EVALUATION OF SUPERIOR CULTURES FOR YIELD AND YELLOW VEIN MOSAIC RESISTANCE IN OKRA

(*Abelmoschus esculentus* (L.) Moench)

NIKITHA J.

(2014 – 11 - 115)

DEPARTMENT OF PLANT BREEDING AND GENETICS

COLLEGE OF AGRICULTURE

VELLAYANI, THIRUVANANTHAPURAM-695 522

KERALA, INDIA

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by

NIKITHA J.

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THESIS

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2016

DECLARATION

I, hereby declare that this thesis entitled **"EVALUATION OF SUPERIOR CULTURES FOR YIELD AND YELLOW VEIN MOSAIC RESISTANCE IN OKRA (*Abelmoschus esculentus* (L.) Moench)"** is a bonafide record of research work done by me during the course of research and the thesis has not previously formed the basis for the award to me of any degree, diploma, associateship, fellowship or other similar title, of any other University or Society.

Vellayani, **Nikitha J.**
Date: (2014 -11-115)

CERTIFICATE

Certified that this thesis entitled **"EVALUATION OF SUPERIOR CULTURES FOR YIELD AND YELLOW VEIN MOSAIC RESISTANCE IN OKRA (*Abelmoschus esculentus* (L.) Moench)"** is a record of research work done independently by Ms. Nikitha J. under my guidance and supervision and that it has not previously formed the basis for the award of any degree, diploma, fellowship or associateship to her.

Vellayani,
Date:

Dr. Arya.K
(Major Advisor, Advisory Committee)
Professor (Plant Breeding and Genetics)
College of Agriculture
Vellayani.

CERTIFICATE

We, the undersigned members of the advisory committee of Ms. Nikitha J., a candidate for the degree of **Master of Science in Agriculture** with major in Plant Breeding and Genetics, agree that the thesis entitled **"EVALUATION OF SUPERIOR CULTURES FRO YIELD AND YELLOW VEIN MOSAIC RESISTANCE IN OKRA (*Abelmoschus esculentus* (L.) Moench)"** may be submitted by Ms. Nikitha J., in partial fulfilment of the requirement for the degree.

Dr. Arya.K
(Chairman, Advisory Committee)
Professor (Plant Breeding and Genetics)
Department of Plant Breeding and Genetics
College of Agriculture**,** Vellayani.

Dr. P. Manju
(Member, Advisory Committee)
Professor and Head
Department of Plant Breeding and Genetics
College of Agriculture, Vellayani.

Dr. Vijayaraghavakumar
(Member, Advisory Committee)
Professor and Head
Department of Agricultural Statistics
College of Agriculture, Vellayani.

Dr. K. Umamaheshwaran
(Member, Advisory Committee)
Professor
Department of Plant Pathology
College of Agriculture, Vellayani

(Name and Address)

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Nikitha J.

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LIST OF ABBREVIATIONS

%	-	Per cent
@	-	At
^{0} C	-	Degree Celsius
ANOVA	-	Analysis of Variance
cm	-	Centimetre
d.f	-	Degrees of freedom
DAE	-	Days after emergence
DAS	-	Days after sowing
et al.	-	And co-workers/co-authors
F_2	-	Second filial generation
F_6	-	Sixth filial generation
g	-	Gram
GCV	-	Genotypic coefficient of variation
GV	-	Genotypic variance
h	-	Hour
H^2	-	Heritability
IU	-	International Unit
i.e.	-	That is
mcg/g	-	Microgram gram^{-1}
mg	-	Milligram
mg/g	-	Milligram gram^{-1}
mt/ha	-	Metric ton hectre^{-1}
OYVMV	-	Okra yellow vein mosaic virus
PCV	-	Phenotypic coefficient of variation
PV	-	Phenotypic variance
R	-	Residual effect
RBD	-	Randomized block design
SE(m)	-	Standard error mean
spp.	-	Species
t/ ha	-	Tons hectre^{-1}
V. I.	-	Vulnerability (severity) index
viz.	-	Namely/ as follows
YVMV	-	Yellow vein mosaic virus
YVMVD	-	Yellow vein mosaic virus disease

Introduction

1. INTRODUCTION

Okra (*Abelmoschus esculentus* (L.) Moench) having an African origin, is one of the most valued vegetable crop grown throughout the world. India is considered as a secondary centre of origin, because wide variability and dominant characters are observed among the existing genotypes and other related species of okra. The crop is often cultivated for its green, non-fibrous and immature fruits. Due to its multiple qualities like high medicinal and nutritive value, easiness in cultivation and portability, year round cultivation, wide adaptability, export potential and high returns, okra has a prominent position among the fruit vegetables.

Being the rich source and good supplement of carbohydrates, proteins, vitamins, minerals and fat, okra is inevitable in human diet. Cooked, boiled and drained okra without salt contains about (3.9g/ 80g) carbohydrates, (2g/ 80g) dietary fibre, (1.9g/ 80g) sugars, (0.2g/ 80g) fats, (1.5g/ 80g) proteins and amino acids, (226IU/ 80g) Vitamin A, (13.0mg/ 80g) Vitamin C, (0.2mg/ 80g) Vitamin E, (32mcg/ 80g) Vitamin K and various minerals (NHB, 2013). The mucilage content in okra also finds applications in the industrial as well as the medical field. Due to its high iodine content, consumption of okra is good for the treatment of goiter. The fibre content in bhindi pods helps to relieve constipation condition by promoting smooth peristalsis of digested food particles (Sindhu *et al.,* 2013).

Okra is tolerant to heat and drought. It is cultivated mainly during rainy (June-September) and summer (February-May) seasons in south India as it is a tropical crop which can withstand hot weather and susceptible to low night temperatures. It is well fitted for multiple cropping systems either as sole crop or intercrop as it is a medium duration annual herb with erect and quick growing nature. Okra cultivation is widely adopted among the marginal, small and large farmers as it has the potential to boost food, nutritional and health security and being a cash crop, it could foster rural development and support sustainable land care.

India is the largest producer of okra in the world (6350.3 thousand tonnes which is approximately 73.25 per cent share of world production) with an area of 530.8 thousand hectare and productivity of 12mt/ ha. In India, Andhra Pradesh is the leading producer of okra with 1184.2 thousand tonnes i.e. 20.5 per cent of the national production (Bagool, 1994). After onion, okra has the major share in revenue generation through export of fresh vegetables (Mastoi and Sahito, 2012). Okra productivity in India is higher (12.00t/ ha) when compared to the world average productivity (7.80t/ ha), but is lower than that of Ghana (20t/ ha) and Egypt (14.00t/ ha) (Kumar and Reddy, 2015).

The accelerated yield potential is often limited by the damage caused by various insects such as fruit and shoot borer, aphids, jassids, ants, whiteflies and diseases like *Fusarium* wilt, powdery mildew, yellow vein mosaic virus (YVMV) disease and nematodes. The study about YVMV disease is very important in okra cultivation since it is a highly destructive viral disease which infects at all the stages of crop growth.

The yellow vein mosaic virus (YVMV) disease is characterized by the presence of a homogenous interwoven network of pale coloured veins mostly yellowish. The presence of green islands in between provides the mosaic appearance. At the early stages of crop growth, we can observe yellowing of only infected leaves whereas, the entire leaves turn to be completely yellow at later stages and no trace of green tissue could be observed in extreme cases. In certain conditions, some raised structures known as enations are observed on the lower surface of infected leaf. When the plants are infected during the early stages, the further growth of the plant will be impaired which remain as stunted. The fruits will be deformed, tough, small and become pale yellow to white in colour. If the plant acquires infection during seedling stage i.e. approximately twenty days after germination, about 50-100 per cent yield loss will be caused (Singh *et al.,* 2014).

This crisis can be overcome with genetic improvement through the development and release of improved varieties having wider genetic base, higher yielding potential, superior pod quality, YVMV disease resistance, better performance under various agro-climatic conditions and also will be able to provide stable and sustainable results with better acceptance by rural, urban and peri-urban farmers in terms of pod yield and quality (Kumar and Reddy, 2015).

In India, continuous efforts were made to develop high yielding as well as YVMV disease resistant varieties of okra. Earlier, Pusa Sawani, an YVMV resistant variety developed by IARI was able to cut down the disease incidence to some extent. But a vast gap exists in the research efforts and the expected outcome. Emerging biotypes of whitefly, new virus strains and breakdown of resistance in the developed varieties/ hybrids are the major challenges which need to be addressed (Bagool, 1994). Consistent resistance performance is not shown by many of the resistant varieties (Prabhu *et al.,* 2007). Hence the need of the hour is to release commercially important varieties having elite combinations of many desirable characteristics.

In this context the present study "Evaluation of superior cultures for yield and yellow vein mosaic resistance in okra (*Abelmoschus esculentus* (L.) Moench) was envisaged with the following objectives:-

1. To assess the extent of variability for yield and yield related traits among the selected genotypes.
2. To assess the level of resistance to YVMV among the selected genotypes through field evaluation and virus transmission studies.

Review of Literature

2. REVIEW OF LITERATURE

2.1 GENETIC VARIABILITY

The characters like number of days taken for first flowering, leaf axil having first flower, number of primary branches, number of fruits, fruit length, fruit girth, fruit weight, yield plant^{-1}, crop duration, count for the population of leaf hopper as well as injury score of leaf hopper exhibited significant differences for all the okra genotypes studied (Sivanandan, 2003).

High genotypic and phenotypic coefficients of variation were recorded for the characters like number of branches plant^{-1}, disease incidence, ascorbic acid content, yield plant^{-1} and weight of fruits among the seventeen characters studies among forty one genotypes of okra (Patro and Ravisankar, 2004).

The genotypic coefficient of variation (GCV), heritability and genetic advance were found to be higher for the biometric characters like yield plant^{-1}, average fruit weight, plant height and length of fruits among the evaluated okra genotypes which may be due to additive gene action. The higher PCV than GCV indicate that these characters were highly dependent on environment (Mehta *et al.,* 2006).

High GCV and PCV were observed for most of the traits while evaluating 101 genotypes of bhindi. High GCV and PCV were noticed in the case of fruit yield and protein content. High heritability was obtained in the case of traits like number of fruits plant $^{-1}$, fruit yield and ridges per plant. High genetic advance was observed for fruit yield and protein content. GCV and PCV were noticed to be high for yellow vein mosaic disease incidence (Sindhumole *et al.,* 2006).

Mean squares of all the traits for seventy genotypes of okra were found to be significant which indicates that genetic variability was present among the genotypes studied. High GCV and PCV were observed for characters like number of branches plant^{-1}, height of the plant, number of fruits plant^{-1} and yield plant^{-1}. Moderate GCV

and PCV were noticed in internodal length, girth and length of fruits. PCV was higher than corresponding GCV indicating that the improvement in these characters would be more effective in selection (Singh *et al.,* 2007).

Choudhary *et al.* (2009) reported highest GCV for yield plant^{-1} followed by leaf number and number of branches in okra plants. Higher PCV compared to GCV was reported which showed that the expression of the selected genotypes were influenced by the environment.

The variability in the selected twelve genotypes of bhindi was found to be maximum as the GCV and PCV were noticed to be high in the trait number of primary branches in a plant (Jindal *et al.,* 2010).

The difference between GCV and PCV were found to be very close which indicate that environmental influence on the selected parameters including yield plant^{-1} among the forty eight okra genotypes were less (Nasit *et al.,* 2010).

Prakash and Pitchaimuthu (2010) attempted to check the genetic variability of various biometric characters in forty four okra genotypes. All the evaluated genotypes were significant for all the characters selected. High value for GCV and PCV was observed for traits including height of the plant.

The genotypes studied for the variability was found to be significant when the okra genotypes were evaluated in a 9 x 9 diallel fashion (Wammanda *et al.,* 2010).

In the trials with genotypes of bhindi, Duggi (2012) noticed that high GCV and PCV were obtained for the traits yield plant^{-1} followed by fruit number and fruit weight. Moderate GCV and PCV were shown by height of plant, crop duration and length of fruits. The characters like girth of fruits and days to 50 per cent flowering were observed to have low magnitude for GCV and PCV.

In the screening studies of okra, the characters like height of the plant, fruit length, fruit girth and weight of fruits were found to have high coefficients of variability, heritability and genetic advance which indicated additive gene effect and hence selection can be based on phenotype (Nwangburuka *et al.,* 2012).

High genetic variability was noticed in characters including number of fruits plant $^{-1}$, yield and yellow vein mosaic disease incidence which indicated greater scope for selecting these traits in okra improvement (Reddy *et al.,* 2012).

Shaikh *et al.* (2013) suggested that in the performance study of okra, the characters such as height of the plant and number of fruits plant $^{-1}$ exhibited high genotypic coefficient of variation, heritability and genetic advance. Hence it is effective to select these characters for yield improvement.

In an experiment with okra genotypes, Ahamed and co workers (2015) observed highest range of variation for average weight of the fruits and yield. The traits days to maturity exhibited low GCV and PCV high for yield of the fruits.

Sharma and Prasad (2015) while working with twenty okra genotypes observed the existence of significant variability among the genotypes. A high environmental influence was reflected in diameter of fruit, number of branches plant^{-1}, days to 50 per cent flowering, fruit weight and days to first harvest as indicated by a high difference between genotypic and phenotypic coefficients of variation.

The variance analysis of twenty six okra genotypes revealed significant difference among themselves for characters studied. PCV was closely associated with GCV for all the characters except first flowering node, length of fruits, girth of fruits, average fruit weight, and number of marketable fruits plant^{-1} indicated that the environmental influence was very low. High value of GCV compared to PCV is favourable for selection process because it shows that the characters are under the genetic control rather than environment. High GCV, high heritability and genetic

advance gave better picture for selection of the genotypes rather than calculating heritability alone (Seth *et al.,* 2016).

2.2 HERITABILITY AND GENETIC ADVANCE

High heritability need not always associate with a high genetic advance for a certain polygenic character. Hence, heritability coupled with genetic advance would be more reliable than calculating heritability alone in selecting the best individual through selection (Johnson *et al.,* 1955).

In a study conducted with bhindi genotypes, Philip (1998) reported that the heritability value was maximum for number of flowers per plant. Maximum genetic advance was exhibited by weight of fruits per plant.

Among the eleven characters under study in okra, very high heritability was exhibited by yield plant^{-1} followed by duration and lowest heritability for leaf hopper injury score. Maximum genetic advance was recorded for number of primary branches followed by yield plant^{-1}. All characters showed high genetic advance (Sivanandan, 2003).

Patro and Ravisankar (2004) reported that while evaluating okra genotypes, high heritability was observed for number of branches plant^{-1} followed by yield plant^{-1} and high genetic advance was recorded for yield plant^{-1}, plant height and germination percentage. Highest genetic advance was recorded for number of branches plant^{-1} which meant that the character is more desirable for improvement through selection.

Singh and co workers (2007) in an experiment with seventy genotypes of okra suggested that the high heritability for various characters revealed that direct selection from the morphological appearance could be effective. The expected genetic advance as per cent of mean was high for number of branches plant^{-1}, plant height, number of fruits plant $^{-1}$, total fruit yield, fruit girth, fruit length and internodal

length. High heritability along with high genetic gain was recorded and the characters other than nodes where the first flower appears, pointing that additive gene effects gain more importance for these traits.

High heritability was noticed in number of branches plant^{-1}, average fruit weight, yield plant^{-1} and length of fruit as reported by Choudhary *et al.* (2009) while conducting studies for variability parameters in okra. Moderate estimates of heritability were recorded for plant height at harvest, leaf number and number of fruits plant^{-1}. The trait number of branches plant^{-1} was having high heritability coupled with high genetic advance. Improvement through hybridization and direct advance for height of plant at harvest and number of fruits plant^{-1} for fruit yield is effective and could be attributed to the role of non-additive gene action behind the genetics of these traits.

Sengupta and Verma, (2009) reported that in bhindi, heritability and genetic advance was found to be high for yield plant^{-1}, days to first picking, days to 50 per cent flowering, fruits plant^{-1} and flowering nodes plant^{-1}, which indicated the involvement of additive gene action for these traits.

Abdelmageed (2010) conducted trials with ladies finger cultivars and concluded that if the heritability value estimated is almost 100 percent, the variability observed is due to genetic factors. The low value for heritability represents the environmental influence of the selected traits and hence selection is not effective for that particular character. The polygenes governing the economically important characters give high heritability values so that equally high genetic gain can be expected. Simple selection for such characters is rewarding in okra improvement.

In a field evaluation with twelve okra genotypes, the characters like number of branches plant^{-1}, total and marketable yield showed high value for heritability and genetic advance is due to additive gene effects. Hence selection in these traits could be effective. The characters like average weight of fruits, height of plant, number of

fruits plant^{-1} and length of fruits showed high heritability with a low value for genetic advance which means that selection has less scope in improving these traits (Jindal *et al.,* 2010).

Nasit and co workers (2010) reported medium to high heritability for most of the characters studied in forty eight okra genotypes. High value obtained for genotypic coefficient of variation, heritability and genetic advance in the biometric characters like number of nodes plant^{-1}, yield plant^{-1} and plant height indicate the presence of additive gene action and these characters possess high selective value. Low value of these parameters were exhibited by days to 50 per cent flowering and days to first fruit picking indicating these characters were highly influenced by environments.

Purelines can be developed from the superior segregations obtained from the F_2 generation by selfing and simple selections (Shanthakumar and Salimath, 2011).

Among the ten characters studied in bhindi, all the characters showed high heritability. The highest heritability was recorded for duration with a moderate genetic advance followed by fruit weight with moderate genetic advance. High value for heritability and genetic advance was observed in height of the plant, fruit length, yield plant^{-1} and number of fruits plant $^{-1}$. The genetic advance for days to 50 per cent flowering and fruit girth was found to be moderate even though their heritability estimates were high (Duggi, 2012).

Nwangburuka *et al.* (2012) in a field evaluation of twenty nine bhindi plants noticed that there was high value for heritability and genetic advance for height of plant, fresh fruit length, girth of fruit, length of mature fruit, number of branches plant^{-1} and weight of fruit revealing the role of additive genes and hence direct selection can be used in crop improvement programmes.

The characters like number of branches plant^{-1}, height of the plant, days to 50 per cent flowering, length of fruit, fruit weight, yield plant^{-1}, number of fruits plant^{-1} and yellow vein mosaic virus disease incidence were having high heritability and high genetic advance revealed that selection for these traits can be used for okra improvement (Reddy *et al.,* 2012).

Mogili *et al.* (2013) conducted a study to identify good cultures of okra with high resistance to yellow vein mosaic virus and desirable yield attributing characters revealed high heritability and genetic advance for plant height and yellow vein mosaic incidence.

The evaluation of okra genotypes showed high heritability coupled with high or moderate degree of genetic advance in number of fruits plant $^{-1}$, height of plant, number of leaves plant^{-1}and yield plant^{-1} (Ahamed *et al.,* 2015).

The characters like weight of fruit, days to 50 per cent flowering, number of fruits plant^{-1} as well as yield plant^{-1} showed moderate heritability with moderate genetic advance and high heritability with moderate genetic advance which indicated that improvement in okra can be done through simple selection (Archana *et al.,* 2015).

Twenty six superior cultures of okra were evaluated and noticed that the traits with high heritability estimates suggest that they have high genetic potential. So the environmental effect is low. All the characters studied exhibited high heritability coupled with the high genetic advance. This can probably be explained as the presence of additive genetic control of these characters and selection based on these parameters would be more desirable (Seth *et al.,* 2016).

2.3 CORRELATION

High positive correlation was recorded for number of fruits plant $^{-1}$, fruit weight, plant height, whereas high negative genotypic correlation was recorded with

fruit length and fruit girth when superior okra genotypes were evaluated. Yield plant^{-1} exhibited high positive genotypic correlation with number of fruits plant $^{-1}$, plant height, fruit weight and crop duration (Philip, 1998).

Number of fruits plant $^{-1}$ was significantly and positively correlated with yield plant $^{-1}$. Hence, fruit yield in okra can be increased by selecting the trait number of fruits plant $^{-1}$. Days to 50 per cent flowering was negatively correlated with number of fruits plant^{-1} and fruit yield indicating only a limited scope in the selection of such traits (Dhankar and Dhankar, 2002).

The number of fruits had a positive correlation with yield (0.8789), but was negatively correlated with fruit girth (-0.4310). Length of fruit was positively correlated with fruit weight (0.3761). Fruit girth had negative correlation with number of fruits. Weight of fruit was positively correlated with both fruit length and yield. Positive significant association was observed for number of fruits and fruit weight in the bhindi genotypes selected (Sivanandan, 2003).

Correlation studies in the selected bhindi genotypes revealed that fruit yield plant^{-1} have significant and positive correlation with number of branches plant^{-1}, number of ridges fruit^{-1}, length of fruit and fruit weight. Significant negative correlation of fruit yield plant^{-1} was recorded with plant height, number of days taken for first pod setting, fruit volume, shape index and longevity of tenderness (Patro and Ravisankar, 2004).

Ahiakpa *et al.* (2006) observed a positive correlation between total fruit production and first fruit producing node, first flowering node and first fruit producing node and number of fruits plant $^{-1}$ and girth of stem in an experiment including thirty accessions of okra.

The evaluation fifteen genotypes of okra revealed that the trait yield plant^{-1} was significantly and positively correlation with number of fruits plant^{-1}, height at flowering, fruit girth and 100-seed weight (Akinyele and Osekita, 2006).

The fruit yield was significant and positively correlated with fruit length and average fruit weight. Thus, the fruit yield in bhendi can be improved by selecting for higher fruit length, fruit girth and average fruit weight simultaneously (Mehta *et al.,* 2006).

Significant differences were observed among the segregating population of ladies finger for pods and branch, seeds pod^{-1}, inter node distance, seeds per ridge, branch length, height at flower bud initiation and height at flowering. A positive correlation was recorded for the number of pods plant^{-1} and seed weight, height at maturity, ridges per pod and seeds per ridge (Adeniji and Aremu, 2007).

Fruit yield in okra had significant positive genotypic and phenotypic correlations with number of fruits plant^{-1}, height of plant and length of fruit. Significant positive genotypic and phenotypic associations was observed by yield plant^{-1} with number of fruits plant $^{-1}$, plant height and fruit length. Which means yield improvement in okra can be made by selecting these characters. Similarly, fruit girth exhibited positive and significant genotypic and phenotypic correlations with number of branches plant^{-1}, internodal length and fruit length (Singh *et al.,* 2007).

Significant positive correlations were recorded between yield plant^{-1} with plant height, internodal length, flowering nodes plant^{-1}, fruits plant^{-1}, branches plant^{-1}, weight of fruit, girth of fruit and length of fruit. Simple selection can be made in okra for effective improvement of these traits (Sengupta and Verma, 2009).

Guddadamath *et al.* (2011) did correlation analysis in three populations of the okra using three different varieties. During selection process in segregating

populations, characters like number of fruits plant $^{-1}$, fruit weight and number of branches plant^{-1} exhibited significant positive association with fruit yield plant^{-1}.

Duggi (2012) evaluated various okra genotypes and reported that the yield plant^{-1} was significantly and positively correlated with number of fruits plant $^{-1}$, fruit weight, and fruit girth at genotypic level. Number of fruits plant $^{-1}$ had highest positive correlation with yield plant^{-1} followed by fruit girth and fruit weight. Days to 50 per cent flowering was negatively associated with yield plant^{-1}. On the other hand, the characters viz., plant height, duration and fruit length was not correlated with yield plant^{-1} at genotypic level. Plant height showed significant positive correlation with duration both at genotypic and phenotypic levels. Correlation analysis also revealed that, positive correlation of number of fruits plant^{-1} with fruit girth and negative correlation with fruit weight both at phenotypic and genotypic levels. Fruit weight in turn was found to be positively correlated with fruit length both at phenotypic and genotypic levels.

The correlation between height of plant at maturity, fruit width, number of seeds pod^{-1} and number of fruits plant^{-1} with seed weight plant^{-1} and pod weight plant^{-1} of twenty nine okra accessions suggests that simple selection of these characters will lead to high seed and fruit yield in okra (Nwangburuka *et al.,* 2012).

Investigations on elite F_5 progenies of okra along with a check variety, Varsha Uphar for studying the genetic variability and correlation of yield contributing characters in the late segregating generations revealed that number of branches plant^{-1}, numbers of seed fruit^{-1}, and fruit yield showed moderate heritability, indicating that they can be selected through simple selection (Sharma *et al.,* 2012).

Mogili *et al.* (2013) conducted a study to identify good cultures of okra with desirable characters and yellow vein mosaic resistance. Correlation analysis revealed

that yield plant^{-1} displayed positive genotypic association with length of fruit and number of fruits plant $^{-1}$

Highly significant variation in all the okra genotypes was observed for characters like number of fruits plant^{-1}, days to pod formation, number of branches plant^{-1}, number of leaves plant^{-1}, fruit length and girth was observed. Genotypic correlation coefficient was significant between a pair of characters indicate their genetic relationship (Simon *et al.,* 2013).

Evaluation in fifty okra genotypes revealed that yield plant^{-1} exerted highly significant and negative association with length of internode as well as positive association with number of fruit plant^{-1} (Umesh *et al.,* 2014).

High positive correlation was observed between number of fruits plant $^{-1}$ and yield plant^{-1}. Significant positive correlations was also noticed between plant height and number of fruits plant $^{-1}$ in the twenty five bhindi genotypes evaluated (Ahamed *et al.,* 2015).

The role of environmental factors in the yellow vein mosaic incidence and population of whiteflies (*Bemesia tabaci)* was estimated on commercial varieties of okra. High humidity with low temperature was observed to have increased the disease severity and whitefly population. The YVMV incidence increased with the rise in temperature and as the relative humidity increases, whitefly population was also increased drastically (Ali *et al.,* 2005).

Yield plant^{-1} was significantly and positively correlated with plant height, and number of fruits plant^{-1} while evaluating twenty six genotypes of bhindi (Archana *et al.,* 2015).

If the genotypic correlation coefficient is found to be higher than the corresponding phenotypic value, it indicates that the particular trait is less influenced by the environment (Sharma and Prasad, 2015).

2.4 PATH ANALYSIS

Among the eleven characters studied in okra, the highest indirect effect was observed through number of fruits plant^{-1} but was negative. The lowest indirect effect was observed through fruit length. Minimum positive indirect effect was exerted through plant duration and minimum through number of fruit. Number of fruits plant^{-1} had a positive direct effect with yield. The highest negative indirect effects were observed through plant duration. The highest positive indirect effect was manifested through fruit girth (Sivanandan, 2003).

Path analysis calculated in seventeen genotypes of bhindi revealed high positive direct effect for weight of fruit, length of fruit, number of ridges, germination percentage, height of plant and number of branches plant^{-1}. A maximum negative direct effect was recorded in fruit weight via number of ridges whereas a maximum negative direct effect was recorded in fruit weight via fruit length (Patro and Ravisankar, 2004).

The highest direct effect towards yield was contributed by fruit girth and fruit length. Hence, the trait yield plant^{-1} in okra can be improved by making selection for these traits (Mehta *et al.,* 2006).

In the evaluation of different bhindi genotypes, the character number of fruits plant^{-1} contributes much to yield since it shows highest genotypic and phenotypic direct effect followed by plant height. Plant height showed the highest genotypic and phenotypic indirect effect on yield followed by fruit length and internodal length. The direct effects of other characters irrespective of their positive or negative contribution were low. Thus, selection can be done for genotypes having more fruit number and branches plant^{-1} (Singh *et al.,* 2007).

Alake *et al.* (2012) evaluated twenty five genotypes of okra for sixteen plant characters and studied variance, correlation and path analyses. The study suggested

that number of fruits plant^{-1} exhibited a high positive direct effect on fruit yield and selection for number of fruits plant^{-1} was the best for improving fruit yield.

Das *et al.* (2012) evaluated okra genotypes for various statistical studies for two seasons. The study revealed that for improving yield, more weightage must be given to selection based on number of fruits plant $^{-1}$ and fruit weight.

The path analysis in fifty two genotypes of okra revealed height of plant, number of branches plant^{-1}, number of first fruiting node, length of fruit, width of fruit and number of fruits plant $^{-1}$ at positive direct effect on yield plant^{-1}. The above finding shows that ideal plant with length of internode, number of fruit plant^{-1}, plant height, length of fruit might be help in improving yield plant^{-1} in okra for formulating desire plant with high yield with superior marketable character (Umesh *et al.,* 2014).

The characters like number of seeds plant^{-1}, number of fruits plant^{-1} showed a positive direct effect towards yield in okra (Ahamed *et al.,* 2015).

The path coefficient analysis showed the presence of very high direct positive effect of fruits plant^{-1}, weight of fruit, height of plant and on yield plant^{-1}. Hence, these characters could be relied upon for selection of high yielding genotypes in okra. The direct effect of fruit length as well as fruit girth on yield through fruit weight were also found to be positive, indicating their importance in exercising selection (Rajkumar and Sundaram, 2015).

The character which showed indirect effects was height of plant through number of fruits plant^{-1}. Positive and negative indirect effect was observed through weight of fruit. The residual effect was estimated to be about 98.82 per cent which indicated that the characters selected for study were enough to explain the variability in yield plant^{-1} (Sharma and Prasad, 2015).

2.5 YELLOW VEIN MOSAIC VIRUS DISEASE

Considering the overall segregating ratios, it could be hypothesized that the inheritance of tolerance is quantitative, with possibly two major factors, and dependent on genes present. The oligogenic resistance in some crops against viruses and the hypothesis that gene dosage dependent resistance is incompletely dominant. As the tolerance of IPSA Okra 1 is assumed to be gene dosage dependent, it might be a symptomless carrier type (Ali *et al.,* 2000).

Batra and Singh in the year 2000 screened okra genotypes during two successive years which included both hybrids and open pollinated ones and revealed that heavy incidence of yellow vein mosaic incidence was observed during summer season.

Maximum rate of yellow vein mosaic virus disease development in okra was recorded between 35-45 DAS, irrespective of varieties in both the years. Initially there was increasing trend and thereafter declining. The YVMV dissemination rate was more during 35-50 DAS which must be supplemented with systemic insecticide to reduce whiteflies population and thereby reducing the disease severity and finally good harvest could be obtained (Bhagat *et al.,* 2001).

Twelve lines of okra were screened for YVMV disease resistance and found that two genotypes were found to be resistant and other four lines showed fairly high degree of tolerance. The disease incidence ranged between 10.00 to 21.25 per cent. The rest of the six lines were found to be highly susceptible approximately 80-100 per cent disease incidence (Rashid *et al.,* 2002).

Prabhu *et al* (2007) conducted an experiment to identify the source of resistance to okra yellow vein mosaic virus in Maharashtra. The study reported that that YVMV in was directly correlated with atmospheric temperature, relative humidity and whitefly population.

The percent incidence of okra yellow vein mosaic virus disease ranged from 0 to 92.45 per cent in different germplasm lines. Six genotypes were completely free and did not produce any symptoms of OYVMV. These six germplasm lines were also screened under artificial inoculation using viruliferous whiteflies under controlled conditions in the glass house. The inoculated plants of these six genotypes were completely devoid of symptoms thereby confirming absence of OYVMV. Hence these were found resistant to OYVMV under artificial inoculation conditions also. These lines were not found to be symptomless carriers of this disease (Mehra *et al.,* 2008).

In the year 2010, Fajinmi and Fajinmi suggested that the bhindi fields must be protected up to at least twenty one days after emergence from the attack from whiteflies for satisfactory yields and yield loss can be reduced by 25-50 per cent.

Benchasri (2011) reported moderate resistance to yellow vein mosaic disease for one variety when he evaluated fifteen valuable accessions of okra.

Deshmukh and co-workers (2011) conducted an experiment with thirty five okra lines and reported that yellow vein mosaic incidence varies from season to season and found to be higher in summer than kharif. Hence, prominent variation is observed due to environmental conditions.

Kishor (2012) conducted a line x tester analysis in okra, and the hybrids obtained showed high yield and resistance to yellow vein mosaic disease.

The fifty susceptible okra seedlings when inoculated with the virus through vector transmission reproduced similar symptoms that were noticed in the field. The symptoms were observed within fifteen days after inoculation and plant showed stunted nature in the later period of crop growth. Vector transmission on healthy okra plants could not reproduce the symptom (Venkataravanappa *et al.,* 2013).

Materials and Methods

3. MATERIALS AND METHODS

The present study entitled "Evaluation of superior cultures for yield and yellow vein mosaic resistance in okra (*Abelmoschus esculentus* (L.) Moench) consisted of field evaluation of selected cultures as well as the confirmatory experiment for disease resistance.

3.1 EXPERIMENTAL SITE

The field evaluation was conducted in the Instructional Farm, College of Agriculture, Vellayani and the confirmatory study for the yellow vein mosaic disease resistance was done under controlled condition i.e. in the glass house of the Department of Plant Pathology, College of Agriculture, Vellayani during 2015-2016.

3.2 EXPERIMENTAL DESIGN

Fifteen genotypes were raised in the field along with two check varieties, Varsha Uphar and Kiran during summer, 2015. The experiment was laid out in Randomized Block Design (RBD) with three replications with spacing of 60 x 30 cm with twenty five plants per treatment per replication. The yellow vein mosaic resistance was scored at three stages of crop growth viz. 30 days after sowing (30 DAS), 50 days after sowing (50 DAS) and 70 days after sowing (70 DAS), by using the rating scale (0-5) developed by Rajamony *et al.* (1990). Also, the vector population and number of leaves with disease symptoms were recorded from first, third and fifth leaves at the above three stages.

3.3 EXPERIMENTAL MATERIALS

Fifteen superior cultures developed from the project entitled "Development of high yielding varieties resistant to yellow vein mosaic

Plate 1. General view of the experimental plot

disease from segregating generations in okra (*Abelmoschus esculentus* (L.) Moench)" funded by the ICAR/ DARE central 100 crore special grant project were used as study material for the present study. The superior cultures include VLYA 1, VLYA 2, VLYA 3, VLYA 4, VLYA 5, VLYA 6, VLYA 7, VLYA 8, VLYA 9, VLYA 10, VLYA 11, VLYA 12, VLYA 13, VLYA 14 and VLYA 15.

3.4 CULTURAL PRACTICES

The field was prepared thoroughly to fine tilth by ploughing, harrowing, clod crushing and leveling. FYM @ 12t/ ha was applied at the time of land preparation and then ridges and furrows were prepared. Ridges were taken 60 cm apart with a height of about 15 cm. Each culture was planted in a row at a distance of 30 cm between plants. Seeds were dibbled at the rate of two to three seeds per hill. After germination and plant establishment, a single healthy plant was maintained at each hill by means of thinning. All other cultural practices were done as per the package of practices recommendation of KAU (2011).

3.5 RECORDING OF OBSERVATIONS

Among the twenty five plants in a row, fifteen were selected from each replication based on their competitiveness. The biometric observations were taken from these selected plants and their mean were recorded for further statistical analysis. The observations were recorded for the following characters

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3.5.1 Biometric Characters

3.5.1.1 Days to 50 Per cent Flowering

The number of days taken for the flowering of 50 per cent of the plants in a row was counted and the mean values were recorded.

3.5.1.2 Number of Fruits Plant^{-1}

The total number of fruits harvested from each plant was counted and the mean was recorded.

3.5.1.3 Fruit Weight (g)

The total weight of fruits of five randomly selected plants was computed and the average was recorded in grams.

3.5.1.4 Fruit Length (cm)

The length of the fruits harvested from each plant was measured in centimeters from the tip to base of the fruit and the mean was recorded.

3.5.1.5 Fruit Girth (cm)

The girth at the middle of the fruit was measured in centimeters and the mean was calculated.

3.5.1.6 Yield Plant^{-1} (g)

The green fruit weight obtained in each harvest was recorded and expressed in grams.

3.5.1.7 Plant Height (cm)

The height of the plant was measured in centimeters from the ground level to the tip of the plant at final harvest using a meter scale and the mean value was expressed.

3.5.1.8 Duration (days)

The number of days from the date of sowing to the final harvest was counted for each observational plant and the mean was calculated.

3.5.2 Pest and Disease Incidence

3.5.2.1 Scoring for YVM Disease

The scoring for YVMV disease incidence was recorded from each of the selected plants based on the characteristic symptoms on the leaves, fruits and stem. Based on the 0-5 disease rating scale (Table 1) proposed by Rajamony *et al.* (1990), the plants were screened as highly resistant, resistant, medium resistant, medium susceptible, susceptible and highly susceptible. The observations were taken at 30, 50 and 70 DAS in the field.

Based on the score obtained, the vulnerability/ severity index (V.I.) was also worked out. The severity index was calculated based on the equation suggested by Sibernagel and Jafri (1974).

$$\text{Vulenerability Index (V.I.)} = \frac{[0n_0 + 1n_1 + 2n_2 + 3n_3 + 4n_4 + 5n_5] \times 100}{n_t\,(n_c - 1)}$$

n_0, n_1,..., n_5 = Number of plants in category 0, 1,….., 5

n_t = Total number of plants

n_c = Total number of categories

Table 1. Disease rating scale

Scale	Description	Category
0	No symptoms	Highly Resistant (HR)
1	Slight vein clearing, very light mottling of light and dark green colour in younger leaves	Resistant (R)
2	Vein thickening and first-chlorosis	Medium Resistant (MR)
3	Yellowing of leaves (chlorosis of leaves, fruit and stem)	Medium Susceptible (MS)
4	Distortion of leaves	Susceptible (S)
5	Stunting of the plant with negligible or no flowering and fruiting	Highly Susceptible (HS)

Table 2. Fruit and shoot borer rating scale

Score	Category
0	Immune
1-5	Resistant
6-15	Moderately Resistant
16-30	Moderately Susceptible
>30	Susceptible

3.5.2.2 Scoring for Fruit and Shoot Borer

The number of fruits damaged in each line was counted and was expressed as percentage value. The scoring for bhindi fruit and shoot borer for various genotypes were done based on the scale (Table 2) given by Gupta and Yadav (1978).

3.5.2.3 Scoring for Other Diseases, if Any

The seventeen genotypes were screened for various diseases affecting the okra plants.

3.5.2.4 Number of Whiteflies on Leaves

The number of whiteflies (*Bemesia tabaci*) was recorded by taking observations from the first, third and fifth leaves of the plant during 30, 50 and 70 DAS of the crop. The total population of whiteflies in the lower side of the leaves in each of the selected plants was counted and means were recorded.

3.6 CONFIRMATORY STUDY

Among the fifteen genotypes evaluated in the field, ten were selected based on high yield and disease resistance and were subjected to confirmatory study in the glass house. The vector and graft transmission experiments were carried out for further screening of resistance to *Bhindi yellow vein mosaic virus* (BYVMV). The vulnerability (severity) index of each culture was recorded and grouped under different categories based on the disease rating scale developed by Rajamony *et al.* (1990).

Plate 2. Whiteflies collected in test tubes

Plate 3. Whiteflies fed with fresh infected YVMV disease

3.6.1 Vector Transmission

The selected ten cultures were sown in poly bags filled with potting mixture containing soil, sand and compost in the ratio 2:1:1 respectively with three replications each. At the two leaf stage, the viruliferous *Bemesia tabaci* at the rate of 10-15 whiteflies per plant were inoculated. The inoculated plants were then kept in insect proof cages and were transferred to the glass house for observation of symptom expression.

3.6.1.1 Maintenance of Whitefly Culture

The whitefly culture of *Bemesia tabaci* was initially maintained in brinjal (*Solanum melongena*). The brinjal plants were raised in poly bags filled with the potting mixture 2:1:1 ratio of soil, sand and compost respectively and these plants were introduced into cages. These cages were maintained at a temperature of 28 to 30 ^{0}C in an insect proof glass house. As a source of vector, the whitefly population colonized under the leaves of these brinjal plants was taken.

3.6.1.2 Collection of Whiteflies

An aspirator made of glass tube with the dimensions 30 cm x 0.5 cm x 40 cm was used to collect the whiteflies and were blown into the test tubes. A starvation period of 3-4 h was given to the collected whiteflies. The disease free whiteflies were used for further transmission studies.

3.6.1.3 Raising of Healthy Okra Seedling

The ten cultures selected from the field experiment were grown in poly bags filled with potting mixture of soil, sand and compost in 2:1:1 the ratio. Three replications of each were planted in a staggered manner. These plants were then kept in insect proof cages.

Plate 4. Vector transmission in the glass house

3.1.1.1 Culture of Bhindi Yellow Vein Mosaic Virus

Naturally infected bhindi plants were selected from the field of Instructional Farm, College of Agriculture, Vellayani. The leaves and twigs of these yellow vein mosaic disease affected bhindi plants were fed to the healthy uninfected whiteflies in the test tubes. After an acquisition period of 24 h, the whiteflies were released into eight day old (two leaf stage) healthy seedlings of selected bhindi cultures. A 24 h inoculation access was given. The *bhindi yellow vein mosaic virus* culture was maintained throughout the experiment by frequently inoculating the healthy plants with viruliferous whiteflies (*Bemesia tabaci*).

3.1.2 Graft Transmission

The cultures which were found to be resistant to yellow vein mosaic disease after the vector transmission studies were subjected to graft transmission studies. Here, the selected genotypes were taken as the root stock. The diseased scion from the YVMV infected plants were cut into 'V' shaped wedge. A vertical cut was made in the healthy plant and the diseased scion was wedge grafted into the healthy root stock. The grafted junction was tied using a polythene strip and the scion was covered using a polythene bag. After the grafting, the inoculated plants were kept in a cool place in the glass house for the symptom expression. Further, the new leaves grown from the root stock were observed for the presence or absence of the YVM disease symptoms. This was taken as a criterion for the confirmation of resistance of the particular cultures.

Plate 5. Graft transmission in the glass house

3.7 STATISTICAL ANALYSIS

3.7.1 Analysis of Variance (ANOVA)

The biometric observations recorded from the field evaluation were subjected to analysis of variance (Panse and Sukhatme, 1985) for the comparison among various cultures and to estimate variance components.

The significance of mean sum of squares for each character was tested against the corresponding error degrees of freedom using F test (Fisher and Yates, 1967).

$$\text{Standard Error of Mean (SE(m))} = \sqrt{\frac{MSE}{r}}$$

Where,

MSE = Mean sum of squares of error

r = Number of replications

If the treatments were found to be significant, critical difference will be calculated for making comparison among the treatments.

$$\text{Critical Difference (CD)} = t_{\alpha} \sqrt{\frac{2MSE}{r}}$$

Where, t_{α} is the student's't' table value at error degrees of freedom, 'α' is the level of significance, 'MSE' is the mean sum of squares of error and 'r' represents the number of replications.

3.7.2 Estimation of Genetic Parameters

3.7.2.1 Genetic Components of Variance.

For each character, the phenotypic and genotypic components of variance were estimated by equating the expected value of mean squares (MS) to the respective variance components (Jain, 1982). The variance components were estimated based on this. It is as follows:

i. Genotypic variance (GV)

$$GV = \frac{MST - MSE}{r}$$

ii. Environmental variance (EV)

$$EV = MSE$$

iii. Phenotypic variance (PV)

$$PV = GV + EV$$

Where, MSE=Mean sum of error, MST= Mean sum of treatments.

3.7.2.2 Coefficients of Variation

The components namely, phenotypic, genotypic and environmental variances were used for estimation of coefficient of variation at both phenotypic and genotypic levels for all the traits were computed by following the formula as suggested by Singh and Chaudhary (1985).

i. Phenotypic coefficient of variation (PCV)

$$PCV = \frac{\sqrt{PV}}{\bar{x}} \times 100$$

ii. Genotypic coefficient of variation (GCV)

$$GCV = \frac{\sqrt{GV}}{\bar{x}} \times 100$$

$\bar{x}$ = The mean of each character estimated over all the treatments.

The PCV and GCV was classified by Subramanian and Menon (1973) as,

Low - (<10%)
Moderate - (10-20%)
High - (>20%)

3.7.2.3 Heritability

For each trait, broad sense heritability (H^2) was calculated as the ratio of genotypic variance to phenotypic variance and expressed as percentage (Allard, 1999).

Heritability (H^2) = $\frac{GV}{PV}$ x 100

Heritability was categorized by Robinson *et al.* (1949) as

Low - (<30%),
Moderate - (31-60%)
High - (>60%)

3.7.2.4 Genetic advance

Genetic advance, which is the measure of genetic gain under selection, depends upon standardized selection differential, heritability and phenotypic standard deviation. The genetic advance was calculated by the method proposed by (Fehr *et al.,* 1987)

Genetic advance (GA) = $k.H^2 \sqrt{PV}$

Where k is the standardized selection differential (2.06 at 5% level of selection)

Genetic advance as percentage mean was estimated using the formula given by Johnson *et al.* (1955).

GA as percentage of mean = $k.H^2 \frac{\sqrt{PV}}{\bar{x}} \times 100$

Genetic advance (% mean) was categorized as per the suggestion of Al-Jibouri *et al.* (1958).

Low	- (0-10%)
Moderate	- (10-20%)
High	- (>20%)

3.7.3 Correlation analysis

Phenotypic, genotypic and environmental correlation coefficients were calculated using the respective variances and co-variances of the characters which showed significant variation in the ANOVA as suggested by Singh and Choudhary (1985).

Phenotypic correlation coefficients, $r_P = \frac{COV_P(X,Y)}{\sqrt{PV(X).PV(Y)}}$

Genotypic correlation coefficient, $r_G = \frac{COV_G(X,Y)}{\sqrt{GV(X).GV(Y)}}$

Where, COV_P (X,Y) and COV_G (X,Y) respectively denotes the phenotypic and genotypic co variances between the two traits X and Y. PV (X) and GV (X) denotes the phenotypic and genotypic variance for X and PV (Y) and GV (Y) indicate the phenotypic and genotypic variance for Y respectively.

3.7.4 Path analysis

Path coefficient analysis partitions the genotypic correlation coefficients into direct and indirect effects. Path coefficient suggested by Wright (1960) was applied to study the cause and effect relationship of yield and yield attributes.

The set of equations obtained from the path diagram were solved to get the information on the direct and indirect contribution of the causal factors on the effect.

The residual effect is computed as $R = 1- (r_{Y1}.P_{Y1} + r_{Y2}.P_{Y2} +\ldots\ldots+ r_{Yn}.P_{Yn})$

$$R = 1- \sum(r_{Yi}.P_{Yi})$$

Where 'r' is the correlation between various traits and the direct effect of X_1 on Y is P_{12} and so on. Indirect effect of X_1 on Y depends on other correlated factors.

The direct and indirect effects were classified based on the scale given by Lenka and Mishra (1973)

>1.0	- Very high
0.3-0.99	- High
0.2-0.29	- Moderate
0.10-0.19	- Low
0.00-0.09	- Negligible

Plate 6. Yellow vein mosaic disease incidence in the field

Results

4. RESULTS

The current investigation entitled “Evaluation of superior cultures for yield and yellow vein mosaic resistance in okra (*Abelmoschus esculentus* (L.) Moench)” was conducted in the Department of Plant Breeding and Genetics, College of Agriculture, Vellayani. The first experiment was the field evaluation of selected genotypes and was done at the Instructional Farm, College of Agriculture, Vellayani. The second experiment constituting the confirmatory studies on the resistance to yellow vein mosaic disease was done in the Department of Plant Pathology, College of Agriculture, Vellayani. The biometric observations and scores were recorded for further statistical analysis.

4.1 EVALUATION OF SUPERIOR CULTURES OF OKRA

4.1.1 Mean Performance

The mean performance of fifteen superior genotypes and two check varieties namely Varsha Uphar and Kiran for the following observations were recorded in Table 3.

4.1.1.1 Days to 50 Per cent Flowering

The days to 50 per cent flowering ranged between 38.33 and 43.00. The highest mean value for the character was observed in the check variety Kiran (43.00) and the lowest value of 38.33 was observed in VLYA 11. Among the seventeen genotypes studied, nine genotypes were having value less than the general mean of 40.82 days.

Table 3. Mean performance of okra genotypes for yield and yield components.

GENOTYPES	DFF	NFPP	FW	FL	FG	YPP	PH	DR
VLYA 1	40.33	16.87	20.86	16.89	4.65	349.56	125.41	92.07
VLYA 2	39.67	17.27	23.14	16.45	6.32	397.51	124.71	90.19
VLYA 3	42.33	12.67	21.39	14.85	5.58	270.63	109.78	91.71
VLYA 4	42.00	14.07	25.89	15.36	6.35	360.80	112.75	94.59
VLYA 5	40.67	16.20	23.75	15.85	5.56	383.87	119.71	91.33
VLYA 6	39.33	17.27	20.11	17.79	5.66	344.55	126.84	90.61
VLYA 7	39.67	16.80	19.06	16.74	4.62	318.20	124.88	89.86
VLYA 8	41.00	15.00	24.48	15.25	6.62	366.07	118.39	112.54
VLYA 9	42.33	11.87	30.83	13.85	4.86	363.99	107.04	94.12
VLYA 10	40.00	16.73	22.83	15.91	6.62	379.28	124.57	93.73
VLYA 11	38.33	19.73	20.11	17.15	6.54	396.40	130.75	90.14
VLYA 12	42.33	10.60	21.56	13.40	5.55	226.09	105.31	91.38
VLYA 13	39.67	17.27	21.69	15.89	5.52	373.71	126.66	90.51
VLYA 14	41.67	14.73	17.21	14.71	1.65	253.01	116.62	96.67
VLYA 15	39.67	17.67	21.59	17.08	6.43	380.72	126.16	90.18
Varsha Uphar	42.00	14.13	21.12	14.40	6.12	297.17	115.39	90.54
Kiran	43.00	9.80	20.34	13.61	5.16	197.90	98.76	101.09
MEAN	40.82	15.22	22.12	15.60	5.52	332.91	118.45	93.60
SE(m)	0.41	0.40	0.26	0.45	0.17	9.33	1.83	0.36
CD	1.17	1.15	0.74	1.28	0.48	26.89	5.27	1.04

DFF=Days to 50% flowering
NFPP= No. of fruits per plant
FW= Fruit weight (g)
FL= Fruit length (cm)
FG= Fruit girth (cm)
YPP= Yield per plant (g)
PH= Plant height (cm)
DR= Duration (days)

4.1.1.2 Number of Fruits Plant^{-1}

The mean number of fruits plant^{-1} ranged from 9.80 to 19.73 with highest value recorded by VLYA 11 and lowest by the check variety Kiran. Nine genotypes were having values greater than the general mean of 15.22.

4.1.1.3 Fruit Weight (g)

The mean weight of fruits showed wide range between 17.21 g and 30.83 g. Six genotypes had a mean fruit weight greater than the general mean value of 22.12 g. The genotype VLYA 9 had the maximum fruit weight of 30.83 g and the minimum was recorded by genotype VLYA 14 (17.21 g).

4.1.1.4 Fruit Length (cm)

The mean range exhibited for length of fruits by the various genotypes was between 13.40 and 17.79 cm. The genotype VLYA 6 had the longest fruit with 17.79 cm whereas the genotype VLYA 12 had the shortest fruit. Nine genotypes were having higher mean fruit length than the general mean of 15.60 cm.

4.1.1.5 Fruit Girth (cm)

The girth of the fruits ranged from 1.65 to 6.62 cm. The highest value was recorded for two genotypes namely VLYA 8 and VLYA 10 and the genotype VLYA 14 recorded the lowest value. Eleven genotypes were showing higher value for fruit girth than the general mean of 5.52 g.

4.1.1.6 Yield Plant^{-1} (g)

The mean values for yield plant^{-1} ranged from 197.90 to 397.51 g. The maximum value was observed for genotype VLYA 2 (397.51 g) and the lowest was for the check variety Kiran. Among the seventeen genotypes, eleven genotypes recorded higher yield plant^{-1} than the general mean of 332.91 g.

4.1.1.7 Plant Height (cm)

The height of the plant ranged between 98.76 and130.75cm. The maximum plant height was recorded by genotype VLYA 11 and the minimum was exhibited by Kiran. Nine genotypes were having the higher plant height than the general mean of 118.45 cm.

4.1.1.8 Duration (days)

The duration of plant ranged between 89.86 and 112.54 days. Highest mean value was recorded for genotype VLYA 8 and the lowest for genotype VLYA 7. Only six genotypes represented higher duration than the general mean of 93.60 days.

4.1.1.9 Scoring for YVM Disease

The number of leaves with disease symptoms in each genotype was recorded and presented as mean value in Table 4. The disease symptom during 30 DAS, 50 DAS and 70 DAS was observed from the first, third and fifth leaves and total mean was calculated. The mean value ranged between 0.00 and 2.18. The disease incidence was found to be more during the late stages i.e. 70 DAS of crop growth than during the early period. The genotypes VLYA5, VLYA11 and VLYA13 showed complete absence of disease symptoms during all the stages of crop growth. The genotypes VLYA 1, VLYA 2, VLYA 4, VLYA 5, VLYA 6, VLYA 10, VLYA 11, VLYA 12, VLYA 13, VLYA 14, VLYA 15, VLYA 16 and Varsha Uphar did not show any disease symptom during the early stages of growth. The maximum mean diseased leaves were observed in VLYA 3. Among the seventeen genotypes, nine genotypes showed mean diseased leaves lesser than the general mean of 1.14.

Table 4. Pest and disease incidence in okra genotypes.

GENOTYPES	Number of whiteflies on leaves				Fruit and shoot borer	Number of diseased leaves			
	30 DAS	50 DAS	70 DAS	MEAN		30 DAS	50 DAS	70 DAS	MEAN
VLYA1	1.07	1.49	0.69	1.49	0.19	0.00	0.82	0.89	0.57
VLYA2	0.49	0.22	0.15	0.22	0.00	0.00	0.13	1.00	0.38
VLYA3	0.91	0.89	1.00	0.89	0.05	0.73	2.67	3.13	2.18
VLYA4	1.40	1.04	1.18	1.04	0.00	0.00	0.00	2.20	0.73
VLYA5	0.69	0.78	0.62	0.78	0.04	0.00	0.00	0.00	0.00
VLYA6	0.69	1.11	0.62	1.11	0.15	0.00	1.80	2.17	1.32
VLYA7	2.09	1.16	0.55	1.16	0.27	0.47	2.29	2.87	1.87
VLYA8	1.22	1.22	1.36	1.22	0.24	1.47	2.02	2.87	2.12
VLYA9	1.04	0.40	1.68	0.40	0.09	1.07	2.27	2.73	2.02
VLYA10	0.76	1.73	0.69	1.73	0.12	0.00	1.67	1.93	1.20
VLYA11	0.98	0.96	0.80	0.96	0.00	0.00	0.00	0.00	0.00
VLYA12	1.44	0.76	1.04	0.76	0.23	0.00	1.80	2.93	1.58
VLYA13	0.38	0.53	0.29	0.53	0.00	0.00	0.00	0.00	0.00
VLYA14	1.07	0.38	1.29	0.38	0.00	0.00	2.47	2.60	1.69
VLYA15	1.11	0.96	0.96	0.96	0.03	0.00	0.40	0.55	0.32
Varsha Uphar	1.22	0.73	0.87	0.73	0.02	0.00	1.60	2.40	1.33
Kiran	2.09	1.36	1.02	1.36	0.20	0.33	2.60	3.13	2.02
SE(M)	---	---	---	0.80	0.98	---	---	---	0.28
CD	---	---	---	NS	NS	---	---	---	0.68

NS = Non Significant
DAS = Days After Sowing

4.1.1.10 Scoring for Fruit and Shoot Borer

The scoring for fruit and shoot borer of seventeen genotypes were done at 30 DAS, 50 DAS and 70 DAS and number of fruits damaged were recorded (Table 4). The general mean was found to be 0.10 and the range was from 0.00 to 0.27. The maximum fruit and shoot borer infestation was in the genotype VLYA 7 and the genotypes viz., VLYA 2, VLYA 4,VLYA 11, VLYA 13 and VLYA 14 were found to be completely devoid of fruit and shoot borer infestation. Ten genotypes were having a score less than the general mean. There was no significant difference among the genotypes for the character.

4.1.1.11 Scoring for Other Diseases, if Any

No other diseases were observed in the genotypes studied during the various stages of crop growth.

4.1.1.12 Number of Whiteflies on Leaves

The number of whiteflies on leaves was counted and the mean data is represented in Table 4. The number was found to be more during early crop growth period i.e. 30 DAS. All the studied genotypes were non-significant for the trait number of whiteflies on leaves. The general mean was found to be 1.09 and ten genotypes were found having lesser mean number of whiteflies on leaves than the general mean. The range of mean values obtained was 0.38 to 2.09. The highest number of whiteflies on leaves was observed in genotype VLYA 7 and Kiran whereas, the least number was observed in genotype VLYA 13.

4.1.2 Analysis of Variance

The ANOVA for the various biometric characters were calculated and recorded in Table 5. All the genotypes were found to be highly significant for all the characters at both 5 % and 1 % level.

Table 5. Analysis of variance for yield and yield components in okra genotypes.

Characters	Mean sum of squares		
	Genotypes	Replication	Error
Days to 50% flowering	5.59**	1.12	0.49
Number of fruits per plant	22.25**	0.14	0.48
Fruit weight (g)	27.84**	0.10	0.20
Fruit length (cm)	5.28**	0.08	0.60
Fruit girth (cm)	4.34**	0.05	0.08
Yield per plant (g)	11540.62**	90.88	261.32
Plant height (cm)	248.85**	8.90	10.03
Duration (days)	97.25**	1.19	0.39

*- Significant at 5% level
**- Significant at 1% level

4.1.2.1 Days to 50 Per cent Flowering

Maximum number of days for the flowering of fifty per cent of the plants in a line was noticed and found that the variety Kiran which was on par with the genotypes VLYA 3, VLYA 4, VLYA 9, VLYA 12 and Varsha Uphar and the minimum number of days for 50 per cent of the plants was shown by the genotype VLYA 11, which was on par with VLYA 6.

4.1.2.2 Number of Fruits Plant^{-1}

The genotype VLYA 11 showed the maximum number of fruits which was found to be highly significant from rest of the genotypes under study. One of the check varieties used, Kiran showed the lowest number of fruits plant^{-1} and was on par with the genotype VLYA 12.

4.1.2.3 Fruit Weight (g)

The weight of the fruits showed a wide range between the genotypes. The maximum fruit weight was noticed in VLYA 9 which was highly significant from the other genotypes. Similarly, the minimum weight for fruits was depicted by VLYA 14.

4.1.2.4 Fruit Length (cm)

The longest fruits were observed in the genotype VLYA 6 which was on par with VLYA 1, VLYA 7, VLYA 11 and VLYA 15. The genotype VLYA 12 showed the shortest fruit. Similar trend was followed by VLYA 9, Varsha Uphar and Kiran.

4.1.2.5 Fruit Girth (cm)

The genotype VLYA 8 was found to have the maximum fruit girth but was on par with VLYA 2, VLYA 4, VLYA 10, VLYA 11, VLYA 15 and Varsha Uphar and a the minimum girth for fruits were shown by VLYA 14.

4.1.2.6 Yield Plant^{-1} (g)

Among the seventeen genotypes, the highest yield plant^{-1} was recorded by VLYA 2 and was on par with VLYA 5, VLYA 10, VLYA 11, VLYA 13 and VLYA 15 and the least yield was observed by the check variety Kiran.

4.1.2.7 Plant Height (cm)

The genotype VLYA 11 with the maximum height, was found to be on par with VLYA 6, VLYA 13 and VLYA 15 whereas, the minimum height was noticed in Kiran.

4.1.2.8 Duration (days)

The longest duration for the crop was noticed for the genotype VLYA 8 and was highly significant from all the other cultures. The shortest duration was shown by genotype VLYA 7 which was on par with genotypes VLYA 2, VLYA 6, VLYA 7, VLYA 11, VLYA 13, VLYA 15 and Varsha Uphar.

4.1.3 Genetic Parameters

The various genetic parameters like GCV, PCV, heritability and genetic advance were calculated for different characters for all the seventeen genotypes and recorded in the Table 6.

Table 6. Estimation of genetic parameters.

Characters	Mean	Range	GV	PV	GCV (%)	PCV (%)	h^2 (%)	GA as % mean
		Min-Max						
Days to 50% flowering	40.82	38.33-43.00	1.70	2.19	3.19	3.63	77.52	5.79
Number of fruits per plant	15.22	9.80-19.73	7.26	7.74	17.70	18.28	93.81	35.32
Fruit weight (g)	22.12	17.21-30.83	9.21	9.41	13.72	13.87	97.89	27.97
Fruit length (cm)	15.60	13.40-17.79	1.56	2.16	8.01	9.41	72.45	14.05
Fruit girth (cm)	5.52	1.65-6.62	1.42	1.50	21.59	22.21	94.00	43.23
Yield per plant (g)	332.91	197.90-397.51	3759.77	4021.08	18.42	19.05	94.00	36.69
Plant height (cm)	118.45	98.76-130.75	79.61	89.64	7.53	7.99	89.00	14.62
Duration (days)	93.60	89.86-112.54	32.29	32.67	6.07	6.11	99.00	12.43

4.1.3.1 Days to 50 Per cent Flowering

The mean for the trait days to 50 per cent flowering for all the genotypes was obtained as 40.82. The GCV (3.19 %) and PCV (3.63 %) showed low values with only slight variation among them. A high value was observed for heritability (77.52 %) with low genetic advance as percentage mean.

4.1.3.2 Number of Fruits Plant^{-1}

The general mean of seventeen genotypes for the character number of fruits plant^{-1} was recorded as 15.22. Moderate GCV (17.70 %) and PCV (18.28 %) were obtained with high heritability (93.81 %) and high genetic advance (35.32 %).

4.1.3.3 Fruit Weight (g)

The minimum to maximum range of values for fruit weight among seventeen genotypes were calculated as 17.21 g and 30.83 g with a general mean of 22.12 g. Fruit weight showed a moderate GCV (13.72 %) and PCV (13.87 %) with only a slight variation. The heritability value was high (97.89 %) with a high genetic advance of 27.97 %.

4.1.3.4 Fruit Length (cm)

The general mean of fruit length was obtained as 15.60 cm. The GCV (8.01 %) and PCV (9.41 %) were found to be low but heritability (72.45 %) was high. The genetic advance was calculated to be moderate (14.05 %).

4.1.3.5 Fruit Girth (cm)

Fruit girth showed a general mean of 5.52 cm. The GCV and PCV obtained were high (21.59 % and 22.21 % respectively). Fruit girth showed high heritability of 94.00 % and the high genetic advance (43.23 %).

4.1.3.6 Yield Plant^{-1} (g)

The yield obtained in each plant was calculated and a minimum of 197.90 g and maximum of 397.51 g with a general mean of 332.91 g was obtained. Moderate values of GCV and PCV obtained were 18.42 % and 19.05 % respectively. Yield plant^{-1} showed a high heritability (94.00 %) coupled with high genetic advance (36.69 %).

4.1.3.7 Plant Height (cm)

The general mean obtained for plant height was 118.45 cm and the range obtained was 98.76 cm to 130.75 cm. Plant height showed a low GCV (7.53 %) and PCV (7.99 %). The heritability calculated was high (89.00 %) and the genetic advance is having a moderate value of 14.62 %.

4.1.3.8 Duration (days)

The general mean for duration was estimated as 93.60 days. GCV and PCV were low (6.07 % and 6.11 % respectively). Eventhough a very high heritability (99.00 %) value was obtained, a moderate genetic advance (12.43 %) was observed for crop duration.

4.1.4 Correlation Studies

The association of yield and yield contributing traits and resistance to yellow vein mosaic resistance was worked out. The genotypic and phenotypic correlation coefficients for the biometric characters and simple correlation for pest and disease incidence were worked out and presented in Tables 7, 8 and 9.

Table 7. Genotypic correlation coefficients for yield, its components and YVMV disease.

Characters	DFF	NFPP	FW	FL	FG	PH	DR	YVMVD	YPP
DFF	1								
NFPP	-0.9164**	1							
FW	0.2855*	-0.2597	1						
FL	-0.9044**	0.9499**	-0.3001*	1					
FG	-0.2895*	0.2186	0.3750**	0.2454	1				
PH	-0.9382**	0.9991**	-0.2881*	0.9690**	0.2029	1			
DR	0.3708**	-0.3458*	0.1902	-0.3766**	-0.0033	-0.3569*	1		
YVMVD	0.7669**	-0.7615**	0.0385	-0.6708**	-0.2697	-0.7187**	0.4434**	1	
YPP	-0.7607**	0.7697**	0.4107**	0.6935**	0.4942**	0.7459**	-0.1739	-0.7145**	1

DFF =Days to 50% flowering
NFPP = No. of fruits per plant
FW = Fruit weight (g)
FL = Fruit length (cm)
FG = Fruit girth (cm)
YPP = Yield per plant (g)
PH = Plant height (cm)
DR = Duration (days)
YVMVD = Yellow vein mosaic virus disease

*- Significant at 5% level
**- Significant at 1% level

4.1.4.1 Days to 50 Per cent Flowering

The character days to 50 per cent flowering recorded high significant negative effect with yield at both genotypic (-0.7607) and phenotypic (-0.6284) levels.

Among the inter-correlations studied, it was found that the trait had highly positive and significant effect with yellow vein mosaic virus resistance (0.7669 and 0.5840 respectively for both levels) and duration (0.3708 and 0.3314 respectively for both levels). Significant positive genotypic correlation was recorded for fruit weight (0.28550) at genotypic level.

The trait had high significant negative correlation with fruit length (-0.9044 and -0.7666), number of fruits plant^{-1} (-0.9164 and -0.8471) and plant height (-0.9382 and -0.8157) respectively for genotypic and phenotypic levels. Fruit girth recorded significant negative association with days to 50 per cent flowering at genotypic level (0.2855) only.

4.1.4.2 Number of Fruits Plant^{-1}

The number of fruits plant^{-1} was significantly and positively correlated with yield plant^{-1} at genotypic (0.7697) and phenotypic (0.7756) levels.

The number of fruits plant^{-1} was found to be positively correlated with fruit length (0.9499 and 0.8623) and plant height (0.9991 and 0.9665) respectively at genotypic and phenotypic levels highly significant and positive with.

A highly significant negative correlation was observed between number of fruits plant^{-1} and yellow vein mosaic disease both genotypically (-0.7615) and phenotypically (-0.7047). Similarly, a negative, but significant relation was observed between number of fruits plant^{-1} and duration (-0.3458 and -0.3318 respectively at genotypic and phenotypic levels).

Table 8. Phenotypic correlation coefficients for yield, its components and YVMV disease.

Characters	DFF	NFPP	FW	FL	FG	PH	DR	YVMVD	YPP
DFF	1								
NFPP	-0.8471**	1							
FW	0.2512	-0.2504	1						
FL	-0.7666**	0.8623**	-0.2501	1					
FG	-0.2464	0.2196	0.3585**	0.2229	1				
PH	-0.8157**	0.9665**	-0.2710	0.8236**	0.1893	1			
DR	0.3314*	-0.3318*	0.1897	-0.3220*	0.0001	-0.3300*	1		
YVMVD	0.5840**	-0.7047**	0.0392	-0.5046**	-0.2400	-0.6480**	0.4043**	1	
YPP	-0.6284**	0.7756**	0.4083**	0.6404**	0.4738**	0.7321**	-0.1648	-0.6520**	1

DFF =Days to 50% flowering
NFPP = No. of fruits per plant
FW = Fruit weight (g)
FL = Fruit length (cm)
FG = Fruit girth (cm)
YPP = Yield per plant (g)
PH = Plant height (cm)
DR = Duration (days)
YVMVD = Yellow vein mosaic virus disease

*- Significant at 5% level
**- Significant at 1% level

4.1.4.3 Fruit Weight (g)

The character fruit weight was found to have high positive significant correlation with yield plant^{-1} both genotypically (0.4107) and phenotypically (0.4083).

The inter-correlation studies of fruit weight revealed that the character fruit girth was highly significantly and positively correlated (0.3750 and 0.3585 respectively at genotypic and phenotypic levels) with fruit weight.

Significant negative correlation was seen between fruit weight and fruit length (-0.3001) and fruit weight and plant height (-0.2881) only genotypically.

4.1.4.4 Fruit Length (cm)

The direct correlation of fruit length with yield was found to be highly significant and positive (0.6935 and 0.6404 respectively at genotypic and phenotypic levels).

The genotypic as well as the phenotypic inter-correlation between fruit length and plant height (0.9690 and 0.8236) was positive and highly significant.

Highly significant and negative correlation was noticed between fruit length with duration at genotypic (-0.3766) level whereas, this was found to be negative and significant at phenotypic (-0.3220) level. The inter-correlation of fruit length with yellow vein mosaic disease was also found to be highly significant and negative at both genotypic (-0.6708) and phenotypic (-0.5046) levels.

4.1.4.5 Fruit Girth (cm)

A highly significant and positive correlation was observed between fruit girth and yield plant^{-1} (0.4942 and 0.4738 respectively at genotypic and phenotypic levels).

4.1.4.6 Plant Height (cm)

Plant height was highly significantly and positively correlated with yield plant^{-1} both (0.7459 and 0.7321 respectively at genotypic phenotypic levels).

A highly significant negative correlation was noticed between height of plant and yellow vein mosaic disease (genotypic and phenotypic levels respectively as -0.7187 and 0.6480). A significant and negative inter-correlation was noticed for plant height and duration (-0.3569 and -0.3300 respectively for genotypic and phenotypic levels).

4.1.4.7 Duration (days)

The character duration was found to be correlated with yellow vein mosaic disease highly significantly and negatively at genotypic (0.4434) and phenotypic (0.4043) levels.

4.1.4.8 Scoring for YVM Disease

A highly significant and negative correlation was observed between yellow vein mosaic disease and yield plant^{-1}. Yellow vein mosaic disease incidence was positively correlated and highly significant both at 5 % and 1 % level with number of whiteflies on leaves and fruit and shoot borer incidence.

4.1.4.9 Scoring for Fruit and Shoot Borer

Fruit and shoot borer incidence was positively correlated with both yellow vein mosaic disease incidence and number of whiteflies on leaves. The correlation between fruit and shoot borer with yellow vein mosaic disease incidence was highly significant both at 5 % and 1 % levels whereas, it was significant with number of whiteflies on leaves at 5 % level only.

Table 9. Simple correlation of pest and disease incidence.

Characters	Fruit and shoot borer	Number of whiteflies on leaves	Yellow vein mosaic virus disease incidence	Yield per plant (g)
Fruit and shoot borer	1			
Number of whiteflies on leaves	0.5929**	1		
Yellow vein mosaic virus disease incidence	0.6101**	0.6841**	1	
Yield per plant (g)	-0.8756**	-0.6003**	-0.7697**	1

*-Significant at 5% level
**-Significant at 1% level

4.1.4.10 Number of Whiteflies on Leaves

The number of whiteflies on leaves was positively correlated highly significantly both at 5 % level and 1 % level with yellow vein mosaic virus disease. It was also found to be positively correlated with fruit and shoot borer incidence but was significant only at 5 % level.

4.1.5 Path Analysis

The direct dependence among the set of characters were analyzed using the path analysis. Here, the dependence of yield plant^{-1} on all the other biometric characters was estimated. The direct and indirect effects of various characters to yield plant^{-1} are recorded in Table 10. The biometric characters viz., days to 50 per cent flowering, number of fruits plant^{-1}, fruit weight, fruit girth, fruit length, fruit girth and duration, having high correlation with yield plant^{-1} were selected for the analysis.

4.1.5.1 Days to 50 Per cent Flowering

Days to 50 per cent flowering represented a negative and moderate (-0.1967) direct effect towards yield plant^{-1}.

Days to 50 per cent flowering was having a high but negative indirect effect through number of fruits plant^{-1}. Positive and low indirect effect to yield plant^{-1} was through fruit weight (0.1767). Positive and negligible indirect effect was exhibited through fruit length (0.0781) and duration (0.0172).

A negative and negligible indirect effect was shown through fruit girth (-0.0114) and yellow vein mosaic virus (-0.0574).

Table 10. Path coefficient analysis.

Characters	Days to 50% flowering	Number of fruits per plant	Fruit weight (g)	Fruit length (cm)	Fruit girth (cm)	Duration (days)	Yellow vein mosaic virus	Correlation coefficient of yield
Days to 50% flowering	-0.1967	0.1999	-0.0562	0.1976	0.0569	-0.0729	-0.1509	-0.7607
Number of fruits per plant	-0.7671	0.7548	-0.1960	0.7170	0.1650	-0.2610	-0.5748	0.7697
Fruit weight (g)	0.1767	-0.1607	0.6188	-0.1857	0.2321	0.1177	0.0238	0.4107
Fruit length (cm)	0.0781	-0.0738	0.0233	-0.0777	-0.0191	0.0293	0.0521	0.6935
Fruit girth (cm)	-0.0114	0.0086	0.0147	0.0096	0.0393	-0.0001	-0.0106	0.4942
Duration (days)	0.0172	-0.0160	0.0088	-0.0174	-0.0002	0.0463	0.0205	-0.1739
Yellow vein mosaic virus	-0.0574	0.0569	-0.0029	0.0502	0.0202	-0.0332	-0.0748	-0.7145
Residual effect	0.0664							

4.1.5.2 Number of Fruits Plant^{-1}

A positive and high direct effect was shown by number of fruits plant^{-1} (0.7548) towards yield plant^{-1}.

A positive low indirect effect (0.1999) was shown through days to 50 per cent flowering. But a positive negligible indirect effect was shown through fruit girth (0.0086) and yellow vein mosaic virus disease incidence (0.0569.

Number of fruits plant^{-1} showed a negative and low indirect effect through fruit weight (-0.1607).

4.1.5.3 Fruit Weight (g)

High direct effect towards yield plant^{-1} of 0.6188 was observed for fruit weight.

A positive but negligible indirect effect was contributed by fruit weight via fruit length (0.0233), fruit girth (0.0147) and duration (0.0088). A negative but low indirect effect was shown through number of fruits plant^{-1} (-0.1960).

Fruit weight showed a negative and negligible indirect effect through days to 50 per cent flowering (-0.0562) and yellow vein mosaic virus disease incidence (-0.0029).

4.1.5.4 Fruit Length (cm)

The direct effect of fruit length was found to be negative and negligible (-0.0777).

A positive and high indirect effect was shown through number of fruits plant^{-1} (0.7170), positive but low indirect effect was exhibited through days to 50 per cent flowering (0.1976) and a positive and negligible indirect effect was felt through

fruit weight (0.0096) and yellow vein mosaic virus disease incidence (0.0502).

Fruit length showed a negative and low indirect effect through fruit weight (-0.1857) and a negative and negligible indirect effect was observed for fruit length through duration (-0.0174).

4.1.5.5 Fruit Girth (cm)

The character fruit girth contributed only a positive negligible direct effect (0.0393) towards yield plant^{-1}.

Fruit girth showed a moderate and positive indirect effect through fruit weight (0.2321), low positive indirect effect through number of fruits plant^{-1} (0.1650) and positive negligible indirect effect through days to 50 per cent flowering (0.0569) and yellow vein mosaic virus disease incidence (0.0202).

A negative and negligible indirect effect was shown through fruit length (-0.0191) and duration (-0.0002).

4.1.5.6 Duration (days)

Duration contributes positively but negligible direct effect (0.0463) towards yield plant^{-1}.

Positive and negligible effect was seen through fruit length (0.0293). Positive and low indirect effect was contributed through fruit weight (0.1177). A moderate but negative indirect effect was shown via number of fruits plant^{-1} (-0.2610).

Negative and negligible indirect effect was exhibited by duration through days to 50 per cent flowering (-0.0729), fruit girth (-0.0001) and yellow vein mosaic virus disease incidence (-0.0332).

4.1.5.7 Scoring for YVM Disease

The direct effect of yellow vein mosaic virus disease incidence was found to be negative and negligible (-0.0748).

.The indirect effect was found to be positive and negligible through fruit weight (0.0238), fruit length (0.0521) and duration (0.0205), whereas, the indirect effect through fruit girth (-0.0106) was found to be negative and negligible and that of days to 50 per cent flowering (-0.1509) was found to be negative and low.

The indirect effect of yellow vein mosaic virus disease incidence was found to be negative and high through number of fruits plant^{-1} (-0.5748).

4.1.6 Scoring for YVM Disease

All the seventeen genotypes were categorized based on the disease scale given by Rajamony *et al.,* 1990 and recorded in Table 11. Among the seventeen genotypes under study, VLYA 5, VLYA 11 and VLYA 13 were found to be highly resistant. The cultures VLYA 4, VLYA 10 and VLYA 15 were found to be resistant. Eight genotypes were under the category moderately resistant they include VLYA 1, VLYA 2, VLYA 3, VLYA 6, VLYA 7, VLYA 8, VLYA 12 and Varsha Uphar. Genotypes viz., VLYA 9, VLYA 14 and Kiran were found to be moderately susceptible. No genotype was found to be susceptible or highly susceptible.

4.1.7 Scoring for Fruit and Shoot Borer

The seventeen genotypes were categorized based on the percentage of fruits attacked by fruit and shoot borer and recorded in Table 12. Among the seventeen genotypes screened, five genotypes (VLYA 2, VLYA 4, VLYA 11, VLYA 13 and VLYA 14) were found to be immune towards okra fruit and shoot borer attack. The genotypes VLYA 3, VLYA 5, VLYA 15 and Varsha Uphar were categorized as

Table 11. Scoring for yellow vein mosaic resistance.

GENOTYPES	30 DAS			50 DAS			70 DAS		
	V.I	Range of score	Reaction	V.I	Range of score	Reaction	V.I	Range of score	Reaction
VLYA 1	0.00	0	HR	25.00	2	MR	31.25	2	MR
VLYA 2	0.00	0	HR	10.42	1	R	35.42	2	MR
VLYA 3	29.17	2	MR	31.25	2	MR	39.58	2	MR
VLYA 4	0.00	0	HR	0.00	0	HR	14.58	1	R
VLYA 5	0.00	0	HR	0.00	0	HR	0.00	0	HR
VLYA 6	0.00	0	HR	22.92	2	MR	29.17	2	MR
VLYA 7	27.08	2	MR	29.17	2	MR	31.25	2	MR
VLYA 8	33.33	2	MR	37.50	2	MR	37.50	2	MR
VLYA 9	33.33	2	MR	35.42	2	MR	41.67	3	MS
VLYA 10	0.00	0	HR	12.50	1	R	16.67	1	R
VLYA 11	0.00	0	HR	0.00	0	HR	0.00	0	HR
VLYA 12	0.00	0	HR	8.33	1	R	37.50	2	MR
VLYA 13	0.00	0	HR	0.00	0	HR	0.00	0	HR
VLYA 14	0.00	0	HR	41.67	3	MS	43.75	3	MS
VLYA 15	0.00	0	HR	4.17	1	R	10.42	1	R
Varsha Uphar	0.00	0	HR	6.25	1	R	20.83	2	MR
Kiran	25.00	2	MR	33.33	2	MR	41.67	3	MS

V.I. = Vulnerability Index
0 = Highly Resistant (HR)
1 = Resistant (R)
2 = Moderately Resistant (MR)
3 = Moderately Susceptible
4 = Susceptible (S)
5 = Highly Susceptible (HS)
No. of plants = 25

Table 12. Scoring for okra fruit and shoot borer.

Genotypes	Percentage Attack	Score	Category
VLYA1	18.67	16-30	MS
VLYA2	0.00	0	I
VLYA3	4.67	1-5	R
VLYA4	0.00	0	I
VLYA5	3.67	1-5	R
VLYA6	15.00	6-15	MR
VLYA7	27.33	16-30	MS
VLYA8	23.67	16-30	MS
VLYA9	8.67	6-15	MR
VLYA10	12.33	6-15	MR
VLYA11	0.00	0	I
VLYA12	23.33	16-30	MS
VLYA13	0.00	0	I
VLYA14	0.00	6-15	I
VLYA15	3.33	1-5	R
Varsha Uphar	1.67	16-30	R
Kiran	19.67	16-30	MS

resistant. Only three genotypes were found to be moderately resistant, they include VLYA 6, VLYA 9 and VLYA 10 and rest of the genotypes like VLYA 1, VLYA 7, VLYA 8, VLYA 12 and Kiran came under the category of moderately susceptible. No genotype was found to be susceptible to okra fruit and shoot borer attack.

4.2 GLASS HOUSE EXPERIMENT

The genotypes screened as highly resistant (VLYA 5, VLYA 11 and VLYA 13) and resistant (VLYA 4, VLYA 10 and VLYA 15) were selected for the confirmatory study in the glass house along with some moderately resistant genotypes having higher yield such as VLYA 1, VLYA 2, VLYA 6 and VLYA 12. The vulnerability index for all the genotypes calculated using the disease scale of Rajamony *et al.* (1990) was recorded in Table 13.

4.2.1 Vector Transmission

All the genotypes except VLYA 4 and VLYA 6 were obtained as highly resistant after the whitefly transmission. The genotype VLYA 4 showed a vulnerability index of 16.66 and was categorized as resistant.

The genotype VLYA 6 recorded vulnerability index of 43.50 and was categorized as moderately susceptible.

4.2.2 Graft Transmission

The graft transmission study revealed the resistance of the genotypes VLYA 5, VLYA 11 and VLYA 13 which were highly resistant to yellow vein mosaic virus disease. The genotype VLYA 4 was confirmed for being resistant to yellow vein mosaic virus disease in both vector and graft transmission studies and also the genotype VLYA 6 which exhibited moderate susceptibility in vector transmission was confirmed to be moderately susceptible after graft transmission. The genotypes VLYA 1, VLYA 2 and VLYA 15 which were highly resistant after vector

Table 13. Scoring for yellow vein mosaic virus disease under glass house experiment.

Genotypes	Vector transmission			Graft transmission		
	V. I.	Range of score	Reaction	V. I.	Range of score	Reaction
VLYA 1	0.00	0	HR	25.00	2	MR
VLYA 2	0.00	0	HR	22.50	2	MR
VLYA 4	16.66	1	R	16.66	1	R
VLYA 5	0.00	0	HR	0.00	0	HR
VLYA 6	43.50	3	MS	50.00	3	MS
VLYA 10	0.00	0	HR	2.50	1	R
VLYA 11	0.00	0	HR	0.00	0	HR
VLYA 12	0.00	0	HR	45.00	3	MS
VLYA 13	0.00	0	HR	0.00	0	HR
VLYA 15	0.00	0	HR	35.45	2	MR

V.I. = Vulnerability Index
No. of plants =10

Plate 7. Successful graft unions of selected genotypes

transmission were noticed to be moderately resistant in the graft transmission study. The genotype VLYA 10 was also observed to be resistant. The genotype VLYA 12 which was found to be highly resistant after vector transmission was confirmed to be moderately susceptible by the graft transmission study.

Hence in the present study entitled “Evaluation of superior cultures for yield and yellow vein mosaic resistance in okra (*Abelmoschus esculentus* (L.) Moench)”, fifteen genotypes screened along with check varieties revealed that the cultures VLYA 5, VLYA 11, VLYA 13 having high yield potential and are highly resistant to yellow vein mosaic virus disease could be further subjected to different trials before releasing for field cultivation.

VLYA 5

VLYA 11

VLYA 13

Plate 8. Selected genotypes

Discussion

5. DISCUSSION

Okra (*Abelmoschus esculentus* (L.) Moench) commonly called as bhendi in India, belongs to Malvaceae family. They are cultivated widely because of high nutritive value and export potentiality. Okra is one of the major vegetable crops grown in the tropics and sub tropics (Kochhar, 1986). Okra is often grown for its tender fruits which are rich in protein, vitamin A, B, C, iodine and minerals (Baloch *et al.,* 1990).

Bhindi is very popular among Indian farmers due to its ease of cultivation and high returns. But the most important hurdle in okra cultivation is the heavy incidence of pests and diseases (Hammon and Sloten, 1989). From time immemorial, developing resistance to pest and disease attack in addition to high yield became an inevitable component in the okra breeding programme (Chattopadhyay *et al.,* 2011).

By the intense breeding programmes, various improved varieties were developed with high yield and resistance towards pests and diseases. But due to the emergence of new biotypes of pests and new races of pathogens, it becomes a necessity to continuously develop new and improved varieties suited for the particular climate and region. Eventhough heterosis breeding had contributed to the development of resistant varieties in okra; due to the hybrid breakdown new hybrids need to be produced inorder to replace the old ones.

The current study was the continuation of a previous work in the department in which various resistant varieties were selected from different local regions of Kerala, Karnataka and Andhra Pradesh and hybridization was carried out among them. These hybrids were evaluated for yield, yellow vein mosaic resistance and various other pests and diseases. The F_6 generation was evaluated for high yield and yellow vein mosaic disease resistance. Knowledge about genetic variability and

correlation studies of various traits are required for improving yield. Hence the information on genetic variability of genotypes will directly help in crop improvement (Dhankar and Dhankar, 2002).

5.1 GENETIC VARIABILITY

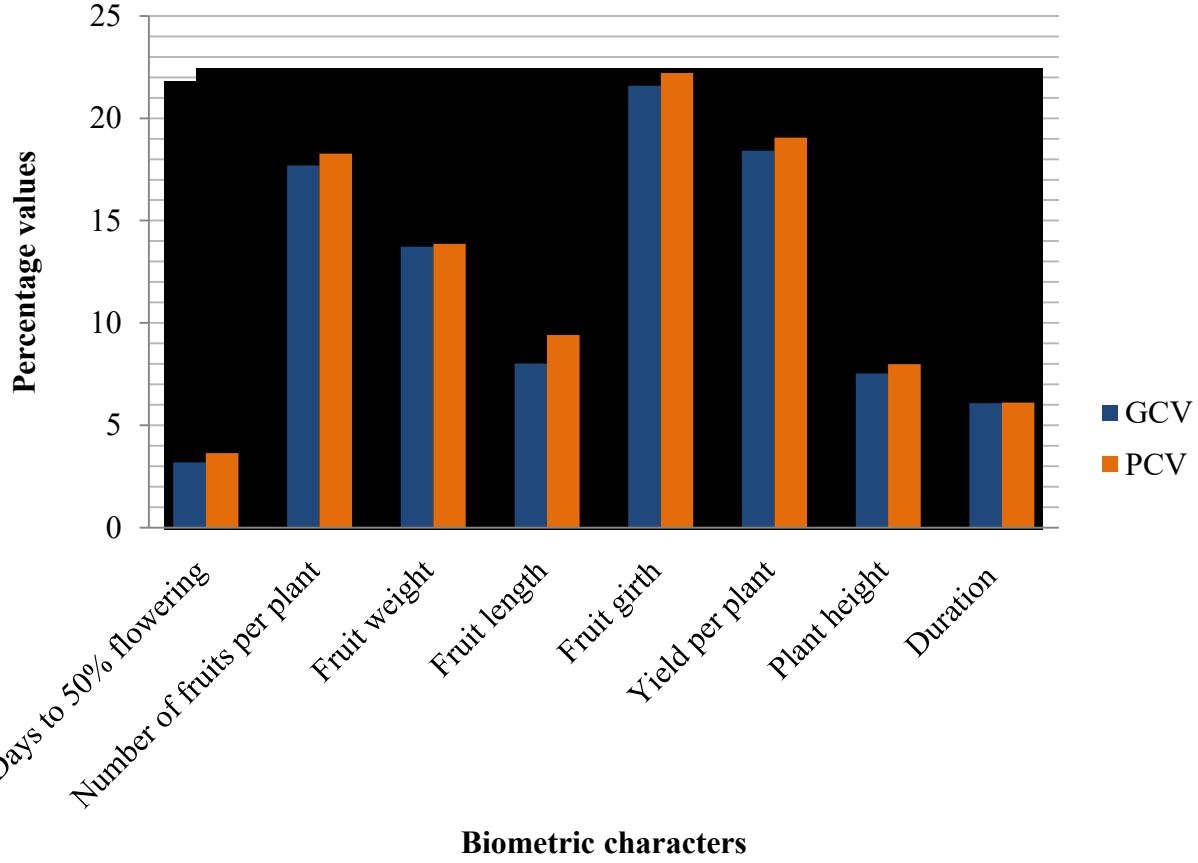
The mean performance of the seventeen okra genotypes were calculated and found that the highest range was observed in yield plant^{-1} followed by plant height, duration and weight of fruit. Similar results were noticed in the works by Saran *et al.* (2007); Choudhary *et al.* (2009); Ahamed *et al.* (2015); Archana *et al.* (2015). Hence, as per Vijay and Manohar (1990), the traits having higher range of variation must be given priority in the selection process of evaluation of genotypes.

The analysis of variance revealed that the selected traits for study viz., days to 50 per cent flowering, number of fruits plant^{-1}, fruit weight (g), fruit length (cm), fruit girth (g), yield plant^{-1} (g), plant height (cm) and duration (days) were found to be highly significant for all the genotypes evaluated which is similar to the results by Wammanda *et al.* (2010).

Significance of the characters under study indicated genetic variability in the experimental material. In the evaluation of cultures or genotypes, variability in the population is a pre-requisite. Inorder to select a particular trait, sufficient amount of variability must be observed for that trait. These results are in concordance with that of the results by Prakash and Pitchaimuthu (2010). Similar results were also recorded for many traits such as number of fruits plant^{-1}, fruit length, fruit girth, fruit weight, yield plant^{-1} and duration by Sivanandan (2003). The genetic variability studies revealed that yield improvement can be done through selection in okra as suggested by Archana *et al.* (2015).

Studies on variability revealed that the phenotypic coefficient of variation was found to be higher than the genotypic coefficient of variation. Similar result

Figure 1. PCV (%) and GCV (%) for various biometric characters of okra genotypes



was obtained for Patro and Ravisankar (2004). The higher value for phenotypic coefficient of variation indicated the influence of environment in the expression of these traits as pointed by Mehta *et al.* (2006).

The range of genetic variability calculated using GCV and PCV indicates the interaction effect of environment on the traits studied. High genotypic coefficient of variation was observed for fruit girth and low genotypic coefficient of variation was evident in days to 50 per cent flowering, fruit length, plant height and duration which is in accordance with the works done by Ahamed *et al.* (2015).

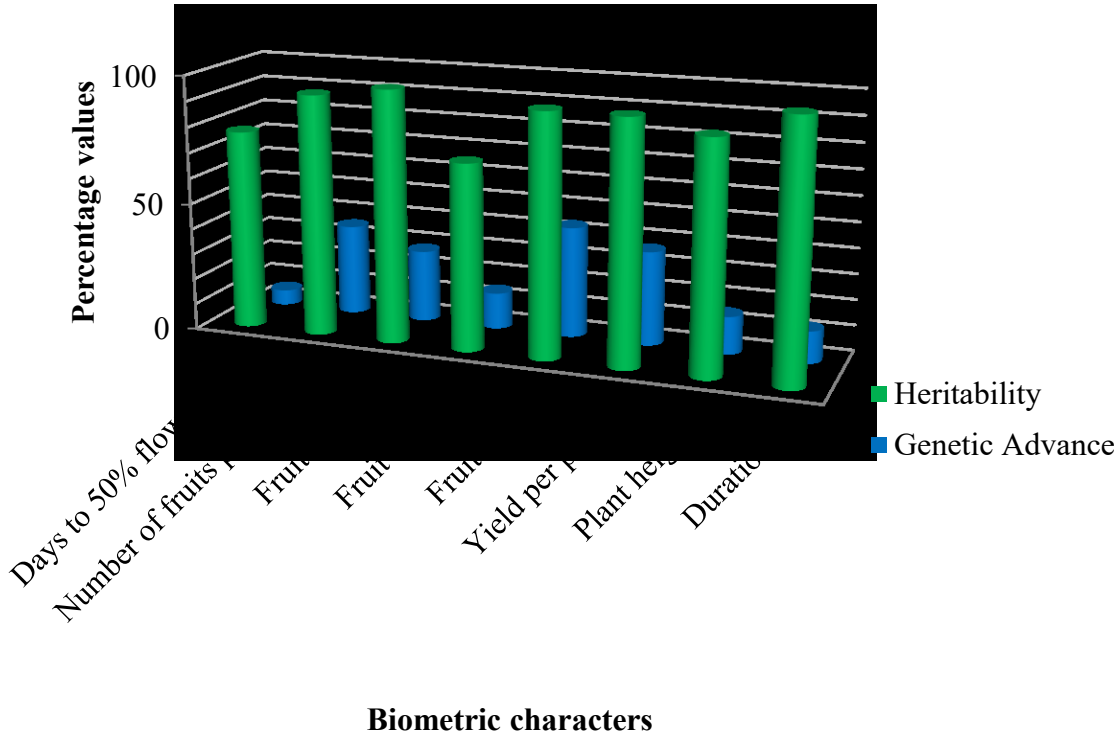
Moderate GCV and PCV were observed in the traits number of fruits plant^{-1}, fruit weight and yield plant^{-1}. The less difference between phenotypic and genotypic coefficients of variation observed in all characters revealed that these characters were least influenced by environment. The high GCV can be used as a criterion for selection. This was in accordance with Singh and Jalikop (1986). The characters having high GCV can be directly selected inorder to improve the yield as reported by Sengupta and Verma (2009). These reports were also provided by Thakur *et al.* (1996).

The difference between phenotypic and genotypic variances were calculated and observed that the traits fruit girth and fruit weight were found to have less difference. The same traits were noticed to have low difference between phenotypic and genotypic variance as reported by Ahamed *et al.* (2015). The higher difference between genotypic and phenotypic variances suggests that those characters are influenced by environment which is in accordance with the findings of Sharma and Prasad (2015).

5.2 HERITABILITY AND GENETIC ADVANCE

Among the eight characters studied, all characters exhibited high heritability. The highest heritability was exhibited by duration followed by fruit

Figure 2. Heritability (%) and Genetic Advance (% mean) for various biometric characters of okra genotypes



weight. Similarly highest heritability was recorded for duration, followed by fruit weight with high genetic advance by Duggi (2012). Hence the character having high heritability can be used for crop improvement through selection as suggested by Patro and Ravisankar (2004).

The character fruit weight showed high heritability in the current study which is in accordance with the reports by Mohamed and Anbu (1997); Hazra and Basu (2000); Saifullah and Rabbani (2009).

The high heritability for various biometric characters was expressed by various researchers. The high heritability for characters like plant height and length of fruits were supported by the works by Murthy and Bavaji (1980); Mehta *et al.* (2006).

Heritability which is usually measured in percentage indicates the gene action present in a particular character. The high value for heritability indicates that the variability noticed is due to genetic factors (Reddy *et al.*, 2012). If the heritability is low it means that the variation obtained is due to environmental factors hence cannot be selected directly. This was similar to the results presented earlier by Vishal *et al.* (2006); Adiger *et al.* (2011).

The high heritability values provide extra strength to the major genes which is used to determine the genetic advance. So it is more reliable to select characters having high heritability and high genetic advance as reported by Abdelmageed (2010).

Characters having high heritability need not be having high genetic advance in the case of polygenic characters. Hence heritability measured along with genetic advance as percentage of mean would be more reliable in selection. The result corroborated with that of Johnson and co-workers (1955).

High genetic advance was shown by fruit girth followed by yield plant^{-1}, number of fruits plant^{-1}, and fruit weight indicating that the selected characters are more reliable for improvement through selection (Sengupta and Verma, 2009). Moderate genetic advance was shown by plant height, fruit length and duration. Days to 50 per cent flowering was found to have low genetic advance, means the trait was highly influenced by environment. This was in accordance with the study conducted by Nasit *et al.* (2010).

High heritability coupled with high genetic advance was observed for number of fruits plant^{-1}, fruit weight, fruit girth and yield plant^{-1} in the present investigation. High heritability coupled with high genetic advance for these characters along with other traits like height of plant, number of branches plant^{-1}, days to 50 per cent flowering, length of fruit and yellow vein mosaic virus infestation on fruits and plants were also reported by Reddy *et al.* (2012). Similar result was reported by Duggi, (2012).

High heritability coupled with high genetic advance indicates that these traits are controlled by additive gene action. So, selection can be done using these parameters which is in accordance with those reported by Dhankar and Dhankar (2002); Mehta *et al.* (2006); Singh *et al.* (2007); Nwangburuka *et al.,* 2012; Seth *et al.,* (2016).

High heritability along with high genetic advance was noticed in characters like length of fruit, duration and height of plant. The characters like height of plant, number of fruits plant^{-1}, leaf length, leaf diameter and yield plant^{-1} were found to have high heritability together with high genetic advance as reported by Ahamed *et al.* (2015). Traits like fruit weight, days to 50 per cent flowering, number of fruits plant^{-1} and yield plant^{-1} exhibited moderate to high heritability coupled with moderate genetic advance as suggested by Archana *et al.,* (2015).

5.3 CORRELATION

For the crop improvement programme to be successful, enough valid information about correlation must be available (Akinyele and Osekita, 2006). Inorder to go for simultaneous improvement of various traits, the genotypic and phenotypic correlation studies must be conducted. Then only the effect of environment on the concerned trait can be evaluated. This was previously reported by Umesh *et al.* (2014).

The yield plant^{-1} was found to be significantly and positively correlated with fruit weight, number of fruits plant^{-1}, length of fruit, girth of fruit and height of plant both at phenotypic and genotypic levels. Number of fruits plant^{-1} was found to have the maximum positive correlation with yield plant^{-1}. Similar results were obtained by Dhall *et al*. (2001); Jaseena *et al.* (2008); Adiger *et al.* (2011); Jagan *et al.* (2013); Ahamed *et al.* (2015); Archana *et al.* (2015). The direct positive correlation of yield with these characters indicate that fruit yield plant^{-1} can be improved by selecting these traits as expressed by Singh *et al.* (2007).

Days to 50 per cent flowering and yellow vein mosaic disease incidence was found to be negatively correlated with yield plant^{-1}. Negative correlation coefficient between days to 50 per cent flowering and number of fruits plant^{-1} suggests that early flowering genotypes could provide more yield plant^{-1}. Hence earliness to flowering can be taken as a criterion for selection. Negative correlation means those characters are independent in selection process for yield improvement. The correlation coefficients obtained were found to be high which means the genotypes selected for evaluation were highly uniform. These findings are in accordance with those of Adeniji and Aremu (2007).

The highest inter-correlation was noticed between height of plant and number of fruits plant^{-1} as reported by Singh *et al.* (2007); Umesh *et al.* (2014),

which means that as the height of the plant increases, the number of fruiting nodes also increases thereby the number of fruits also increases. This is similar to the research findings of Archana *et al.* (2015). Another explanation for the same was given by Sharma and Prasad (2015) as the height of the plant increases, more nodes will emerge for the development of new branches as a result of accumulation of more photosynthates.

The trait days to 50 per cent flowering was correlated with the characters number of fruits plant^{-1}, weight of fruit and girth of fruit highly significantly and negatively. This finding is in concordance with the findings of Akinyele and Osekita (2006) and Sengupta and Verma (2009).

Fruit weight was significantly and positively correlated with fruit length and fruit girth which reveals that as the length of the fruit and fruit girth increases, the fruit weight will gradually increases thereby increasing the yield. These results add to the results by Akinyele and Osekita (2006).

The yellow vein mosaic disease was found to be significantly and negatively correlated with number of fruits plant^{-1} which indicated that when there is yellow vein mosaic disease incidence, the fruit number reduces. Similar results were obtained for Ndunguru and Rajabu (2004).

More significant correlation was obtained between two characters when the genotypic correlation coefficients were calculated indicating that such characters have more relations genotypically as suggested by Simon *et al*. (2013).

The genotypic correlation between traits were found to be higher than the corresponding phenotypic correlation except correlation between number of fruits plant^{-1} and girth of fruit, yield plant^{-1} and between weight of fruit and yellow vein mosaic disease. Higher the genotypic correlation between characters they are less influenced by environment. This was earlier explained by Sagar (1992); Dhankar

and Dhankar (2002); Singh *et al.* (2007). Hence the difference in the correlation coefficients can also be considered for varietal improvement as these indicate less involvement of environment. These results are in accordance with that of Sharma and Prasad (2015).

5.4 PATH ANALYSIS

The positive direct effect towards yield plant^{-1} was contributed by number of fruits plant^{-1}, fruit weight, fruit girth and duration among which number of fruits plant^{-1} and fruit weight were found to have high positive direct effect towards yield. This means selection for these characters will directly increase yield. The number of fruits plant^{-1} showed maximum positive direct effect towards yield as suggested by Vijay and Manohar (1990); Dhankar and Dhankar (2002); Adiger *et al.* (2011); Ahamed *et al.* (2015); Rajkumar and Sundaram (2015). The major contribution of traits like number of fruits plant^{-1} and fruit weight was earlier recorded by Singh *et al.* (2007); Sharma and Prasad (2015).

The highest negative direct effect towards yield was contributed by days to 50 per cent flowering which was in concordance with the report by Umesh *et al.* (2014); Rajkumar and Sundaram (2015).

The highest indirect effect was contributed by number of fruits plant^{-1} through length of fruit. The indirect effect of weight of fruit through length of fruit and girth of fruit were found to be positive which emphasize the importance of fruit length and fruit girth in selection. Similar result was observed in the work by Adiger *et al.* (2011); Kumar *et al.* (2012); Rajkumar and Sundaram (2015). The indirect effect of other characters was found to be low, which could not be considered which is in association with the reports by Umesh *et al.* (2014).

Yield was positively correlated with fruits plant^{-1}, fruit weight, fruit length, fruit girth and plant height. But among this, fruit length was found to have negative

direct effect with yield and the direct effect of fruit girth towards yield plant^{-1} was found to be negligible. The possible explanation for this was provided by Singh and Choudhary (1985). They explained that the negative or negligible direct effect of characters like fruit length and fruit girth may be because the correlation present might be due to the indirect effects.

The residual effect was found to be 0.0664 which is approximately equal to one indicating that the selected traits were sufficient for explaining yield plant^{-1}. Low residual effect was obtained by Ahamed *et al*. (2015) which he explained as the characters selected in the study contributed to major portion of yield. Another explanation for the same was given by Sharma and Prasad (2015).

5.5 YELLOW VEIN MOSAIC VIRUS DISEASE

Ten superior genotypes selected from the field evaluation, vector transmission and graft transmission studies were carried out in the green house. Out of the ten genotypes, eight were categorized as highly resistant after vector transmission. But the graft transmission studies revealed that only three genotypes were found to be highly resistant to yellow vein mosaic disease. Similar report was provided by Ali *et al.* (2005) where two varieties exhibited mild symptoms in the greenhouse eventhough no symptoms appeared after inoculation. The artificial inoculation of okra genotypes under controlled condition could not produce yellow vein mosaic disease symptoms which confirmed the absence of the virus as reported by Mehra *et al.* (2008).

The existence of yellow vein mosaic disease resistant superior cultures pointed that there was transfer of desirable genes from wild relatives that were hybridized with the local varieties. This was earlier reported by Jaseena *et al.* (2008) and explained that these selected cultures could be further utilized for releasing yellow vein mosaic disease resistant varieties.

The yellow vein mosaic incidence was positively and significantly correlated with the number of whiteflies on leaves which is in accordance with the reports by Prabhu *et al.* (2007). The healthy okra plants were not contaminated with whitefly cultures used for transmission studies as reported by Venkataravanappa *et al.* (2013).

Summary

6. SUMMARY

The present study entitled "Evaluation of superior cultures for yield and yellow vein mosaic resistance in okra (*Abelmoschus esculentus* (L.) Moench)" was carried out in the Department of Plant Breeding and Genetics, College of Agriculture, Vellayani during 2014-2016, with the objective of identifying high yielding and yellow vein mosaic resistant cultures of okra from advanced cultures developed through an inter-varietal hybridization programme.

In order to realize the objectives two experiments were undertaken. The first experiment consisted of field evaluation of the fifteen superior okra cultures selected for the study viz., VLYA 1, VLYA 2, VLYA 3, VLYA 4, VLYA 5, VLYA 6, VLYA 7, VLYA 8, VLYA 9, VLYA 10, VLYA 11, VLYA 12, VLYA 13, VLYA 14 and VLYA 15. The cultures were obtained from the previous project undertaken in the department. Varsha Uphar and Kiran were used as checks. The field design was Randomized Block Design (RBD) with three replications during the summer season of 2015. The biometric observations viz., days to 50 per cent flowering, number of fruits plant^{-1}, fruit weight (g), fruit length (cm), fruit girth (g), yield plant^{-1} (g), plant height (cm) and duration (days) as well as the scoring for yellow vein mosaic disease, scoring for fruit and shoot borer, scoring for number of whiteflies on leaves and scoring for other diseases were recorded and statistical analyses were done.

The mean performance of seventeen genotypes for all the characters studied were calculated and found that the trait yield plant $^{-1}$ was found to have the maximum range of mean values followed by plant height and duration. Among the various characters studied, selection was mainly based on the yield performance as well as yellow vein mosaic disease resistance.

The analysis of variance revealed that all the characters were highly significant for all the genotypes evaluated. Estimation of genetic parameters revealed that fruit girth recorded the highest coefficients of variation. Moderate GCV and PCV were observed for traits like number of fruits plant^{-1}, fruit weight and yield plant $^{-1}$. Low GCV and PCV were observed for the characters days to 50 per cent flowering, fruit length, plant height and duration. All the biometric characters studied were found to have high heritability among which the highest heritability was noticed for duration followed by weight of fruit, yield plant $^{-1}$ and fruit girth. High genetic advance was observed for number of fruits plant^{-1}, fruit weight, fruit girth and yield plant $^{-1}$ whereas, the moderate and low genetic advance was noticed for the traits fruit length, plant height, duration and days to 50 per cent flowering respectively. High heritability coupled with high genetic advance was noticed for number of fruits plant^{-1}, fruit weight, fruit girth and yield plant $^{-1}$. High heritability with moderate genetic advance was recorded for fruit length, plant height and duration. The trait days to 50 per cent flowering had high heritability coupled with low genetic advance.

The yield plant^{-1} was found to be significantly and positively correlated with number of fruits plant^{-1}, fruit weight, length of fruit, girth of fruit and height of plant both at genotypic and phenotypic levels. The traits days to 50 per cent flowering and yellow vein mosaic disease were found to be negatively correlated with yield plant $^{-1}$. Among the inter-correlations studied, very high positive and significant correlation was noticed between plant height and number of fruits plant^{-1}.

The trait days to 50 per cent flowering had high positive and significant correlation with yellow vein mosaic virus disease and duration. Significant positive genotypic correlation was recorded with fruit weight at genotypic level. The trait had high significant negative correlation with fruit length, number of fruits plant^{-1} and plant height at both genotypic and phenotypic levels.

Number of fruits plant^{-1} was found to be significantly and positively correlated with height of plant and length of fruit both at genotypic and phenotypic levels. A highly significant negative correlation was observed between number of fruits plant-^{1} and yellow vein mosaic disease both genotypically and phenotypically. Similarly, a negative and significant inter-correlation was observed between number of fruits plant^{-1} and duration at genotypic and phenotypic levels.

The inter-correlation studies of weight of fruit revealed that it had a highly significant and positive correlation with girth of fruit both at genotypic and phenotypic levels. A significant negative correlation was seen between weight and length of fruit and between weight of fruit and height of plant at genotypic level only. The genotypic as well as the phenotypic inter-correlation between fruit length and plant height was positive and highly significant. Highly significant and negative correlation was noticed between fruit length with duration at genotypic level. The inter-correlation of fruit length with yellow vein mosaic disease was also found to be highly significant and negative at both genotypic and phenotypic levels.

A highly significant and negative correlation was observed between height of plant and yellow vein mosaic disease at both genotypic and phenotypic levels. A significant and negative inter-correlation was noticed for plant height and duration at genotypic and phenotypic levels. The character duration was found to be highly significantly and negatively correlated with yellow vein mosaic disease at genotypic and phenotypic levels. The simple correlation revealed that the traits yellow vein mosaic disease and number of whiteflies on leaves were significantly and positively correlated. In many of the correlation coefficients it was found that the genotypic correlation coefficients were higher than the corresponding phenotypic correlation coefficients.

The path analysis showed that the characters number of fruits plant^{-1}, weight and girth of fruit and duration were found to have positive direct effect towards

yield among which number of fruits plant^{-1} and fruit weight showed the maximum positive direct effect towards yield. The indirect effects of all the characters were also found out and the number of fruits plant^{-1} had high indirect effect towards yield through fruit length. Similarly, number of fruits plant^{-1} had a high but negative indirect effect towards yield through days to 50 per cent flowering.

The number of diseased leaves was observed and the vulnerability index was calculated for all the seventeen genotypes. This revealed that the genotypes VLYA 5, VLYA 11 and VLYA 13 were resistant to the disease during all stages of crop growth. The genotypes VLYA 4, VLYA 10 and VLYA 15 were categorized as resistant. Hence the genotypes which recorded higher yield as well as disease resistance viz., VLYA 1, VLYA 2, VLYA 4, VLYA 5, VLYA 6, VLYA 10, VLYA 11, VLYA 12, VLYA 13 and VLYA 15 were further taken for the second experiment for the confirmation of disease resistance.

In the glass house experiment, vector transmission and graft transmission studies were conducted and the vulnerability index was calculated. In vector transmission studies, even though the genotypes VLYA 1, VLYA 2, VLYA 5, VLYA 10, VLYA 11, VLYA 12, VLYA 13 and VLYA 15 were found to be highly resistant, after the graft transmission, it was found that only the genotypes VLYA 5, VLYA 11 and VLYA 13 were highly resistant. This confirmed that the genotypes VLYA 5, VLYA 11 and VLYA 13 were resistant to yellow vein mosaic disease.

Hence the present investigation revealed that the superior cultures VLYA 5, VLYA 11 and VLYA 13 were having high yield and yellow vein mosaic disease resistance. These selected cultures can be used for further trials.

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EVALUATION OF SUPERIOR CULTURES FOR YIELD AND YELLOW VEIN MOSAIC RESISTANCE IN OKRA

(*Abelmoschus esculentus* (L.) Moench)

by

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ABSTRACT

The present study entitled "Evaluation of superior cultures for yield and yellow vein mosaic resistance in okra (*Abelmoschus esculentus* (L.) Moench)" was carried out in the Department of Plant Breeding and Genetics, College of Agriculture, Vellayani during 2014-2016, with the objective to identify high yielding and yellow vein mosaic resistant cultures of okra from those evolved through inter-varietal hybridization programme.

Fifteen superior cultures of okra obtained from the previous project in the Department viz., VLYA 1, VLYA 2, VLYA 3, VLYA 4, VLYA 5, VLYA 6, VLYA 7, VLYA 8, VLYA 9, VLYA 10, VLYA 11, VLYA 12, VLYA 13, VLYA 14 and VLYA 15 along with two check varieties Varsha Uphar and Kiran were evaluated in a Randomized Block Design (RBD) with three replications during summer season of 2015. The analysis of variance was calculated for the traits under study *viz.,* days to 50 per cent flowering, number of fruits plant^{-1}, fruit weight (g), fruit length (cm), fruit girth (g), yield plant^{-1} (g), plant height (cm) and duration (days) and these were found to be highly significant for all the genotypes evaluated.

The maximum yield was recorded by the genotype VLYA 2 which was on par with genotypes VLYA 5, VLYA 10, VLYA 11, VLYA 13 and VLYA 15 and the minimum yield was observed by the check variety Kiran. The yield plant^{-1} exhibited moderate GCV (18.42%) and PCV (19.05%), high heritability (94.00%) coupled with high genetic advance (36.69%). The yield plant^{-1} was found to be significantly and positively correlated with number of fruits plant^{-1}, fruit length, fruit girth, fruit weight and plant height both at genotypic and phenotypic levels. Days to 50 per cent flowering and yellow vein mosaic disease incidence was found to be negatively correlated with yield plant^{-1}. Very high positive and significant inter-correlation was noticed between height of plant and number of fruits plant^{-1}.

The path analysis showed that number of fruits plant^{-1} and fruit weight showed the maximum positive direct effect towards yield. The number of fruits plant^{-1} had high indirect effect through fruit length.

The scoring for yellow vein mosaic disease and the vulnerability index revealed that the genotypes VLYA 5, VLYA 11 and VLYA 13 were resistant to the disease during all stages of crop growth. Number of white flies was found to be highest in VLYA 10 and lowest in VLYA 2. The incidence of fruit and shoot borer was also scored and five genotypes viz., VLYA 2, VLYA 4, VLYA 11, VLYA 13 and VLYA 14 were found to be immune and VLYA 3, VLYA 5, VLYA 15 and Varsha Uphar were found to be resistant.

The glass house experiment of vector transmission and graft transmission was conducted for the confirmation of disease resistance and the vulnerability index was calculated to check the severity of the disease. The genotypes VLYA 5, VLYA 11 and VLYA 13 received a score '0' which indicated that these genotypes were highly resistant. Hence the genotypes which obtained a vulnerability index of '0' during both field evaluation and glass house experiment were confirmed to be resistant to yellow vein mosaic disease.

Hence the present study revealed that the cultures VLYA 5, VLYA 11 and VLYA 13 were having high yield and yellow vein mosaic disease resistance. So these genotypes can be used for further trials before releasing for field cultivation.