif, S. O., Parvin, S., Rony, M. M. H., Islam, M. S. and Hossain, M. S. (2018). Genetic variability, heritability, character association and morphological diversity in okra (*Abelmoschus esculentus* L. Moench). *International Journal of Plant and Soil Science,* 1-11.

Tao, D. C. (1952). *Design and Analysis of Double Crank 5-Bar Linkage* (Doctoral dissertation, Purdue University).

Tattanakorn, M. and Kumar, P. (2004). Baseline survey export okra production in Thailand. *Inter-Country Program for Vegetable IPM in South and SE Asia Phase II, Food and Agriculture Organization of United Nations June*.

Temam, N., Mohamed, W. and Aklilu, S. (2020). Agro morphological characterization and evaluation of Okra [*Abelmoschus esculentus* (L.) Moench] genotypes for yield and other variability components at Melkassa, Central Ethiopia. *MOJ Ecological and Environmental Sciences.* 5(2): 80–87.

Thirupathireddy, M., Hari, B. K., Ganesh, M., Reddy, K., Begum, H., Purushothama, B. 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). *Journal of Agricultural Technology, 8*(2): 639-655.

Thulasiram, L. B., Bhople, S. R. and Ranjith, P. (2017). Correlation and path analysis studies in okra. *Electronic Journal of Plant Breeding*, *8*(2): 620-625.

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 Journal of Applied Ecology,* 9: 7-18.

Tripathi, K. K., Govila, O. P., Ranjini, W. and Vibha, A. (2011). Biology of Okra [*Abelmoschus esculentus* (L). (Moench]. series 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.

Vachhani, J. H. and Shekhat, H. G. (2008). Gene action in okra [*Abelmoschus esculentus (*L). (Moench]. *Agriculture Science Digest*, 28(2): 84-88.

Vavilov, N. I. (1951). The origin, variation, immunity and breeding of cultivated plants. Chronica Botanica, 13: 1-366

Vekariya, R. D., Patel, A. I., Modha, K. G. and Mali, S. C. (2019). G x E interaction and stability analysis in okra [*Abelmoschus esculentus* (L.) Moench]. *IJCS, 7*(4): 3146-3150.

Verma, V., Singh, B., Singh, M. K. and Singh, S. K. (2018). Studies on genetic variability, heritability and genetic advance in Okra [*Abelmoschus esculentus* (L.) Moench.]. *Journal of Pharmacognosy and Phytochemistry, 7*(4): 1114-1115.

Vinithra, S., Sindhuja, K., Senthilkumar, N., Thangavel, P., Ponsiva, S. T., Kandasamy, R. and Thirugnanakumar, S. (2019). Studies on genetic parameters, correlation and causation among biometrical traits in bhendi. *Electronic Journal of Plant Breeding*, *10*(4): 1541-1546.

Wakode, M. M., Bhave, S. G., Navhale, V. C., Dalvi, V. V., Devmore, J. P. and Mahadik, S. G. (2016). Combining ability studies in okra (*Abelmoschus esculentus* L. Moench). *Electronic Journal of Plant Breeding*, *7*(4): 1007-1013.

Walling, N., Kanaujia, S. P., Alila, P., Sharma, M. B. and Ozukum, C. (2020) Genetic variability and correlation studies in Okra (*Abelmoschus esculentus* L. Moench) Genotypes Under Foothill Conditions of Nagaland. *International Journal of Recent Sciences and Research.* 11(02), pp. 37651-37654.

Wammanda, D. T., Kadams, A. M. and Jonah, P. M. (2010). Combining ability analysis and heterosis in a diallel cross of okra (*Abelmoschus esculentus* (L.) Moench). *African Journal of Agricultural Research.* 5(16): 2108-2115.

Weerasingh, O. R., Perera, A. L. T., de Costa, W. A. J. M., Jinadase, D. M. and Vishnukarthasingham, R. (2004). Production of tomato hybrids for dry zone conditions of Sri Lanka using combining ability analysis, heterosis and DNA testing Procedure. *Tropical Agriculture Research.* 16: 79-90.

Wright, S. (1921). Systems of mating. I. The biometric relations between parent and offspring. *Genetics*, *6*(2): 111.

Yadav, A., Mishra, K. K. and Yadav, A. (2020). Studies on combining ability through Line × Tester analysis in Okra [*Abelmoschus esculentus* (L.) Moench]. International journal of current microbiology and appliued Sciences. 9(06): 494-499.

Yogendra, Y., Praveen, K. M., Tridip, B., Swadesh, B. and Arup, C., (2018). First evidence on heterotic affinity and combining ability of cultivated Okra [*Abelmoschus esculentus* (L.) Moench] inbred lines for tolerance to enation leaf curl virus disease. *Agricultural Research and Technology Open Access Journal.* 18(5): 556071.

Yonas, M., Garedew, W. and Debela, A. (2014). Variability and association of quantitative characters among okra [*Abelmoschus esculentus* (L.) Moench] collection in south western Ethiopia. *Journal of Biological Sciences*, *14*(5): 336-342.

APPENDICES

Appendix I: Mean sum of square and significant level of variety and genotype X environment interection for homogenety of different characters of okra

Bartletts Anova Table

Components	df	PH 100	LN 100	First Flower	50% Flower	Node of 1st Flower	1st Edible harvest	Length	Diameter	Fruit weight	Fruit/Plant	Yield/Plant	Seed/Fruit	100 Seed Weight
Varieties	7	298.65	27.88	8.002	7.46	1.11	11.52	0.65	0.0087	2.47	13.78	9565.21	20.88	0.51
G X E	21	456.32	79.42	7.41	7.95	6.07	12.11	0.96	0.0075	4.91	30.13	17317.52	49.37	1.91
Errors (Pooled)	56	2.38	2.33	0.52	0.33	0.12	0.79	0.098	0.0081	0.148	1.03	428.09	0.7	0.0038
F (Varieties)		**	**	**	**	**	**	**	NS	**	**	**	**	**
F (G X E)		**	**	**	**	**	**	**	NS	**	**	**	**	**

** 1% level of significant

Appendix II: Mean performance of different yield contributing character of Okra

Genotype	PH25	PH50	PH75	PH100	LN25	LN50
G1	7.63	31.60	70.87	107.67	6.80	13.73
G2	7.80	27.40	60.00	96.53	5.73	10.67
G3	9.53	25.87	51.93	76.00	6.40	16.53
G4	9.93	30.33	65.00	107.07	6.53	12.53
G5	7.80	20.73	46.60	84.13	6.47	24.53
G6	9.80	29.07	61.60	94.47	6.13	15.20
G7	12.47	36.73	79.27	123.73	6.40	18.53
G8	11.90	37.13	75.80	103.80	6.73	12.60
G9	9.77	27.47	53.20	72.87	6.60	24.67
G10	12.33	34.40	67.60	100.07	6.33	13.73
G11	11.43	35.67	79.07	115.67	6.27	13.73
G12	9.67	32.07	73.20	96.33	5.93	18.27
G13	12.40	52.07	143.40	190.33	6.13	22.73
G14	11.90	44.40	111.80	174.93	6.47	15.07
G15	11.00	42.20	109.07	162.27	6.27	15.33
G16	11.27	41.33	117.80	179.93	7.00	17.67
G17	11.47	41.67	101.33	142.13	6.67	17.00
G18	9.20	35.80	110.73	131.80	5.40	14.67
G19	11.03	39.73	110.07	172.00	6.60	17.60
G20	12.67	47.47	114.20	161.53	6.47	18.87
G21	11.27	50.93	118.40	147.93	6.47	17.07
G22	9.87	38.27	88.20	112.33	6.27	15.33
G23	11.93	43.27	108.67	142.00	6.73	19.33
G24	10.13	40.80	118.47	180.07	6.80	17.73
G25	11.37	44.00	116.13	191.67	6.47	16.60
G26	11.53	43.47	109.40	162.07	6.67	22.47
G27	11.53	38.80	121.93	187.20	6.87	24.93
G28	12.80	44.87	105.07	152.60	6.67	21.47
G29	10.40	38.47	91.47	138.67	6.20	14.73
G30	10.60	41.73	118.07	184.73	6.87	28.33

G31	9.93	35.00	76.53	108.93	6.13	16.07
G32	12.33	38.47	88.73	155.60	6.87	20.00
G33	10.23	34.47	86.40	125.13	6.40	15.20
G34	12.73	41.73	116.53	163.20	6.40	18.13
G35	11.53	45.47	109.53	133.07	6.47	19.40
G36	10.20	32.60	73.13	91.20	6.07	13.00
G37	11.63	40.47	96.80	134.20	6.93	23.67
G38	10.80	45.47	118.07	147.07	6.40	17.47
G39	11.20	40.33	111.80	152.60	6.67	23.47
G40	9.63	35.00	88.60	124.93	6.13	23.93
G41	11.47	38.40	90.60	133.33	6.40	20.93
G42	12.20	44.13	109.67	144.93	6.13	16.00
G43	10.77	34.60	81.87	127.53	6.33	12.40
G44	11.40	38.33	103.20	150.13	6.60	23.00
G45	10.60	37.40	94.87	139.13	6.67	17.67
G46	11.97	39.27	108.20	167.00	6.33	18.13
G47	11.27	46.33	131.57	165.20	6.53	17.87
G48	10.57	36.60	96.33	142.53	6.73	23.20
G49	9.87	35.20	83.27	121.07	6.00	13.40
G50	12.47	42.27	99.53	154.00	6.53	19.47
Minimum	**7.63**	**20.73**	**46.60**	**72.87**	**5.40**	**10.67**
Maximum	**12.80**	**52.07**	**143.40**	**191.67**	**7.00**	**28.33**

PH25= Plant height at 25 days (cm), PH50= Plant height at 50 days (cm), PH75= Plant height at 75 days (cm), PH100= Plant height at 100 days (cm), LN25= Leaf number at 25 days, LN50= Leaf number at 50 days

Continuation....

Genotype	LN75	LN100	FFI	50FI	NFF	FEFH
G1	35.13	44.33	40.67	42.00	4.53	46.67
G2	23.80	33.80	45.00	47.00	4.73	52.33
G3	41.13	66.20	42.00	43.67	4.73	48.00
G4	31.93	47.07	42.67	44.33	5.00	49.67
G5	85.13	114.20	45.67	47.67	5.20	51.33
G6	34.20	46.67	41.00	42.00	4.80	48.00
G7	41.67	54.27	41.33	43.00	5.13	46.67
G8	29.33	42.93	44.33	46.00	4.93	51.33
G9	69.13	66.60	40.33	41.67	4.47	46.00
G10	34.00	43.93	41.00	42.33	4.67	46.33
G11	27.80	35.27	40.33	42.00	4.87	47.00
G12	68.60	72.00	41.00	42.33	4.40	46.00
G13	52.67	63.73	40.67	42.67	4.53	47.33
G14	31.93	47.13	42.33	44.00	4.93	48.33
G15	43.27	60.80	42.67	43.67	4.40	49.00
G16	41.33	56.73	41.33	43.00	4.80	47.33
G17	39.53	53.47	39.33	40.00	4.67	45.33
G18	40.20	43.60	43.67	46.00	5.00	49.00
G19	38.87	47.53	41.33	42.67	4.87	47.67
G20	53.40	63.33	40.33	41.67	4.47	47.00
G21	40.07	39.00	38.33	40.00	4.53	45.33
G22	42.60	40.93	38.67	40.00	3.87	45.67
G23	51.87	63.27	39.33	41.00	4.67	46.00
G24	40.00	44.87	40.33	41.67	4.73	48.00
G25	46.00	66.33	42.33	44.00	5.00	49.00
G26	46.13	51.87	40.67	42.33	4.60	47.67
G27	64.20	70.40	41.67	42.67	5.20	48.00
G28	57.33	67.00	40.00	41.33	4.73	47.33
G29	44.40	59.13	40.67	41.67	4.53	47.33
G30	69.07	74.40	41.00	42.33	4.80	48.33

G31	45.33	49.87	39.67	40.33	3.73	44.67
G32	59.77	80.47	43.67	45.00	6.40	51.67
G33	35.07	37.73	40.67	41.67	3.80	45.67
G34	39.47	42.27	40.00	42.00	4.67	46.00
G35	38.53	43.00	39.33	41.00	4.73	46.67
G36	27.93	34.60	41.00	42.33	4.47	48.33
G37	65.93	62.53	40.00	41.33	4.33	46.33
G38	39.47	44.67	40.67	42.00	4.47	47.00
G39	58.20	64.00	44.00	44.67	5.80	49.67
G40	59.13	62.13	40.00	41.33	4.60	47.67
G41	49.40	54.20	39.33	41.33	4.53	46.67
G42	36.13	39.93	40.00	41.67	4.47	46.67
G43	43.73	49.93	40.67	42.00	4.40	47.33
G44	58.00	62.47	41.00	42.67	4.73	47.33
G45	45.00	60.87	39.67	41.00	4.73	45.67
G46	45.33	54.53	41.00	42.67	4.40	47.33
G47	43.67	44.27	39.67	41.67	4.60	46.67
G48	55.67	54.60	40.00	41.33	4.67	47.00
G49	31.20	42.73	41.67	43.00	4.60	47.67
G50	44.00	57.87	39.33	41.00	4.73	46.33
Minimum	**23.80**	**33.80**	**38.33**	**40.00**	**3.73**	**44.67**
Maximum	**85.13**	**114.20**	**45.67**	**47.67**	**6.40**	**52.33**

LN75=Leaf number at 75 days, LN 100=Leaf number at 100 days, FFI=First female flower ignition days, 50FI= days to 50% flowering , NFF=Number of first female flower and FEFH=First edible fruit harvesting days

Continuation.....

Genotypes	Fruit length (cm)	Fruit diameter (cm)	Fruit weight (g)	RG	Number of Fruits per plant
G1	13.93	2.00	21.40	5.00	20.37
G2	11.87	2.07	20.73	5.00	17.33
G3	12.67	2.10	19.13	8.00	20.17
G4	13.33	2.03	20.33	5.00	12.67
G5	13.73	1.97	19.33	5.00	35.43
G6	13.00	2.07	19.33	5.00	23.33
G7	15.27	1.93	21.17	5.00	20.30
G8	12.73	2.07	22.13	5.00	23.80
G9	12.53	2.00	17.27	5.00	31.93
G10	13.07	2.07	21.97	6.33	17.53
G11	13.67	2.00	20.00	5.00	22.50
G12	13.93	2.67	17.47	5.00	27.60
G13	15.07	2.00	20.80	5.00	31.53
G14	12.33	2.07	18.53	5.00	27.77
G15	15.20	2.00	20.60	5.00	23.13
G16	14.27	2.00	20.13	5.00	33.27
G17	13.27	2.03	21.43	5.00	25.93
G18	12.93	2.10	17.13	5.00	26.60
G19	13.80	2.10	22.33	5.00	22.97
G20	13.60	2.00	18.13	5.00	30.87
G21	13.00	2.00	17.40	5.33	20.73
G22	13.87	1.93	19.80	5.00	22.67
G23	13.73	2.00	19.13	5.00	32.73
G24	13.20	2.13	23.07	5.00	27.73
G25	14.40	1.97	21.73	5.00	35.80
G26	13.60	2.13	22.20	5.00	31.20
G27	13.47	2.00	18.00	5.00	33.40
G28	15.27	1.97	20.40	5.00	29.80

G29	15.33	1.90	19.93	5.00	29.67
G30	13.73	2.00	22.33	5.00	36.67
G31	15.20	1.83	16.33	5.67	26.13
G32	20.07	1.70	19.27	5.00	42.33
G33	13.60	1.97	19.20	5.00	23.00
G34	13.53	2.00	19.80	5.00	30.93
G35	13.93	1.90	17.27	5.00	26.73
G36	13.60	2.03	21.87	5.00	21.93
G37	14.80	2.00	20.47	5.00	37.47
G38	13.33	1.93	18.07	5.00	24.67
G39	14.27	1.97	19.20	5.00	34.93
G40	12.33	2.13	17.20	5.00	28.57
G41	13.73	1.90	18.93	5.00	31.07
G42	14.20	2.03	20.00	5.00	24.27
G43	12.67	1.97	15.60	5.00	22.53
G44	13.93	2.00	19.93	5.00	33.40
G45	14.47	2.00	19.87	5.00	35.07
G46	12.87	2.03	19.67	5.00	33.13
G47	13.70	1.83	17.00	5.00	25.33
G48	12.87	2.00	18.00	5.00	27.27
G49	14.60	1.93	18.93	5.00	26.60
G50	13.73	1.97	19.07	5.00	34.13
Min	11.87	1.70	15.60	5.00	12.67
Max	20.07	7.67	23.07	8.00	42.33

Continution....

Genotypes	Seeds per fruits	100 Seed weight (g)	Fruits yield per plant (g)
G1	64.73	6.79	420.24
G2	37.27	6.17	386.00
G3	64.57	6.40	399.40
G4	27.13	7.37	286.27
G5	47.43	5.88	691.96
G6	46.53	7.23	465.55
G7	56.53	7.17	419.97
G8	69.53	6.36	552.01
G9	74.27	6.27	547.56
G10	26.40	7.67	417.05
G11	65.13	6.90	468.33
G12	44.07	7.41	502.43
G13	41.90	7.32	624.95
G14	44.67	7.91	479.09
G15	45.93	7.16	503.81
G16	53.23	7.44	694.77
G17	48.63	7.25	498.16
G18	72.13	7.57	462.49
G19	52.30	7.26	563.20
G20	65.63	7.90	560.68
G21	55.73	7.19	504.36
G22	53.87	8.08	479.48
G23	73.30	7.30	612.53
G24	55.30	7.48	636.13
G25	53.47	7.44	828.57
G26	62.83	7.58	641.73
G27	73.63	6.39	616.59
G28	47.53	8.15	631.67
G29	53.37	7.15	586.84

G30	63.70	7.45	828.13
G31	54.07	7.81	356.60
G32	43.80	6.27	861.47
G33	64.13	7.24	447.67
G34	51.73	7.31	628.09
G35	60.37	8.62	469.37
G36	77.43	6.71	468.63
G37	43.93	7.87	777.93
G38	71.10	7.00	540.04
G39	68.03	7.01	703.55
G40	48.50	6.86	502.60
G41	71.80	7.57	631.64
G42	70.70	6.40	522.13
G43	56.10	6.04	366.75
G44	67.17	6.73	670.00
G45	59.07	7.60	689.25
G46	56.93	7.10	652.53
G47	58.43	7.83	419.27
G48	63.70	7.18	480.87
G49	66.30	6.54	486.67
G50	55.97	7.59	656.52
Min	26.40	5.88	286.27
Max	77.43	8.62	861.47

Appendix III: Weather report of R and D Farm, Metal Agro Limited Debigonj, Panchagarh from 2014 to 2017

Weather Report: January - December/2014

Month	Temperature(^{o}C)		Relative Humidity (%)	
	Maximum	Minimum	Maximum	Minimum
January	19.37	14.67	91.33	73.83
February	21.97	16.52	82.39	58.22
March	27.9	21.31	68.64	44.56
April	32.64	26.44	58.95	42.83
May	32.13	27.54	78.08	62.04
June	31.78	28.3	89.95	71.91
July	31.74	28.74	92.1	75.1
August	29.57	28.55	91.1	75.89
September	31.42	28.22	88.45	72.81
October	30.62	26.22	81.58	62.05
November	26.92	21.4	80.43	55.73
December	22.36	16.59	83.13	61.34

Weather Report: January - December/2015

Month	Temperature(^{o}C)		Relative Humidity (%)	
	Maximum	Minimum	Maximum	Minimum
January	19.28	14.61	85.32	73.36
February	24.21	17.58	82	56.27
March	28.27	22.69	68.58	47.67
April	29.12	24.67	76.65	59.35
May	31.31	27.42	80	65
June	31.64	28.23	88.79	74.5
July	33.04	29.44	86.21	66.95
August	31.87	28.19	89.29	75.38
September	32.26	28.82	91	74.15
October	32.16	27.18	77.75	56.71
November	27.7	22.35	78.58	56.96
December	22.15	16.23	83.13	63.09

Weather Report: January - December/2016

Month	Temperature(^{o}C)		Relative Humidity (%)	
	Maximum	Minimum	Maximum	Minimum
January	20.18	13.95	84.32	67.04
February	24.94	27.89	78.95	50.69
March	28.9	23.05	70.18	48.59
April	31.71	26.41	72.27	57.09
May	30.37	26.17	83.81	65.59
June	31	28.77	91.86	72.72
July	30.34	27.91	94.22	84
August	33.32	29.72	83.41	67.29
September	30.48	27.43	95.38	82.38
October	31.72	27	84.31	62.5
November	29.29	22.12	78.32	52.68
December	23.52	17.67	83.27	63.18

Weather Report: January - December/2017

Month	Temperature(^{o}C)		Relative Humidity (%)	
	Maximum	Minimum	Maximum	Minimum
January	21.82	14.95	76.57	58.65
February	24.72	17.77	75.21	48.63
March	25.74	20.52	73.25	55.04
April	29.63	24.87	77.16	60.96
May	31.45	27.02	83.37	66.37
June	32.56	28.56	83.37	65.18
July	31.05	28.71	91.11	76.96
August	31.89	28.9	91.65	74.5
September	32.21	28.69	89.94	72.88
October	29.48	26.25	90.12	74.62
November	27.25	21.3	75.26	54.5
December	23.61	17.8	81.95	65

Appendix IV: Mean and range of seven parental line of okra.

Parents	PH100	LN100	FFI	50FI	NFF	FEFH	LENGTH	DM	WEIGHT	F/PT	YIELD	S/F	100SW
P1	80.00	50.93	48.00	49.00	6.67	54.00	11.74	2.00	15.37	19.93	360.00	60.67	4.20
P2	55.20	60.00	45.67	48.00	7.50	51.67	12.18	2.01	16.13	19.33	345.67	75.30	4.00
P3	143.00	49.67	53.00	56.00	8.47	54.67	12.13	1.97	14.99	21.47	307.16	57.20	4.13
P4	114.40	52.67	57.00	59.00	9.50	64.00	13.44	1.97	15.47	22.13	413.33	54.17	3.90
P5	130.40	60.00	53.67	58.00	9.13	62.00	14.21	2.15	20.13	24.00	395.00	80.10	4.40
P6	122.60	66.60	57.00	59.67	8.60	61.67	13.58	2.17	15.93	29.40	481.33	71.73	4.03
P7	139.73	75.47	55.67	58.67	8.67	62.67	12.57	2.12	15.03	24.13	450.73	74.60	4.37
Min	**55.20**	**49.67**	**45.67**	**48.00**	**6.67**	**51.67**	**11.74**	**1.97**	**14.99**	**19.33**	**307.16**	**54.17**	**3.90**
Max	**143.00**	**75.47**	**57.00**	**59.67**	**9.50**	**64.00**	**14.21**	**2.17**	**20.13**	**29.40**	**481.33**	**80.10**	**4.40**
Mean	**112.19**	**59.33**	**52.86**	**55.48**	**8.36**	**58.67**	**12.84**	**2.05**	**16.15**	**22.91**	**393.32**	**67.68**	**4.15**

Appendix V: Mean and range of 21 hybrid of okra

F1	PH100	LN100	FFI	50FI	NFF	FEFH	LENGTH	DM	WEIGHT	F/PT	YIELD	S/F	100SW
1	82.00	61.60	49.33	53.67	8.33	61.00	12.95	2.04	17.45	27.73	432.91	76.13	4.67
2	143.40	63.07	54.00	57.67	8.40	61.00	13.55	2.08	18.84	33.20	512.51	66.27	4.70
3	111.00	80.53	53.33	56.67	8.73	61.33	13.12	2.12	17.93	35.70	541.24	72.17	5.00
4	136.53	53.87	53.67	57.00	8.70	61.00	15.45	2.16	20.40	33.13	626.29	72.10	4.63
5	99.53	70.93	55.67	57.67	8.60	63.67	14.42	2.12	19.33	29.53	503.07	73.50	4.87
6	149.07	69.07	56.67	59.67	8.70	65.00	12.53	2.09	16.19	33.13	486.83	62.00	4.50
7	142.60	57.87	54.00	59.00	8.87	61.33	13.37	2.13	21.20	33.00	670.91	75.40	4.83
8	110.00	78.67	51.33	55.33	8.63	59.67	14.11	2.12	17.99	41.80	779.41	84.63	4.87
9	180.20	68.87	53.33	55.67	8.47	61.00	14.58	2.15	19.03	42.27	745.00	69.37	4.60
10	152.00	69.80	58.33	58.00	9.07	66.33	14.41	2.04	17.67	33.07	611.00	72.57	4.60
11	127.00	65.80	54.00	56.00	9.13	60.33	13.47	2.03	17.22	30.87	461.20	73.60	4.77
12	152.00	86.80	53.00	56.67	8.93	62.00	14.81	2.15	20.40	33.73	654.09	64.27	4.53
13	155.93	62.47	55.33	59.00	8.47	62.67	14.55	2.14	20.39	34.27	697.41	62.53	4.63
14	162.67	78.20	56.00	59.33	8.93	63.67	14.24	2.12	17.80	36.13	711.40	68.33	4.13
15	169.67	61.13	53.00	56.00	9.40	60.67	14.48	2.17	19.13	37.47	796.67	76.60	5.30
16	125.47	60.87	53.33	56.33	8.57	60.33	14.55	2.08	20.53	26.93	502.99	75.03	4.50
17	80.80	62.40	51.67	55.33	8.63	60.33	12.32	2.11	22.60	35.00	703.33	74.33	4.30
18	160.27	64.60	56.67	59.33	8.73	64.67	14.52	2.21	22.77	39.07	692.33	63.73	4.17
19	151.53	87.87	56.33	59.33	9.20	65.67	14.16	2.07	18.93	41.47	756.29	72.33	4.40
20	151.00	66.20	53.67	57.67	8.67	62.33	13.49	2.15	17.20	35.33	597.60	81.93	4.73
21	144.80	67.47	56.00	59.67	8.80	62.67	14.96	2.17	20.60	32.33	555.87	73.43	4.80
Min	**80.80**	**53.87**	**49.33**	**53.67**	**8.33**	**59.67**	**12.32**	**2.03**	**16.19**	**26.93**	**432.91**	**62.00**	**4.13**
Max	**180.20**	**87.87**	**58.33**	**59.67**	**9.40**	**66.33**	**15.45**	**2.21**	**22.77**	**42.27**	**796.67**	**84.63**	**5.30**
Mean	**137.50**	**68.48**	**54.22**	**57.38**	**8.76**	**62.22**	**14.00**	**2.12**	**19.22**	**34.53**	**620.87**	**71.92**	**4.64**

Picture plates of my research work

Picture plate 1. A flower bud at appropriate stage for emasculation

Picture plate 2. The process of emsculation without making any injury to the stigma

Picture plate 3. A completely emasculated flower bud

Picture plate 4. Process of bagging of emasculated flower bud

Picture plate 5. Complete bagging after emasculation of flower bud

Picture plate 6. Process of pollination through rubbing the stigma with pollens

Picture plate 7. Complete pollination of emasculated flower bud

Picture plate 8. Supervisor and co-supervisor are in the research field

Picture plate 9. Supervisor, co-supervisor and research assistants are in the research field

Picture plate 10. I am with my supervisor and co-supervisor in research field