Genetic Divergence in Okra (*Abelmoschus esculentus* (L.) Moench)

THESIS

Submitted to the

Jawaharlal Nehru Krishi Vishwa Vidyalaya, Jabalpur

In partial fulfillment of the requirements for
the Degree of

MASTER OF SCIENCE

In

AGRICULTURE
(PLANT BREEDING AND GENETICS)

By

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2012

CERTIFICATE – I

This is to certify that the thesis entitled **“Genetic Divergence in Okra (*Abelmoschus esculentus* (L.) Moench)”** submitted in partial fulfillment of the requirements for the degree of **MASTER OF SCIENCE IN AGRICULTURE (Plant Breeding and Genetics)** of Jawaharlal Nehru Krishi Vishwa Vidyalaya, Jabalpur is a record of the bonafide research work carried out by **Mr. Deepak Kumar Saryam** under my guidance and supervision. The subject of the thesis has been approved by the Student’s Advisory Committee and the Director of Instruction.

No part of the thesis has been submitted for any other degree or diploma (Certificate awarded etc.) or has been published / published part has been fully acknowledged. All the assistance and help received during the course of the investigation have been fully acknowledged by him.

Place : Jabalpur
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Chairman Advisory Committee

THESIS APPROVED BY THE STUDENT’S ADVISORY COMMITTEE

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Member	**Dr. K. S. Kushwaha**	…………………………………

CERTIFICATE – II

This is to certify that the thesis entitled **“Genetic Divergence in Okra (*Abelmoschus esculentus* (L.) Moench)”** submitted by **Mr. Deepak Kumar Saryam** to the Jawaharlal Nehru Krishi Vishwa Vidyalaya, Jabalpur in partial fulfillment of the requirements for the degree of **MASTER OF SCIENCE IN AGRICULTURE** in the Department of **Plant Breeding and Genetics** has been, after evaluation, approved by the External Examiner and by the Student’s Advisory Committee after an oral examination on the same.

Place: Jabalpur
Date:……/……/………

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Head of the Department (Dr. D. K. Mishra)……………………………......

Director of Instruction (Dr. P. K. Mishra) ………………………………….

ACKNOWLEDGEMENT

First of all, I would like to pranam at the foot of god of Saptagiri hills SHRI VANKATESWRA SWAMI and Thanks to Almighty God for giving me this opportunity to express my heartfelt gratitude to all the dedicated people whose support and kind co-operation encouraged me during the course of investigation.

It is my proud privilege to express my venerable regards and profound sense of gratitude to Dr. S. K. Mittra, Sr. Scientist (Plant Breeding & Genetics),Department of Horticulture, College of Agriculture, JNKVV, Jabalpur for his precious, able guidance, convincing suggestions and constant encouragement during the tenure of investigation and preparation of the manuscript as a chairman of my advisory committee.

I am extremely grateful to all the respected members of my advisory committee, Dr. A. K. Mehta, Professor, Department of Plant Breeding & Genetics, Dr. K. S. Kushwaha, Associate Professor, Department of Mathematics and Statistics, College of Agriculture Engineering, JNKVV, Jabalpur for their valuable suggestions during the study and preparation of this manuscript.

I express my warmest feeling and deep sense of gratitude and regard to Prof. V. K. Gour, Dr. A. N. Shrivastava, Dr. D. Khare, Dr. R. S. Shukla, Dr. P. K. Moitra, Dr. Sarad Tiwari Dr. R. K. Dubey, Dr. S. K. Biliaya, Dr. J. P. Lakhani, Dr. A. S. Gontia, Dr. M. S. Bhale, Dr. Sanjay Singh, Dr. (Mrs.) Anita Babbar, Dr. M. K. Shrivastava and Dr. Sunita Pandey, and Shri B. K. Verma without whose benevolent guidance and constant motivation it would not have been possible to complete this project.

My cordial thanks to Prof. V. S. Tomar, Hon'ble Vice Chancellor, Dr. S. K. Rao, Dean Faculty of Agriculture, Dr. S. S. Tomar, Director of Rsearch Services, Dr. K. K. Saxena, Director of Extension Services, Dr. P. K. Mishra, Director of Instruction, Dr.N.N. Pathak, Director Farm, Dr. P. K. Bisen, Dean Student

Welfare and Dr. R. S. Khampariya Dean, College of Agriculture Jabalpur for providing necessary facilities during this investigation.

I express my gratitude to all the teaching and non teaching staff of the Department for providing all possible facilities needed for my investigation during the course of my study. I also evince my sincere thanks Mr. B.K. Verma the skilled Research associate and other field staff for their valuable help, responsibility and care in carrying out the field work.

I extend my thanks to the project entitled R.K.V.Y. on development of vegetable hybrids for providing facilities and NBPGR New Delhi for graciously providing genetic material for the study.

Words are not enough to express my gratitude and regards to my beloved father Shri Guruprasad Saryam and mother Smt. Rekha Saryam for their blessing and good wishes without which I could not be able to fulfill this study. I would like to thank my maternal aunty Mrs. Tilakvati and maternal uncle Mr. Ajarshah and Brijesh, I would like to thank my sisters Shanti and Priyanka and my brother Umendra for giving their valuable support during the period of study.

Last but not the least, I express my sincere thanks to my seniors Mr. Vijay Katara, Miss. Priya Nair, Miss. Stuti Mishra, Komal Singh Keram, K. P. Singh, Kamlesh Pawar, Mukesh Aldak, P. S. Utti and Swapnil for thier guidance and friends specially Sandeep, Pankaj, Anant, Sanjay, Arun and last but not the least, I express my sincere thanks to my juniors Mr. Vikas Kumar, Vikas Verma, Nitin, Hussain, Umashankar, Deepak, Jitendra, Neha Dhuria, Preeti Vanskar, Dheerendra, Niranjan and Nilesh for their friendly support.

Above all, I thank the Almighty God for this countless blessings. I express my sincere thank to the Department of Horticulture, Department of Plant Breeding & Genetics, I/C Librarian and the Department of Agricultural Meteorology, CAE, JNKVV, Jabalpur for providing the necessary facilities and the weather data. Confer my thanks to Mr. B.K.Verma and R.K.V.Y.

Place : Jabalpur
Date : / /2012 ***(Deepak Kumar Saryam)***

LIST OF ABBRIVIATIONS

et al.,	:	And others
%	:	Percentage
X^{-1}	:	Per
@	:	At the rate of
Cm	:	Centimeters
M	:	Meter
Σ	:	Summation
mm	:	Millimeter
PCV	:	Phenotypic coefficient of variation
GCV	:	Genotypic coefficient of variation
Fig.	:	Figure
Kg	:	Kilograms
h^2b	:	Broad sense heritability
e.g.,	:	Example
D^2	:	Genetic divergence
Max.	:	Maximum
Mini.	:	Minimum
g or gm	:	Gram (s)
FYM	:	Farm yard manure
Ha	:	Hectare
d.f.	:	Degree of freedom
i.e.,	:	That is
Λ	:	Wilk’s criterion
GA	:	Genetic advance
No.	:	Number
Viz.,	:	Namely
CD	:	Critical difference
SE	:	Standard Error

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Introduction

Okra [*Abelmoschus esculentus* (L.) Moench] has occupied a prominent position among vegetables; it is one of the choicest fruit vegetable grown extensively in the subtropical to tropical warm area of the world including India, Africa, Turkey and other neighbouring countries. Vavilov, considered it to be a native of Ethopian region but according to Murdoc its origin is in West Africa. It is widely grown during summer and rainy seasons for its tender green fruits, is one of the most important vegetable crops of India, however its tender green leaves are also eaten in the far east countries. It is also known by many local names in different parts of the world. It is called Lady's finger in England, Gumbo in the U.S.A. and Bhindi in northern India. It is a polyploid, belonging to the family Malvaceae with 2n = 130 - 2n = 8x =72 or 144 chromosomes. It is an often cross pollinated crop, with out crossing to an extent of 4–19 per cent with the maximum of 42.2 per cent under insect assisted pollination. In India 60 per cent share of export goes to okra among fresh vegetables.

Edible fresh and mature okra fruits contain 88 per cent moisture and large number of chemical components including vit. A, B and C. Its unripe 100 g fruits contain 3100 calorie energy, 1.8 g protein, 90 mg. calcium and 1.0 mg iron. It has many medicinal properties, and is an excellent source of iodine for control of goiter; its leaves are used for preparing a medicament to reduce inflammation. Okra is widely cultivated in plains of the India with average of over 452.5 thousand ha and production 4803.3 thousand MT and 10.6 MT ha^{-1} productivity. In Madhya Pradesh okra is grown in 8.8 thousand ha and 52,800 tons production with productivity of 6.00 tons ha^{-1}. *(Anons.,* 2010-11).

In our country there exists a wide variation amongst the okra varieties expressing wide degree of variation for quantitative and qualitative traits *viz.,* plant height, number of primary branches plant^{-1}, number of fruits plant^{-1}, size of fruit *i.e.*, length, breadth and weight etc. are the yield contributing characters while, colour of fruit and fiber content determine the quality of fruit.

The foremost challenge of the agriculturist has always been to produce adequate quantity of food from the available acreages, to meet the requirements of ever expanding world population. The rate of yield gain in crop improvement programme must match the rate of population growth so as to overcome malnutrition and hunger.

A logical way to start any crop improvement programme is to assess the variation existing in the available materials. It is said that genetic variability is the "*sine qua non*" of any such programme. Selection is said to be effective in a population having large heritable variability. The genetic variability and its components are the genetic fractions of observed variability that provides measures of transmissibility of the variation and response to selection. The knowledge on pattern of inheritance of various characters of economic importance is essential, while determining the most appropriate breeding procedures for crop improvement. The breeder's choice of the material for any improvement work consequently depends on the amount of genetic variability present. The phenotype which is a manifestation of genotype, environment and interaction of both is often not true indicator of its genotype, thus heritability gives an estimate of degree of influence of the environmental factors over the genotype and genetic advance measures the extent of improvement in one cycle of selection.

The degree of positive or negative association amongst the yield and yield contributing traits, help in determining the traits contributing to increase in yield. Thus information on coefficient of correlation and path coefficient analysis are important attributes before initiating a crop improvement programme as path coefficient analysis partitions the relationship among the associated traits into direct and indirect effects. D^2 statistics originally developed by P.C. Mahalanobis in 1928 is one of the patent technique of measuring genetic divergence is extensively used in plant breeding, helps the plant breeder in assessment of the genetic diversity and in choosing appropriate parents in hybridization programme.

The present investigation entitled “Genetic Divergence in Okra (*Abelmoschus esculentus* (L.) Moench)” has been designed with the following objectives on yield, yield attributing and fruit quality traits.

1. To estimate genetic parameters of yield and its components.
2. To estimate coefficient of correlation and path coefficient analysis for yield and its components.
3. To estimate genetic divergence for identification of putative lines.
4. Screening for incidence of yellow vein mosaic virus.

REVIEW OF LITERATURE

An attempt has been made to study “Genetic Divergence in Okra [*Abelmoschus esculentus* (L.) Moench]”; the main objective to study the inheritance pattern of the characters is to strengthen crop improvement programme to increase the yielding ability and fruit quality traits of okra. Information on inheritance pattern of various quantitative traits is helpful in architecture of crop improvement techniques. The success of any breeding programme mainly depends on the amount and nature of genetic variability present in the population under study. The relevant and available literature related to the various aspects of the present investigations has been discussed under the following heads:

2.1 To estimate genetic parameters of yield and its components.

2.2 To estimate coefficient of correlation and path coefficient analysis for yield and its components.

2.3 To estimate genetic divergence for identification of putative lines.

2.4 Screening for incidence of yellow vein mosaic virus.

2.1 To estimate genetic parameters of yield and its components

Presence of genetic variation in populations under crop improvement is of immense importance to make the crop improvement programme effective. Lush (1940) defined the broad sense heritability as the ratio of genetic variance to total variance.

2.1.1 Genotypic and phenotypic coefficients of variation:

Variability refers to the presence of phenotypic differences among the individuals of plant population. Variability results due to differences either in the genetic constitution of the individuals of a population or in the environment in which they were grown. Magnitude of genetic variability present in a population is of paramount importance to a plant breeder for starting a judicious breeding programme. Selection is only effective when there is genetic variability among the genotypes in a population. The genotypic coefficient of variation (GCV) measures the extent of genetic variability present in a crop species and also enables to quantify the extent of variability present in different characters. The phenotypic coefficient of variation (PCV) of a character is the manifestation of genotypes, environment and interaction between the genotypes and environment. The success of a crop improvement programme depends upon the extent and magnitude of variability existing in the germplasm.

Singh *et al.* (1975) observed high GCV for plant height, number of effective nodes, number of branches plant^{-1}, and fruit yield plant^{-1} in okra. High estimates of PCV were observed for girth of fruit and number of effective nodes while, low estimates of PCV were observed for days to 50 per cent flowering and first fruiting.

Korla and Sharma (1984) revealed that plant height exhibited the greatest variability, while the node of first fruit set the least. Studied traits expressed low to moderate coefficient of variability. While, Reddy *et al.* (1985) reported that GCV and PCV were highest for fruit yield plant^{-1} followed by plant height, indicating wide variability. Similarly, Yadav (1986) in an assessment of 26 *A. esculentus* cultivars for eight characters revealed that plant height, yield plant^{-1} and number of seeds fruit^{-1} showed high GCV followed by moderate GCV for number of fruits plant^{-1} and length of fruits. On the contrary Vijay and Manohar (1990) revealed high GCV estimates for 50 per cent flowering, number of effective nodes, branches plant^{-1} and fruit yield, while it was low for internodal length.

Singh *et al.* (1998) okra varieties Parbhani Kranti, Hisar Unnat and Satdhari; were treated with four doses of gamma rays and four doses of ethyl methane sulfonate. High GCV and PCV were observed for number of fruits plant^{-1}, yield plant^{-1} and plant height.

Pathak and Singh (1999) reported that the estimates of PCV were higher than the GCV for germination, plant height, plant spread, stem diameter, number of branches, earliness, 50 per cent flowering, number of fruits, fruit length, diameter and weight, fruit yield, and consumption period, indicating influence of environment on expression of character. Highest variation was noted at both genotypic and phenotypic levels for plant spread and number of branches plant^{-1}. While, Hazra and Basu (2000) studied the genetic variability among different characters and obtained moderate GCV for plant height, leaves plant^{-1}, fruit weight, fruits plant^{-1}, seeds fruit^{-1}, and fruit yield plant^{-1}. These characters proved the existence of justifiable genetic distance among the different cultivars. Similarly, Dhall *et al.* (2001 and 2003) revealed that the estimates of PCV and GCV were high for plant height, total and marketable yield plant^{-1}, number of fruits plant^{-1} and virus incidence.

Gandhi *et al.* (2001) studied 44 okra genotypes collected from NBPGR for 13 traits, *viz.,* branches plant^{-1}, fruit yield plant^{-1} and height at first fruit set showed high GCV and PCV estimates. Wide differences between GCV and PCV were observed for branches plant^{-1} and seed yield plant^{-1}, indicating the role of environment in the expression of these characters. While, Yadav *et al.* (2002) reported highest GCV for yield plant^{-1}, followed by fruit width, fruit weight, plant height, number of fruits plant^{-1} and number of nodes plant^{-1}. The GCV was generally lower than the PCV. Similarly, Bendale *et al.* (2003) revealed that PCV for all the characters was higher than the GCV. The number of branches plant^{-1}, yield plant^{-1} and number of fruits plant^{-1} showed high GCV and PCV estimates. While, Singh and Singh (2003) and Verma *et al.* (2004) observed high GCV and PCV for number of primary branches plant^{-1} and yield plant^{-1}. However, Sarkar *et al.* (2004) revealed that fruit yield plant^{-1}, number of fruits plant^{-1}, fruit weight, fruit dry weight and number of leaves plant^{-1} at first flower showed high value of GCV and PCV.

Mehta *et al.* (2006) studied 22 diverse genotypes of okra for fruit yield and its component traits, estimates of PCV were higher than those of GCV for all the seven traits indicating influence of environment in expression of these traits. Estimates of GCV were higher for fruit yield, fruit weight, plant height and fruit length revealing presence of substantial genetic variability for these traits.

Similarly, Naidu *et al.* (2007) observed high degree of variability for plant height, number of fruits plant^{-1}, fruit weight and fruit yield plant^{-1}.

Saifullah and Rabbani (2009) studied 121 okra genotypes collected from different parts of Bangladesh were characterized and evaluated for different quantitative and qualitative traits. The GCV and the PCV were very close for most of the characters studied, indicating lessen influence of environment on the expression of characters *viz.,* days to first flowering, plant height, number of primary branches plant^{-1}, number of internodes plant^{-1}, number of fruits plant^{-1}, fruit weight, number of seeds fruits^{-1} and fruit yield plant^{-1}. These estimates provided the basis for phenotypic selection for development of new variety.

Akotkar *et al.* (2010) observed high values of GCV and PCV for number of fruiting nodes, number of ridges fruit^{-1} and plant height, indicated presence of substantial genetic variability controlling inheritance of these traits. However, Akinyele and Osekita (2011) observed high GCV for number of branches plant^{-1}, number of fruits plant^{-1} and seed yield. While, Sanjay *et al.* (2012) reported high GCV for no. of fruits plant^{-1} followed by yield plant^{-1}, no. of flowers plant^{-1}, no. of leaves plant^{-1}, no. of branches plant^{-1}, plant height and stem diameter. The GCV was less than the PCV, indicating the influence of environment in the expression of these traits.

2.1.2 Heritability and genetic advance

Heritability in broad sense is the ratio of genotypic variance to total phenotypic variance and gives us an estimate of extent of influence of the environment in the expression of a character, while genetic advance gives us an estimate of extent of genetic gain in one cycle of selection in a trait. High estimates of heritability (h^2b) and genetic advance (GA) reveal that the trait under reference is under the influence of additive gene action, while high h^2b with low GA reveals that the trait is influenced by non-additive genes. Whereas low estimates for h^2b and GA reveal influence of environment in the expression of such traits.

Vashistha *et al.* (1982) obtained high values for h^2b and GA for fruits plant^{-1}, plant height and root length indicating scope for improving these characters by selection due to preponderance of additive genes. Similarly, Reddy *et al.* (1985) reported high h^2b and GA for fruit yield plant^{-1}, branch number and plant height.

Yadav (1986) in an assessment of eight characters in 26 *A. esculentus* cultivars revealed moderate to high h^2b and GA for number of fruits plant^{-1} and length of fruits. Similarly, Patil and Dalal (1992) reported high h^2b estimates for yield and its components in seven *A. esculentus* genotypes and their F_1 hybrids. Fruit attributes revealed moderate h^2b estimates.

Patil *et al.* (1996) observed relatively high GA for characters *e.g*., plant height, number and weight of good fruits per plant indicates likely effectiveness of selection for such characters. Similarly, Panda and Singh (1997) reported high estimate of h^2b and GA for plant height, number of fruits and total fruit yield plant^{-1} and opined to improve these traits though selection.

Singh *et al.* (1998) treated three genotypes of okra *e.g*., Parbhani Kranti, Hisar Unnat and Satdhari with four each doses of gamma rays and ethyl methane sulpfonate respectively. High h^2b and GA were observed for yield plant^{-1}, plant height, number of seeds fruit^{-1} and number of fruits plant^{-1}. While, Pathak and Singh (1999) recorded very high h^2b and GA for fruit diameter, plant spread, fruit weight, fruit yield plant^{-1} and earliness.

Hazra and Basu (2000) revealed that plant height, fruit weight, ridges fruit^{-1}, dry weight of fruit and seeds fruit^{-1} were highly heritable, while primary branches plant^{-1}, leaves plant^{-1}, days to first flower, fruit length, fruits plant^{-1} and fruit yield plant^{-1} were moderately heritable. Primary branches plant^{-1}, seeds plant^{-1}, seeds fruit^{-1} and fruit weight had high h^2b values with above average to high GA. Whereas, Dhall *et al.* (2001) and Dhall *et al.* (2003) revealed predominance of additive factors due to high estimates of h^2b and GA in fruit length, plant height, number of fruits plant^{-1} and virus incidence.

John *et al.* (2001) expressed high h^2b with very high GA for number of branches plant^{-1} and number of seeds fruit^{-1} in all the irradiated treatments. High h^2b with very high GA was observed in 20 kR dose for leaf number, flowers plant^{-1} and fruits plant^{-1} while for fruit yield plant^{-1} the h^2b and GA were high, similar findings were obtained in 30 kR on above listed traits and pollen sterility and plant duration. The estimates of h^2b and GA were low for incidence of YVMV in all treatments while it was moderate in the cultivated parent.

Gandhi *et al.* (2001) evaluated 44 genotypes of okra from NBPGR for 13 different characters. Fruit length, height at first fruit set and fruit girth showed high h^2b estimates, however these characters were coupled with varied GA estimates ranging from high-low suggesting, complexity of genetic mechanism in expression of these characters. Predominance of additive genetic variance was expressed by height at first fruit set, internodal length, fruit length, number of fruits plant^{-1} plant height and number of branches plant^{-1}.

Dhankhar and Dhankar (2002) reported that fruit yield, number of fruits plant^{-1} and plant height showed high to moderate heritability in both years. The GA was recorded moderate to low for all characters, indicating limited scope for further improvement through selection.

Singh and Singh (2002) treated seeds of three okra cultivars *viz.,* Parbhani Kranti, Hisar Unnat, and Satdhari with gamma rays and ethyl methane sulfonate. High h^2b and GA were observed for yield plant^{-1}, plant height, and number of seeds fruit^{-1} in M_2 and M_3 generations. While, Singh and Singh (2003) reported high h^2b with high-low GA for yield plant^{-1}, 1000 seed weight and days to 50 per cent flowering in both generations.

Bendale *et al.* (2003) recorded medium to high and high h^2b for yield and yield-contributing characters *viz.,* first flowering node, days to first harvest, fruit length, fruit weight, plant height, nodes plant^{-1}, internodal length, branches plant^{-1}, moisture content in fruit, fruiting period, seeds fruit^{-1}, 100 seed weight, fruits plant^{-1} and yield plant^{-1}. Whereas Verma *et al.* (2004) observed high estimates of h^2b and GA for no. of seeds fruit^{-1} and plant height.

Sarkar *et al.* (2004) observed high h^2b coupled with high GA for number of fruits plant^{-1}, fruit weight and fruit yield plant^{-1}, indicating that these characters were controlled by additive genes. Similarly, Indurani and Veeraragavathatham (2005) observed high h^2b coupled with high GA for characters *e.g*., plant height at first flower bud appearance, number of fruits plant^{-1}, fruit weight and yield plant^{-1} suggesting that due importance could be given for these characters in selection programme.

Bello *et al.* (2006) obtained high h^2b and GA estimates for fruit diameter and number of branches plant^{-1} reveals that these characters are governed by additive genes. Mehta *et al.* (2006) in a study of 22 diverse genotypes of okra for fruit yield and its component traits for h^2b and GA as percentage of mean, the estimates were higher for fruit yield, fruit weight, plant height and fruit length. Whereas Sunil *et al.* (2007) reported high h^2b coupled with moderated GA for days to flowering, number of node plant^{-1}, internodal length, number of fruits plant^{-1} and yield plant^{-1}. High h^2b coupled low GA was observed for fruit length indicating predominance of non-additive gene action. While, Naidu *et al.* (2007) revealed high estimate of h^2b and GA in number of nodes to first flower, fruits plant^{-1}, number of seeds fruit^{-1} and fruit yield plant^{-1}.

Saifullah and Rabbani (2009) characterized and evaluated 121 okra genotypes of Bangladesh for different quantitative and qualitative traits, high h^2b estimates along with considerable GA were noticed in days to first flowering, plant height, no. of primary branches plant^{-1}, internodes plant^{-1}, fruits plant^{-1}, fruit weight, seeds fruits^{-1} and fruit yield plant^{-1}.

Akotkar *et al.* (2010) revealed high h^2b and GA as percentage of mean for number of fruiting nodes, number of ridges fruit^{-1}, plant height and number of fruiting nodes indicating these characters to be controlled by additive genes. However, Shanthakumar and Salimath (2010) studied h^2b and GA in three double crosses and four single cross F_2 population of okra. Heritability in (BS) and GA were high for all the characters indicating effectiveness of selection due to the involvement of additive type of gene action in controlling these characters.

Jindal *et al.* (2010) crossed 12 okra genotypes in diallel fashion excluding reciprocals to generate 66 one-way hybrids. Estimates of high h^2b coupled with high GA were obtained for number of branches plant^{-1}; total and marketable yield plant^{-1}. Presence of high h^2b coupled with low GA for days to fruit picking, average fruit weight, plant height, internodal length, number of fruits plant^{-1}, fruit diameter and average fruit length. It revealed that direct selection has limited scope for further improvement of these traits due to predominance of non-additive genes. However, Adiger *et al.* (2011) in a study of 163 genotypes (43 parents and 120 crosses) of okra to determine the h^2b and GA as percentage of mean, the estimates were high for plant height, fruit yield plant^{-1}, fruit weight and days to 50 per cent flowering. While, Ramanjinappa *et al.* (2011) recorded high h^2b for all the characters studied, however days to 50 per cent flowering exhibited moderate h^2b. The characters *viz.,* plant height, number of branches plant^{-1}, nodes plant^{-1}, intermodal length, fruits plant^{-1}, seeds fruits^{-1} and total yield plant^{-1} exhibited high h^2b coupled with high GA as percentage of mean.

Sanjay *et al.* (2012) studied 20 diverse genotypes of okra, revealed high GA along with high h^2b for fruit yield plant^{-1} followed by number of flowers plant^{-1}, fruits plant^{-1}, leaves plant^{-1}, plant height and days to flower. It indicated preponderance additive genes controlling these characters, indicating selection to be effective.

2.2 Coefficient of correlation analysis for yield and its components

Correlation studies are of considerable importance in plant breeding. Coefficient of correlation describes the degree of association between two variables. The correlation between yield and its component traits gives an idea for selection pressure, which could profitably be exercised to obtain increase in yield. As such, it is necessary to estimate the correlation coefficients, as it aids in estimating the true associations due to genetic causes. A brief review related to these aspects is being reviewed as follows:

Singh *et al.* (1975) reported moderate to high positive correlation between days to flowering and maturity, plant height with internodal length and fruit length with fruit width. Ajimal *et al.* (1979) observed positive correlation of yield with number of fruits, nodes and length of internode. Similarly, Mahajan and Sharma (1979) reported that yield had positive association with plant height, number of fruits plant^{-1} and fruit length. While, Koul *et al.* (1979) observed significant differences for all the 15 characters studied. Seed yield was observed to have positive relationship with fruit yield.

Singh and Singh (1979) observed that the fruit yield was positively related with plant height, number of branches plant^{-1}, fruit length and fruits plant^{-1}. Similarly, Yadav (1986) revealed positive relationship of fruit yield with plant height, fruits plant^{-1} and fruit length. While, Shukla (1990) observed positive association of fruit yield with number of fruits plant^{-1}, nodes plant^{-1} and fruit length.

Mandal and Dana (1994) reported that fruit yield was positively associated with number of fruits plant^{-1} and fruit length, while it showed negative association with days to 50 per cent flowering. Similarly, Gondane *et al.* (1995) revealed positive relationship of fruit yield plant^{-1} with number of fruits plant^{-1}, weight of edible fruit^{-1}, stem thickness and plant height.

Sood *et al.* (1995) studied correlation among 12 traits and observed that nodes plant^{-1}, duration of edible fruits, plant height and fruit length had strong positive correlation with yield. While, Dash and Misra (1995) recorded positive correlation of fruit yield plant^{-1} with number of branches plant^{-1}, fruit length, fruit girth, fruit weight, no. of seeds fruit^{-1} and seed weight fruit^{-1}.

Yadav (1996) observed positive correlation between yield plant^{-1} and number of fruits plant^{-1}, while days to first fruiting showed positive correlation with fruit length and fruit width. Plant height showed positive association with fruit length. Whereas, Rajani and Manju (1997) reported strong positive correlation of nodes plant^{-1}, fruiting span, plant height and fruit length with fruit yield. Similarly, Singh *et al.* (1998) reported strong positive correlation of yield plant^{-1} with of fruits plant^{-1}, fruit length, fruit girth, number of seeds fruit^{-1} and plant height suggested the importance of these characters in the improvement of okra.

Whereas, Hazra and Basu (2000) reported that fruit yield plant^{-1} was positively associated with plant height while, days to first flowering showed negative relationship with number of fruits plant^{-1}.

Dhall *et al.* (2000) revealed positive relationship of marketable yield plant^{-1} with total yield plant^{-1}, fruit weight, fruit length, number of fruits plant^{-1} and plant height. It indicates that due emphasis should be given on such characters to improve the yield potential.

Niranjan and Mishra (2003) reported that in general, the genotypic correlations were higher than the corresponding phenotypic correlation for all the character combinations. Fruit yield was positively correlated with edibility period of fruits, fruits plant^{-1}, fruit length, seeds fruit^{-1}, fruit weight, plant height and branches plant^{-1} at both genotypic and phenotypic levels. Associations were significant at the genotypic level only between edibility period of fruits and number of branches plant^{-1}. All characters expressed positive association among each other at both levels. Similarly, Bendale *et al.* (2003) revealed that fruit length, fruit weight, plant height, nodes plant^{-1} and number of fruits plant^{-1} were positively associated with fruit yield.

Jaiprakashnarayan and Mulge (2004), Sarkar *et al.* (2004) and Sureshbabu *et al.* (2004) reported positive association of yield plant^{-1} with number of fruits plant^{-1}, average fruit weight, nodes on main stem, fruit length, plant height (at 60 and 100 DAS) and number of leaves (at 45 and 100 DAS) on the contrary Patro and Ravishankar (2004) revealed negative relationship of fruit yield plant^{-1} with plant height and days taken to first fruit setting.

Bhalekar *et al.* (2005) observed that fruit length, internodal length, fruits plant^{-1} and branches plant^{-1} had strong positive correlation with fruit yield, while Ghosh (2005) reported that fruit yield plant^{-1} was positively correlated with fruiting span, internodal length, number of seeds fruit^{-1}, plant height at maturity and weight of fruit.

Pawar (2005), Mehta *et al.* (2006) & Singh *et al*. (2007) reported that the yield plant^{-1} was positively correlated with fruits plant^{-1}, fruit weight, fruit length and girth. Similarly, Mohapatra *et al.* (2007) evaluated 23 genotypes for different yield contributing traits and incidence of YVMV estimated that total fruit yield plant^{-1} had a positive phenotypic and genotypic relationship with number of fruits plant^{-1}, fruit girth, internodal distance and fruit weight.

Verma *et al.* (2007) revealed, yield plant^{-1} exhibited positive correlation with fruits plant^{-1}, fruit weight, fruit length, and girth while, negative association was observed with 100 seed weight, days to first flowering and days to 50 per cent flowering.

Sanjay and Annapurna (2009) reported that flower plant^{-1} was positively related with leaves plant^{-1}, diameter of stem and days to flower at both genotypic and phenotypic levels. While, fruits branch^{-1}, fruits plant^{-1} and days to flower were positively correlated at both genotypic and phenotypic levels.

Balakrishnan and Sreenivasan (2010) revealed that fruit yield was positively associated with number of fruits, internode number, fruit weight and fruit length. Hence selection of genotypes with short growth habit, short flowering period and short fruit length will help to minimize the shoot and fruit borer infestation. Similarly, Adiger *et al.* (2011) reported that fruit yield expressed positive relationship with plant height, number of branches plant^{-1}, internodal length, fruit length, fruit weight and number of fruits plant^{-1} at both genotypic and phenotypic levels, indicating mutual association of these traits. Whereas, Sanjay *et al.* (2012) revealed that the values of correlations at genotypic level were higher than the phenotypic correlations indicating, strong inherent association between the various characters studied. Yield plant^{-1} showed positive association with number of flowers plant^{-1}, fruits branches^{-1}, fruits plant^{-1}, length of fruit and weight at genotypic and phenotypic levels. This indicated that fruit yield could be improved by making selection on the basis of flowers plant^{-1}, fruit branch^{-1}, fruits plant^{-1} and length of fruits.

2.2.1 Path coefficient analysis

A number of factors are involved in correlation studies, thus their association becomes more complex and confusing, under such circumstances. Path coefficient analysis helps in removing the complication by measuring the direct and indirect influences of one variable upon the other by partitioning the correlation coefficients into the components of direct and indirect effects. This has also an advantage to point out the true yield determinants for genetic improvement of crops.

Ajimal *et al.* (1979) observed that the number of days to first flowering showed direct contribution to yield followed by number of nodes and fruits plant^{-1}, while Koul *et al.* (1979) studied 15 characters, primary branches plant^{-1} had greatest direct effect on the fruit yield. While, Reddy *et al.* (1985) reported that fruits plant^{-1} had the highest positive direct effect on fruit yield, while plant height revealed high direct and indirect effects on yield, where as branch number had an indirect effect. Selection for these last two traits was seen as the most effective method for improving yield. Whereas, Gondane *et al.* (1995) reported that weight of edible fruit and number of fruits plant^{-1} were observed to be the most important variables contributing towards fruits yield. Similarly, Choudhary and Sharma (1999) revealed that weight of fruit had maximum direct genotypic effect on yield followed by branches plant^{-1}, plant height and fruits plant^{-1}. Findings of Dhall *et al.* (2000) revealed that the marketable yield plant^{-1}, number of fruits plant^{-1}, fruit weight, fruit length and plant height expressed high direct effect on the total yield are in agreement with the above findings indicated that due emphasis should be given on such characters to improve the yield potential.

Niranjan and Mishra (2003) revealed that fruit weight exerted highest genotypic correlation value (0.975) and highest positive direct effect (0.507) on fruit yield plant^{-1} followed by number of seeds fruit^{-1}, fruit length, fruits plant^{-1} and branches plant^{-1}. Similarly, Jaiprakashnarayan and Mulge (2004) revealed that the average fruit weight, nodes on main stem and fruits plant^{-1} had high positive direct effect on total yield plant^{-1}. Whereas, Sureshbabu *et al.* (2004) reported that fruits plant^{-1} showed the highest positive direct effect on yield followed by plant height, days to flower, fruit length, fruit girth and fruits plant^{-1}. Findings of Pawar (2005) are in agreement with the present findings, *i.e.*, number of fruits plant^{-1} and seeds fruit^{-1} contributed on yield plant^{-1} owing to their high direct and indirect effects for all the characters.

Akinyele and Osekita (2006) in path coefficient analysis revealed that number of fruits plant^{-1} and height at flowering had the highest direct effect on seed yield. This suggested that the two attributes had a strong influence on seed yield. Hence, fruits plant^{-1} and height at flowering are the main determinants for seed yield plant^{-1}. On the contrary Mehta *et al.* (2006) reported that fruit girth had the maximum direct effect followed by fruit length towards fruit yield. Thus, the fruit yield in okra could be improved by selecting for higher fruit length, fruit girth and average fruit weight simultaneously.

Verma *et al.* (2007) revealed that number of fruits plant^{-1} had highest positive direct effect on yield plant^{-1} followed by number of nodes to first flower. The indirect effects of most the components towards yield were negligible in magnitude except in case of nodes to first flower via plant height and fruit length, days to first flowering via days to 50 per cent flowering, days to 50 per cent flowering via fruit length; days to first picking via days to 50 per cent flowering, number of fruits plant^{-1} via fruit length and plant height.

Adiger *et al.* (2011) positive direct contribution of fruit weight was maximum towards fruit yield followed by number of fruits plant^{-1}, plant height and number of branches plant^{-1}. Days to 50 per cent flowering exhibited highest negative direct effect followed by test weight and fruit diameter. Findings of Akinyele and Osekita (2011) were not in agreement with this study, the findings revealed that plant height at flowering, final plant height and number of seeds fruit^{-1} showed positive direct genotypic effect on fruit yield plant^{-1}. Number of fruits plant^{-1} and seeds fruit^{-1} showed very high direct genotypic effect on yield. Thus, fruits plant^{-1} was a prime character contributing to fruit yield, this was closely followed by height at flowering and then number of seeds fruit^{-1}.

2.3 Genetic divergence

“The separation of population gene pool may occur from the gene pools of other populations due to selection and the phenomenon of mutation, migration and genetic drift. Continued divergence can lead to speciation”. The pattern of genetic variation is of great importance both to germplasm conservationists and also to the plant breeders. Specific accessions identified, could be passed on to breeders for utilization in crop improvement programmes.

Genetic divergence is the process, in which two or more populations of ancestral species accumulate independent genetic changes through time; often the populations become reproductively isolated over a period of time. Sometimes subpopulations giving in ecologically distant peripheral environment may exhibit genetic divergence from the remainder of a population.

In plant breeding programmes, assessment of the genetic diversity is done by the D^2 statistics devised by Mahalanobis in 1928. Now this technique is extensively used in variability related plant breeding studies. This is one of the patent techniques of measuring genetic divergence. Rao in 1952 suggested the application of this technique for the assessment of genetic diversity in plant breeding, genetic diversity plays a very important role, because hybrids between lines of diverse origin, generally display a greater heterosis compared to closely related parents.

Ariyo (1987) reported that 30 okra genotypes of diverse eco-geographical origin were studied for 14 characters were subjected to analysis by Mahalanobis D^2 technique. Genetic divergence among the genotypes was quantitatively measured. The genotypes were grouped into five clusters. There was no relationship between clustering pattern and eco-geographic distribution. Effect of genetic divergence on the choice of parental stock in hybridization was discussed.

Bisht *et al.* (1995) studied genetic diversity for a range of morphological characters pubescence and pigmentation of various plant parts, among qualitative descriptors, seemed to be most significant in the analysis of variability.

The multivariate analysis, mainly on quantitative descriptors, using principal component and non-hierarchical cluster analysis suggested that days to flowering, plant height, and various fruit characteristics were important components of variability and contributed significantly to the total variation. Only two of the 10 principal components had given values more than one and together accounted for 54.52 per cent of the total variation. The accessions were grouped into eight distinct clusters which further emphasized the relative contribution of various quantitative characters to the total variability.

Hazra *et al.* (2002) studied 22 genotypes of okra for 13 fruit yield and other related characters to determine genetic divergence following D^2 analysis, the genotypes were grouped into five clusters with highest of 16 genotypes in cluster I. Most of the genotypes were not much divergent based on character constellation but were highly variable for individual character. A genotype apprehended to be under the species other than *A. esculentus* showed the widest divergence and belonged to the separate cluster. On the basis of high yield, important yield components and fruit quality, four diverse and desirable genotypes *e.g.,* MDO-10, LORM-1, KS-410 and MDO-6 were selected.

Bendale *et al.* (2003) in a study comprising 25 okra genotypes using Mahalanobis D^2 analysis observed the nature of divergence and to assessed the importance of a set of quantitative characters related to economic yield in genetic differentiation. The genotypes were grouped into 8 clusters. Cluster I was largest with 13 genotypes. The highest genetic distance was found between clusters III and VII. Ascorbic acid content and yield plant^{-1} had the largest contribution to divergence followed by a substantial variation in cluster means for plant height. Crosses among genotypes of clusters IV, VII and VIII were recommended to develop desirable high yielding okra cultivars / hybrids.

Mamta Kumari and Choudhury (2006) analyzed D^2 values, on 40 genotypes during the summer and rainy seasons were classified into 11 clusters during the rainy season and into 9 clusters during the summer. The genetic distance was greatest between clusters IX and VI during the rainy season, and between clusters VII and V during the summer. The intra-cluster distance was high for clusters IV and VIII during the rainy and summer seasons, respectively. Among the yield components, fruit length had the greatest effect on divergence, followed by fruit yield plant^{-1} during the rainy season, whereas fruit yield plant^{-1} had the greatest effect on divergence, followed by number of primary branches, during the summer. The results suggested that greater emphasis should be given to fruit yield plant^{-1}, fruit length, and number of primary branches during selection for high yielding genotypes of okra.

Sharma *et al.* (2008) in a study of 39 okra genotypes for genetic divergence that, they were grouped in to eight clusters, cluster I was the largest with 14 genotypes followed by cluster II with 8, cluster III with 5, cluster IV and V with 4 in each and cluster VI with 2 genotypes, while cluster VII and VIII were monogenotypic. The clustering pattern indicated that there was no association between geographical distribution of genotypes and genetic divergence. The intra-cluster distance was noted maximum in cluster IV, while inter-cluster distance was recorded maximum between cluster VIII and VI followed by VII and VI and are the good sources for attempting hybridization for creation of new variability. Maximum divergence was revealed by number of seeds per fruit, fruit width, average fruit weight, plant height, node at which 1st flower appears, number of fruits per plant and fruit length, therefore, selection of diverse parents based on these characters were recommended for getting good hybrids or segregates in okra.

Prakash and Pitchaimuthu (2010) reported that D^2 analysis, of 44 genotypes were grouped into 12 clusters. The cluster III was the largest with eight genotypes followed by cluster I and VIII with seven, cluster II with five, cluster XII with three while remaining clusters were with two genotypes each. The intra-cluster distance was maximum in cluster XII, while inter cluster distance was maximum between cluster VI and VIII followed by I and IX, thus being a good source for attempting hybridization. Genotypes *viz.,* IIHR-238, IIHR-241 showed maximum number of fruits plant^{-1} and total yield plant^{-1}. The characters *e.g*., days to 50 per cent flowering,100 seed weight, number of seeds fruit^{-1} and average fruit weight directly contributed towards maximum divergence and therefore, selection of divergent parents based on these characters is recommended for getting good hybrids or segregates in okra.

Akotkar *et al.* (2010) carried out D^2 analysis and revealed that 50 genotypes could be grouped into five clusters. Cluster I consisted of 45 genotypes was the largest followed by cluster II with two genotypes, remaining clusters were monogenotypic. Plant height expressed the highest contribution toward total genetic divergence. The highest intra-cluster distances were recorded in cluster I followed by cluster II. The maximum inter-cluster distance was recorded between cluster IV and cluster II, followed by cluster V and cluster II. Among all the genotypes studied, IC-332454 showed the highest cluster mean for fruit yield plant^{-1} and number of fruits plant^{-1}. The genotypes in cluster V, III and II also exhibited significant performance for fruit yield plant^{-1}, number of fruits plant^{-1} and plant height. On the basis of groupings of individual genotypes into different clusters, contribution of individual character towards total genetic divergence, inter-cluster distance and cluster mean, the genotypes *e.g.,* IC-9856B, IC-331157, IC-342075, IC-332453 and IC-43736 were found promising for crop improvement programme.

Garg *et al.* (2011) revealed that 53 germplasm lines of okra representing different regions were evaluated to assess the extent of genetic diversity employing Mahalanobis D^2 statistics. The genotypes were classified into 11 discrete clusters and the entire collection was allocated to different clusters. No parallelism between genetic and geographic divergence was observed. Substantial variation in cluster means was observed for all characters studied. Considering extent of diversity among genotypes and cluster means for various characters, crosses among genotypes of clusters XI, X, VI, VII and I might give rise to heterotic hybrids and wide spectrum of variability in subsequent segregating generations. Genotypes POS^{-}16, JOL-2, K-19, POS-8, VRO-22, VRO-10, POS-18, POS-27, Hisar Unnat and Punjab-8 were observed to be potential parents for future okra breeding programmes.

Prakash *et al.* (2011) reported that genetically diverse population was grouped into 12 clusters. The cluster III was the largest with eight genotypes followed by cluster I and VIII each with seven, cluster II with five, cluster XII with three while, the remaining clusters were bigenotypic. 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 XII, while inter-cluster distance was maximum between cluster VI and VIII followed by I and IX. Days to 50 per cent flowering, 100 seed weight, number of seeds fruit^{-1} and average fruit weight directly contributed towards maximum divergence hence, selection of divergent parents based on these characters was recommended for getting good hybrids or segregates in okra.

Verma *et al.* (2011) reported significant variability among the genotypes for all the characters under study. Based on D^2 analysis, the genotypes were grouped into seven clusters irrespective of geographical diversity. Cluster I contributed maximum of 16 genotypes followed by cluster IV with 11, cluster II with 7, while cluster III, V, VI, were mono genotypic. The maximum intra-cluster distance was observed in cluster II followed by cluster I and IV. The maximum inter-cluster distance was noticed between cluster II and VII followed by cluster II and IV, cluster II and III, cluster VI and cluster VII and cluster V and cluster II. Characters *viz.,* plant height, fruit yield plant^{-1}, flowering nodes plant^{-1}, days to 50 per cent flowering and branches plant^{-1} contributed maximum to divergence and have a major role in improvement of fruit yield in okra. Crossing between genotypes belonging to cluster II and VII as well as cluster II and IV and cluster II and III are expected to give maximum variability.

Reddy *et al.* (2012) revealed considerable genetic diversity among 100 genotypes of okra for all the seventeen quantitative characters 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 characters fruit length, internodal length and number of marketable fruits plant^{-1} were the potent factors in differentiating the germplasm. 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 could 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.

2.4 Incidence of yellow vein mosaic virus

Yellow vein mosaic is the most destructive viral disease of okra, it infects the crop at all the stages of growth which ultimately reduces growth and yields. Okra incurs severe losses in yield throughout India due to the disease transmitted by vector *Bemisia tabaci* (Gen.). Presently there is no definite control against YVMV as most of the public sectors varieties / hybrids are susceptible to this disease and it is the major problem of all okra growing areas. To overcome this malady, breeding work on this aspect has been taken up at many centers and some promising varieties tolerant to this disease with high yields have been released by different states, however the resistance is not durable.

Dhankhar *et al.* (1996) reported that Parbhani Kranti and 11 hybrids were highly resistant to yellow vein mosaic virus followed by P-7 which was moderately resistant, while, the remaining genotypes expressed susceptibility. Whereas, Pathak *et al.* (1999) reported that out of 72 cross progenies, 59 were found to be either resistant or moderately resistant against yellow vein mosaic virus.

Ali *et al.* (2000) reported that IPSA Okra 1 was tolerant to YVMV was crossed to 3 susceptible genotypes *viz.,* Parbhani Kranti, SL-44 and SL-46 to determine the nature of inheritance of tolerance of IPSA Okra 1. It was revealed from the results of grafting test that the tolerance in IPSA Okra 1 is genetic and not due to escape. The F_1 hybrids were tolerant to YVMV. From the segregation pattern for disease reaction in F_2 and BC_1 generations the crosses, it could be hypothesized that the tolerance to YVMV in IPSA Okra 1 is quantitative, with possibly two major factors, and dependent on gene dosage with incompletely dominant gene action.

Rashid *et al.* (2002) reported that lines OK-292 and OK-285 showed resistant to YVMV in both season and OK-315, OK-316 and OK- 317 were found tolerant. Highest yield was observed in OK-292 followed by OK-285 while, OK-310 recorded the lowest yield.

Dhall *et al.* (2001) studied genetic variability, h^2b and GA for 10 quantitative characters, significant differences among genotypes were observed for all characters except for virus incidence. Estimates of PCV and GCV were high for virus incidence. It exhibited high h^2b along with high GA, indicating the predominance of additive factors.

Vijaya (2004) reported that VRO-5 and VRO-6 recorded the lowest mean disease incidence for YVMV incidence. Zulfeghar and Patil (2004) reported that Arka Anamika recorded the lowest disease incidence and the highest yield, while the susceptible control Pusa Sawani recorded the highest disease incidence and the lowest yield. None of the genotypes were immune to the disease. Arka Anamika, Hybrid 8 and Hybrid 10 were resistant, while Soumya F_1 and Reshma were moderately resistant.

Nizar *et al.* (2004) reported in his experiments that screening of germplasm for YVMV incidence under natural epiphytotic conditions revealed that none of the accessions were ‘immune’ or ‘highly resistant’, three accessions *viz.,* IC 218887, IC 69286 and EC 305619 were ‘resistant’ 43 were ‘moderately resistant ’and the rest were susceptible. The results also revealed that none of the yellow vein mosaic virus disease resistant accessions were exceptionally high yielding or vice versa.

Sharma *et al.* (2007) concluded that cultivars P-7 and Prabhani Kranti were the top yielders in spring-summer season whereas, Varsha Uphaar (117.30q ha^{-1}) and Prabhani Kranti (110.40q ha^{-1}) with low disease incidence (<10%) were the most promising for the rainy season.

Saifullah and Rabbani (2009) evaluated 121 okra genotypes during summer 2004 for qualitative characters. Wide range of variation was also observed amongst the okra genotypes. Majority of the genotypes were susceptible to YVMV. Some genotypes were also found to be high yielding and also tolerant to the disease.

Tiwari *et al.* (2012) observed that VRO-6 was YVMV. Beside that moderate resistance was observed in VRO-3 and HRB-9-2 under field conditions. Pusa sawni showed high susceptibility to the disease. Pusa makhmali was found moderately susceptible under field conditions.

MATERIAL AND METHODS

This chapter comprises the details of the materials used and the methods adopted during the course of present investigation entitled “Genetic Divergence in Okra [*Abelmoschus esculentus* (L.) Moench]” was carried out during *Kharif* season of the year 2011.

3.1 Experimental site

The experiment was conducted at Vegetable Research Farm, Maharajpur, Department of Horticulture, Jawaharlal Nehru Krishi Vishwa Vidyalaya, Jabalpur (M.P.).

3.1.1 Soil

The soil of the experimental field was clayey loam with good drainage and uniform texture with medium NPK status.

3.1.2 Climate and weather conditions

Jabalpur is situated on ‘Kymore Plateau and Satpura hills’ agro-climatic zone of Madhya Pradesh at 23.910 North latitude, and 79.50 East longitude, at an altitude of 411.78 meters above the mean sea level. The tropic of cancer passes through the middle of the district. Climate of the region is typically semi arid and sub tropical having extreme winter and summer with average annual rainfall received during June – October is around 1350 mm. The average maximum temperature is 46^0c and minimum temperature 6^0c. The average annual relative humidity is 74 per cent.

The meteorological parameters were recorded at JNKVV Meteorological observatory, Jabalpur during the crop season on parameters *viz.,* minimum and maximum temperature, sunshine hours, rainfall in mm, number of rainy days and relative humidity are presented in Table 3.1

Table3.1: Data showing meteorological week wise information of Jabalpur during the entire *period of experimentation* of the year 2011.

Months	Meteorolo-gical WEEK	TEMPERATURE (°C)		RELATIVE HUMIDITY (%)		WIND VELOCITY km/hr	SUNSHINE HOURS	RAIN FALL (mm)	NO. OF RAINY DAYS
		MAX	MIN	I	II				
July	**26**	27.4	22.8	90	80	09.5	00.4	091.3	04
	27	33.1	22.8	86	61	05.7	04.9	015.2	02
	28	31.7	23.5	92	71	06.2	03.1	046.4	03
	29	33.5	22.8	93	83	07.3	02.5	429.1	06
August	**30**	30.7	22.7	90	70	06.3	09.4	119.2	03
	31	31.5	23.6	92	82	05.3	03.9	140.0	05
	32	31.9	22.7	93	85	06.7	01.5	118.5	06
	33	33.3	22.7	92	78	06.4	04.0	057.6	03
Septembe	**34**	32.9	22.9	93	70	03.2	06.3	014.6	03
	35	33.5	22.8	96	71	04.5	05.8	150.6	07
	36	33.0	22.6	94	80	05.3	01.2	221.6	04
	37	31.9	22.4	93	73	05.1	03.9	092.2	03
October	**38**	30.4	21.9	93	67	05.7	05.1	041.0	04
	39	32.0	20.8	86	56	05.1	06.9	000.0	00
	40	32.3	18.6	90	47	03.1	09.0	005.2	01
	41	32.7	19.1	92	43	02.3	08.3	000.0	00
	42	31.8	15.8	89	31	02.5	09.3	000.0	00
November	**43**	30.9	13.9	87	30	02.5	08.9	000.0	00
	44	29.3	11.0	86	24	02.4	09.0	000.0	00
	45	30.3	12.1	89	29	02.5	08.3	000.0	00
	46	31.5	12.4	89	28	02.4	08.0	000.0	00
December	**47**	29.7	11.3	92	33	02.3	08.7	000.0	00
	48	29.2	09.6	89	36	02.2	07.3	000.0	00
Total								**1542.5**	**54**

The climate was favorable however there was very heavy rainfall in end of July 2011 continuing to rain heavily till mid August and again heavy rains from mid September to third week. The rainfall ceased after middle of October, two irrigations were given at the end at fortnightly intervals. The climate was more or less favorable and the crop condition was good.

3.2 Experimental material

The experimental material comprised of 55 exotic and indigenous genotypes of okra collected from NBPGR, New Delhi and five checks *viz.,* Phule Utkarsh, Hisar Unnat, VRO-5, VRO-6 and Pusa A4. Genotypes are presented in Table 3.2.

Table 3.2 List of genotypes studied

S. No.	Name of genotype	S. No.	Name of genotype	S. No.	Name of genotype
1	EC 305617	21	EC 329397	41	IC 018542
2	EC 133336	22	EC 329400	42	IC 018960-B
3	EC 305622	23	EC 329418	43	IC 018960-C
4	EC 169319	24	EC 550848	44	IC 018973-A
5	EC 305634	25	IC 006485	45	IC 018975
6	EC 329379	26	IC 007472	46	IC 022237-A
7	EC 305664	27	IC 007952	47	IC 024906-A
8	EC 169443-A	28	IC 009856-C	48	IC 027831
9	EC 169333	29	IC 013995-A	49	IC 027881-A
10	EC 169364	30	IC 014600	50	IC 027889
11	EC 329356	31	IC 014845-B	51	IC 028359
12	EC 329357	32	IC 033344	52	IC 029119-B
13	EC 169398	33	IC 015036-B	53	IC 029191
14	EC 169515	34	IC 015435	54	IC 031850
15	EC 329366	35	IC 016262-A	55	IC 031932-A
16	EC 329368	36	IC 018473-A	56	Pusa A4
17	EC 329369	37	IC 018533	57	VRO-5
18	EC 305637	38	IC 018534	58	VRO-6
19	EC 305616	39	IC 018540	59	Phule utkarsh
20	EC 033122	40	IC 018541-A	60	Hissar unnat

3.3 Experimental details:

3.3.1 Design of experiment

The experiment was laid out in Randomized Complete Block Design (RCBD) with 60 treatments (55 genotypes + 5 checks) in three blocks. The experimental details are as follows:

Design	:	RCBD
Block	:	Three
Genotypes	:	Sixty
Row length	:	3.0 m
Spacing	:	60 X 30 cm
Number of row/ accession	:	2
Net area of experimental field	:	648 m^2
Gross area of experimental field	:	813.6 m^2
Distance between blocks	:	0.5 m
Season	:	*Kharif*, 2011
Date of sowing	:	12th July 2011
Manures	:	10 tons FYM ha^{-1}
Fertilizer dose (N: P: K)	:	80:50:50 kg ha^{-1}

3.3.2 Field preparation, sowing and management of crop

One cross cultivation was done by tractor drawn cultivator followed by two harrowing and leveling in order to get good tilth of the soil for sowing. Seeds were hand dibbled. Two weeks after sowing thinning was done to maintain plant to plant distance. All the recommended package of practices was followed to raise a healthy crop. Hand weeding was done as and when needed to keep the experimental plots weed free.

3.3.3 Fertilizer application

A dose of 80kg N, 50kg P_2O_5 and 50kg K_2O ha^{-1} was applied along with FYM @10 tons ha^{-1}. FYM was applied prior to sowing and 1/3rd dose of nitrogen and entire quantity of P, K was applied at sowing. Remaining dose of nitrogen was applied in two splits at 30 and 60 days after sowing.

3.4 Sampling

Sampling was done at 30 days to harvest time for growth analysis. Five competitive plants were randomly selected from each plot for the study; average of five plants was recorded as treatment mean.

3.5 Observation

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

(A) Morphological characters:

3.5.1 Leaf blade length (cm)

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

3.5.2 Leaf blade width (cm)

The width of leaf blade was measured on the leaves used for recording length of leaf blade, using a scale and then average was recorded.

3.5.3 Petiole length (cm)

The petiole length was measured on the leaves used for recording length of leaf blade, using a scale and then average was recorded.

3.5.4 Internodal length (cm)

The length between two nodes from different places such as base, middle and top with the help of scale was recorded on observational plants and average was worked out for each plot.

3.5.5. Number of branches plant^{-1}

Number of branches per plant was recorded at final harvest.

3.5.6 Stem diameter (mm)

It was measured from randomly selected five plants from each plot with the help of a Vernier calliper and then average was recorded.

3.5.7 Plant height (cm)

Height of plant was recorded in cm at physiological maturity, from the base just above the soil surface to growing point of the plant at final harvest.

3.5.8 Flower length (cm)

It was measured from randomly selected five flowers from every plot with the help of scale and then average was recorded.

3.5.9 Flower width (cm)

The width of flower was measured from randomly selected five flowers with the help of scale and then average was recorded.

(B) Phenological characters:

3.6.1 Node at first flower appears

Recorded the node at which first flower was borne on the main stem.

3.6.2 Days to 50 percent flowering (days)

Number of days required for 50 per cent of the plants to flower in each plot was recorded.

3.6.3 Fruiting span (days)

Duration of fruiting from each genotype was recorded.

3.6.4 Days to maturity (days)

Average number of days required to maturity was recorded.

(C) Yield parameters:

3.7.1 Number of fruits plants^{-1}

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

3.7.2 Fruit length (cm)

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

3.7.3 Fruit diameter (mm)

The diameters of the randomly selected fruits were recorded at different positions *i.e*., at the base, at middle and at top with the help of digital Vernier caliper and average was worked out.

3.7.4 Fruit weight (g)

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

3.7.5 Number of locules fruit^{-1}

Number of locules fruit^{-1} on observational plants was recorded.

3.7.6 Number of seeds fruit^{-1}

The number of seeds in five randomly selected fruits from observational plants was counted and average seeds fruit^{-1} was calculated.

3.7.7 100 seed weight (g)

The 100 seed weight was recorded separately with the help of weighing balance and average was worked out for each plot.

3.7.8 Fruit yield plant^{-1} (g)

Fresh marketable fruits were picked up from the observational plants separately throughout the harvesting period at an interval of three days and average yield per plant was worked out.

(D) Other observations:

3.8.1 Incidence of yellow vein mosaic virus:

The number of plants affected due to YVMV was counted at 90 DAS and percentage of incidence was worked out in each treatment. Percentage value is converted by using angular transformation statistics.

3.9 Statistical analysis:

The data in respect of various characters studied were subjected to the following analysis:

3.9.1 Analysis of variance

3.9.2 Estimation of parameters of genetic variability *i.e*., mean, range, genotypic and phenotypic coefficient of variation, heritability, expected genetic advance and genetic advance as percentage of mean.

3.9.3 Correlation coefficient analysis

3.9.4 Path coefficient analysis

3.9.5 Genetic divergence

3.9.1 Analysis of variance

The data on yield and quality traits were statistically analyzed on the basis of model described by Cochran and Cox (1950) for randomized complete block design. In order to test the significance of treatments Critical difference was computed (Fisher and Yates, 1963).

$$Y_{ij} = \mu + b_i + t_j + e_{ij}$$

Where,

Y_{ij} = Performance of j^{th} genotype in i^{th} block

μ = General mean

b_i = True effect of i^{th} block

t_j = True effect of j^{th} treatment

e_{ij} = Random errors which are supposed be identically and independently distributed with normal distribution having mean zero and variance σ^2_e.

Table 3.3 ANOVA for Randomized Complete Block Design

Source of variation	**d.f.**	**Sum of squares**	**Mean squares**	**Expected mean squares**
Replication	(r-1)	rss	M1	$\sigma^2_e + g\,\sigma^2_r$
Genotypes	(g-1)	gss	M2	$\sigma^2_e + r\sigma^2_g$
Error	(r-1)(g-1)	ess	M3	σ^2_e
Total	(rg-1)			

1. Genotypic variance (σ^2_g) = $\dfrac{M_2 - M_3}{r}$
2. Phenotypic variance (σ^2_p) = $\dfrac{M_2 - M_3}{r} + M_3$
3. Environmental variance (σ^2_e) = M_3

Where,

r = number of replications

g = number of genotypes

M_1= mean square due to replication

M_2= mean square due to genotypes

M_3= mean square due to error

3.9.2 Parameters of genetic variability

3.9.2.1 Mean

Mean is calculated by the following formula:

$$\bar{X} = \frac{\sum Xi}{N}$$

Where,

Σxi = Sum of all the observations of i^{th} trait

N= Total number of observations

3.9.2.2 Range

Range is the difference between the smallest and the greatest term of a series of observation and thus provides the information about the variability present in the genotypes.

3.9.2.3 Genotypic and phenotypic coefficient of variation

Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were calculated by the method suggested by Burton (1952).

3.9.2.4 Phenotypic coefficient of variation (PCV)

Since, $\sigma^2_p = \sigma^2_g + \sigma^2_e$

$PCV = (\sigma_p/\bar{X}) \times 100$ where,

$$\sigma_p = \sqrt{\sigma^2_p}$$

3.9.2.5 Genotypic coefficients of variation (GCV)

$GCV = (\sigma_g/\bar{X}) \times 100$ where,

$$\sigma_g = \sqrt{\sigma^2_g}$$

Where,

σ^2_p = Phenotypic variance

σ_p = Phenotypic standard deviation

σ^2_g = Genotypic variance

σ_g = Genotypic standard deviation

σ^2_e = Environmental variance

$\bar{X}$ = General mean

The estimates of PCV and GCV were classified as low, moderate and high according to Sivasubramanian and Madhavamenon (1973).

< 10 per cent	=	low
10-20 per cent	=	moderate
> 20 per cent	=	high

3.9.2.6 Heritability

It is the ratio of genotypic variance to the total phenotypic variance. Broad sense heritability was calculated in by adopting the formula as suggested by Hanson *et al.* (1956).

$$h^2b \ \% = \frac{\sigma^2_g}{\sigma^2_p} \times 100$$

Where,

h^2b = Heritability in broad sense

σ^2_g = Genotypic variance

σ^2_p = Phenotypic variance

Heritability per cent in broad sense was calculated for each character is classified into four groups:

Very high	> 90%
High	70 -90%
Medium	50% to 70%
Low	< 50%

3.9.2.7 Expected genetic advance

Improvement in the mean genotypic value of selected plants over the parental population is known as genetic advance. Expected genetic advance was calculated by the method suggested by Johnson *et al.* (1955).

$$GA = K\ \sigma_p\ h^2\ (bs)$$

Where,

GA = Genetic Advance

K = Constant (Standard selection differential) having the value of 2.06 at 5 per cent selection intensity

h^2b = Heritability of the character

σ_p = Phenotypic standard deviation

3.9.2.8 Genetic advance as percentage of mean

It was calculated by the following formula:

$$\text{GA as percentage of mean} = \frac{\text{Genetic advance}}{\text{General mean}} \times 100$$

GA as percentage of mean was categorized as:

< 25 per cent = low

25-35 per cent = moderate

>35 per cent = high

3.9.3 Correlation analysis

Correlation coefficients were calculated for all quantitative character combinations at phenotypic, genotypic and environmental levels by the formula given by Miller *et al.* (1958).

$$\mathbf{r}\,(X_iX_j) = \frac{\mathrm{COV}\,(X_iX_j)}{\sqrt{\mathrm{Var}\,(X_i)\ \mathrm{Var}(X_j)}}$$

Where,

$r\ (x_i\ x_j)$ = Coefficient of correlation between Xith and Xjth traits

COV (Xi Xj) = Covariance between Xith and Xjth traits

Var Xi = Variance of Xith trait

Var Xj = Variance of Xjth trait

Genotypic, phenotypic and environmental correlations were computed by substituting corresponding variance and covariance in the above formula. The estimation of covariance between two traits was derived in the same way as for corresponding variance components.

Testing of correlations:

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

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

Where,

n= Number of treatments.

r = phenotypic correlations coefficient.

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

3.3.4 Path coefficient analysis

The direct and indirect contribution of various characters to yield were calculated through path coefficient analysis as suggested by Wright (1921) and elaborated by Dewey and Lu (1959).

The following set of simultaneous equations were formed and solved for estimating direct and indirect effects.

$r_1Y = P_1Y + r_{12}\,P_2Y + r_{13}\,P_3\,Y + \ldots\ldots\ldots\ldots\ldots + r_1i\,P_1Y.$

$r_2Y = r_{21}\,P_1Y + P_2\,Y + r_{23}\,P_3Y + \ldots\ldots\ldots\ldots\ldots + r_{21}\,p_1Y.$

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$r_kY = r_{k1}\,P_1Y + r_{k2}\,P_2Y + r_{k3}P_3Y + \ldots\ldots\ldots\ldots + r_kP_kY.$

Where,

r_1Y to r_kY = Coefficient of correlation between causal factors 1 to i and dependent character Y

P_1Y to P_kY = Direct effect of characters 1 to i on character Y.

r_{12} to $r_{k-1,}$ = Coefficient of correlation among causal factors.

The above equations were written in a matrix form as under:

$$\underset{A}{\begin{bmatrix} r_1Y \\ r_2Y \\ \vdots \\ r_kY \end{bmatrix}} \qquad \underset{C}{\begin{bmatrix} 1 & r_{12} & r_{13}\ldots\ldots\ldots\ldots\ldots r_1 \\ r_{21} & 1 & r_{23}\ldots\ldots\ldots\ldots\ldots r_{2i} \\ \vdots & & \\ r_{k1} & r_{k2} & r_{k3}\ldots\ldots\ldots\ldots\ldots 1 \end{bmatrix}} \qquad \begin{bmatrix} P_1Y \\ P_2Y \\ \vdots \\ P_kY \end{bmatrix}$$

Then,

$$B = [C]^{-1}\,A$$

Where,

$$[C]^{-1} = \begin{bmatrix} C_{11} & C_{12} & C_{13}\ldots\ldots\ldots\ldots C_{1i} \\ C_{21} & C_{22} & C_{23} \qquad\quad C_{2i} \\ \vdots & & \\ C_{i1} & C_{i2} & C_{i3} \qquad\quad C_{ii} \end{bmatrix}$$

Then the direct effects were calculated as follows:

$$\overset{k}{\underset{i=1}{P_1}}Y = \sum C_{1i}\ r_i y$$

$$\overset{k}{\underset{i=1}{P_2}}Y = \sum C_{2i}\ r_{iy}$$

$$\overset{k}{\underset{i=1}{P_k}}Y = \sum C_{ki} r_k y$$

Residual effect was obtained as per for formula given below:

$$R = \sqrt{1 - \sum d_i r_{ij}}$$

Where,

di = Direct effect of the i^{th} character

rij = Correlation coefficient of the i^{th} character with j^{th} character.

Path coefficient were to be rated based on the scales given below. (Lenka and Mishra, 1973).

> 1.0	Very high
0.30 – 0.99	High
0.2 – 0.29	Moderate
0.1 – 0.19	Low
0.00 – 0.09	Negligible

3.9.4 Genetic divergence

The data collected on different characters were analyzed through Mahalanobis's generalized distance D^2 (1936).

3.9.4.1 Test of significance:

After testing the difference between genotypes for each of the characters, a simultaneously test of significance for differences in the mean value of number of correlated variables with regard to the pooled effect of 15 characters was carried out using ‘V’ statistic which in turn utilizes Wilk’s ‘Λ’ criterion. The sums of squares and sums of products of error and error + variety were used for this purpose. The estimation of ‘Λ’ (Wilk’s criterion) was done using the following relationship.

$$\text{‘}\Lambda\text{’} = (E)/(E+V)$$

Where,

(E) = Determination of error sum of squares and sum of products matrix.

(E+V) = Determination of error + Varieties sum of squares a sum of products matrix.

The significance of “Λ” was tested by X^2 as

$$X^2\, pq = V = -m \log e\, \Lambda$$

Where,

m = n-(p+q+1/2) with pq degrees of freedom

n = Total number of observation-1

p = Number of characters

q = k-1

k = number of populations

Computation of D^2 values

Mahalanobis’s D^2 statistics (1936) was used for assessing the genetic divergence between populations. The generalized distances between any two populations is defined as

$$\Delta^2 = (\lambda ij)\ di \times dj$$

Where,

λij = Reciprocal matrix to the common dispersion matrix.

di = Difference between the mean values of the two populations for the i^{th} character.

dj = difference between the mean values of the two populations for j^{th} character.

The quantity is estimated by the D^2 statistic as

D^2 = (S^{ij}) didj

Where,

Sij = sample estimate of ij^{th} character.

Since the formula for computation requires the inversion of the matrix of 14th order, transformation of the original correlated unstandardized character mean to standardized uncorrelated variables was done to simplify the computational procedure. The information was effected by pivotal condensation method (Rao, 1952).

3.9.4.2 Determination of group constellations or clusters:

Grouping of the populations into various clusters was done by using Tocher's method as described by Rao, (1952). The criterion used in clustering by this method is that any two variables belonging to the same cluster should at least on an average, show a smaller D^2 value than those belonging to different clusters. For this purpose D^2 values of the combinations of each genotype were arranged in ascending order of their magnitudes in a tabular form as described by Singh and Choudhary (1977). To start with, two populations having the smallest distance from each other were considered, to which a third population having the smaller D^2 value from the first two populations was added. Similarly, next the nearest fourth population was considered and this procedure was continued. At certain stage when it was felt that after adding a particular population there was an abrupt increase in the average D^2, that population was not considered for, in that cluster. The groups of the first cluster were then omitted and the rest were treated in a similar way. This process was continues till all the populations were included into one or the other cluster. After the formation of the clusters, the averages inter and intra cluster divergences (distance) were calculated. The square root of the D^2 value obtained from the above, represent the (D) between and within clusters.

3.9.4.3 Average intra-cluster distance:

For the measurement of intra-cluster distances, the formula used was $\Sigma iDi^2/n$ where, ΣiDi^2 was the sum of distances between all possible combinations (n) of the populations included in a cluster.

3.9.4.4 Average inter-cluster distances:

Clusters are taken one by one and their distances from other clusters were calculated. The distance between two clusters was the sum of the D^2 values between the members of the other cluster divided by the product of number of genotypes in both the clusters under consideration.

3.9.4.5 Contribution of individual characters towards divergence

In all the combinations each cluster was ranked on the basis of its combination towards divergence between two entries (di = Yii-Yjj). Rank one is given to the highest mean difference and rank 'P' to the lowest difference. Where, 'P' is the total number of characters. Percentage contribution of each character (X) towards genetic divergence was calculated using the formula.

$$X = Nx100/M$$

Where,

N = Number of genotype combinations where the character was ranked first.

M = All possible combinations of number of genotypes

3.10 Angular transformation or arcsine:

Angular transformation is used with percentage and proportion *i.e.,* 70*%*. This transformation produces values that are numerically close to the original % values over most of the percentage range while retaining all of the desirable statistical properties of the arcsine transformation according to Freeman and Turkey (1950).

$$Y = \mathrm{Sin}^{-1}\sqrt{\%}$$

$$Y = \mathrm{Sin}^{-1}\sqrt{0.70}$$

RESULTS

Experimental findings of the present investigation entitled "Genetic Divergence in Okra (*Abelmoschus esuleutus* (L) Moench)" are presented under the following hands:

4.1 Mean performance of the genotypes

4.2 Analysis of variance

4.3 Genetic Variability

- 4.3.1 Genotypic and phenotypic coefficient of variation
- 4.3.2 Broad sense heritability and Genetic advance as percentage of mean.

4.4 Correlation Coefficient analysis

4.5 Path coefficient analysis

4.6 Genetic divergence

4.7 Incidence of yellow vein mosaic virus

4.1 Mean performance of the genotypes

Range and mean performance of the 60 genotypes for all the 22 characters are presented in Table 4.1.

Plant height (cm)

Plant height ranged from 80.70 to 111.70 cm, with mean of 94.99 cm. The maximum plant height was recorded in genotypes IC033344 and minimum was observed in EC305634.

Stem diameter (mm)

Stem diameter varied from 12.69 to 23.90 mm with average of 17.33 mm. The maximum stem diameter was observed in EC305622 while, it was recorded minimum in EC329357.

Number of branches plant^{-1}

Genotype IC022237-A (6.0) recorded maximum branches plant^{-1} while, it was recorded the least in IC018960-C (1.25). Average for the trait branches plant^{-1} was 2.51.

Internodal length (cm)

Internodal length ranged between 5.04 in genotype IC018540 to 9.57 in IC031850 cm with an average of 7.18 cm.

Petiole length (cm)

Petiole length recorded an average of 19.83 cm. Maximum petiole length was noted in IC018542 (27.84), while genotype IC009856-C (16.61) revealed smallest petiole length.

Leaf blade length (cm)

Leaf blade length ranged between 14.17 in IC016262-A to 22.30 cm in IC018542 with a mean of 18.78 cm.

Leaf blade width (cm)

Leaf blade width recorded an average of 24.11 cm. It was highest in IC018542 (31.10) while, it was the least in IC015036-B (17.51).

Node to first flower appears

The maximum nodes to first flowering was noted in EC329366 (11.45) while, it was lowest in Hisar Unnat (5.40). This trait revealed a mean of 7.43.

Flower length (cm)

Flower length varied from 4.04 cm to 6.14 cm with mean of 5.16 cm. Genotype EC305664 produced longest flowers while, EC305616 recorded smallest flowers.

Flower diameter (cm)

The maximum (6.76 cm) flower diameter was exhibited by genotype EC329379 while, it was minimum in IC014845-B (4.49 cm). The average recorded was 5.72 cm.

Table 4.1: Mean performance of the genotypes for yield and ancillary characters in okra.

S. No.	Accession	Plant height (cm)	Stem diameter (mm)	No. of branches plant^{-1}	Internodal length (cm)	Petiole length (cm)	Leaf blade length (cm)	leaf blade width (cm)	Node at 1st flower appears	Flower length (cm)	Flower diameter (cm)	Fruit length (cm)
01	EC305617	89.4333	20.3600	3.1000	8.0800	17.2800	17.2800	22.6500	7.1667	4.2000	5.7267	12.1167
02	EC133336	91.8333	19.2800	2.1667	7.1500	19.7467	19.9267	29.0000	6.0167	4.6667	5.2067	14.6033
03	EC305622	108.3333	23.9000	3.1000	7.2400	18.8500	18.8500	22.9267	7.0000	5.3900	5.9600	18.7500
04	EC169319	83.8667	20.5133	2.4000	5.9000	19.5000	19.1000	25.8633	6.8000	4.5467	5.6000	17.2500
05	EC305634	80.7067	20.3200	5.2000	6.0100	19.3900	19.8300	24.6967	7.3600	5.5000	5.0500	13.2000
06	EC329379	87.5000	20.8700	3.1000	7.2600	21.1800	18.2200	23.3567	8.6000	4.3400	5.4800	11.6300
07	EC305664	84.2000	16.4900	2.8000	6.0000	19.1600	15.9000	23.4167	7.4000	6.1400	6.6200	15.2500
08	EC169443-A	82.4833	16.8100	1.6000	6.8133	18.9133	21.8400	27.3400	6.4000	5.6600	5.7500	15.7500
09	EC169333	93.4333	16.6400	1.7667	6.6900	17.3400	16.9300	22.6967	7.1000	4.6200	5.3867	14.5500
10	EC169364	91.1000	18.6967	2.5667	6.1200	17.8667	18.2000	25.8000	6.6500	4.1500	5.2333	15.9500
11	EC329356	96.3000	15.9100	2.7000	8.0867	21.0900	15.2600	20.4567	8.4000	5.6700	5.7200	16.7800
12	EC329357	90.3667	12.6933	2.2000	6.8800	19.1500	17.2300	22.0000	6.0267	4.8467	5.5600	13.0000
13	EC169398	107.3000	19.0800	2.4000	6.6600	22.4933	20.9133	27.4000	6.2500	4.8500	5.1867	17.0400
14	EC169515	80.8333	15.7133	1.9667	5.9900	21.2800	20.8100	27.8267	6.1000	5.5733	4.8467	16.6000
15	EC329366	94.3667	18.6467	1.7000	7.3200	22.1567	20.8200	22.2500	11.4500	5.1100	5.1900	16.2500
16	EC329368	102.8667	16.4633	2.4000	7.5300	20.0533	19.6500	22.3000	8.4000	5.2500	6.0400	15.8667
17	EC329369	88.7333	13.5833	3.4000	7.5600	17.0400	20.7900	22.4233	7.0567	5.3400	5.7467	12.7733
18	EC305637	90.0000	17.8867	1.7000	8.1200	18.5400	18.5700	22.2067	7.9500	5.6200	6.7600	16.8500
19	EC305616	95.5000	16.4467	1.8000	6.7700	17.8000	17.1333	24.2000	6.7333	4.0400	5.6467	15.9900

20	IC033122	109.4333	18.8200	1.9000	8.0000	22.1567	18.8333	26.4067	7.4000	5.4333	5.9200	17.5267
21	EC329397	93.0667	18.8267	4.7000	6.7600	21.2600	20.2400	23.5400	8.1500	4.4200	6.0600	14.9000
22	EC329400	101.7667	20.0600	1.4000	7.9600	19.8200	17.1000	20.1700	6.1000	5.6800	6.5800	15.0500
23	EC329418	96.5533	16.8300	1.7000	8.1000	17.1900	15.3900	19.1200	8.3500	5.8800	6.1867	19.4167
24	EC550848	109.8333	17.9633	2.3000	6.5200	20.9000	20.9300	27.7667	6.2500	5.6200	5.8200	17.5000
25	IC006485	87.2667	17.3433	1.5000	7.1000	22.0500	15.1300	19.4133	8.0000	5.4100	5.6467	15.9000
26	IC007472	98.7667	15.3700	1.5500	7.8400	20.0700	20.2500	23.3400	6.8100	4.3300	5.1300	16.9900
27	IC007952	97.0000	16.4600	2.7000	6.8200	21.8300	20.1500	22.2967	7.0433	5.2700	5.9800	16.4100
28	IC009856-C	94.9000	17.7700	3.0000	7.7800	16.6100	14.2200	17.7767	6.8000	5.3000	6.6233	14.7900
29	IC013995-A	85.5000	16.6500	1.6000	6.8167	20.3000	18.5100	21.4133	7.2000	5.3400	5.5067	15.6567
30	IC014600	96.9333	17.4500	2.6000	7.0300	20.9567	21.0500	22.6333	8.8000	4.7800	5.0400	12.7000
31	IC014845-B	87.6333	17.6500	3.7000	6.6900	18.7867	15.4700	18.5733	10.8000	4.9100	4.4900	12.6800
32	IC033344	111.7000	18.5167	2.1000	7.1300	22.2767	20.7000	26.3700	7.0000	5.7933	6.2067	17.8200
33	IC015036-B	85.9000	15.0567	1.7767	7.3600	18.6300	14.6600	17.5133	8.2267	5.5600	6.0133	15.2500
34	IC015435	86.6333	15.4367	1.7333	7.0100	20.8000	18.3600	22.0100	8.2000	5.3200	5.6300	15.1000
35	IC016262-A	98.4667	17.3000	2.5000	7.8000	18.9000	14.1700	17.8600	8.3000	5.2600	5.7400	13.4167
36	IC018473-A	99.9333	13.7600	1.5333	6.6900	18.5333	18.2200	20.6700	7.4000	5.2300	5.8467	14.5000
37	IC018533	93.7667	17.4467	3.7000	6.9100	20.0133	20.1000	22.5533	11.3000	5.2800	5.9167	12.0500
38	IC018534	86.3000	16.0100	2.0000	7.2200	19.4700	18.4000	20.7333	7.2767	5.3500	5.7333	15.6000
39	IC018540	89.7667	15.2567	3.0000	5.0400	17.2200	16.3800	20.0200	10.7267	3.6900	4.9667	18.6500
40	IC018541-A	96.2333	16.8533	2.6500	8.2200	20.0300	19.5000	24.1133	7.1767	5.3900	5.7000	18.0833
41	IC018542	103.6667	18.9267	3.0000	6.1700	27.8433	22.3000	31.1000	8.2000	5.4100	5.9000	15.0467
42	IC018960-B	104.1667	15.4300	1.7333	8.6800	21.2700	19.3500	26.6167	5.3000	5.2600	5.9200	16.2300
43	IC018960-C	93.3000	16.1567	1.2500	7.1900	18.9000	18.8000	26.0033	6.3000	4.5067	5.8500	19.6700
44	IC018973-A	87.1000	13.3400	1.3500	7.4800	18.4000	18.9000	27.4600	6.6000	4.5100	5.8800	11.4400

45	IC018975	98.0667	19.6133	3.7000	8.6267	21.6000	19.2000	25.7667	8.6000	5.1800	5.9900	13.3333
46	IC022237-A	87.4000	18.6233	6.3333	7.5267	17.3333	21.5000	28.3367	10.9500	5.4200	5.7600	12.4633
47	IC024906-A	91.8667	17.9967	4.5000	6.7200	18.8000	20.6200	28.1000	7.6000	5.4700	5.7467	15.6200
48	IC027831	91.4667	16.3433	4.5000	5.2700	19.1100	20.0000	25.2000	7.7000	5.3600	5.6267	14.1100
49	IC027881-A	91.8333	15.1333	2.9000	7.2100	19.7000	17.6000	23.3000	6.7000	5.2600	6.0200	16.7367
50	IC027889	102.3000	17.4033	2.7000	7.2300	17.2667	19.3000	27.3333	8.2000	5.1500	5.7333	14.9867
51	IC028359	91.9333	17.3167	2.3000	6.5100	17.0000	19.9267	28.5600	6.7000	5.4100	5.7733	11.9000
52	IC029119-B	96.9333	16.1767	2.0000	7.6000	19.1200	16.4000	24.2500	6.1000	4.5867	5.4733	14.7600
53	IC029191	105.7667	15.9800	1.4333	8.1700	19.5667	18.7500	25.3267	6.6000	5.1900	5.2800	13.1600
54	IC031850	97.2667	15.8200	1.6000	9.5767	20.3700	18.7000	27.3000	7.5000	5.5400	4.6933	13.4167
55	IC031932-A	99.8667	16.4333	3.4333	7.4767	18.1000	19.3000	24.1000	6.9800	5.9000	6.1800	15.8900
56	Pusa A4	101.1000	17.1833	1.5000	7.7700	19.8000	21.6600	28.5000	6.7000	5.3100	5.7800	15.7000
57	VRO-5	108.1333	18.7800	2.4000	6.6400	25.4500	21.0300	27.3833	5.7500	5.5700	6.0600	17.5500
58	VRO-6	100.9333	17.5700	2.0000	8.1233	22.3700	18.5000	25.7333	5.4900	5.7500	6.0800	22.5100
59	Phule Utkarsh	98.2333	18.3200	2.1000	6.6000	19.9600	19.6000	26.5000	6.4000	5.2400	6.0333	19.5000
60	Hisar Unnat	101.6000	20.2700	2.6000	7.5000	21.3367	20.9300	27.1667	5.4000	5.0500	6.1067	15.7267
	Minimum	**80.7067**	**12.6933**	**1.2500**	**5.0400**	**16.6100**	**14.1700**	**17.5133**	**5.3000**	**3.6900**	**4.4900**	**11.4400**
	Maximum	**111.7000**	**23.9000**	**6.3333**	**9.5767**	**27.8433**	**22.3000**	**31.1000**	**11.4500**	**6.1400**	**6.7600**	**22.5100**
	G. Mean	**94.9907**	**17.3325**	**2.5174**	**7.1841**	**19.8322**	**18.7897**	**24.1190**	**7.4323**	**5.1639**	**5.7222**	**15.4990**
	CD 5%	14.5339	1.6205	0.7110	0.5607	1.1629	1.0942	1.4930	0.6614	0.3284	0.7529	1.2554
	CD 1%	19.2153	2.1425	0.9400	0.7413	1.5375	1.4466	1.9739	0.8744	0.4342	0.9955	1.6598

S. No.	Accession	Fruit diameter (mm)	No. of locules fruit^{-1}	Fruit weight (g)	No. of fruits plant^{-1}	No. of seeds fruit^{-1}	100 seed weight (g)	Days to 50 %flowering	Fruiting span (days)	Days to maturity	Incidence of YVMV	Fruit yield plant^{-1} (g)
01	EC305617	15.8700	7.1000	16.1200	7.3000	55.7333	5.7267	49.0000	47.000	101.0000	63.923	115.4667
02	EC133336	16.4400	5.0000	17.2200	6.4667	58.1333	5.5900	47.0000	45.000	103.0000	34.923	183.6667
03	EC305622	19.2500	5.4000	15.6167	11.6000	50.4000	5.5767	49.0000	53.550	102.5000	74.996	255.4000
04	EC169319	16.8067	5.0000	16.4000	10.3000	59.2000	4.6500	49.3333	47.500	103.0000	44.996	166.6067
05	EC305634	19.7633	7.0333	13.2833	9.9333	50.3000	5.8100	49.6667	47.500	98.5000	46.920	219.8333
06	EC305637	17.7200	6.9000	14.3333	7.8000	29.2000	5.6767	56.0000	48.500	100.5000	56.990	118.0333
07	EC305664	15.3267	6.9000	14.7367	6.5000	53.2000	7.7767	53.3333	49.100	101.5000	52.766	119.0700
08	EC169443-A	16.1067	5.0000	15.9533	10.1667	47.4333	4.8500	46.3333	49.500	100.0000	39.146	148.6000
09	EC169333	17.0467	5.6333	14.6033	9.4333	56.8000	4.8000	46.3333	44.500	99.0000	38.850	152.1000
10	EC169364	18.7167	5.0000	13.9667	10.6000	52.3667	4.5000	46.3333	47.500	100.5000	30.290	160.2333
11	EC329356	17.4600	5.0000	13.7633	14.7333	46.0000	5.8267	53.3333	46.000	97.5000	58.996	216.9667
12	EC329357	15.4667	5.0000	11.6900	8.2000	34.0000	5.7267	53.3333	49.000	99.5000	58.996	116.6667
13	EC169398	17.2800	5.0000	14.4000	11.1333	39.1667	4.7000	49.3333	49.500	97.5000	42.990	152.1333
14	EC169515	18.4067	5.0000	14.0333	9.2333	47.8000	4.8000	49.0000	46.500	101.0000	36.930	134.0000
15	EC329366	19.2300	5.0000	16.2733	7.0000	48.8000	5.8967	47.6667	50.000	103.5000	56.990	112.4867
16	EC329368	18.6633	5.0000	16.8500	7.0667	50.3000	5.9267	47.6667	46.500	101.0000	56.990	139.6000
17	EC329369	15.2833	6.4333	17.2900	6.5333	46.2000	7.8400	55.3333	52.500	109.0000	56.990	108.8333
18	EC305637	15.8133	5.0000	13.6567	7.3000	53.6000	5.8367	45.6667	46.500	96.5000	56.990	125.0600
19	EC305616	17.3200	5.0000	14.3667	9.4333	57.1000	4.8500	47.6667	49.500	100.6667	14.996	138.2667
20	IC033122	17.1333	5.0000	14.8000	9.4667	50.2000	4.3000	52.3333	47.500	106.3333	39.146	141.8667
21	EC329397	18.6767	7.8667	16.4500	12.6667	61.1000	5.7767	46.6667	54.000	106.5000	56.990	292.5000
22	EC329400	18.5700	5.4000	17.6533	7.0000	51.9000	7.4500	50.0000	47.000	102.5000	56.990	118.6000

23	EC329418	16.5400	5.0000	16.1467	11.5000	54.0000	7.3933	51.6667	50.000	103.5000	63.923	201.4667
24	EC550848	17.7267	5.0000	17.8100	16.1667	67.7000	6.4767	47.3333	47.000	104.0000	6.1433	332.1000
25	IC006485	17.6900	5.0000	14.9067	12.0000	56.5667	7.4600	50.6667	50.000	100.5000	54.773	198.0000
26	IC007472	18.6567	5.5000	17.0733	10.4000	54.4000	6.9567	50.3333	48.000	103.0000	56.990	188.6333
27	IC007952	16.0700	5.0000	15.2933	11.2333	42.9000	7.5567	49.6667	53.500	101.5000	56.990	182.7000
28	IC009856-C	14.9700	5.0000	17.0300	11.5000	51.1000	5.7100	49.0000	50.000	97.5000	63.923	204.0000
29	IC013995-A	18.1200	5.0000	15.7800	6.6000	45.6000	5.8800	50.3333	47.000	96.0000	56.990	110.3867
30	IC014600	15.6600	5.0000	18.0833	9.1333	39.2000	5.8000	48.6667	50.000	97.5000	50.846	127.3000
31	IC014845-B	16.1633	5.0000	13.8667	6.5333	36.7000	3.9900	54.6667	45.500	98.0000	74.996	105.1333
32	IC033344	18.4100	5.2333	14.2000	11.1667	47.5667	4.6500	48.3333	46.500	96.5000	47.003	160.2000
33	IC015036-B	16.9000	5.1000	13.4800	12.2667	39.0000	6.7000	51.0000	44.500	96.5000	56.990	176.2667
34	IC015435	17.4300	5.1667	15.4800	11.5333	57.1000	5.9600	51.0000	51.500	99.5000	56.990	160.3667
35	IC016262-A	17.4033	5.0000	15.9633	10.1333	58.8667	6.9967	48.6667	46.500	98.5000	56.990	147.3333
36	IC018473-A	17.2700	5.0000	15.7900	11.8000	52.1333	7.2567	49.0000	45.500	102.5000	50.846	213.5000
37	IC018533	15.4533	5.0000	16.8900	6.5333	44.8000	5.7800	56.3333	47.000	97.5000	63.923	108.1667
38	IC018534	16.0367	5.0000	16.2867	7.3333	47.8333	7.4900	51.6667	45.000	98.0000	54.983	116.7333
39	IC018540	18.3667	5.0000	16.6933	9.4667	48.3000	7.1467	54.6667	45.500	100.5000	56.990	148.6667
40	IC018541-A	18.3067	6.0333	17.6600	8.0000	51.6000	5.9467	53.0000	50.000	95.5000	54.773	129.5667
41	IC018542	17.8067	5.0000	16.1967	7.1000	48.7000	6.4900	48.6667	47.500	100.5000	50.846	135.7667
42	IC018960-B	17.9200	5.0000	14.7867	9.7333	45.5000	7.5567	48.0000	47.500	98.5000	63.923	142.0667
43	IC018960-C	18.7633	5.0000	16.9500	10.8000	47.7000	5.9067	48.3333	47.000	101.5000	55.070	194.6000
44	IC018973-A	20.2667	5.0000	17.9900	11.6000	42.6667	7.7967	49.6667	44.000	101.5000	52.766	220.9167
45	IC018975	16.5967	5.0000	14.6667	12.0667	33.8000	3.9767	53.0000	47.500	101.0000	56.990	174.9333
46	IC022237-A	15.6500	5.0000	14.3467	9.8333	35.4000	5.9467	57.3333	49.500	99.5000	56.990	164.8500
47	IC024906-A	17.7133	5.0000	13.9500	12.4000	58.9000	3.9900	49.6667	46.000	99.0000	61.213	211.7000
48	IC027831	14.1033	5.0000	13.4200	9.0000	44.8000	5.9300	48.0000	47.000	98.5000	58.996	128.2667

49	IC027881-A	17.5467	5.0000	13.4000	13.0000	40.4000	5.8467	50.6667	41.500	102.5000	63.923	200.8500
50	IC027889	17.1067	5.1000	15.2167	10.4667	39.3000	5.7900	51.0000	46.500	101.5000	56.990	164.5000
51	IC028359	16.1367	5.0000	13.2533	11.0000	31.7000	5.6767	49.3333	41.500	100.3333	50.846	152.4000
52	IC029119-B	16.5633	5.0000	14.0033	13.2000	51.2333	7.4900	50.0000	45.500	102.5000	48.840	195.5667
53	IC029191	18.5533	5.0000	14.8733	11.9333	31.8000	7.4400	49.6667	44.500	101.0000	56.990	190.5000
54	IC031850	17.5567	5.1000	13.6933	11.0000	47.7000	5.9767	50.0000	45.000	99.0000	56.990	153.9000
55	IC031932-A	14.8833	5.0000	13.2733	10.1000	48.8000	6.4767	48.3333	47.500	100.3333	56.990	154.2333
56	Pusa A4	18.9367	5.0000	17.6400	15.3667	56.2000	6.9900	47.0000	46.000	106.0000	6.1433	234.2000
57	VRO-5	18.2400	5.0000	17.8333	16.2333	56.9000	7.2800	47.3333	53.000	100.0000	26.066	312.5000
58	VRO-6	19.8600	5.0000	16.9967	16.5000	46.3000	8.0500	49.0000	49.000	101.3333	12.286	217.1067
59	Phule Utkarsh	18.5233	5.0000	17.3800	17.5000	49.6333	7.7167	46.0000	49.500	103.6667	14.996	323.5000
60	Hisar Unnat	18.4833	5.0000	17.8933	15.2667	42.4000	6.9900	48.3333	45.500	105.6667	14.996	214.2667
	Minimum	**14.1033**	**5.0000**	**11.6900**	**6.4667**	**29.2000**	**3.9767**	**45.6667**	**41.500**	**95.5000**	**6.1433**	**105.1333**
	Maximum	**20.2667**	**7.8667**	**18.0833**	**17.5000**	**67.7000**	**8.0500**	**57.3333**	**54.000**	**109.0000**	**74.996**	**332.1000**
	G. Mean	**17.3456**	**5.2650**	**15.4943**	**10.4544**	**48.2356**	**6.139**	**49.9278**	**47.635**	**100.6889**	**49.762**	**172.2189**
	CD 5%	1.1579	0.3441	1.4103	1.5239	6.4520	0.6072	3.0383	3.1674	3.7267	12.6567	26.3203
	CD 1%	1.5309	0.4550	1.8646	2.0147	8.5303	0.8027	4.0169	4.1877	4.9270	16.7335	34.7982

Fruit length (cm)

Fruit length varied from 11.44 cm in IC018973-A to 22.51 in VRO-6 cm with mean of 15.49 cm.

Fruit diameter (mm)

The maximum (20.26 mm) fruit diameter was exhibited by genotype IC018973-A while, it was the least in IC027831 (14.10 mm) with an average of 17.34 mm.

Number of locules fruit^{-1}

An average of 5.26 was recorded for the trait number of locules fruit^{-1}, 44 genotypes recorded 5.0 locules fruit^{-1} while, EC 329397 recorded the highest numbers of locules 7.86 remaining genotypes recorded more than 5 locules.

Fruit weight (g)

Average for the trait fruit weight was 15.49 g. The genotype IC014600 (18.03) exhibited maximum fruit weight while EC329357 (11.69) recorded the least fruit weight.

Number of fruits plant^{-1}

The maximum 17.50 fruits plant^{-1} were recorded in genotypes Phule Utkarsh while, it was the least in genotype EC133336 (6.46) with mean of 10.45.

Number of seeds fruit^{-1}

Seeds fruit^{-1} ranged between 29.20 to 67.70 seeds fruit^{-1}, with an average of 48.23.The maximum seeds per fruit were observed in EC550848 however it was recorded the least in EC305637.

Days to 50 per cent flowering (days)

Genotype EC305637 was recorded shortest duration to (45.66) days to 50 per cent flowering while, IC022237-A (57.33) recorded the maximum for the trait, the average was 49.92 days.

Fruiting span (days)

Fruiting span ranged from 41.5 to 54.0 with mean of 47.63 days. Genotype EC329397 revealed the maximum while, IC027881-A and IC028359 recorded shortest duration of fruiting span.

Days to maturity (days)

Genotype IC018541-A was observed to be earliest in maturity (95.50) while genotype EC329369 recorded maximum duration to maturity (109.00) with an average of 100.68 days.

100 seed weight (g)

Average for the trait was 6.13. Highest 100 seed weight was recorded in VRO 6 (8.05) while it was least in IC 018975 (3.97).

Fruit yield plant^{-1} (g)

Highest fruit yield^{-1} plant was recorded in EC 550848 (332.10 g) while, it was the lowest in IC117078 (105.13 g) with an average 172.21 g.

Incidence of YVMV

Average incidence 49.76 for YVMV incidence was recorded, incidence was recorded highest in EC305622 and IC014845-B (74.99) while the incidence was least in EC550848 and Pusa A4 (6.14).

4.2 Analysis of variance

The analysis of variance for all the characters studied has been presented in Table 4.2. Results reveal that there is presence of substantial variability amongst the genotypes as evident from the very high level of significance for treatments in the findings.

4.3 Genetic variability

4.3.1 Coefficient of variation

Estimation of components of genetic parameters of variation for yield and its contributing characters exhibited a wide range of variation for the characters studied (Table 4.2). Results indicated that the values of PCV were of higher magnitude than those of GCV for all the characters indicating influence of environment over the genotype.

The highest PCV was observed in four character *viz*., No. of branches (42.91), followed by incidence of YVMV (34.15), fruit yield plant^{-1} (32.05) and No. of fruits plant^{-1} (27.67).

Moderate PCV was recorded for node at 1st flower appears (19.28) followed by 100 seed weight (18.69), number of seeds fruit^{-1} (18.06), fruit length (15.04),leaf blade width (13.59), stem diameter (12.54), number of locules (12.54), internodal length (12.11), plant height (11.20), fruit weight (11.16), leaf blade length (11.13), petiole length (10.70), flower length (10.37) and flower diameter (10.35).

The PCV was low for four characters *viz*., fruit diameter (8.59), fruiting span (6.50), days to 50 per cent flowering (6.24) and days to maturity (3.34).

4.3.2 Heritability (broad sense)

The estimate of heritability (broad sense) for all the characters has been presented in Table 4.2. It was classified as very high (> 90%), high (70-90%), medium (50-70%) and low (<50%). Heritability ranged from 37.7 per cent for days to maturity to 99.92 per cent for plant height.

The broad sense heritability was very high for leaf blade width (92.00%), node at 1st flower appears (91.80%), fruit yield plant^{-1} (91.30%). However, it was recorded high for no. of locules (89.60%), leaf blade length (89.50%), no. of fruits plant^{-1} (89.30%), 100 seed weight (89.3%), fruit length (88.90%), petiole length (88.50%), flower length (85.60%), internodal length (84.10%), no. of branches (83.4%), no. of seeds fruit^{-1} (79.00%), YVMV incidence (78.78%), stem diameter (78.70%), fruit diameter (76.90%), and fruit weight (74.50%). Moderate heritability was exhibited by the traits *e.g.*, days to 50 per cent flowering (63.70%), fruiting span (60.00%) and days to maturity (53.10%). Flower diameter (38.20%) and plant height (28.73%). recorded low estimates of heritability.

Table 4.2: ANOVA, genetic components of variances, heritability, genetic advance for yield and yield contributing traits in okra.

Source of variation	d.f.	Mean sum of square for quantitative traits										
		Plant height (cm)	Stem diameter (mm)	No. of branches plant^{-1}	Internodal length (cm)	Petiole length (cm)	Leaf blade length (cm)	leaf blade width (cm)	Node at 1st flower appears	Flower length (cm)	Flower diameter (cm)	Fruit length (cm)
Replication	2	57.84	0.017	0.049	0.037	0.029	0.084	0.023	0.052	0.016	.0005	0.036
Genotype	59	178.52**	12.18**	3.113**	2.033**	12.48**	12.22**	30.54**	5.828**	0.779**	0.619**	15.11**
Error	118	80.79	1.004	0.193	0.120	0.517	0.457	0.852	0.167	0.041	0.216	0.602
GCV		6.008	11.138	39.192	11.113	10.071	10.541	13.044	18.482	9.605	6.404	14.189
PCV		11.209	12.549	42.909	12.118	10.704	11.139	13.594	19.284	10.379	10.355	15.047
h^2b		28.730	78.700	83.100	84.100	88.500	89.500	92.00	91.800	85.600	38.200	88.900
GA		6.302	3.529	1.856	1.508	3.871	3.861	6.218	2.712	0.945	0.466	4.271
GA as % of mean		6.634	20.363	73.743	21.002	19.520	20.540	25.783	36.490	18.310	8.158	27.562
CD 5%		14.533	1.620	0.711	0.560	1.162	1.094	1.493	0.661	0.328	0.752	1.255
CD 1%		19.215	2.142	0.940	0.741	1.537	1.446	1.973	0.874	0.434	0.995	1.659

Source of variation	d.f.	Mean sum of square for quantitative traits										
		Fruit diameter (mm)	No. of locules fruit^{-1}	Fruit weight (g)	No. of fruits plant^{-1}	No. of seeds fruit^{-1}	100 seed weight (g)	Days to 50 % flowering	Fruiting span (days)	Days to maturity	Incidence of YVMV	Fruit yield plant^{-1} (g)
Replication	2	0.210	0.0005	0.012	0.176	6.883	0.002	0.005	0.442	0.405	52.071	81.001
Genotype	59	5.641**	1.219**	7.458**	23.33**	195.98**	3.670**	22.125**	21.117**	23.396**	743.77**	8610.23**
Error	118	0.512	0.045	0.760	0.888	15.923	0.141	3.530	3.837	5.312	61.27	264.988
GCV		7.537	11.880	9.643	26.163	16.061	17.668	4.986	5.038	2.438	30.310	30.625
PCV		8.594	12.549	11.166	27.673	18.066	18.697	6.247	6.503	3.344	34.149	32.050
h^2b		76.900	89.600	74.500	89.300	79.000	89.300	63.700	60.000	53.100	78.780	91.300
GA 5%		2.362	1.219	2.658	5.327	14.187	2.111	4.093	3.830	3.687	27.578	103.816
GA as % of mean		13.618	23.168	17.155	50.956	29.413	34.394	8.198	8.040	3.662	55.420	60.281
CD 5%		1.157	0.344	1.410	1.523	6.452	0.607	3.038	3.167	3.726	12.656	26.320
CD 1%		1.530	0.455	1.864	2.014	8.530	0.802	4.016	4.187	4.927	16.73	34.798

4.3.3 Genetic advance

Genetic advance as percentage of mean was calculated to predict the expected genetic gain in one cycle of selection (Table 4.2). It was classified as very high (>50%), high (>50-35%), moderate (20-35%) and low (<20%).

The highest estimate of genetic advance as percentage of mean was recorded for no. of branches (73.74%) followed by fruit yield plant^{-1} (60.28%), YVMV incidence (55.42%) no. of fruits plant^{-1} (50.95%) were classified as very high, while node at 1st flower appears (36.49%) was high, whereas, the estimates were moderate for 100 seed weight (34.39%), no. of seeds fruit^{-1} (29.41%), fruit length (27.56%), and leaf blade width (25.78%) no. of locules (23.16%), internodal length (21.00%), leaf blade length (20.54%) and stem diameter (20.36%). However, the estimates were low for petiole length (19.52%), flower length (18.31%), fruit weight (17.15%), fruit diameter (13.61%), days to 50 per cent flowering (8.19%), flower diameter (8.15%), fruiting span (8.04%), while plant height (6.63%) and days to maturity (3.66%), recorded very low estimates of GA as percentage of mean.

4.4 Correlation coefficient analysis:

Coefficients of correlation were analyzed for all possible combinations of yield and yield contributing characters are presented in (Table 4.3).

Plant height

Plant height revealed very strong positive association with petiole length (0.2928), fruit length (0.2675) and no. of fruits plant^{-1} (0.2672), however it showed strong positive relationship with internodal length (0.2183), while no. of locules (-0.1965) expressed strong negative association with plant height. Whereas, traits *viz.,* stem diameter (0.1593), leaf blade length (0.1570) leaf blade width (0.1690) and node at 1st flower appears (0.1629) revealed positive relationship. However, its association was negative with days to 50 per cent flowering (-0.1617) and incidence of YVMV (-0.1843). Remaining traits did not express any relationship with plant height.

Stem diameter

Highly strong positive association of stem diameter was reveled with no. of branches (0.2860) however, it revealed negative relationship of same magnitude with hundred seed weight (-0.2806). Positive association of this trait petiole length (0.2231), number of locules fruit^{-1} (0.2162) and fruiting span (0.2122) were strong, while leaf blade width (0.1892) and leaf blade length (0.1861) revealed positive relationship. However, association was highly negative and strong with 100 seed weight (-0.2806).

Number of branches plant^{-1}

Number of branches plant^{-1} showed highly positive association with nodes at 1st flower appears (0.3926), number locules fruit^{-1} (0.3477) and days to 50% flowering (0.3015), however it revealed negative relationship of same magnitude with fruit length (-0.2771). It also indicated strong positive association with incidence of YVMV (0.2159). Negative relationship of same magnitude was observed between this trait and 100 seed weight (-0.2381), fruit diameter (-0.2373), internodal length (-0.225) and fruit weight (-0.2145). However, it revealed positive association with leaf blade length (0.1910) whereas, it indicated very highly negative association with fruit length (-0.2771).

Internodal length

The correlation of internodal length was strong with flower length (0.2104) followed by positive association with flower diameter (0.1671) and 100 seed weight (0.1500).

Petiole length

Petiole length showed very strong positive association with leaf blade length (0.3553), leaf blade width (0.3024) and fruit diameter (0.2686), however it expressed strong positive relationship with fruit length (0.2303), flower length (0.1969) and fruiting span (0.1964).It also indicated negative relationship of same magnitude with incidence of YVMV (-0.2109). Number of fruits plant^{-1} (0.1694) revealed positive relationship with petiole length.

Table 4.3 Estimates of genotypic, phenotypic and environmental coefficients of correlation among yield and its contributing characters in okra

			2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21
			Stem diameter (cm)	No. of branches plant^{-1}	Internodal length (cm)	Petiole length (cm)	Leaf blade length (cm)	leaf blade width (cm)	Node at 1st flower	Flower length (cm)	Flower diameter (cm)	Fruit length (cm)	Fruit diameter (mm)	No. of locules fruit^{-1}	Fruit weight	No. of fruit plant^{-1}	No. of seed fruit^{-1}	100 seed weight (g)	Days to 50 % flowering	Fruiting span	Days to maturity	Incidence of YVMV
1	**Plant height**	G	0.2998	-0.2892	0.4604	0.5176	0.3006	0.3249	-0.3205	0.2618	0.4920	0.4379	0.3833	-0.3558	0.3623	0.5057	0.1156	0.1178	-0.3943	0.1535	0.2870	-0.3013
		P	0.1593*	-0.1157	0.2183**	0.2928***	0.1570*	0.1690*	-0.1629*	0.0670	0.0767	0.2675***	0.1188	-0.1965**	0.1347	0.2672***	0.0454	0.0962	-0.1617*	0.0476	0.0961	-0.1843*
		E	0.0428	0.0754	-0.0240	0.1110	0.0165	0.0078	0.0073	-0.1967	-0.1303*	0.1641	-0.1514	-0.0585	-0.0776	0.0395	-0.0251	0.1324	0.0138	-0.0303	-0.0278	-0.1053
2	**Stem diameter**	G		0.3387	-0.0422	0.2424	0.2042	0.2224	0.0451	-0.0107	0.1591	0.1097	0.1980	0.2472	0.1552	0.0306	0.1482	-0.3758	-0.1887	0.2722	0.0986	-0.1218
		P		0.2860***	-0.0235	0.2231**	0.1861*	0.1892*	0.0568	-0.0159	0.0383	0.0866	0.1405	0.2162**	0.1113	0.0447	0.0948	-0.2806***	-0.1041	0.2122**	0.0722	-0.0980
		E		0.0610	0.0593	0.1330	0.0977	-0.0015	0.1405	-0.0408	-0.1353*	-0.0339	-0.0615	0.0572	-0.0329	0.1268	-0.1045	0.2291*	0.1066	0.0859	0.0268	-0.0099
3	**No. of branches**	G			-0.2884	-0.1195	0.1877	0.0907	0.4297	0.0149	-0.0524	-0.3402	-0.3058	0.3935	-0.2229	-0.0966	-0.1641	-0.2855	0.4185	0.2483	-0.0767	0.2781
		P			-0.2254**	-0.0847	0.1910*	0.0815	0.3926***	0.0124	-0.0100	-0.2771***	-0.2372**	0.3477***	-0.2145**	-0.1063	-0.1176	-0.2381**	0.3015***	0.1323	-0.0465	0.2159**
		E			0.0998	0.1307	0.2186*	0.0169*	0.1408	-0.0013	0.0613	0.1176	0.0398	0.0571	-0.1883	-0.1730	0.0837	0.0625	-0.0145	-0.1686*	0.0162	-0.0510
4	**Internodal length**	G				0.0021	-0.1465	-0.0890	-0.1026	0.2207	0.2347	-0.0295	0.0636	-0.0656	0.0862	0.0948	-0.1368	0.1649	0.0912	-0.0459	0.0379	0.1713
		P				0.0014	-0.1427	-0.0909	-0.1029	0.2104**	0.1671*	-0.0382	0.0790	-0.0320	0.0745	0.0848	-0.0745	0.1500*	0.0521	-0.0429	-0.0141	0.1407
		E				-0.0029	-0.1205	-0.1116	-0.1117	0.1529	0.1086	-0.0950	0.1458	0.1944**	0.0312	0.0197	0.2031*	0.0543*	-0.0608	-0.0409	-0.1447	0.0068
5	**Petiole length**	G					0.4238	0.3420	-0.0886	0.2230	0.0078	0.2407	0.3614	-0.0885	0.1759	0.1783	0.0357	0.0408	-0.1558	0.2811	0.0152	-0.2441
		P					0.3553***	0.3024***	-0.0852	0.1969**	-0.0085	0.2303**	0.2686***	-0.0644	0.1390	0.1694*	0.0102	0.0555	-0.1082	0.1964**	-0.0069	-0.2109**
		E					-0.2008*	-0.0657*	-0.0553	0.0215	-0.0490	0.1484*	-0.1818*	0.1326	-0.0234	0.0980	-0.1269	0.1738*	0.0431	-0.0393	-0.0746	-0.0452
6	**Leaf blade length**	G						0.7793	-0.1172	0.0858	-0.1306	0.0136	0.1707	-0.0146	0.2793	0.0539	-0.0416	-0.1304	-0.2632	0.2112	0.2779	-0.3551
		P						0.7224***	-0.1054	0.0635	-0.0623	0.0126	0.1421	-0.0094	0.2074**	0.0423	-0.0676	-0.1284	-0.1881*	0.1254	0.1794*	-0.2897***
		E						0.1627*	0.0091	-0.0952	0.0556	0.0045	0.0027	0.0357	-0.1278	-0.0563	-0.2198*	-0.1115*	0.0550	-0.1442	-0.0555	0.0574
7	**leaf blade width**	G							-0.3708	0.0216	-0.1059	0.0548	0.2399	-0.0999	0.0597	0.2447	-0.0289	-0.1874	-0.3258	-0.1319	0.2670	-0.5183
		P							-0.3341***	0.0270	0.0763	0.0383	0.1740*	-0.0997	0.0264	0.2112**	-0.0491	-0.1731*	-0.2112**	-0.0822	0.1814*	-0.438***
		E							0.0852	0.0729	-0.0605	-0.1209	-0.2063**	-0.0982	-0.1623*	-0.1173	-0.1899*	-0.0343	0.2259*	0.0889*	-0.0281	0.0235
8	**Node at 1st flower**	G								-0.0834	-0.2795	-0.2943	-0.2005	0.0290	-0.0721	-0.3828	-0.1952	-0.2074	0.5668	0.0541	-0.2275	0.4917
		P								-0.0687	-0.1735*	-0.2741***	-0.1739*	0.0371	-0.0810	-0.3609***	-0.1736*	-0.1825*	0.4475***	0.0299	-0.1618*	0.4067***
		E								0.0487	-0.0347	-0.0863	-0.0397	0.1176	-0.1485*	-0.1507*	-0.0563	0.0565	0.0807	-0.0568	-0.0147	-0.0879
9	**Flower length**	G									0.4113	-0.2562	0.2454	0.4269	-1256.0	0.1374	-0.0055	0.1866	0.0119	0.0696	-0.1558	0.0259
		P									0.3207***	0.1616*	-0.1264	-0.1397	-0.1182	0.1184	0.0065	0.1753*	0.0332	0.0457	-0.1265	0.0278
		E									-0.0168	0.0465	0.0366	-0.0030	-0.0935	-0.0146	0.0633	0.0977	0.1069	-0.0175	-0.0824	0.0371

Leaf blade length

Highly strong and positive association of leaf blade length was reveled with leaf blade width (0.7224) however, it revealed negative relationship of same magnitude with incidence of YVMV (-0.2897). Association of leaf blade length was strong with fruit weight (0.2074) followed by days to maturity (0.1794) revealing positive relationship, while it indicated negative relationship of same magnitude with days to 50 per cent flowering (-0.1881).

Leaf blade width

Leaf blade width showed good positive relationship with number of fruits plant^{-1} (0.2112) whereas, days to maturity (0.1814) and fruit diameter (0.1740) revealed positive association with this trait. However, incidence of YVMV (-0.4383) and node at first flower appears (-0.3341) showed strong highly negative association with this character followed by strong negative association with days to 50 per cent flowering (-0.2112).

Node at 1st flower appears

Node at first flower appears showed very strong positive association with days to 50 per cent flowering (0.4475), incidence of YVMV (0.4067), while it revealed negative relationship of same magnitude with number of fruits plant^{-1} (-0.3609) and fruit length (-0.2741). However, association was negative with hundred seed weight (-0.1825), fruit diameter (-0.1739), seed fruit^{-1} (-0.1736), flower diameter (-0.1735) and days to maturity (-0.1618).

Flower length

Flower length showed very strong positive association with flower diameter (0.3207) however, 100 seed weight (0.1753) and fruit length (0.1616) also revealed positive relationship.

Flower diameter

It expressed strong positive association with 100 seed weight (0.2011) and fruit length (0.1957).

Fruit length

The trait fruit length showed very strong positive association with number of fruits plant^{-1} (0.3965), fruit diameter (0.3305) and no of seeds per fruit (0.3279) however, its relationship was highly strong and negative with incidence of YVMV (-0.3048) and days to 50 per cent flowering (-0.2530) followed by number of locules (-0.2389) expressing strong negative correlation, on the contrary fruit weight (0.1905) and fruiting span (0.1895) revealed positive relationships.

Fruit diameter

Very strong positive relationship of fruit diameter was exhibited with no. of fruit plant^{-1} (0.3134) and fruit weight (0.2617) while, days to maturity (0.1805), and no. of seeds fruit^{-1} (0.1617) revealed positive associations. However, its association was highly strong and negative with days to 50 per cent flowering (-0.2601) followed by strong and negative correlation with incidence of YVMV (-0.2427).

Number of locules fruit^{-1}

Number of locules fruit^{-1} showed strong positive relationship with fruiting span (0.2338), while it revealed negative relationship of same magnitude with number of fruits plant^{-1} (-0.2139).

Fruit weight

Highly strong and positive association of fruit weight was revealed with 100 seed weight (0.3487), days to maturity (0.3137) and number of seeds fruit^{-1} (0.2970). However, it revealed negative relation of same magnitude with incidence of YVMV (-0.2632). Its relationship with fruiting span (0.1846) was positive, while it also revealed negative relationship with days to 50 per cent flowering (-0.1901).

Number of fruits plant^{-1}

Number of fruits plant^{-1} indicated strong positive relationship with hundred seed weight (0.2205) and days to maturity (0.1953) while, it exhibited negative association with incidence of YVMV (-0.4667) and days to 50 per cent flowering (-0.2585).

Number of seeds fruit^{-1}

Days to maturity (0.1670) and fruiting span (0.1647) showed positive relationship with number of seeds fruit^{-1} while, it revealed highly negative association with days to 50 per cent flowering (-0.3769) and incidence of YVMV (-0.2660).

100 seed weight

Correlation coefficient for hundred seed weight was strong and positive with days to maturity (0.2199).

Days to 50 per cent flowering

Positive correlation of this trait with incidence of YVMV (0.3441) was highly significant.

Fruiting span

The character fruiting span did not showed any significant relationship with any other character.

Days to maturity

Highly negative association of Days to maturity with incidence of YVMV (-0.2817) was observed.

Fruit yield plant^{-1}

This trait expressed highly strong positive association with no. of fruits plant^{-1} (0.8033), fruit diameter (0.3767) fruit length (0.3496), no. of seeds fruit^{-1} (0.3164), days to maturity (0.3019), fruit weight (0.2742) while, plant height (0.2277), leaf blade width (0.2199), 100 seed weight (0.2195), flower diameter (0.1540), fruiting span (0.1526), petiole length (0.1519) and stem diameter (0.1505) indicated positive relationship. Highly negative association was observed with incidence of YVMV (-0.3892), days to 50 per cent flowering (-0.3195) and node at first flower appears (-0.3070).

4.5 Path coefficient analysis:

The estimates of path coefficients for yield attributing traits and fruit quality on fruit yield are furnished in table 4.4. The character wise results obtained from present investigation for direct and indirect effects are presented as:

Direct Effects

The phenotypic path coefficient analysis of different yield contributing and associated traits on fruit yield plant^{-1} revealed that traits *viz.,* number of fruits plant^{-1}(0.733), recorded high estimate of positive direct effect followed by low direct effect of number of seeds fruit^{-1} (0.165), branches plant^{-1} (0.147), fruit diameter (0.133) while, the contribution of fruit weight (0.097), days to maturity (0.058), fruiting span (0.056), 100 seed weight (0.055), stem diameter (0.027) and plant height (0.023) were negligible. The negative direct effect were also negligible for node at first flower appears (-0.051), fruit length (-0.069) and internodal length (-0.096).

Indirect Effects

Plant height

Plant height showed negligible positive direct effect on fruit yield plant^{-1} (0.0233). However, its indirect effects manifested through fruit length (0.0062), no. of fruits plant^{-1} (0.0062), internodal length (0.0051), stem diameter (0.0037), fruit weight (0.0031), fruit diameter (0.0028), hundred seed weight (0.0024), days to maturity (0.0022), number of seeds fruit^{-1} (0.0013) and fruiting span (0.0011) were negligible. Its negative indirect effect through number of branches (-0.0027) and node at 1st flower appears (-0.0038) were also negligible.

Stem diameter

The direct contribution of this trait on fruit yield plant^{-1} (0.0277) was negligible but positive. The positive indirect effects were also negligible via number of branches plant^{-1}(0.0079), fruiting span (0.0059), plant height (0.0044), fruit diameter (0.0039), number seed fruit^{-1} (0.0036), fruit weight (0.0031), fruit

Table 4.4: Estimates of path coefficients analysis showing direct and indirect effect on fruit yield plant^{-1} in okra.

Character	Plant height (cm)	Stem diameter (cm)	No. of branches plant^{-1}	internodal length (cm)	Node at 1st flower appears	Fruit length (cm)	Fruit diameter (cm)	Fruit weight (g)	No. of fruit plant^{-1}	No. of seed fruit^{-1}	100 seed weight (g)	Fruiting span	Days to maturity
Plant height (cm)	**0.0233**	0.0037	-0.0027	0.0051	-0.0038	0.0062	0.0028	0.0031	0.0062	0.0013	0.0024	0.0011	0.0022
Stem Diameter (mm)	0.0044	**0.0277**	0.0079	-0.0007	0.0016	0.0024	0.0039	0.0031	0.0012	0.0036	-0.0081	0.0059	0.0020
No. of Branches plant^{-1}	-0.0170	0.0421	**0.1472**	-0.0332	0.0578	-0.0408	-0.0349	-0.0316	-0.0156	-0.0121	-0.0343	0.0195	-0.0069
Internodal length (cm)	-0.0211	0.0023	0.0218	**-0.0966**	0.0099	0.0037	-0.0076	-0.0072	-0.0082	0.0095	-0.0148	0.0041	0.0014
Node at 1st flower appears	0.0084	-0.0029	-0.0203	0.0053	**-0.0518**	0.0142	0.0090	0.0042	0.0187	0.0083	0.0089	-0.0015	0.0084
Fruit length (cm)	-0.0186	-0.0060	0.0193	0.0027	0.0191	**-0.0695**	-0.0230	-0.0132	-0.0276	-0.0242	-0.0081	-0.0132	-0.0063
Fruit diameter (mm)	0.0158	0.0187	-0.316	0.0105	-0.0232	0.0440	**0.1332**	0.0348	0.0417	0.0171	0.0163	-0.0014	0.0240
Fruit weight (g)	0.0132	0.0109	-0.0210	0.0073	-0.0079	0.0186	0.0256	**0.0977**	0.0120	0.0266	0.0334	0.0180	0.0306
No. of fruit plant^{-1}	0.1958	0.0328	-0.0779	0.0621	-0.2646	0.2907	0.2297	0.0902	**0.7330**	0.0760	0.1517	0.0206	0.1432
No. of seeds fruit^{-1}	0.0094	0.0214	-0.0136	-0.0163	-0.0267	0.0576	0.0212	0.0451	0.0172	**0.1655**	0.0009	0.0331	0.0256
100 seed weight (g)	0.0057	-0.0163	-0.0130	0.0085	-0.0096	0.0065	0.0068	0.0191	0.0116	0.0003	**0.0559**	0.0031	0.0121
Fruiting span	0.0027	0.0120	0.0075	-0.0024	0.0017	0.0107	-0.0006	0.0104	0.0016	0.0113	0.0032	**0.0564**	0.0067
Days to maturity	0.0057	0.0042	-0.0027	-0.0008	-0.0095	0.0053	0.0106	0.0184	0.0115	0.0091	0.0128	0.0070	**0.0588**
Fruit yield plant^{-1} (g)	**0.2277**	**0.1505**	**0.0208**	**-0.0485**	**-0.3070**	**0.3496**	**0.3767**	**0.2742**	**0.8033**	**0.2924**	**0.2202**	**0.1526**	**0.3019**
Partial R^2	**0.0053**	**0.0042**	**0.0031**	**0.0047**	**0.0159**	**-0.0243**	**0.0502**	**0.0268**	**0.5889**	**0.0484**	**0.0123**	**0.0086**	**0.0178**

R square = 0.7617 Residual effect = 0.488

length (0.0024), days to maturity (0.0020), node at first flower appears (0.0016) and number of fruits plant^{-1} (0.0014). Negative indirect effects if this trait were observed through 100 seed weight (-0.0081) and internodal length (-0.0007), were negligible.

Number of branches plant^{-1}

This trait expressed low positive direct effect on fruit yield plant^{-1} (0.1472). Its indirect effect through node at 1st flower appears (0.0578); stem diameter (0.0421) and fruiting span (0.0195) were positive and negligible. Negative indirect effects if this trait observed through days to maturity (-0.0069), number of seeds fruit^{-1} (-0.0121), fruits plant^{-1} (-0.0156), plant height (-0.0170), fruit weight (-0.0316), internodal length (-0.0332), hundred seed weight (-0.0343), fruit diameter (-0.0349) and fruit length (-0.0408) were negligible.

Internodal length

Internodal length showed negative direct effect on fruit yield plant^{-1} (-0.0966). This character exhibited positive indirect effects via number of branches plant^{-1} (0.0218), node at 1st flower appears (0.0099), number of seeds fruit^{-1} (0.0095), fruiting span (0.0041), fruit length (0.0037), stem diameter (0.0023) and days to maturity (0.0014) were negligible. However, its negative indirect effect through fruit weight (-0.0072), fruit diameter (-0.0076), number of fruits plant^{-1} (-0.0082), 100 seed weight (-0.0148) and plant height (-0.0211) were negligible.

Node at 1st flower appears

The direct contribution of this trait on fruit yield plant^{-1} was negative and negligible (-0.0518). However, it exhibited positive negligible indirect effect through number of fruits plant^{-1} (0.0187), fruit length (0.0142), fruit diameter (0.0090), 100 seed weight (0.0089), plant height (0.0084), days to maturity (0.0084), number of seeds fruit^{-1} (0.0083), internodal length (0.0053) and fruit weight (0.0042). Negative indirect effects exhibited through fruiting span

(-0.0015), stem diameter (-0.0029) and number of branches plant^{-1} (-0.0203) were negligible.

Fruit length

This trait revealed negative direct effect on fruit yield plant^{-1} (-0.0695), its indirect effect through number of branches plant^{-1} (0.0193), node at 1st flower appears (0.0191) and internodal length (0.0027) were positive but negligible. It also showed negligible negative indirect effects through stem diameter (-0.0006), days to maturity (-0.0063), hundred seed weight (-0.0081), fruit weight (-0.0132), fruiting span (-0.0132), plant height (-0.0186), fruit diameter (-0.0230), number of seed fruit (-0.0242) and number of fruits plant^{-1} (-0.0276).

Fruit diameter

The direct contribution of fruit diameter on fruit yield plant^{-1} was low positive (0.1332) followed by negligible positive indirect effect through fruit length (0.0440), no. of fruit plant^{-1} (0.0417), fruit weight (0.0348), days to maturity (0.0240), stem diameter (0.0187), number of seeds fruit^{-1} (0.0171), 100 seed weight (0.0163), plant height (0.0158) and internodal length (0.0105). While, negligible indirect effects of fruiting span (-0.0014), node at first flower appears (-0.0232) and number of branches plant^{-1} (-0.0316) were negative.

Fruit weight

Direct effect of this trait on fruit yield plant^{-1} was negligible positive (0.0977). The positive indirect effects were also negligible via 100 seed weight (0.0334), days to maturity (0.0306), number of seeds fruit^{-1} (0.0266), fruit diameter (0.0256), fruit length (0.0186), fruiting span (0.0180), plant height (0.0132), number of fruits plant^{-1} (0.0120), stem diameter (0.0109) and internodal length (0.0073). Its negative indirect effect through node at 1st flower appears (-0.0079) and number of branches plant^{-1} (-0.0210) were negligible.

Number of fruits plant^{-1}

Number of fruits plant^{-1} showed high positive direct effect on fruit yield plant^{-1} (0.7330) its indirect effects through fruit length (0.2907) was moderate for fruit diameter (0.2297) while it was negligible via plant height (0.1958), 100 seed weight (0.1517), days to maturity (0.1432), fruit weight (0.0902), number of seeds fruit^{-1} (0.0760), internodal length (0.0621), stem diameter (0.0328) and fruiting span (0.0206) were positive. It indicated negative indirect effect through number of branches plant^{-1} (-0.0779) and node at first flower appears.

Number of seeds fruit^{-1}

It expressed low positive direct effect on fruit yield plant^{-1} (0.1655). It also showed negligible positive indirect effects through fruit length (0.0576), fruit weight (0.0451), fruiting span (0.0331), days to maturity (0.0256), stem diameter (0.0214), fruit diameter (0.0212), number of fruits plant^{-1} (0.0172), plant height (0.0094) and 100 seed weight (0.0009). Whereas, negative indirect effects via number of branches (-0.0136), internodal length (-0.0163) and node at 1st flower appears (-0.0267) were also negligible.

100 seed weight (g)

The direct contribution of 100 seed weight on fruit yield plant^{-1} was positive but negligible (0.0559) while, its positive indirect effect through fruit weight (0.0191), days to maturity (0.0121), number of fruits plant^{-1} (0.0116), internodal length (0.0085), fruit diameter (0.0068), fruit length (0.0065), plant height (0.0057), fruiting span (0.0031), and number of seeds fruit^{-1} (0.0003) were negligible. It also exhibited negligible negative indirect effects via node at 1st flower appears (-0.0096), number of branches plant^{-1} (-0.0130) and stem diameter (-0.0163).

Fruiting span

Fruiting span showed negligible positive direct effect on fruit yield plant^{-1} (0.0564) whereas, its indirect effects were negligible and positive through stem diameter (0.0120), number of seeds fruit (0.0113), fruit length (0.0107), fruit weight (0.0104), number of branches plant^{-1} (0.0075), days to maturity (0.0067), 100 seed weight (0.0032), plant height (0.0027), node at first flower appears (0.0017) and number of fruits plant^{-1} (0.0016). Fruiting span also showed very negligible negative indirect effects via fruit diameter (-0.0006) and internodal length (-0.0024).

Days to maturity (days)

The direct contribution of this trait on fruit yield plant^{-1} was positive and negligible (0.0588). Positive indirect effects this trait through fruit weight (0.0184), 100 seed weight (0.0128), number of fruits plant^{-1} (0.0115), fruit diameter (0.0106), number of seeds fruit^{-1} (0.0091), fruiting span (0.0070), plant height (0.0057), fruit length (0.0053), and stem diameter (0.0042) were negligible. It also showed negative indirect effects through internodal length (-0.0008), number of branches plant^{-1} (-0.0027) and node at 1st flower appears (-0.0095).

4.6 Genetic Divergence:

The quantitative assessment of genetic divergence has been studied using Mahalanobis's D^2 statistics and canonical analysis technique on 60 genotypes over 22 yield and yield contributing agronomic characters. Results are presented below:

Mahalanobis generalize distance (D^2)

The analysis of variance showed highly significant differences within the population for all the 22 characters studied. The V statistics indicated V = 7769.70200. The value of Wilk's criterion was 10113.444, the degrees of freedom was 1298. The D^2 values corresponding to possible comparison among 60 genotypes taking two genotypes at a time were computed separately in the analysis.

4.6.2 Contribution of individual characters towards genetic divergence

The percentage contribution towards genetic divergence by all the characters is presented in Table 4.5(a) The character no. of locules contributed most towards genetic divergence (12.37%) followed by remaining characters in descending order *viz.,* 100 seed weight (11.41 %), leaf blade length (9.44 %), node at 1st flower appears (9.32%), fruit yield plant^{-1} (9.04%), fruit length (6.21%), leaf blade width (5.65%), no. of fruits plant^{-1} (5.54%), no. of seeds fruit^{-1} (5.08%), flower length (4.75%), petiole length (4.75 %), internodal length (3.56%), fruiting span (2.88%), incidence of YVMV (2.54%), fruit diameter (2.32%), no. of branches (2.26%) and stem diameter (1.41 %). whereas, magnitude of genetic divergence was less than one per cent for days to 50 percent flowering, fruit weight (g), days to maturity, flower diameter and plant height.

Table 4.5(a): Contribution of fruit yield and ancillary characters towards divergence in okra (%)

S. No.	Character	Times ranked 1st	Percentage contribution towards divergence (%)
01	No. of locules fruit^{-1}	219	12.37
02	100 seed weight (g)	202	11.41
03	Leaf blade length (cm)	167	9.44
04	Node at 1st flower appears	165	9.32
05	Fruit yield plant^{-1}	160	9.04
06	Fruit length (cm)	110	6.21
07	leaf blade width (cm)	100	5.65
08	No. of fruit plant^{-1}	98	5.54
09	No. of seeds fruit^{-1}	90	5.08
10	Flower length (cm)	84	4.75
11	Petiole length (cm)	84	4.75
12	Internodal length (cm)	63	3.56
13	Fruiting span	51	2.88
14	Incidence of YVMV	45	2.54
15	Fruit diameter (mm)	41	2.32
16	No. of branches plant^{-1}	40	2.26
17	Stem diameter	25	1.41
18	Days to 50 % flowering	11	0.62
19	Fruit weight (g)	11	0.62
20	Days to maturity	3	0.17
21	Flower diameter (mm)	1	0.06
22	Plant height (cm)	0	0.00

4.6.3 Grouping of genotypes into different clusters

The study comprised of 24 exotic, 31 indigenous accessions and five checks *viz.,* Phule Utkarsh, Hisar Unnat, VRO-5, VRO-6 and Pusa A4 were assessed for nature and magnitude of genetic divergence based on 22 quantitative traits following Mahalanobis's D^2 statistic and Anderson's canonical analysis. On the basis of D^2 values, the 60 genotypes were grouped into 12 clusters following Tocher's method, 3 clusters were polygenotypic (Cluster I was the largest cluster with 40 genotypes followed by Cluster VIII with seven genotypes while, Cluster IV comprised of only four genotypes) while, remaining nine clusters were mono-genotypic. Cluster wise distribution of genotypes is summarized in Table 4.5(b)

4.6.4 Intra and inter cluster divergence D^2 values

The average intra and inter-cluster D^2 values estimated as per the procedure given by Singh and Choudhary (1979) are presented in Table 4.5(c) and the cluster mean values are summarized in Table 4.5(d). Cluster VIII showed maximum intra cluster D^2 value (D^2 = 336.27) followed by Cluster I (D^2 = 208.73) and Cluster IV (D^2 = 133.64). Cluster II, III, V, VI, VII, IX, X, XI and XII were mono-genotypic hence, showed no intra cluster divergence.

The highest inter cluster divergence was observed between genotypes of cluster IV and X (D^2 = 1144.12), followed by cluster VI vs XI (D^2 = 1070.73) and II vs X (D^2 = 1004.12).

Cluster I (D^2 = 208.73) was the largest cluster with 40 genotypes, was nearest to cluster VII (D^2 = 284.32) followed in descending order by cluster III (D^2 = 292.15), II (D^2 = 306.65), VI (D^2 = 347.40), V (D^2 = 366.77), VIII (D^2 = 386.74) and IX (D^2 = 395.36) whereas, it was distantly placed to cluster IV (D^2 = 406.76), XII (D^2 = 440.76), X (D^2 = 462.3) and XI (D^2 = 467.26).

Cluster II (0.00) was mono-genotypic, it was nearest to cluster IV (D^2 = 126.21) followed by clusters *viz.,* IV (D^2 = 306) and XI (D^2 = 378.84), however it was distantly placed to clusters VII (D^2 = 474.31), IX (D^2 = 496.07), VIII (D^2 = 583.38), III (D^2 = 604.30), V (D^2 = 644.10), and VI (D^2 = 682.07) XII (D^2 = 745.76) and X (D^2 = 1004.12).

Table 4.5(b): Distribution of okra genotypes in different clusters

Cluster	Number of genotypes	Genotypes
I	40	EC169364, EC305616, EC169333, EC169319, IC018960-C, EC169398, IC027889, EC169443-A, EC169515, EC133336, IC033344, IC033122, EC329368, IC013995-A, IC015435, EC329379, IC018541-A, IC007472, IC031932-A, IC018960-B, IC018534, IC027881-A, IC018473-A, IC007952, IC029119-B, IC006485, IC031850, IC029191, EC329400, IC014600, IC028359, IC027831, IC024906-A, Hisar Unnat, IC016262-A, EC329356, IC018975, EC329357, EC305622, IC018973-A
II	1	Pusa A4
III	1	IC015036-B
IV	4	EC550848, VRO-5, Phule Utkarsh, VRO-6,
V	1	IC018533
VI	1	IC009856-C
VII	1	EC329418
VIII	7	EC305617, EC305637, EC305664, EC305634, EC329397, EC329369, IC022237-A
IX	1	EC329366
X	1	IC014845-B
XI	1	IC018542
XII	1	IC018540

Cluster III (0.00) was closest to cluster VI (D^2 = 124.19) had only one genotype followed by clusters *e.g.,* VII (D^2 = 135.22), X (D^2 = 246.41), I (D^2 = 292.15), XII (D^2 = 330.02) and V (D^2 = 377.73). While, the remaining clusters *viz.,* VIII (D^2 = 442.84), IX (D^2 = 569.28), II (D^2 = 602.30) IV (D^2 = 647.49) and XI (D^2 = 919.57) were placed distantly to Cluster III.

Cluster IV (D^2 = 133.64) comprised of four genotypes, it was nearest to cluster I (D^2 = 406.76) while, remaining clusters *e.g.,* VII (D^2 = 498.83), XI (D^2 = 513.25), III (D^2 = 647.49), VI (D^2 = 684.06), VIII (D^2 = 690.46), IX (D^2 = 706), XII

Table 4.5(c): Intra and inter-cluster divergence (D^2) for fruit yield and associated traits in okra

Cluster Number	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII
I	**208.73**	306.65	292.15	406.76	366.77	347.40	284.32	386.74	395.36	462.30	467.26	440.15
II		**0.00**	604.30	126.21	644.10	682.07	474.31	583.38	496.07	**1004.12**	378.84	745.76
III			**0.00**	647.49	377.73	124.19	135.22	442.84	569.28	246.41	919.57	330.02
IV				**133.64**	840.20	684.06	498.83	690.46	706.00	**1144.12**	513.25	836.04
V					**0.00**	452.42	396.97	403.86	208.50	216.75	501.15	331.11
VI						**0.00**	161.32	433.37	782.07	321.31	**1070.73**	456.14
VII							**0.00**	436.87	474.77	417.74	855.41	334.17
VIII								**336.27**	602.49	511.58	714.20	487.19
IX									**0.00**	479.47	314.07	436.40
X										**0.00**	953.89	318.93
XI											**0.00**	876.62
XII												**0.00**

(D^2 = 836.04) and V (D^2 = 840.20) were distantly placed to the cluster, whereas, cluster X (D^2 = 1144.12) was at wide distance from Cluster IV.

Cluster V (0.00), comprised of only genotype IC018533. It was nearest to Clusters *e.g.* IX (D^2 = 208.50), X (D^2 = 216.75), XII (D^2 = 331.11), I (D^2 = 366.77), III (D^2 = 377.73) and VII (D^2 = 396.97), while clusters VIII (D^2 = 403.86), VI (D^2 = 452.42), XI (D^2 = 501.15), II (D^2 = 644.10) and IV (D^2 = 840.20) were more distantly situated to cluster V.

Cluster VI (0.00) comprised of one genotype IC009856-C only. It was nearest to Cluster III (D^2 = 124.19), VII (D^2 = 161.32), X (D^2 = 321.31) and I (D^2 = 347.40), remaining clusters *viz.,* VIII (D^2 = 433.37), V (D^2 = 452.42), XII (D^2 = 456.14), II (D^2 = 682.07), IV (D^2 = 684.06), (D^2 = 782.07) and XI (D^2 = 1070.73) were distantly placed to the cluster VI.

Cluster VII (0.00), was a mono-genotypic cluster comprised of genotype (EC329418), it was nearest to Cluster III (D^2 = 135.22) followed by cluster VI (D^2 = 161.32), I (D^2 = 284.32), XII (D^2 = 334.17) and V (D^2 = 396.97) whereas, clusters X (D^2 = 417.74), VIII (D^2 = 436.87), II (D^2 = 474.31), IX (D^2 = 474.77), V (D^2 = 498.83) and XI (D^2 = 855.41) revealed distant placement of clusters.

Cluster VIII (D^2 =336.27) comprised of seven genotypes *viz.,* EC305617, EC305637, EC305664, EC305634, EC329397, EC329369, and IC022237-A, it was closest to cluster I (D^2 = 386.74). However the remaining clusters were distantly placed to it e.g. V (D^2 = 403.86), VI (D^2 = 433.37), VII (D^2 = 436.87), III (D^2 = 442.84), XII (D^2 = 487.19), X (D^2 = 511.58), II (D^2 = 583.38), IX (D^2 = 602.49), IV (D^2 = 690.46) and XI (D^2 = 714.20).

Genotype EC329366 was the only entry in Cluster IX (0.00). It was nearest to Cluster V (D^2 = 208.50) followed by XI (D^2 = 314.07) and I (D^2 = 395.36), while, cluster XII (D^2 = 436.40), VII (D^2 = 474.77), X (D^2 = 479.47), II (D^2 = 496.07), III (D^2 = 569.28), VIII (D^2 = 602.49), IV (D^2 = 706.00) and VI (D^2 = 782.07) were distantly placed to cluster IX.

Cluster X (0.00), also a mono-genotypic cluster consisted of genotype IC014845-B only. This cluster was closest to Cluster V (D^2 = 216.75), III (D^2 = 246.41), XII (D^2 = 318.93) and VI (D^2 = 321.31) whereas clusters *viz.,* VII (D^2 = 417.74), I (D^2 = 462.30), IX (D^2 = 479.47), VIII (D^2 = 511.58), IX (D^2 = 953.89) II (D^2 = 1004.12) and IV (D^2 = 1144.12) were distantly placed to it.

Mono-genotypic Cluster XI (0.00) comprised of genotype IC018542. It was close to Cluster IX (D^2 = 314.07) and II (D^2 = 378.84), remaining clusters *e.g.*, I (D^2 = 467.26), V (D^2 = 501.15), IV (D^2 = 513.25), VIII (D^2 = 714.20), VII (D^2 = 855.41), XII (D^2 = 876.62), III (D^2 = 919.57), X (D^2 = 953.89) and VI (D^2 = 1070.73) revealed moderate to wide distances to this cluster.

Cluster XII (0.00) with genotype IC 018540 was also a mono-genotypic cluster. Clusters *viz.,* X (D^2 = 318.93), III (D^2 = 330.02), V (D^2 = 331.11) VII and (D^2 = 334.17) were close to this cluster. However, the remaining clusters *e.g.*, IX (D^2 = 436.40), I (D^2 = 440.15), VI (D^2 = 456.14), VIII (D^2 = 487.19), II (D^2 = 745.76), IV (D^2 = 836.04) and XI (D^2 = 876.62) revealed distance from this cluster.

4.6.5 Cluster mean showing importance of grouped characters:

Cluster I

This cluster did n not record low / high values for any of the yield contributing character. Cluster I is mixed cluster with moderate value for all the morphological traits.

Cluster II

This cluster showed least value for number of branches plant^{-1} (15.06), days to 50 per cent flowering (47.00) and incidence of YVMV (6.14). It also showed high cluster mean values for fruit weight (17.64), number of seeds fruit^{-1} (56.20) and days to maturity (106.00).

Cluster III

This cluster recorded least value for traits *e.g.*, plant height (85.90), stem diameter (15.06), leaf blade width (17.51), fruit weight (13.48), fruiting span (44.50) and days to maturity (96.50).

Cluster IV

This cluster showed low values for node at first flower appears (5.97) while, it revealed highest value for plant height (104.28), number of fruits plant (16.60) and fruit yield plant^{-1} (296.30).

Cluster V

Low values of cluster means were recorded for fruit length (12.05) and number of fruits plant^{-1} (6.53) in this cluster. It also showed maximum value for days to 50 per cent flowering (56.33).

Cluster VI

This cluster showed least values for petiole length (16.61), leaf blade length (14.22) and fruit diameter (14.97) while it revealed maximum value for flower diameter (6.62) and fruiting span (50.00).

Cluster VII

Highest values of cluster mean for flower length (5.88) fruit length (19.42), 100 seed weight (7.39) and fruiting span (50.00) were observed in this cluster.

Cluster VIII

It showed highest values cluster mean for number of branches plant^{-1} (4.09), internodal length (7.03) and number of locules fruit^{-1} (6.75).

Cluster IX

This cluster expressed high cluster mean values for node at first flower appears (11.45), fruit diameter (19.23) and fruiting span (50.00).

Table 4.5(d): Cluster mean values for different yield and associated characters in okra

Cluster No.	Plant height (cm)	Stem diameter (mm)	No. of branches plant^{-1}	Internodal length (cm)	Petiole length (cm)	Leaf blade length (cm)	leaf blade width (cm)	Node at 1st flower appears	Flower length (cm)	Flower diameter (cm)	Fruit length (cm)	Fruit diameter (mm)	No. of locules fruit^{-1}	Fruit weight (g)	No. of fruits plant $^{-1}$	No. of seeds fruit $^{-1}$	100 seed weight (g)	Days to 50 per cent flowering (days)	Fruiting span (days)	Days to maturity (days)	Incidence of YVMV	Fruit yield plant $^{-1}$ (g)
I	95.59	17.09	2.26	7.27	19.76	18.81	24.35	7.07	5.15	5.70	15.52	17.34	5.09	15.22	10.33	47.87	5.95	49.45	47.14	100.31	51.00	164.58
II	101.10	17.18	**1.50**	7.77	19.80	21.66	28.50	6.70	5.31	5.78	15.70	18.94	5.00	**17.64**	15.37	**56.20**	6.99	**47.00**	46.00	**106.00**	**6.14**	234.20
III	**85.90**	**15.06**	1.78	7.36	18.63	14.66	**17.51**	8.23	5.56	6.01	15.25	16.90	5.10	**13.48**	12.27	39.00	6.70	51.00	**44.50**	**96.50**	56.99	176.27
IV	**104.28**	18.16	2.20	6.97	22.17	20.02	26.85	**5.97**	5.55	6.00	19.27	18.59	5.00	17.51	**16.60**	55.13	7.38	47.42	49.63	102.25	14.87	**296.30**
V	93.77	17.45	3.70	6.91	20.01	20.10	22.55	11.30	5.28	5.92	**12.05**	15.45	5.00	16.89	**6.53**	44.80	5.78	**56.33**	47.00	97.50	63.92	108.17
VI	94.90	17.77	3.00	7.78	**16.61**	**14.22**	17.78	6.80	5.30	**6.62**	14.79	**14.97**	5.00	17.03	11.50	51.10	5.71	49.00	**50.00**	97.50	63.92	204.00
VII	96.55	16.83	1.70	8.10	17.19	15.39	19.12	8.35	**5.88**	6.19	**19.42**	16.54	5.00	16.15	11.50	54.00	**7.39**	51.67	**50.00**	103.50	63.92	201.47
VIII	87.29	18.44	**4.09**	**7.03**	18.95	19.11	24.06	8.10	5.05	5.78	13.19	16.90	**6.75**	15.22	8.65	47.30	6.36	52.48	49.73	102.36	55.94	162.66
IX	94.37	18.65	1.70	7.32	22.16	20.82	22.25	**11.45**	5.11	5.19	16.25	**19.23**	5.00	16.27	7.00	48.80	5.90	47.67	**50.00**	103.50	56.99	112.49
X	87.63	17.65	3.70	6.69	18.79	15.47	18.57	10.80	4.91	**4.49**	12.68	16.16	5.00	13.87	6.53	**36.70**	**3.99**	54.67	45.50	98.00	**75.00**	**105.13**
XI	103.67	**18.93**	3.00	6.17	**27.84**	**22.30**	**31.10**	8.20	5.41	5.90	15.05	17.81	5.00	16.20	7.10	48.70	6.49	48.67	47.50	100.50	50.85	135.77
XII	89.77	15.26	3.00	**5.04**	17.22	16.38	20.02	10.73	**3.69**	4.97	18.65	18.37	5.00	16.69	9.47	48.30	7.15	54.67	45.50	100.50	56.99	148.67

Cluster X

Highest cluster mean values for incidence of YVMV (75.00) was revealed, it also showed the least values for flower diameter (4.49), number of seeds fruit^{-1} (36.70), hundred seed weight (3.99) and fruit yield plant^{-1}(105.13).

Cluster XI

It showed highest values of cluster means for leaf blade width (31.10) petiole length (27.84), leaf blade length (22.30) and stem diameter (18.93).

Cluster XII

This cluster recorded least values for internodal length (5.04), flower length (3.69).

4.6.6 Canonical analysis

Canonical analysis was also carried out to verify the group constellations obtained through D^2 statistics (Rao, 1952). The values of the first four canonical vectors and their roots are presented in Table 4.5(e). The first and second canonical roots have accounted for 27.69 and 13.72 per cent of total variation respectively, thus 41.41 per cent of total variation was expressed by the first two canonical roots. The third and fourth canonical roots have expressed 10.289 and 9.541 per cent of total variation respectively, thus the sum of these two vectors accounted for 19.83 per cent of the total variation expressed. The five and six canonical roots have accounted for 7.51161 and 6.47583 per cent of total variation respectively, these together accounts for 13.987 per cent of the total variation. The seventh canonical root accounted for 5.01146 of total variation.

With respect to the relative predominance of different characters under study, it would be apparent from the absolute size of coefficients that leaf blade length (0.361), leaf blade width (0.355) and fruit yield plant^{-1} (0.347) were predominant in the primary axis of differentiation however, in secondary axis fruit yield plant^{-1} (0.53434), number of fruits plant^{-1} (0.38991) and hundred seed weight (0.23747) were preponderant. In the third axis of absolute size of coefficient, internodal length (0.30887), hundred seed weight (0.27488) and node at 1st flower appears (0.22728) were important, while in the fourth axis there was predominance of characters *viz.,* leaf blade width (0.14514), stem diameter (0.13959) and incidence of YVMV (0.07338). In the fifth axis of differentiation there was predominance of node at first flower appears (0.50534), number of fruits plant^{-1} (0.48002) and number of branches plant^{-1} (0.37873). Whereas, in the sixth axis of there was predominance of fruit length (0.59813), number of seeds fruit^{-1} (0.34892) and node at first flower appears (0.18827). In the seventh axis of differentiation predominance of characters *viz.,* flower length (0.75555), flower diameter (0.22770) and number of seeds fruit^{-1} (0.15944) was observed. Clustering by Tocher's method and three dimensional representation of the relative position of genotypes is

Table 4.5(e): Values of the canonical vectors and roots for yield and ancillary traits in okra.

S. No.	Characters	1 vector	2 vector	3 vector	4 vector	5 vector	6 vector	7 vector
01	Plant height (cm)	0.06266	0.00141	0.05826	0.00525	0.04021	0.00677	0.02782
02	Stem diameter (mm)	0.06746	-0.07161	-0.22087	**0.13959**	0.13982	0.16286	0.11726
03	No. of branches plant^{-1}	-0.09943	-0.03385	-0.34050	-0.00405	**0.37873**	-0.13671	0.01062
04	Internodal length (cm)	0.00529	0.06731	**0.30887**	-0.03100	-0.04706	-0.13953	0.01010
05	Petiole length (cm)	0.22759	-0.27644	0.18262	-0.10687	0.09090	0.01057	0.10253
06	Leaf blade length (cm)	**0.36166**	-0.41632	0.02701	-0.18198	0.02927	-0.33043	0.00077
07	leaf blade width (cm)	**0.35598**	-0.14428	-0.17844	**0.14514**	-0.03972	-0.42663	-0.16273
08	Node at 1st flower appears	-0.27803	-0.35324	**0.22728**	-0.04160	**0.50534**	**0.18827**	-0.22733
09	Flower length (cm)	0.06862	0.06182	0.11876	-0.08185	0.19379	-0.10442	**0.75555**
10	Flower diameter (cm)	0.04735	0.06580	-0.01623	-0.02152	0.03746	0.05642	**0.22770**
11	Fruit length (cm)	0.21479	0.07604	0.18839	0.04316	-0.08930	**0.59813**	-0.03330
12	Fruit diameter (mm)	0.30522	-0.10554	0.00876	0.00984	0.00252	0.17320	-0.33240
13	No. of locules fruit^{-1}	-0.06883	0.13431	-0.65624	-0.27260	-0.17915	0.11411	-0.00668
14	Fruit weight (g)	0.14034	-0.14480	-0.02472	-0.25617	0.16996	0.10520	-0.05557
15	No. of fruit plant^{-1}	0.21212	**0.38991**	-0.08247	-0.01647	**0.48003**	-0.12706	-0.22602
16	No. of seeds fruit^{-1}	0.30464	-0.17360	-0.16899	-0.13274	-0.02745	**0.34892**	**0.15944**
17	100 seed weight	-0.05102	**0.23747**	**0.27488**	-0.64621	-0.23291	-0.17120	-0.14034
18	Days to 50 % flowering	-0.22162	0.01848	-0.01741	-0.17079	0.11249	0.02268	-0.21088
19	Fruiting span (days)	-0.02350	-0.03713	-0.09467	-0.52334	0.23193	0.09766	0.09350
20	Days to maturity (days)	0.05749	-0.05728	-0.05371	-0.12503	-0.02137	0.01651	0.01549
21	Incidence of YVMV	-0.33164	-0.02640	0.00913	**0.07338**	0.16628	-0.06506	0.09612
22	Fruit yield plant^{-1}	**0.34778**	**0.53434**	0.12062	0.05982	0.28147	0.02877	-0.01598
Values of canonical roots		2641.095	1308.995	981.400	910.057	716.434	617.644	477.978
Percentage of variation expressed		27.69112	13.72444	10.28970	9.54169	7.51161	6.47583	5.01146
Cumulative (%) of variation expressed		27.69112	41.41556	51.70526	61.24695	68.75856	75.23439	80.24585

4.7 Incidence of yellow vein mosaic virus:

The genotypes were classified into highly susceptible, susceptible, tolerant, moderately resistant and resistant to yellow vein mosaic virus incidence, angular transformation value is presented in the Table 4.5(f). Genotypes Pusa A4 and EC 550848 were observed to be resistant under field conditions, while genotypes VRO-6, Phule utkarsh, Hisar unnat, EC 305616 and VRO-5 exhibited moderate resistance to this disease. However, 11 genotypes revealed tolerance to the disease, 33 genotypes were susceptible while 09 genotypes expressed high degree of susceptibility to the disease.

Table 4.5(f): Categorization for incidence of yellow vein mosaic virus in okra.

YVMV Incidence	Genotypes
Highly susceptible	IC024906-A, IC027881-A, IC018960-B, IC018533, IC009856-C, EC329418, EC305617, IC014845-B, EC305622
Susceptible	IC028359, IC018542, IC018473-A, IC014600, IC018973-A, EC305664, IC018541-A, IC006485, IC018534, IC018960-C, IC031932-A, IC031850, IC029191, IC027889, IC022237-A, IC018975, IC018540, IC016262-A, IC015435, IC015036-B, IC013995-A, IC007952, IC007472, EC329400, EC329397, EC329369, EC329368, EC329366, EC305637, EC305637, IC027831, EC329357, EC329356
Tolerant	EC169364, EC133336, EC169515, EC169333, IC033122, EC169443-A, EC169398, EC169319, EC305634, IC033344 and IC029119-B
Mod. resistant	VRO-6, Phule utkarsh, Hisar unnat, EC 305616, VRO-5
Resistant	Pusa A4, EC 550848

DISCUSSION

The experimental findings of the present investigation "Genetic Divergence in Okra (*Abelmoschus esuleutus* (L) Mrench)" has been discussed under the following heads:

5.1 Analysis of Variance

5.2 Genetic variability

    5.2.1 Mean performance of the genotypes

    5.2.2 Genotypic and phenotypic coefficient of variation

    5.2.3 Heritability and genetic advance

5.3 Association analysis

    5.3.1 Correlation coefficient analysis

    5.3.2 Path coefficient analysis

5.4 To estimate genetic divergence for identification of putative lines.

5.5 Incidence of yellow vein mosaic virus

5.1 Analysis of Variance

The main objective of the present investigation was to study the genetic variability present in okra experimental materials under study. The estimates of mean sum of square due to genotypes were highly significant for all the characters, except for days to 50 percent flowering and days to maturity. (Table 4.2) indicates the presence of substantial genetic diversity in the existing material. The findings of Patro and Ravisankar (2004), Naidu *et al.* (2007), Shanthakumar and Salimath (2010) and Reddy *et al.* (2012) are similar to the findings of the present study.

2 Genetic variability

5.2.1 Mean performance of the genotypes

Range and mean of 60 genotypes for all the 22 characters are presented in Table 4.1.

Plant height (cm)

The maximum plant height was recorded in genotypes IC 033344 and minimum was observed in EC305634 with the mean value of 94.99 cm, 29 genotypes exhibited above the mean value. The findings were similar to the studies of Bendale *et al.* (2003), Sanjay Kumar *et al.* (2012) and Reddy *et al.* (2012).

Stem diameter (mm)

Stem diameter was observed to be maximum in EC305622 and it was minimum in EC329357, 23 genotypes revealed above mean values of 17.33 mm. The findings of Pathak and Singh (1999) were quite similar to the present investigation.

Number of branches plant^{-1}

The genotype IC022237-A recorded maximum branches plant^{-1}, while, genotype IC018960-C exhibited least branches plant^{-1}, 26 genotypes expressed above the mean value of 2.51 branches. The findings of Bendale *et al.* (2003) and Reddy *et al.* (2012) were quite similar to the present study.

Internodal length (cm)

The shortest internodal length was observed in genotype IC018540, while, it was maximum in genotype IC031850. Thirty one genotypes exceeded the mean value (7.1841). The findings were quite similar to Bendale *et al.* (2003) and Reddy *et al.* (2012).

Petiole length (cm)

Petiole length was recorded the maximum in IC018542 while, genotype IC009856-C (16.61) revealed smallest petiole length mean recorded for the trait was 23.16cm.

Leaf blade length (cm)

Genotypes IC018542 recorded considerably long leaf blade while, genotype IC016262-A expressed smallest leaf blade. Thirty genotypes revealed values above the mean value (18.78cm).

Leaf blade width (cm)

This trait was found to be highest in IC 018542, it was recorded to be lowest in IC015036-B. Thirty genotypes exhibited values above the mean value of 24.11cms.

Node to first flower appears

Mean value recorded for the trait was 7.43, 22 genotypes exceeded the mean. The maximum nodes to first flowering was noted in EC329366 while, it was observed minimum in Hisar Unnat. The findings were quite similar to the study of Bendale *et al.* (2003).

Flower length (cm)

Genotype EC305664 produced longest flower while, EC305616 revealed smallest flower. Twenty two genotypes exceeded the mean value 5.16 cm.

Flower diameter (cm)

The maximum flower diameter was exhibited by genotype EC329379 while, it was minimum in IC014845-B while, 27 genotypes recorded above the mean value 5.72 cm.

Fruit length (cm)

Genotype VRO-6 produced longest fruit while, smallest fruit was recorded in IC018973-A. Mean value of 15.49 cms was exceeded by 31 genotypes. The findings of Farghali *et al.* (1994), Bendale *et al.* (2003) and Shanthkumar and Salimath (2010) support the findings of this investigation.

Fruit diameter (mm)

The maximum fruit diameter was exhibited by genotype IC018973-A while, it was recorded minimum in IC027831. Mean value of 17.34 mm was exceeded by 31 genotypes. The findings were in agreement with Farghali *et al.* (1994), Sanjaykumar *et al.* (2012) and Reddy *et al.* (2012).

Number of locules fruit^{-1}

Genotype EC329397 recorded locules fruit^{-1} while least *i.e*., locules fruit^{-1} was recorded in 44 genotypes, only 16 genotypes expressed values above the mean (5.26). The findings of Naidu *et al.* (2007) support the present observations.

Fruit weight (g)

Average weight of fruit recorded was 15.49g. Genotype IC014600 exhibited maximum fruit weight, while, genotype EC329357 recorded the minimum, values above the mean were recorded in 34 genotypes. The findings were quite similar to Farghali *et al.* (1994), Sood (1999), Bendale *et al.* (2003) and Reddy *et al.* (2012).

Number of fruits plant^{-1}

The maximum fruits plant^{-1} was recorded in genotypes Phule Utkarsh. While, it was least in genotype EC133336 and 29 genotypes recorded above the mean value (10.45). The findings were quite similar to as reported by Bendale *et al.* (2003), Sanjaykumar *et al.* (2012)

No. of seeds fruit^{-1}

The maximum seeds fruit^{-1} was observed in EC550848 and it was the least in EC305637, average for the trait was 48.23 and 32 genotypes were above the mean value. Bendale *et al.* (2003) recorded similar observations.

Days to 50 per cent flowering

Genotype EC305637 attained 50 per cent flowering in (45.66 days) was recorded early while, IC022237-A was observed late (57.33 days) for the trait, mean value of 49.92 days was surpassed by 21 genotypes. The findings were quite similar to the studies of Sood (1999), Adiger *et al.* (2011) and Reddy *et al.* (2012).

Fruiting span (days)

This trait ranged between 41.50 to 54.00 days with mean of 47.63 days. EC329397 exhibited maximum fruiting span, while IC027881-A and IC028359 expressed minimum.

Days to maturity (days)

Genotype IC018541-A was earliest in maturity, while genotype EC329369 was late days, 37genotype recorded values above the mean value of 100.68 days. The findings of Sood (1999) and Bendale *et al.* (2003) agree with the present investigation.

100 seed weight (g)

EC058704 revealed highest 100 seed weight, whereas it was in least in IC117078. The average for the trait was 6.13 g and 32 genotypes exceeded the mean value. The findings were quite similar to of those Bendale *et al.* (2003).

Fruit yield plant^{-1} (g)

Highest fruit yield plant^{-1} was recorded in EC550848 while it was found to be lowest in IC014845-B, 27 genotypes exhibited values above the mean value (172.21 gm). The findings were quite similar the reports by Patil *et al.* (1996), Sood (1999), Bendale *et al.* (2003), Naidu *et al.* (2007), Adiger *et al.* (2011), Sanjaykumar *et al.* (2012) and Reddy *et al.* (2012).

5.2.2 Genotypic and phenotypic coefficient of variation

Analyses of variance for different characters under study revealed that mean sum of squares due to the genotypes were highly significant for all the characters indicating existence of high genetic variability in the population. Presence of such variability in the genetic constitution of the individuals is desirable and can be utilized for crop improvement. The success of breeding programme depends largely upon directional shift from available genetic variability for crop improvement.

Significant estimates of genetic variability for fruit yield and its components were observed for all the characters studied. In general, the values of phenotypic variance and phenotypic coefficient of variations (PCV) were of higher magnitude than those of genotypic variance and genotypic coefficient of variations (GCV) for all the characters studied, revealing that the environment had an important role to play in influencing the expression of these characters.

Coefficient of variation:

The highest PCV was observed in four characters *viz.,* number of branches, followed by incidence of YVMV, fruit yield plant^{-1} and number of fruits plant^{-1}. The highest value of PCV and GCV were obtained for number of branches plant^{-1} followed by incidence of YVMV, fruit yield plant^{-1} and number of fruits plant^{-1}. These findings are in agreement with the finding of Singh *et al.* (1974), Vijay and Manohar (1990), Pathak and Singh (1999), Gandhi *et al.* (2001), Bendale *et al.* (2003), Verma *et al.* (2004), Saifullah and Rabbani (2009), Jindal *et al.* (2010) and Sajay Kumar *et al*.(2012). High estimates of PCV and GCV indicate presence of substantial genetic variability in controlling these traits, it also indicates good correspondence between the genotype and phenotype due to negligible environmental influence in the expression of these traits. Node at 1st flower appears, 100 seed weight, number of seeds fruit^{-1}, fruit length, leaf blade width, stem diameter, no. of locules, internodal length, plant height, fruit weight, leaf blade length, petiole length, flower length and flower diameter also recorded moderate PCV estimates due to the influence of environment in the expression of these traits. Findings of Sarkar *et al.* (2004) 100 seed weight, Shanthakumar and Salimath (2010) for number of seeds fruit^{-1} while, Hazra and Basu (2000), Yadav *et al.* (1986) and Pathak and Singh (1999) for fruit length support the findings of present investigation.

Stem diameter recorded a moderate PCV and GCV estimates which are not in agreement with the findings of Pathak and Singh (1999) and Shanthakumar and Salimath (2010). They reported high value of PCV and GCV for this trait. Internodal length recorded a moderate value of PCV and GCV this contradicts the findings of Vijay and Manohar (1990).

Plant height revealed a moderate values of PCV and GCV these observations confirm the findings of Hazra and Basu (2000) while, these are in disagreement with Singh *et al.* (1974), Korla and Sharma (1984), Reddy *et al.* (1985), Yadav (1986), Singh *et al.* (1998), Pathak and Singh (1999), Dhall *et al.* (2001), Yadav *et al.* (2002), Dhall *et al.* (2003), Mehta *et al.* (2006), Naidu et al (2007), Saifullah and Rabbani (2009), Akotkar *et al.* (2010), Adiger *et al.* (2011) and Sanjaykumar *et al.* (2012) as they reported high value of PCV and GCV for this trait.

Moderate GCV and PCV were recorded for fruit weight. Findings of Hazra and Basu (2000) are in agreement with the present study, whereas, Pathak and Singh *et al.* (1998), Yadav *et al.* (2002), Sarkar *et al.* (2004), Mehta *et al.* (2006), Naidu *et al.* (2007), Saifullah and Rabbani (2009), Adiger *et al.* (2011) reported high value of PCV and GCV for this trait. Leaf blade length, petiole length, flower length, flower diameter, showed moderate value of PCV and GCV. Low PCV was observed in characters *e.g.*, fruit diameter, fruiting span and days to 50 per cent flowering while, days to maturity expressed lowest PCV revealing very low possibility of genetic improvement of these traits due to the greater influence of environment in expression of these traits while, Singh *et al.* (1974), Pathak and Singh (1999) and Sanjaykumar *et al.* (2012) reported high values for fruit diameter. Findings of Singh *et al.* (1974) are in agreement for days to 50 per cent flowering, however the observations of Vijay and Manohar (1990), Pathak and Singh *et al.* (1998) and Adiger *et al.* (2011) were in agreement with the present findings as they reported high values of PCV and GCV for this character.

5.2.3 Heritability and genetic advance

Heritability

Heritability denotes the proportion of genetically controlled variability to the phenotypic variance; it is a very important biometrical tool for guiding plant breeder for adoption of appropriate breeding procedures. High heritability is helpful in identifying appropriate character for selection. The estimated values of heritability in broad sense were classified as very high (>90%), high (> 70%-90), medium (50-70%) and low (<50%).

Very high estimates of heritability were obtained for characters *viz.,* leaf blade width, node at 1st flower appears and fruit yield plant^{-1} followed by high estimates for number of locules fruit^{-1}, leaf blade length, number of fruits plant^{-1}, 100 seed weight, fruit length, petiole length, flower length, internodal length, number of branches plant^{-1}, number of seeds fruit^{-1}, incidence of YVMV, stem diameter, fruit diameter and fruit weight. The results were in close proximity to those of Chandra *et al.* (1996) for no. of seeds fruit^{-1}, Panda and Singh (1997), Dhankar and Dhankar (2002), Reddy *et al.* (2012) for fruit yield plant^{-1}, Bendale *et al.* (2003) for intermodal length and Naidu *et al.* (2007) for number of nodes to first flower, Vashistha *et al.* (1982), Korla and Sharma (1984), Singh *et al.* (1998), Dhall *et al.* (2001), John *et al.* (2001), Dhall *et al.* (2002), Indurani and Veeraragavathaatham (2005), Naidu *et al.* (2007), Solankey and Singh (2009), Saifullah and Rabbani (2009), Santhkumar and Salimath (2010), Jindal *et al.* (2010), Ramanjinappa *et al.* (2011), Sanjaykumar *et al.* (2012) for number of fruits plant^{-1}. Higher values of heritability (broad sense) of these characters expressed that they were less influenced by the environmental factors. It reflected that the phenotypes were the near representative of their genotypes and selection based on phenotypic performance would be reliable.

Moderate estimates of heritability were recorded for days to 50 per cent flowering, fruiting span, days to maturity, which indicated that selection based on phenotypic performance would be rewarding on partitioning of environmental variances. These findings are in accordance with Yadav *et al.* (2002), Singh and

Singh (2003), for days to 50 per cent flowering, whereas Reddy *et al.* (2012) reported high value of h^2b for days to 50 per cent flowering.

Estimates of heritability were recorded low for flower diameter and plant height. This is indicative of the fact that characters are rather more influenced by the environment and may not respond much to selection. Findings of Panda and Singh (1997), Dhankar and Dhankar (2002) and Sureshbabu *et al.* (2004) support the present findings but are in disagreement with the results of Reddy *et al.* (2012) as they reported high heritability .

Genetic Advance

Heritability however, indicates only the effectiveness with which selection of a genotype can be based on phenotypic performance, but fails to indicate the genetic progress. Heritability estimates along with genetic gains are more effective and reliable in predicting the improvement through selection (Johnson *et al.* 1955). Estimates of genetic advance predict the extent of improvement that can be achieved in one cycle of selection for improving the different characters.

In the present study, the characters *e.g.*, number of branches, fruit yield plant^{-1}, incidence of YVMV, number of fruits plant^{-1}, and node at 1st flower appears recorded high values of genetic advance as percent of mean indicates higher response to selection. However, the moderate genetic advance as percent of mean was observed in 100 seed weight followed by no. of seeds fruit^{-1}, fruit length and leaf blade width revealed comparatively less response to selection. Low genetic advance was observed for number of locules fruit^{-1}, internodal length, leaf blade length, stem diameter, petiole length, fruit weight, fruit diameter, days to 50 per cent flowering, flower diameter, fruiting span, plant height and days to maturity expresses low response to selection in improvement of these traits. The findings were similar to Patil *et al.* (1996) for plant height and fruits plant^{-1}, Chandra *et al.* (1996) for plant height, Panda and Singh (1997) and Naidu *et al.* (2007) for plant height and number of fruits plant^{-1}.

High heritability coupled with high genetic advance as percentage of mean for traits like, node at first flower appears, fruit yield plant^{-1}, no. of fruits plant^{-1}, branches plant^{-1} and incidence of YVMV suggested the preponderance of additive genes. It also indicated higher response for selection of high yielding genotypes as these characters are governed by additive genes. These results are in close proximity with the findings of Vashistha *et al.* (1982), Reddy *et al.* (1985), Yadav (1986), Patil and Dalal (1992), Patil et al.(1996), Chandra *et al.* (1996), Panda and Singh (1997),Singh *et al.* (1998), Pathak and Singh (1999), Dhall *et al.* (2001), John *et al*. (2001), Yadav *et al*. (2002), Singh and Singh (2002), Dhankhar and Dhanker (2002), Dhall *et al*. (2003), Sarkar *et al.* (2004), Sureshbabu *et al.* (2004), Indurani and Veeraragavathatham (2005), Bello *et al.* (2006), Mehta *at al.* (2006), Naidu *et al.* (2007), Saifullah and Rabbani (2009), Santhkumar and Salimath (2010), Jindal *et al.* (2010), Adiger *et al.* (2011) and Sanjaykumar *et al.* (2012).

High estimates of heritability coupled with low genetic advance as percentage of mean were observed by petiole length, flower length, fruit diameter and fruit weight. It infers that this character was regulated by non additive gene action. The heritability is being exhibited due to the low influence of environment over the genotype and simple selection will not be rewarding due to the predominance of non-additive genes. However, these traits can be improved in heterosis breeding programme by development of hybrid and also by exploitation of transgressive segregants. This result was in close proximity to that of Jindal *et al.* (2010) for fruit diameter and fruit weight.

Low heritability along with low genetic advance was observed for flower diameter and plant height indicating high influence of environment and consequently its selection may not be effective.

5.3 Association analysis:

4.3.1 Correlation coefficient analysis

Coefficients of correlation were analyzed for all possible combinations of 22 characters are presented in (Table 4.3).

Plant height

Plant height revealed very strong positive association with petiole length, fruit length and number of fruits plant^{-1}; however it showed strong positive relationship with internodal length. While number of locules expressed strong negative association with plant height. Whereas, traits *viz.,* stem diameter, leaf blade length and width and node at 1st flower appears revealed positive relationship. However, its association was negative with days to 50 per cent flowering and incidence of YVMV. These results are in close conformity with the findings of Singh *et al.* (1975) and Adiger *et al.* (2011). However, Bello *et al.* (2006) reported strong positive association between plant height and days to 50 per cent flowering.

Stem diameter

Highly strong positive association of stem diameter was reveled with number of branches plant^{-1} however; it revealed negative relationship of same magnitude with hundred seed weight. Positive associations of stem diameter with petiole length, number of locules fruit^{-1} and fruiting span were strong, while leaf blade width and length revealed positive relationship. However, association was highly negative and strong with 100 seed weight. Strong positive association of this trait with fruiting span could be of use in breeding genotypes with long fruiting span to realize high fruit yield.

Number of branches plant^{-1}

Number of branches plant^{-1} showed highly positive association with node at 1st flower appears, number locules fruit^{-1} and days to 50 per cent flowering, however it revealed negative relationship of same magnitude with fruit length. While, this trait indicated strong positive association with incidence of YVMV, however it revealed negative relationship of same magnitude with 100 seed weight, fruit diameter, internodal length and fruit weight. However, it revealed positive association with leaf blade length whereas; it indicated highly negative association with fruit length. However, its association with days to 50 per cent flowering was in confirmation with the findings of Bello *et al.* (2006), while, fruit diameter was in agreement with the findings of Adiger *et al.* (2011). Negative association of this trait with fruit length and fruit weight reveals that a negative selection for this trait may yield an increase in fruit length and weight.

Internodal length

The correlation of internodal length was strong with flower length followed by positive association with flower diameter and 100 seed weight.

Petiole length

Petiole length showed very strong positive association with leaf blade length, leaf blade width and fruit diameter, however it expressed strong positive relationship with fruit length, flower length and fruiting span. It also indicated negative relationship of same magnitude with incidence of YVMV while, fruits plant^{-1} revealed positive relationship with petiole length. No association of this trait with any of the remaining traits was observed. Its positive relationship with fruit length, fruiting span and fruits plant^{-1} revealed that this relationship could be of importance for improvement of fruiting span, no. of fruits and fruit length.

Leaf blade length

Highly strong and positive association of leaf blade length was revealed with leaf blade width; however this trait revealed negative relationship of same magnitude with incidence of YVMV. Association of leaf blade length was strong with fruit weight followed by days to maturity revealing positive relationship, while it indicated negative relationship of same magnitude with days to 50 per cent flowering.

Leaf blade width

Leaf blade width showed strong positive relationship with number of fruits plant^{-1} whereas, days to maturity and fruit diameter revealed positive association with this trait. However, incidence of YVMV and node at first flower appears showed very strong negative association with this character it also exhibited strong negative association with days to 50 per cent flowering.

Node at 1st flower appears

Node at first flower appears showed very strong positive association with days to 50 per cent flowering, incidence of YVMV, while it revealed negative relationship of same magnitude with fruits plant^{-1} and fruit length. However, association was also negative with 100 seed weight, fruit diameter, number of seeds fruit^{-1}, flower diameter and days to maturity.

Flower length

Flower length showed very strong positive association with flower diameter, however 100 seed weight and fruit length also revealed positive relationship.

Flower diameter

It expressed strong positive association with 100 seed weight and fruit length. Remaining associations were non significant.

Fruit length

The trait fruit length showed very strong positive association with fruit plant^{-1} and fruits diameter and seeds fruit^{-1}, however its relationship was highly strong and negative with incidence of YVMV and days to 50 per cent flowering followed by number of locules expressing strong negative correlation, while fruit weight and fruiting span revealed significant positive relationship. These results are in close conformity with the findings of Adiger *et al.* (2011) for fruits plant^{-1}. Negative association of this trait with incidence of YVMV and its positive associations with number of fruits plant^{-1}, fruit weight and fruiting span could be effectively applied in the improvement of fruit yield and resistance to YVMV.

Fruit diameter

Very strong positive relationship of fruit diameter was exhibited with number of fruits plant^{-1} and fruit weight while, days to maturity, and seeds fruit^{-1} revealed positive association. However, its association was highly strong and negative with days to 50 per cent flowering, while incidence of YVMV expressed strong and negative correlation.

Number of locules fruit^{-1}

Number of locules fruit^{-1} showed strong positive relationship with fruiting span, while it revealed negative relationship of same magnitude with number of fruits plant^{-1}.

Fruit weight

Highly strong and positive association of fruit weight was revealed with 100 seed weight, days to maturity and number of seeds fruit^{-1}. However, it revealed negative relationship of same magnitude with incidence of YVMV. Its relationship with fruiting span was positive, while it revealed negative relationship with days to 50 per cent flowering.

Number of fruits plant^{-1}

Number of fruits plant^{-1} indicated strong positive relationship with hundred seed weight and days to maturity while, it exhibited negative association with incidence of YVMV and days to 50 per cent flowering. Selection for higher no of fruits may yield genotypes with low incidence of YVMV.

Number of seeds fruit^{-1}

Days to maturity and fruiting span showed positive relationship with number of seeds fruit^{-1} while, it revealed highly negative association with days to 50 per cent flowering and incidence of YVMV.

100 seed weight

Correlation coefficient for 100 seed weight was strong and positive with days to maturity.

Days to 50 per cent flowering

Positive correlation of this trait with incidence of YVMV was highly significant.

Fruiting span

The character fruiting span did not showed any significant relationship with any other character.

Days to maturity

Highly negative association with incidence of YVMV was observed.

Fruit yield plant^{-1}

This trait expressed highly strong positive association with number of fruits plant^{-1}, fruit diameter, fruit length, seeds fruit^{-1}, days to maturity and fruit weight. However it revealed positive relationship with plant height, leaf blade width, 100 seed weight, flower diameter, fruiting span, petiole length and stem diameter. Similar results have been reported by Mandal and Dana (1994), Gondane *et al.* (1995), Yadav (1996), Rajani and Manju (1997), Paiva *et al.* (1998), Dhall *et al.* (2000) Gandhi *et al.* (2002), Bandale *et al.* (2003), Jaiprakashnarayan and Mulge (2004), Verma *et al.* (2004), Bhalekar *et al.* (2005) Verma *et al.* (2007), Balakrishnan and Sreenivasan (2010), Adiger *et al.* (2011), Kumar *et al.* (2011) and Sanjay Kumar *et al.* (2012). Highly negative association was observed with incidence of YVMV, days to 50 per cent flowering and node at first flower appears. Strong positive association of this trait with number of fruits plant^{-1}, fruit length, fruit weight and fruiting span and its highly negative association with incidence of YVMV could be used in development of high yielding YVMV resistant genotypes.

5.2.2 Path coefficient analysis:

Coefficients of correlations are the indication of simple association between two variables. In a biological system the relationship may exist from a simple to a very complex form. It is therefore, essential to study the relationship among variables in a comprehensive way. Path coefficient analysis is a powerful tool, it enables partitioning of the given relationships into direct and indirect effects *i.e.,* it takes into account not only the relationship of component characters with the dependent traits, but simultaneously takes care of its relationship with other components also. Thus, it helps in understanding the causal system in a better way because it enables partitioning of the total correlation coefficients into direct and indirect effects of various characters.

In the present investigation, path coefficient analysis was carried out for characters under study using phenotypic coefficient and taking yield plant^{-1} as dependent variables, in order to see the causal factor and so as to identify the components which are responsible for producing yield plant^{-1}.

Direct Effects:

The phenotypic path coefficient analysis of different yield contributing and associated traits on fruit yield plant^{-1} revealed that traits *viz.,* number of fruits plant^{-1}, recorded high estimate of positive direct effect followed by low direct effect of number of seeds fruit^{-1}, branches plant^{-1} and fruit diameter. The results are in close harmony with Ajimal *et al.* (1979), Reddy *et al.* (1985), Dhall *et al.* (2000), Sureshbabu *et al.* (2004), Pawar (2005), Akinyele and Osekita (2006) and (2011) Verma *et al.* (2007), for number of fruits plant^{-1}, Niranjan and Mishra (2003), Pawar (2005) and Akinyele and Osekita (2011) for seed fruits^{-1}, Koul *et al.* (1979) and Niranjan and Mishra (2003) for branches plant^{-1}, Sureshbabu *et al.* (2004) and Mehta *et al.* (2006) for fruit diameter while, the findings of Adiger *et al.* (2011) are not in agreement for this trait. They reported negative direct effect. Whereas, the direct effects of fruit weight and plant height were negligible. The negative direct effects revealed by node at first flower appears (-0.051), fruit length (-0.069) and internodal length (-0.096) were also negligible.

Indirect Effects:

Plant height

Plant height showed negligible positive direct effect on fruit yield plant^{-1} (0.0233). However, its indirect effects recorded values smaller than 0.1 via fruit length, no. of fruits plant^{-1}, internodal length, stem diameter, fruit weight, fruit diameter, 100 seed weight, days to maturity, number of seeds fruit^{-1} and fruiting span hence they were negligible.

Stem diameter

The direct contribution of this trait on fruit yield plant^{-1} was negligible but positive. the positive indirect effects were also negligible via number of branches plant^{-1}, fruiting span, plant height, fruit diameter, seeds fruit^{-1}, fruit weight, fruit length, days to maturity, node at first flower appears and number of fruits plant^{-1}.

Number of branches plant^{-1}

This trait expressed low positive direct effect on fruit yield plant^{-1} (0.1472). indirect effect obtained were negligible via node at 1st flower appears, stem diameter and fruiting span while the negative indirect effects via days to maturity, number of seeds fruit^{-1}, fruits plant^{-1}, plant height, fruit weight , internodal length, 100 seed weight, fruit diameter and fruit length were also negligible.

Internodal length

Internodal length showed negligible negative direct effect on fruit yield plant^{-1} (-0.0966). The positive indirect effects via branches plant^{-1}, node at 1st flower appears, seed fruit^{-1}, fruiting span, fruit length, stem diameter and days to maturity were also negligible.

Node at 1st flower appears

The direct contribution of this trait on fruit yield plant^{-1} was negligible and negative (-0.0518). However, it positive indirect effect exhibited through fruit plant^{-1}, fruit length, fruit diameter, 100 seed weight, plant height, days to maturity, seed fruit^{-1}, internodal length and fruit weight were also negligible.

Fruit length

This trait recorded negligible negative direct effect on fruit yield plant^{-1} (-0.0695). However its indirect effects through branches plant^{-1}, node at 1st flower appears and internodal length were also negligible.

Fruit diameter

Positive direct contribution of fruit diameter on fruit yield plant^{-1} was low (0.1332), followed by negligible positive indirect effect via fruit length, fruit plant^{-1}, fruit weight, days to maturity, stem diameter, seed fruit^{-1}, 100 seed weight, plant height and internodal length.

Fruit weight

Direct effect of this trait on fruit yield plant^{-1} was negligibly positive. The positive indirect effects were also negligible via 100 seed weight, days to maturity, seed fruit^{-1}, fruit diameter, fruit length, fruiting span, plant height, fruit plant^{-1}, stem diameter and internodal length.

Number of fruits plant^{-1}

High positive direct effect fruit plant^{-1} on fruit yield plant^{-1} was revealed; its indirect effects via fruit diameter and length were moderate.

Number of seeds fruit^{-1}

Positive direct effect on fruit yield plant^{-1} was low. Positive indirect effects through fruit length, fruit weight, fruiting span, days to maturity, stem diameter, fruit diameter, fruit plant^{-1}, plant height and 100 seed weight were negligible.

100 seed weight (g)

The direct contribution of 100 seed weight on fruit yield plant^{-1} was negligible but positive, similarly, its positive indirect effect through fruit weight, days to maturity, fruit plant^{-1}, internodal length, fruit diameter, fruit length, plant height, fruiting span, and seed fruit^{-1} were negligible.

Fruiting span

Fruiting span showed negligible positive direct effect on fruit yield plant^{-1} whereas, its indirect effects were also negligible and positive through stem diameter, seed fruit, fruit length, fruit weight, branches plant^{-1}, days to maturity, 100 seed weight, plant height, node at first flower appears and number of fruits plant^{-1}.

Days to maturity

Positive direct contribution of this trait on fruit yield plant^{-1} was negligible. However, the positive indirect effects this trait via fruit weight, 100 seed weight, number of fruits plant^{-1}, fruit diameter, number of seeds fruit^{-1}, fruiting span, plant height, fruit length, and stem diameter (0.0042) were negligible.

5.4 Genetic divergence:

Presence of substantial genetic variability for traits of economic importance in a prebreeding population is of immense importance for crop improvement. Study of genetic variability becomes difficult while selecting parents for improvement of a set of traits, due to complex developmental behavior of the genotypes. Selection of elite parents is rather a difficult task for a plant breeder in any breeding programme. Selection of parents on the basis of performance is good but, there is a possibility of related lines being chosen resulting in limited or no advances under selection and therefore, there is a need for emphasis on a wide genetic base. Selection of the parents on the basis of geographical diversity is another way of choosing parents, but this has its own limitations due the complexity in inheritance pattern and their reactions with the complex environmental factors, hence it needs to be supplemented with genetic diversity.

Formulating successful breeding programme for evolving superior cultivars, knowledge of genetic divergence among parents is of immense importance, as the hybrid of genetically diverse parents is likely to express high heterotic effect and also a broad spectrum of variability could be expected in the segregating generations.

The quantitative assessment of genetic divergence has been studied using Mahalanobis's D^2 statistics and canonical analysis technique on 60 genotypes over 22 yield and yield contributing characters are discussed as follows:

The analysis of variance showed highly significant differences within the population for all the 22 characters studied. The V statistics indicated V = 7769.70200. The value of Wilk's criterion was 10113.444. The degree of freedom for the study was 1298. The D^2 values corresponding to possible comparison among 60 genotypes taking two genotypes at a time were computed separately in the analysis.

Contribution of individual characters towards genetic divergence

The percentage contribution towards genetic divergence by all the characters revealed that, number of locules contributed most towards genetic divergence followed by remaining characters in descending order *viz.,* 100 seed weight, leaf blade length, node at 1st flower appears, fruit yield plant^{-1}, these five traits accounted for 51.58 per cent of total variability, while, fruit length, leaf blade width, number of fruits plant^{-1}, no. of seeds fruit^{-1}, flower length, petiole length, internodal length, fruiting span, incidence of YVMV, fruit diameter, no. of branches and stem diameter contributed to remaining part of the total variability. Bendale *et al.* (2003), Prakash and Pitchaimuthu (2010), Prakash *et al.* (2011), Pachiyappan and Saravanan (2012) reported that fruit yield plant^{-1} was an important characteristic responsible for grouping of genotypes, these findings are in close proximity to the present study.

Grouping of genotypes into different clusters

The study comprised of 24 exotic, 31 indigenous accessions and five checks were assessed for nature and magnitude of genetic divergence based on 22 quantitative traits following Mahalanobis's D^2 statistic and Anderson's canonical analysis. On the basis of D^2 values, the 60 genotypes were grouped into 12 clusters following Tocher's method. Three clusters were polygenotypic. Cluster I was the largest cluster with 40 genotypes followed by Cluster VIII with seven genotypes while, Cluster IV comprised of only four genotypes while, remaining nine clusters were mono-genotypic. Many cultivars collected from same place have been grouped into different clusters. This suggested that genetic drift, natural selection and diverse environmental conditions within a country cause more diversity than geographical isolation. The findings are in accordance to Garg *et al*. (2011), Prakash *et al*. (2011), Verma *et al*. (2011), Pachiyappan and Saravanan (2012).

Intra and inter cluster divergence D^2 values

The average intra and inter-cluster D^2 values estimated as per the procedure given by Singh and Choudhary (1979) the cluster VIII showed maximum intra cluster D^2 value (D^2 = 336.27) followed by Cluster I (D^2 = 208.73) and Cluster IV (D^2 = 133.64). Cluster II, III, V, VI, VII, IX, X, XI and XII being mono-genotypic showed no intra cluster divergence.

The highest inter cluster divergence was observed between genotypes of cluster IV and X, followed by cluster VI vs XI and II vs X.

Cluster I was the largest cluster with 40 genotypes, was nearest to cluster VII followed in descending order by cluster III, II, VI, V, VIII and IX whereas, it was distantly placed to cluster IV, XII, X and XI.

Cluster II was mono-genotypic, it was nearest to cluster IV followed by clusters IV and XI, however it was distantly placed to clusters VII, IX, VIII, III, V, VI, XII and X.

Cluster III was closest to cluster VI had only one genotype, followed by clusters VII, X, I, XII and V. While, the remaining clusters *viz.,* VIII, IX, II, IV and XI were placed distantly to this cluster.

Cluster IV comprised of four genotypes, it was nearest to cluster I while, remaining clusters e.g. VII, XI, III, VI, VIII, IX, XII and V were distantly placed to this cluster, cluster X was at wide distance to it.

Cluster V comprised of only genotype IC018533. It was nearest to clusters e.g. IX, X, XII, I, III and VII, while remaining clusters were more distantly situated.

Cluster VI was monogenotypic with entry IC009856-C. It was nearest to cluster III, VII, X and I, remaining clusters were distantly placed to the cluster VI.

Cluster VII, a mono-genotypic cluster comprised of genotype EC329418, it was nearest to Cluster III followed by clusters VI, I, XII and V whereas, clusters X, VIII, II, IX, V and XI revealed distant placement with the cluster.

Cluster VIII comprised of seven genotypes *viz.,* EC305617, EC305637, EC305664, EC305634, EC329397, EC329369, and IC022237-A, it was closest to cluster I. However, the remaining clusters were distantly placed to it.

Genotype EC329366 was the only entry in cluster IX. It was nearest to cluster V followed by XI and I, while, clusters *viz.,* XII, VII, X, II, III, VIII, IV and VI were distantly placed to cluster IX.

Cluster X, a mono-genotypic cluster consisted of only one genotype *i.e.,* IC014845-B. This cluster was closest to cluster V, III, XII and VI whereas the remaining clusters were distantly placed to it.

Mono-genotypic cluster XI comprised of genotype IC018542. It was close to Cluster IX and II, while the remaining clusters revealed moderate to wide distances from this cluster.

Cluster XII with genotype IC 018540 was also mono-genotypic. Clusters *viz.,* X, III, V and VII were close to this cluster. However, the remaining clusters *e.g*., IX, I, VI, VIII, II, IV and XI revealed distance from this cluster.

Cluster means showing importance of grouped characters:

Cluster II recorded low incidence of YVMV with high fruit weight, while genotypes of cluster IV were identified as good donors for plant height, number of fruits plant and fruit yield plant^{-1}, similarly cluster VII for fruit length, thus selection of genotypes / parents from these clusters for crop improvement could be useful in increasing fruit yield with resistance to YVMV.

Canonical analysis

Canonical analysis was also carried out to verify the group constellations obtained through D^2 statistics (Rao, 1952). The first and second canonical roots have accounted for 27.69 and 13.72 per cent of total variation respectively, thus 41.41 per cent of total variation was expressed by the first two canonical roots. The third and fourth canonical roots have expressed 10.289 and 9.541 per cent of total variation respectively, thus the sum of these two vectors accounted for 19.83 per cent of the total variation expressed. The fifth and sixth canonical roots have accounted for 7.511 and 6.475 per cent of total variation respectively, these together accounts for 13.987 per cent of the total variation. The seventh canonical root accounted for 5.011 of total variation.

With respect to the relative predominance of different characters under study, it would be apparent from the absolute size of coefficients that leaf blade length, leaf blade width and fruit yield plant^{-1} were predominant in the primary axis of differentiation however, in secondary axis fruit yield plant^{-1}, number of fruits plant^{-1} and 100 seed weight were preponderant. In the third axis of absolute size of coefficient, internodal length, 100 seed weight and node at 1st flower appears were important, while in the fourth axis there was predominance of characters *viz.,* leaf blade width, stem diameter and incidence of YVMV. In the fifth axis of differentiation there was predominance of node at first flower appears, fruit plant^{-1} and branches plant^{-1}. Whereas, in the sixth axis there was predominance of fruit length, seed fruit^{-1} and node at first flower appears. In the seventh axis of differentiation predominance of characters *viz.,* flower length, flower diameter and number of seeds fruit^{-1} was observed.

5.7 Incidence of yellow vein mosaic virus:

The genotypes were classified into highly susceptible, susceptible, tolerant, moderately resistant and resistant to yellow vein mosaic virus incidence under field conditions. The genotypes Pusa A4 and EC 550848 were observed to be resistant, while VRO-6, Phule utkarsh, Hisar unnat, EC 305616 and VRO-5 exhibited moderate resistance to this disease. However, 11 genotypes revealed tolerance to the disease, 33 genotypes were susceptible while 09 genotypes expressed high degree of susceptibility to the disease. These findings are in accordance with the findings of Nizar *et al.* (2004) and Tiwari *et al.* (2012).

5.8 Identification of putative lines

It is revealed from the data obtained, the most putative lines are as follows:

EC 550848

It has resistant to YVMV disease, highest fruit yield plant^{-1}, long fruit with penta locular, high no. of fruits plant^{-1} and it identified as superior line for selection / recombination breeding / heterosis breeding.

Pusa A4

Fruits long with 5 locules, average fruit yield plant^{-1} and resistant to YVMV disease.

VRO-6

It has longest fruit length**,** 5 locular, high no. of fruits plant^{-1}, long fruiting span with high fruit yield plant^{-1} it is moderate resistant to YVMV disease.

Phule utkarsh

It is moderate resistant to YVMV disease has long fruits, five locular with highest no. of fruits plant^{-1} with high fruit yield plant^{-1}**.**

VRO-5

Fruits long with five locules, high number of fruits plant^{-1}, and high fruit yield plant^{-1}. It is tolerant to YVMV disease.

SUMMARY, CONCLUSION AND SUGGESTIONS FOR FURTHER WORKS

6.1 Summary

The present investigation entitled "Genetic Divergence in Okra (*Abelmoschus esculentus* (L.) Moench)" was carried out during *Kharif* season of 2011 at the Vegetable Research Farm, Department of Horticulture, College of Agriculture, J.N.K.V.V., Jabalpur (MP). The experimental material for the present investigation comprised 60 genotypes of okra. These genotypes were sown in Randomized Complete Block Design with five blocks in three replications. The objectives of the study was to estimate genetic parameters of yield and its components, to estimate coefficient of correlation and path coefficient analysis for yield and its components, to estimate genetic divergence for identification of putative lines and screening for incidence of YVMV. Observations were recorded on five random competitive plants selected from each genotype separately for morphological, phenological, yield and yield contributing traits were evaluated as per standard procedure.

Salient findings of the present investigation:

The mean sums of squares due to genotype were considerably very high for all the characters indicated presence of substantial genetic variability amongst the genotypes studied. Plant height, stem diameter, number of branches plant^{-1}, internodal length, node at first flower appears, leaf blade length, leaf blade width, petiole length, flower length, flower diameter, days to 50 per cent flowering, fruiting span, days to maturity, fruit length, fruit diameter, number of locules fruit^{-1}, fruit weight, number of fruits plant^{-1}, number of seeds fruit^{-1}, 100 seed weight, fruit yield plant^{-1} and incidence of YVMV.

The estimates of PCV were higher than the corresponding GCV for all the traits which might be due to interaction of the genotypes with the environment to some degree or other unexplained environmental factors influencing expression of these characters. Highest PCV and GCV were observed for number of branches plant^{-1} followed by incidence of YVMV, fruit yield plant^{-1} and number of fruits plant^{-1} suggesting presence of substantial phenotypic and genotypic variability among the genotypes for improvement.

High heritability coupled with high genetic advance as percentage of mean was observed in four traits *i.e.,* node at first flower appears, fruit yield plant^{-1}, number of fruits plant^{-1}, and incidence of YVMV suggested preponderance of additive genes. It also indicated higher response to selection for high yield with resistance to YVMV disease due to the predominance of additive gene action.

High heritability coupled with low genetic advance as percentage of means was observed by petiole length, flower length, fruit diameter and fruit weight. This revealed predominance of non-additive gene action in expression of these characters. It being exhibited due to favourable influence of environment rather than genotype and selection for such traits may not be rewarding.

Low heritability along with low genetic advance as percentage of mean was observed for flower diameter and plant height indicated low response to selection due to highly influence of environment on the genotypes and selection would be ineffective.

The phenotypic correlation coefficients were higher in magnitude than their corresponding genotypic ones, indicating thereby strong inherent association between different traits studied. The phenotypic expression of correlation was lessened possibly due to multiple influences of environmental components. In view of their correspondence, selection on phenotypic basis would be effective.

The fruit yield plant^{-1} showed highly strong positive association with number of fruits plant^{-1}, fruit length, days to maturity and fruit weight indicated positive relationship are the major contributors towards fruit yield. It indicated that effective improvement in okra fruit yield through these components. The yield attributing characters exhibited varying trend amongst themselves.

The phenotypic path coefficient analysis of different yield contributing and associated traits on fruit yield plant^{-1} revealed that traits *viz.*, number of fruits plant^{-1}, recorded high estimate of positive direct effect followed by low direct effect of number of seeds fruit^{-1}, branches plant^{-1}, fruit diameter. It indicated that possibility of effective improvement in okra fruit yield through these components could be achieved. The yield attributing characters exhibited varying trend amongst them.

Regarding the percentage contribution towards genetic divergence the character no. of locules showed maximum contribution towards total genetic divergence followed by 100 seed weight, leaf blade length, node at 1st flower appears, fruit yield plant^{-1}, fruit length, leaf blade width, no. of fruits plant^{-1}, no. of seeds fruit^{-1}, flower length, petiole length, internodal length, fruiting span, incidence of YVMV, fruit diameter, no. of branches plants and stem diameter.

On the basis of D^2 values, the 60 genotypes were grouped into 12 clusters following Tocher's method, 3 clusters were polygenotypic. Cluster I was the largest cluster with forty genotypes followed by Cluster VIII with seven genotypes while, Cluster IV comprised of only four genotypes while, remaining nine clusters were mono-genotypic.

Cluster II showed least incidence of YVMV with high cluster mean values for fruit weight and days to maturity. While, Cluster III recorded least value for dwarfness, fruit weight, fruiting span and days to maturity. Cluster IV revealed highest values for plant height, number of fruits plant and fruit yield plant^{-1}. Cluster VI expressed maximum value for flower diameter and fruiting span. Highest values of cluster mean for flower length, fruit length, 100 seed weight and fruiting span was observed in Cluster VII. However, Cluster VIII showed highest values for number of branches plant^{-1}, internodal length and number of locules fruit^{-1}. Cluster IX an expressed high cluster mean value for node at first flower appears, fruit diameter and fruiting span. Cluster X recorded highest cluster mean values for incidence of YVMV was revealed, it also showed the least values for flower diameter, number of seeds fruit^{-1}, hundred seed weight and fruit yield plant^{-1}.

Resistance to YVMV

Genotypes Pusa A4 and EC 550848 were observed to be resistant under field conditions, while genotypes VRO-6, Phule utkarsh, Hisar unnat, EC 305616 and VRO-5 exhibited moderate resistance to this disease. However, 11 genotypes revealed tolerance to the disease.

Putative lines identified on the basis of relevant data obtained are as follows:

EC 550848

It recorded highest fruit yield plant^{-1} with long fruits and resistant to YVMV disease. It is identified as superior line for selection / recombination breeding / heterosis breeding.

Pusa A4

It has average no. fruits plant^{-1}, fruits are long penta locular with high fruit yield plant^{-1} and resistant to YVMV disease.

VRO-6

It has longest fruit length, fruits are penta locular with long fruiting span**,** higher number of fruits plant^{-1} and high fruit yield plant^{-1}. It is moderately resistant to YVMV disease.

Phule utkarsh

It is moderately resistant to YVMV disease, fruits are long penta locular with highest number of fruits plant^{-1} resulting to high fruit yield plant^{-1}.

VRO-5

It has long fruits with five locules with more number of fruits plant, and average fruit yield plant^{-1}. It is tolerance to YVMV disease.

6.2 Conclusion

The variance due to genotypes were highly significant for all the economical characters, phenological traits and fruit quality parameters *viz.,* plant height, stem diameter, node at first flower appears, number of branches, internodal length, leaf blade length, leaf blade width, petiole length, flower length, flower diameter, days to 50 per cent flowering, fruiting span, days to maturity, fruit length, fruit diameter, number of locules fruit^{-1}, fruit weight, number of fruits plant^{-1}, number of seeds fruit^{-1}, 100 seed weight, fruit yield per plant^{-1} and incidence of YVMV revealed the presence of genetic variability among genotypes.

The highest PCV were observed for number of branches, incidence of YVMV, fruit yield plant^{-1} and number of fruits plant^{-1}. It suggests greater phenotypic and genotypic variability among the genotypes and responsiveness of the attributes for making further improvement by recombination and selection.

High heritability coupled with high genetic advance as percentage of mean was observed for node at first flower appears, fruit yield plant^{-1}, number of fruits plant^{-1}, number of branches plant^{-1} and incidence of YVMV suggested the preponderance of additive genes. It also indicated higher response for selection of high yielding genotypes as these characters are governed by additive genes.

Fruit yield plant^{-1} had highly strong positive association with no. of fruits plant^{-1}, fruit diameter, fruit length, number of seeds fruit^{-1}, days to maturity and fruit weight. It indicated that effective improvement in okra. Fruit yield can be achieved using some of these components. The yield attributing characters exhibited varying trend amongst them.

The genetic architecture of fruit yield and quality is based on the balance or overall net effect produced by various components interacting with on another. Based on the studies of path analysis, it may be concluded that no. of fruit plant^{-1}, exhibited maximum positive direct effect on fruit yield plant^{-1}, followed by low direct effect of no. of seeds fruit^{-1}, branches plant^{-1}, fruit diameter, fruit weight, days to maturity, fruiting span, 100 seed weight and stem diameter. Seem to be primary yield contributing characters and could be relied upon for selection of parent/genotypes to improve genetic yield potential of okra.

Intra cluster distance was the highest in cluster VIII while, it was lowest cluster IV. Inter cluster distance value was highest between cluster IV and X while, it was lowest between clusters III & VI. By selecting diverse parents from cluster II, IV and VII for crop improvement work in okra can be strengthened.

It is revealed from the research work that the EC 550848, Phule utkarsh, VRO-6 and Pusa A4 have been identified as superior lines and can be utilized for recombination breeding / heterosis breeding.

6.3 Suggestions for further work

1. The genotypes showing greater adaptability, higher fruit yield potential with other desirable fruit qualities may be tested under different agro-climatic conditions and elite genotypes may be used in recombination or heterosis breeding with resistance to YVMV.
2. Characters having desirable association and direct effects with fruit yield should be given due to consideration for genetic improvement in okra.
3. An umbrageous characteristics pattern of elite okra genotypes should be obtained through DNA finger printing.

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Table 4.3: Estimates of genotypic, phenotypic and environmental coefficients of correlation among yield and its contributing characters in okra

			2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21
			Stem diameter (cm)	No. of branches plant^{-1}	Internodal length (cm)	Petiole length (cm)	Leaf blade length (cm)	leaf blade width (cm)	Node at 1st flower appears	Flower length (cm)	Flower diameter (cm)	Fruit length (cm)	Fruit diameter (mm)	No. of locules fruit^{-1}	Fruit weight (g)	No. of fruits plant^{-1}	No. of seeds fruit^{-1}	100 seed weight (g)	Days to 50 % flowering (days)	Fruiting span (days)	Days to maturity (`days)	Incidence of YVMV
1	Plant height (mm)	G	0.2998	-0.2892	0.4604	0.5176	0.3006	0.3249	-0.3205	0.2618	0.4920	0.4379	0.3833	-0.3558	0.3623	0.5057	0.1156	0.1178	-0.3943	0.1535	0.2870	-0.3013
		P	0.1593*	-0.1157	0.2183**	0.2928***	0.1570*	0.1690*	-0.1629*	0.0670	0.0767	0.2675***	0.1188	-0.1965**	0.1347	0.2672***	0.0454	0.0962	-0.1617*	0.0476	0.0961	-0.1843*
		E	0.0428	0.0754	-0.0240	0.1110	0.0165	0.0078	0.0073	-0.1967	-0.1303*	0.1641	-0.1514	-0.0585	-0.0776	0.0395	-0.0251	0.1324	0.0138	-0.0303	-0.0278	-0.1053
2	Stem diameter (mm)	G		0.3387	-0.0422	0.2424	0.2042	0.2224	0.0451	-0.0107	0.1591	0.1097	0.1980	0.2472	0.1552	0.0306	0.1482	-0.3758	-0.1887	0.2722	0.0986	-0.1218
		P		0.2860***	-0.0235	0.2231**	0.1861*	0.1892*	0.0568	-0.0159	0.0383	0.0866	0.1405	0.2162**	0.1113	0.0447	0.0948	-0.2806***	-0.1041	0.2122**	0.0722	-0.0980
		E		0.0610	0.0593	0.1330	0.0977	-0.0015	0.1405	-0.0408	-0.1353*	-0.0339	-0.0615	0.0572	-0.0329	0.1268	-0.1045	0.2291*	0.1066	0.0859	0.0268	-0.0099
3	No. of branches plant^{-1}	G			-0.2884	-0.1195	0.1877	0.0907	0.4297	0.0149	-0.0524	-0.3402	-0.3058	0.3935	-0.2229	-0.0966	-0.1641	-0.2855	0.4185	0.2483	-0.0767	0.2781
		P			-0.2254**	-0.0847	0.1910*	0.0815	0.3926***	0.0124	-0.0100	-0.2771***	-0.2372**	0.3477***	-0.2145**	-0.1063	-0.1176	-0.2381**	0.3015***	0.1323	-0.0465	0.2159**
		E			0.0998	0.1307	0.2186*	0.0169*	0.1408	-0.0013	0.0613	0.1176	0.0398	0.0571	-0.1883	-0.1730	0.0837	0.0625	-0.0145	-0.1686*	0.0162	-0.0510
4	Internodal length	G				0.0021	-0.1465	-0.0890	-0.1026	0.2207	0.2347	-0.0295	0.0636	-0.0656	0.0862	0.0948	-0.1368	0.1649	0.0912	-0.0459	0.0379	0.1713
		P				0.0014	-0.1427	-0.0909	-0.1029	0.2104**	0.1671*	-0.0382	0.0790	-0.0320	0.0745	0.0848	-0.0745	0.1500*	0.0521	-0.0429	-0.0141	0.1407
		E				-0.0029	-0.1205	-0.1116	-0.1117	0.1529	0.1086	-0.0950	0.1458	0.1944**	0.0312	0.0197	0.2031*	0.0543*	-0.0608	-0.0409	-0.1447	0.0068
5	Petiole length (cm)	G					0.4238	0.3420	-0.0886	0.2230	0.0078	0.2407	0.3614	-0.0885	0.1759	0.1783	0.0357	0.0408	-0.1558	0.2811	0.0152	-0.2441
		P					0.3553***	0.3024***	-0.0852	0.1969**	-0.0085	0.2303**	0.2686***	-0.0644	0.1390	0.1694*	0.0102	0.0555	-0.1082	0.1964**	-0.0069	-0.2109**
		E					-0.2008*	-0.0657*	-0.0553	0.0215	-0.0490	0.1484*	-0.1818*	0.1326	-0.0234	0.0980	-0.1269	0.1738*	0.0431	-0.0393	-0.0746	-0.0452
6	Leaf blade length (cm)	G						0.7793	-0.1172	0.0858	-0.1306	0.0136	0.1707	-0.0146	0.2793	0.0539	-0.0416	-0.1304	-0.2632	0.2112	0.2779	-0.3551
		P						0.7224***	-0.1054	0.0635	-0.0623	0.0126	0.1421	-0.0094	0.2074**	0.0423	-0.0676	-0.1284	-0.1881*	0.1254	0.1794*	-0.2897***
		E						0.1627*	0.0091	-0.0952	0.0556	0.0045	0.0027	0.0357	-0.1278	-0.0563	-0.2198*	-0.1115*	0.0550	-0.1442	-0.0555	0.0574
7	leaf blade width (cm)	G							-0.3708	0.0216	-0.1059	0.0548	0.2399	-0.0999	0.0597	0.2447	-0.0289	-0.1874	-0.3258	-0.1319	0.2670	-0.5183
		P							-0.3341***	0.0270	0.0763	0.0383	0.1740*	-0.0997	0.0264	0.2112**	-0.0491	-0.1731*	-0.2112**	-0.0822	0.1814*	-0.4383***
		E							0.0852	0.0729	-0.0605	-0.1209	-0.2063**	-0.0982	-0.1623*	-0.1173	-0.1899*	-0.0343	0.2259*	0.0889*	-0.0281	0.0235
8	Node at 1st flower appears	G								-0.0834	-0.2795	-0.2943	-0.2005	0.0290	-0.0721	-0.3828	-0.1952	-0.2074	0.5668	0.0541	-0.2275	0.4917
		P								-0.0687	-0.1735*	-0.2741***	-0.1739*	0.0371	-0.0810	-0.3609***	-0.1736*	-0.1825*	0.4475***	0.0299	-0.1618*	0.4067***
		E								0.0487	-0.0347	-0.0863	-0.0397	0.1176	-0.1485*	-0.1507*	-0.0563	0.0565	0.0807	-0.0568	-0.0147	-0.0879
9	Flower length	G									0.4113	-0.2562	0.2454	0.4269	-1256.0	0.1374	-0.0055	0.1866	0.0119	0.0696	-0.1558	0.0259
		P									0.3207***	0.1616*	-0.1264	-0.1397	-0.1182	0.1184	0.0065	0.1753*	0.0332	0.0457	-0.1265	0.0278
		E									-0.0168	0.0465	0.0366	-0.0030	-0.0935	-0.0146	0.0633	0.0977	0.1069	-0.0175	-0.0824	0.0371
10	Flower diameter (cm)	G										0.0486	0.3269	0.3886	0.2307	0.2561	0.2296	0.3919	-0.1648	0.2620	0.1256	0.0004
		P										0.1957**	-0.0772	0.0551	0.1210	0.0865	0.0998	0.2011**	-0.1048	0.0855	0.0898	-0.0506
		E										0.1135	0.0881	0.1156	-0.0057	-0.2471	-0.0735	-0.1084	-0.0495	-0.0805	0.0617	-0.1404
11	Fruit length (cm)	G											0.4113	-0.2562	0.2454	0.4269	0.3974	0.1321	-0.3446	0.2661	0.1515	-0.3684
		P											0.3305***	-0.2389**	0.1905*	0.3965***	0.3279***	0.1259	-0.2530***	0.1895*	0.0903	-0.3048***
		E											-0.0601	-0.0948	-0.0557	0.1472	-0.0341	0.0747	0.0317	-0.0231	-0.0609	0.0225
12	Fruit diameter (mm)	G												0.0486	0.3269	0.3886	0.1711	0.1392	-0.2945	-0.0398	0.2064	-0.3485
		P												0.0473	0.2617***	0.3134***	0.1617*	0.1165	-0.2601***	-0.0109	0.1805*	-0.2427**
		E												0.0453	0.0580	-0.0564	0.1287	0.0068	-0.1865*	0.0531	0.1474*	0.1291
13	No. of locules fruit^{-1}	G													0.0213	-0.2234	0.1446	0.0344	0.1696	0.3566	0.2395	0.1678
		P													0.0162	-0.2139**	0.1181	0.0312	0.1068	0.2338**	0.1367	0.1350
		E													-0.0074	-0.1330	-0.0239	0.0042	-0.1101	-0.1358	-0.1299	-0.0403
14	Fruit weight (g)	G														0.1340	0.3985	0.4257	-0.1416	0.3190	0.3995	-0.3443
		P														0.1231	0.2970***	0.3487***	-0.1901*	0.1846*	0.3132***	-0.2632***
		E														0.0831	-0.0389	0.0078	-0.3047*	"0.0904	0.1787*	0.0033
15	No. of fruits plant^{-1}	G															0.1417	0.2293	-0.3437	0.0442	0.2766	-0.5552
		P															0.1203	0.2205**	-0.2585***	0.0280	0.1953**	-0.4667***
		E															0.0081	0.1466*	0.0046	-0.0211	0.0209	-0.0049
16	No. of seeds fruit^{-1}	G																0.0654	-0.5386	0.2669	0.2843	-0.3408
		P																0.0674	-0.3769***	0.1647*	0.1670*	-0.2660***
		E																0.0833	0.0192	-0.0661	-0.0552	0.0138
17	100 seed weight (g)	G																	0.0212	0.1247	0.2920	-0.0998
		P																	0.0241	0.0484	0.2199**	-0.0809
		E																	0.0411	-0.2072*	0.0837*	0.0191
18	Days to 50 % flowering (days)	G																		0.0367	-0.0869	0.5315
		P																		-0.0083	-0.1095	0.3441***
		E																		-0.0813	-0.1429	-0.1170
19	Fruiting span (days)	G																			0.2304	-0.0159
		P																			0.1186	0.0413
		E																			-0.0267	0.1793
20	Days to maturity (days)	G																				-0.3752
		P																				-0.2817***
		E																				-0.1233
21	Fruit yield plant^{-1}	G	0.1856	0.0289	-0.0282	0.1668	0.1266	0.2464	-0.3431	0.0877	0.2582	0.3924	0.4448	-0.0129	0.3040	0.8793	0.3674	0.2534	-0.4120	0.1933	0.3943	-0.4718
		P	0.1505*	0.0208	-0.0485	0.1519*	0.1233	0.2199**	-0.3070***	0.0602	0.1540*	0.3496***	0.3767***	0.0009	0.2742***	0.8033***	0.3164***	0.2195**	-0.3195***	0.1526*	0.3019***	-0.3892***
		E	-0.0507	-0.0369	-0.2026**	0.0191	0.0921	-0.0712	0.0862	-0.1550*	0.0061	-0.0402	0.0276	0.1331	0.1606*	0.0932	0.0323	-0.0964	-0.0298	0.0508	0.1347	0.0807

VITA

The author of this thesis **Deepak Kumar Saryam** S/o Shri Guruprasad Saryam and Smt. Rekha Bai Saryam was born on 25th April 1985 at Chhindwara (MP). He passed his higher secondary school certificate examination from Semi-Govt. Danielson Higher Secondary School, Chhindwara with first division (71.5%) he joined the College of Agriculture, Jawahar Lal Nehru Krishi Vishwa Vidyalaya, Jabalpur (M.P.) in the year 2004-05 and successfully completed the degree of B.Sc. (Ag.) during the year 2008-09 with 6.76 OGPA at 10 point scale.

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