ASSESSMENT OF GENETIC VARIABILITY FOR YVM RESISTANCE IN OKRA (*Abelmoschus esculentus* (L.) Moench)

by

Abdul Basir

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THESIS

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2020

DEDICATED TO

My Beloved

Mother &

Wife

DECLARATION

I hereby declare that the thesis entitled **'Assessment of genetic variability for YVM resistance in okra (*Abelmoschus esculentus* (L.) Moench)'** is a bonafide record of research work done by me during the course of research and that it has not been previously formed the basis for the award to me of any degree, diploma, fellowship or other similar title, of any other University or Society.

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CERTIFICATE

Certified that the thesis entitled **'Assessment of genetic variability for YVM resistance in okra (*Abelmoschus esculentus* (L.) Moench)'** is a record of research work done independently by **Mr. Abdul Basir** under my guidance and supervision and that it has not previously formed the basis for the award of any degree, diploma, associateship, fellowship to him.

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LIST OF ABBREVIATED TERMS

Abbreviation	Full name
GOI	Government of India
YVM	Yellow Vein Mosaic
YVMD	Yellow Vein Mosaic Disease
YVMV	Yellow Vein Mosaic Virus
PCV	Phenotypic Coefficient of Variation
GCV	Genotypic Coefficient of Variation
GA	Genetic Advance
GAM	Genetic Advance as percentage of Mean
H^2	Broad sense heritability
KAU	Kerala Agricultural University
NBPGR	National Bureau of Plant Genetic Resources
ICAR	Indian Council of Agricultural Research
PDI	Percentage of Diseases Incidence
PDS	Percentage of Disease Severity
CI	Coefficient of Infection
cm^2	Square centimeter
CD	Critical differences
cm	Centimeter
m	Meter
^0C	Degree celcius
%	Per cent
g	Gram

Introduction

1. INTRODUCTION

Okra (*Abelmoschus esculentus* (L.) Moench.) is an annual vegetable crop, originated in tropical Africa, belonging to the family Malvaceae. It is extensively cultivated in various parts of the world mostly for human consumption and also for industrial use as fibre (Alegbejo *et al.*, 2008).

Almost all parts of okra are economically utilisable. When compared with other crops such as tomato, brinjal and most of the cucurbits, okra is considered as nutritionally richer. The tender fruits of okra contain considerable amount of minerals such as calcium, magnesium, potassium, iodine and iron. The fresh pods are mainly used as vegetable for many culinary preparations and also processed into canned, frozen and dehydrated forms. Besides its nutritive values, it is medicinally important also.

India is leading in okra production in the world with 5.51 million tons (62 per cent of the total world production in 2016-17) from 0.49 million ha land (GOI, 2018). Gujarat was the leading state in okra production (921,720 MT) from an area of 75,270 ha with a productivity of 12 tonnes/ha) followed by West Bengal (GOI, 2018).

Okra is highly susceptible to yellow vein mosaic disease (YVMD), leading to significant yield losses in okra cultivation. In India, cultivation of okra has been challenged by severe incidence of YVMV. This virus belongs to the genus Begomovirus and family *Geminiviradeae* which contains many of the crop viruses. It infects almost all stages of lifecycle of the crop and consequently leads to severe effects not only on plant growth but also on the fruit yield. The virus is manifested typically by vein yellowing and thickening of leaves which eventually forms a network of mottled veins and vein lets in the infected leaves. In the early phase of the disease, the leaves exhibit only mild yellow coloured veins, but during the severe stage of infection, the leaves become completely chlorotic and turn yellow. There is significant lessening in the leaf chlorophyll and the infected plants are stunted and produce small-sized pale yellow fruits (Gupta and Paul, 2001). In nature, the virus is not transmitted either by sap or by seed; it is rather transmitted through the insect vector, white

fly (*Bemisia tabaci*). Sastry and Singh (1974) reported that the production losses due to YVMV ranged from 50-90 per cent.

The easy way to manage YVMD is the use of resistant genotypes. For developing resistant varieties, suitable okra lines must be identified initially from the available germplasm, which can be used for further breeding programmes. Hence the present investigation was conducted with the following objectives:

- To study the genetic variability in okra germplasm for yield and yield components
- To assess the yellow vein mosaic virus incidence and whitefly population in various okra genotypes
- To select the best okra line (s) resistant / tolerant to YVMD.

Review of literature

2. REVIEW OF LITERATURE

The investigation on **'Assessment of genetic variability for YVM resistance in okra (*Abelmoschus esculentus* (L.) Moench)'** was carried out in the Department of Plant Breeding and Genetics, College of Horticulture, Kerala Agricultural University, Vellanikkara.

A detailed review on the available literature is presented below:

2.1 Introduction

Okra is the most popular vegetable crops in India and it has high iron and rich in other nutrients among all the vegetables (Rosevellina *et al*., 2020). Okra (*Abelmoschus esculentus* (L.) Moench) is the member of family Malvaceae and known as Lady's finger. It is grown in tropical and sub-tropical part of the world (Rosevellina *et al*., 2020).

There is significant variation in the number of chromosomes and ploidy levels in different species of okra. The highest number of chromosome (2n= 200) reported in *A. caillei* (Siemonsma, 1982) and lowest chromosome number is associated to *A. angulosus* (2n = 56) (Ford, 1938). Even within *Abelmoschus esculentus,* chromosome numbers 2*n* = 72, 108, 120, 132 and 144 occurs in regular series of polyploids with *n* = 12 (Datta and Naug, 1968).

Okra, first found in Abyssinia (present Ethiopia) and distributed to the Caribbean, South America, North America, Africa, India and Eastern Mediterranean in the later time (Indian Horticulture Database, 2011). Most noticeable varieties of okra being grown in India are: Pusa Makhmali, Pusa Sawani, Punjab Padmini, Arka Anamika, Parbhani Kranti, Selection-2 *etc*. For the purpose of export, the hybrids are mostly used (Indian Horticulture Database, 2011). Young okra fruit is known to contain good amount of vitamins A, B, C as well as protein, carbohydrates, fats, minerals, iron and iodine. 100 g of fresh okra fruit can provide 20 per cent, 15 per cent and 50 per cent of the daily requirement of calcium, iron and ascorbic acid respectively. The old mature fruits can be used in processed products (Ali *et al.,* 2000). In spite of its high nutritive value, well acceptability among end users and wide range of available genetic variability, India is still lagging behind countries such as Ghana

and Egypt in terms of productivity of okra fruit (Ali *et al.,* 2000). This is mainly due to that the crop is affected by various biotic and abiotic diseases. Among biotic diseases, yellow vein mosaic virus is regarded as most serious disease and is capable of causing substantial yield losses (80-90%) (Ali *et al.,* 2000). Okra Yellow Vein Mosaic Virus (OYVMV) is believed to be originated from Indian land (Usha, 2008).

The pressure of disease on Okra was high in rainy season due to high humidity and rainfall along with more multiplication of whiteflies (*Bemisia tabaci* Gen.), which transmits YVM disease of okra (Chakrabarty *et al.*, 1997).

The virus attack all the above ground plant parts and finally the disease is characterized by a homogenous knots, yellow veins and yellowish or creamy colored leafs, stunted plant growth and bear very few deformed small fruits (Ali *et al.,* 2012).

2.2 Pests and diseases of okra

The major constraints of the quality and quantity of okra produced are pests and diseases which bring about 35-40 per cent yield losses. Farmers are endangering environment and public health by using synthetic pesticides to control the pests (Mohankumar *et al*., 2016).

Okra is considered as a robust crop which has been under large scale commercial production for long period. The yield losses are very high due to the incidence of a number of biotic and abiotic stresses. During wet season, okra is tolerant to most insect pests because of the profuse growth of foliage, but diseases are common because of the wet-warm condition of the environment. Moreover, during summer or second crop, whiteflies are the most critical and devastating pest characterised with the infrequent diseases. Among the greatest problems observed in production is the increasing occurrence of insect pests, diseases and nematodes, often leading to significant yield loss (Vinutha, 2015).

There are several pests that can cause serious damages on okra including Tomato Fruit Worm (TFW) (*Helicoverpa armigera*), the most destructive pest of okra. Root rot and powdery mildew are becoming serious problems. *Cercospora* leaf spot causes complete

defoliation in seed crop with a yield loss of up to 43.6 per cent (Pandey and Pandey, 2003). Serious yield reduction is caused by Jassids, mites and fruit borers up to 54-66 per cent at different stages of the crop (Satpathy *et al.,* 2004).

During summer, mite causes maximum yield loss of up to 25 per cent. Shoot and fruit borer infests okra both in the vegetative and fruiting stage of the crop and damage ranged from 23-51 per cent in different states of India (Satpathy and Rai, 1998).

Appiah *et al*. (2020) revealed that losses between 20-30 per cent recorded with the single infection of Okra yellow vein mosaic virus (OYVMV) but when in combination with Okra mosaic virus (OkMV) complete yield losses may occur.

2.2.1 Yellow vein mosaic virus disease

Among the different constraints in okra, viral disease, mainly yellow vein mosaic is a major one (Oraon *et al*., 2020) which is transmitted by white fly (*Bemisia tabaci*) (Ali *et al*., 2012). The incidence of this disease was first reported by Kulkarni (1924) in Bombay of British India. Then, it was reported from Uttar Pradesh (Tripathi and Joshi, 1967), Bihar (Jha and Mishra, 1955), Assam (Nath and Saikia, 1992), Gujarat (Tsering and Patel, 1990) and West Bengal (Mukhopadhyay *et al*., 1994). This disease was found to be in epidemic and endemic forms in the all growing states of India. Infection of 100 per cent plants in a field is very normal and yield losses ranged from 50- 94 per cent depending on the stage of crop growth at which infection occurs (Sastry and Singh, 1975).

Okra is susceptible to at least nineteen plant viruses throughout its life cycle (Brunt *et al.,* 1990). These viruses play a devastating effect on okra production in terms of yield and fruit quality. The viruses including yellow vein mosaic virus (YVMV) causes significant losses in the okra production. Nearly all cultivars and land races of okra succumb to YVMV, indicating the absence of resistance to this virus in *A. esculentus.* Tolerance or resistance to viruses is exhibited by several varieties at the time of release, but this tolerance or resistance has broken down with time (Kousalya, 2005).

2.2.1.1 Symptoms of YVM

The viral nature of disease was first established by Uppal *et al.* (1940), who identified it as yellow vein mosaic. The symptomatology and host range was described by Capoor and Verma (1950). Das *et al.* (2012) found that the high infection rate of YVMV disease was recorded due to the early symptoms of disease.

The most common characteristic symptoms of this disease are homogenous interwoven network of yellow vein enclosing islands of green tissues within. Initially the leaves exhibit only yellow coloured veins but in the later stages, the entire leaf turns completely yellow or at times becomes fully cream coloured. The chlorophyll content of the leaf is been partly or completely destroyed. Small leaves are common to infected plants and also remain stunted. Most of the affected plants exhibit thickening of veins on their lower sides. The infected plants has one or few fruits, often deformed, small, pale in colour and tough in texture (Singh, 1990).

According to Niraja *et al.* (2018) accession 2014\OKYVRES-1 exhibited moderate number of fruits (11.20), fruit girth (5.81 cm), fruit length (12.63 cm) average fruit weight (8.53 cm) with highest total yield (4.39 kg plot-1) and significant tolerance to YVMD up to 30-45 DAS of incidence.

2.2.1.2 Assessment of losses due to YVM disease

If the okra plant is infected within 20 days after germination the loss in yield recorded was up to 98 per cent (Sastry and Singh, 1975). However, for plants that were infected at 35 and 50 days following germination, the loss was estimated to be 83 and 49 per cent respectively. The damages caused by yellow vein mosaic in bhendi are severe especially when the infection occurs in 30 days after sowing (Arumugam and Muthukrishan, 1980). The estimated loss due to yellow vein mosaic virus is reported to be between 50-90 per cent. Nath and Saikia (1992) also reported the relationship between crop age and yield losses caused by okra yellow vein mosaic virus at maximum 94.42 per cent and minimum yield losses 32.65 per cent for plants infected at 35 and 63 days after sowing. Aparna *et al.* (2012)

reported that the disease can infect plant at all stages of crop growth and severely reduces growth and yield by 50 to 94 per cent.

2.2.1.3 Screening for resistance to YVM disease

In the screening experiment on YVMD Naraini and Seth (1958) inferred that the wild species *viz., Hibiscus manihot* var. *pungens, H crinitus, H. vititolius* and *H. panduraetormis* were immune to YVM. Sandhu *et al.* (1974) in their screening test found that accession E 31830, Asuntem Koko' from Ghana (*A. manihot* (L) Medicus ssp. *Manihot*) was immune to YVMV.

Crop management using chemicals proves less economical and environmentally not safer than crop improvement by developing YVM disease resistant varieties. Earlier efforts led to the development and release of cultivars like Pusa Sawani and MDU-1 which is field resistant to YVMV (Singh *et al.,* 1962).

Nath and Saikia (1992) screened fourteen okra genotypes for resistance against YVMD by artificial inoculation and natural infection. None of the entries was immune to the disease.

'Varsha Uphar', a YVMD resistant okra variety was developed (Dhankar, 1996) from a cross between Lam Selection I x Parbhani Kranti. Pathak *et al.* (1997) reported that the crosses Parbhani Kranti x HR-55 and Parbhani Kranti x EC 1651 were found to be resistant to YVMD.

Fugro and Rajput (1999), using a partial diallel mating system involving nine genotypes, developed 36 F_1 hybrids. Among these, Sel-4 x Parbhani Kranti, Pusa Sawani x Punjab-7, Sel-4 x BO-1, Sel-4 x Punjab-7 and Sel-4 x Sel-10 were free from YVMD. (Deo *et al.,* 2000) understands that Parbhani Kranti and its hybrid Parbhani Kranti x HRB-9-2 were highly resistant to YVMD. Rattan and Bindal (2000) developed okra hybrids which are resistant to YVMD and further found that lines 407, 409, 417, 430 were completely resistant.

Ragupathi *et al.* (2000) screened twelve okra genotypes, including the highly susceptible Pusa Sawani and MDU-1 and concluded that the disease was absent in the highly

resistant cultivars BO.1 and HRB-55. They further concluded that resistant cultivars were KS-404, HRB 9-2, Hy.8, P-7, Parbhani Kranti, Sel-10 and Sel-4. The cultivar BO-2 was susceptible and MDV-1 and Pusa Sawani recorded 90.83 and 91.53 per cent infection, respectively.

Singh *et al*. (2002) conducted an experiment during *kharif* season under Chhattisgarh condition and Parbhani Kranti was found to be susceptible to YVMD (51.2%) whereas, Arka Anamika was moderately resistant to YVMD (32.2%).

The work carried out by Vijaya (2004) concluded that VRO-5 exhibited the lowest disease incidence of 2.7 per cent with a yield of 58.6 q ha^{-1} and no disease with yield of 60.57 q ha^{-1} in the following year. On the other hand, Parbhani Kranti showed high susceptibility to YVMD with 26.1 per cent and 43.55 per cent frequencies in both years, respectively.

Okra hybrids screened by Neeraj *et al*. (2004) for YVMD and reported highest yield in NOH-15 hybrid (74.8q ha-1) with 11.9 per cent YVMD incidence. Further, NOH-15, JNODH-1, AROH-47 and HYOH-1 were found to share nearly same result with each other for yield and YVMV disease incidence.

Narayanan and Muthiah (2016) carried out a screening study on thirty okra accessions against YVMV disease under Tamil Nadu conditions. This study concluded that accession IC 15027 along with eight other okra accessions were found to be resistant, whereas accessions IC 90214, IC 90213, IC 90203 and IC 90202 displayed moderately resistant reaction. Other accessions and a variety Pusa Sawani showed susceptibility to YVMD disease. In another study by Seth *et al.* (2016), an evaluation was done on twentysix lines of okra including twenty-four of *A. esculentus*, one each of *Abelmoschus manihot* and *Abelmoschus caillei* in one of the hot spots of YVMD disease in West Bengal in order to identify suitable parents for resistant breeding programme. The results showed that six genotypes *viz.,* BCO-1, *Abelmoschus manihot*, *Abelmoschus caillei*, 11/RES-6, VNR Green and 12/RES-2 were found to be highly resistant to YVMV disease along with desirable attributes.

A study was carried out by Kumar and Tayde (2018) on eight okra genotypes with diverse morphological characters. Based on disease scale against YVMV showed completely free/ immune in VRO-5 to YVM disease incidence, whereas IC117216, 1C140934 and Parbhani Kranti genotypes were moderate resistant while two other genotypes 1C433695 and 1C140906 were found to be tolerant against YVMD . On the contrary, the genotype VRO - 4 was found susceptible.

Prakash *et al*. (2017) screened Pusa Sawani as susceptible check variety along with sixty okra genotypes for YVMD resistance under field conditions. Coefficient of infection and per cent disease incidence were calculated for all the genotypes. Per cent diseases incidence ranged from 10 to 100 per cent, whereas coefficient of infection varied from 5 to 100 per cent. Out of sixty okra genotypes, seven were resistant, fifteen moderately resistant, sixteen were moderately susceptible, thirteen susceptible and nine were highly susceptible.

Manju *et al*. (2018) conducted a field screening for the YVMD resistance with 25 okra germplasm accessions. Out of these accessions, one wild accession 1C344598 and two cultivated accessions *viz.,* PSRJ-12952 and RJR-124 exhibited immune reaction (0%) for YVMD infection throughout the crop period and recorded the maximum yield. Okra accessions, PSRJ-13040 and RJR-193 exhibited highly susceptible reaction, recording 84.1 and 83.33 per cent YVMD incidencerespectively and also recorded the lowest yield.

Kumari *et al*. (2018) studied the reaction of YVMD on twenty okra genotypes including four checks Kashi Kranti, Kashi Satdhari, Kashi Lalima and Arka Anamika using whole-plant scoring at the intervals of 30, 45 and 60 days respectively. The genotypes were screened and evaluated in open field conditions in rainy season. Out of the twenty genotypes, five were observed to show resistant reaction, while eight others were moderately resistant to this disease. The remaining genotypes showed susceptible and moderately susceptible reaction. The five resistant genotypes exhibited highest resistant reaction were Kashi Kranti (18.35%), Kashi Satdhari (19.39%), Kashi Lalima (20.34%), Kashi Mohini (20.81%) and Punjab 8 (21.45%). A significantly high

incidence of YVMD was found to be during the months of April and May due to high temperature coupled with high rainfall.

Jamir *et al*. (2020) identified genotype BCO-1 as resistant among 565 genotypes screened, while two genotypes IC433616 and IC111551 were reported to be moderately susceptible against enation leaf curl virus disease up to 60 days after sowing.

Oraon *et al*. (2020) screened three okra varieties *viz*., Arka Abhay, Arka Anamika and Pusa Makhmali and showed minimum per cent of YVMV incidence in Pusa Makhmali at different stages of crop gorwth (3 per cent at flowering stage, 5 per cent at fruiting stage and 7 per cent at maturity stage). Arka Abhay was reported as moderately resistant against YVMV.

2.2.1.4 Genetics of YVM resistance

Varma (1952) studied the relationship between YVMD and its vector white fly population. Despite the fact that a single insect was able to transmit the virus, the minimum number of flies required to produce hundred per cent infection was about 10. The first visual symptom is the clearing of small veins, which usually starts at various points near the leaf margins in about 15 up to 20 days after inoculation of plants. Affected plants produce flowers early and chemical control of the disease proves to be difficult. Destruction of alternative hosts, control of whitefly and other sucking insects, uprooting and burying of infected plants are some of the drastic measures taken to reduce the vector population and also the diseased plants. Wild Okra species such as *A. pungens, A.crinitus, H. vitifolius, H. panduriformis* were immune to this virus.

A number of research workers since 1962 studied the inheritance of this disease. There was no definite conclusion as to the nature of resistance to YVMD in okra genotypes, which may be due to complexity of the disease and more so on getting congenial environment for the establishment of its vector, the whitefly. Nevertheless, there were continuing efforts in order to deter the spread of this deadly viral disease by involving wild relatives as a source of resistance at several Institutions (Dhankar and Kumar, 2012).

According to Niraja *et al.* (2018), the genetic studies of fifteen quantitative traits showed that direct selection through characters such as days to 50 per cent flowering, plant height, fruit length, number of fruits per plant and the incidence of YVMD at 30, 75 and 90 DAS would be effective for improvement in okra to develop a resistance genotype against YVMD.

2.3 Genetic variability

Genetic variability was assessed by Singh and Singh, (1979) in 30 strains of okra and reported high genotypic coefficient of variation (GCV), heritability and genetic advance for first fruiting node, number of pod bearing branches, number of pods per plant and fruit yield per plant,.

Balakrishnan and Balakrishnan (1988) based on their work on the evaluation of bhindi germplasm, reported high phenotypic and genotypic variances for yield per plant followed by plant height and lower variances for number of ridges per fruit and fruit girth. The study further reported high heritability coupled with high genetic advance for plant height, fruit weight, number of fruits per plant, number of seeds per fruit and yield per plant.

A considerably wider coefficient of variation was noticed for yield contributing characters in bhindi genotypes, high genotypic coefficient of variation was recorded for hundred seed weight, pod weight and number of pods per plant. The genetic advance and heritability were found to be higher for yield per plant, number of pods per plant, pod length and pod weight (Jeyapandi and Balakrishnan, 1992).

Mondal and Dana (1993) evaluated ten okra genotypes for nine yield components grown in three consecutive seasons. They observed highly significant differences between seasons, genotypes and season x genotype for all the nine yield components. The highest heritability was observed for number of seeds per fruit, while the lowest for number of nodes on main stem. The genotypic coefficient of variation was low for days to 50 per cent flowering and high for branches per plant. Genetic advance was the highest for yield per plant and the lowest for crude fibre content.

Gondane and Lal (1994) observed a high level of variability for eleven yield components in bhindi. A considerably moderate heritability coupled with high level of genetic advance for pods per plant, primary branches per plant and leaves per plant were observed.

Genotypic and phenotypic variances coefficients of variation and heritability were estimated by Patil *et al.* (1996) for eleven characters in 171 okra genotypes. This study revealed considerable differences for some characters in two seasons. Number and weight of good pods per plant and borer infested pods per plantshowed seasonal difference. In general, genotypic and phenotypic variance was found to be higher in *kharif* than *rabi* season. PCV and GCV values was low for number of days to flowering and high for the weight of borer infested pods. The research further revealed a considerably high genetic advance for characters such as number of good pods per plant, plant height and weight of good pods per plant which served as indicators for the effective selection.

Gandhi *et al.* (2001) evaluated forty four genotypes of okra for thirteen quantitative characters. High GCV and PCV were found for number of branches per plant, height at first fruit set and dry fruit yield per plant. Wide difference between GCV and PCV were observed for characters like branches per plant and seed yield per plant, which indicated the role of environment in the expression of characters. High heritability estimates were seen for fruit length, fruit girth and plant height at first fruit set. Additive genetic variance was reported for characters like plant height, height at first fruit set, length of internode, number of branches per plant, fruit length and number of fruits per plant.

Dhankhar and Dhankar (2002) used fifteen advanced lines of okra and studied PCV, GCV, heritability and genetic advance of fruit yield and its components *viz.*, number of fruits per plant, days to 50 per cent flowering, number of branches per plant, plant height and first fruiting node on stem. Low GCV and PCV were reported for all the characters studied. Moderate GCV, PCV and heritability were estimated for fruits per plant and plant height, and genetic advance was also moderate for all the characters which indicated a limited scope for further improvement through selection.

Mulge *et al.* (2004) studied the genetic variability of 69 okra genotypes for different fruit and yield parameters. The study showed that the genotypic and phenotypic variation were high for number of seeds per fruit and total yield per plant, moderate for number of ridges per fruit, fruits per plant, fruit length, locules per fruit, fruit diameter and average fruit weight, whereas fruit circumference exhibit low GCV and PCV. High heritability and high genetic advance were recorded for ridges per fruit, fruits per plant, total yield per plant, seeds per fruit and locules per fruit.

Jaiprakashnarayan *et al.* (2006) evaluated 69 okra genotypes and reported high GCV and PCV variations for branches per plant, plant height at 100 DAS and internode length. Moderate GCV and PCV were observed for nodes on main stem, leaves at 100 DAS and node number at first flowering. However, days to first flowering and days to 50 per cent flowering showed low GCV and PCV. High heritability with high genetic advance were observed for plant height at 100 DAS, nodes on main stem, internodal length, number of leaves at 45 DAS and node number at first flowering. High heritability and low genetic advance were observed for days to first flowering and days to 50 per cent flowering.

Mehta *et al.* (2006) estimated the genetic variability in 22 diverse okra genotypes for fruit yield and its components and the study revealed that PCV was higher than GCV for all the seven traits and therefore indicated the influence of environment in the expression of these characters. The GCV, heritability as well as genetic advance expressed as percentage of mean were found to be higher for plant height, fruit yield, average fruit weight and fruit length attributed to additive gene action resulting in their inheritance. The fruit yield was significant and positively associated with fruit length and average fruit weight.

In a study carried out by Sachan (2006) involving six popular okra genotypes (Parbhani Kranti, Puss Sawani, Satdhari, Punjab-7, K-21 amd Arka Anamika) for yield performance, the highest plant height, number of nodes per plant and number of pods per plant were noticed in Arka Anamika, followed by Parbhani Kranti. Satdhari exhibited the highest pod weight and green pod yield along with minimum disease incidence and hence proved to be the most promising cultivar of Sikkim.

Sarkar *et al.* (2006) evaluated 25 genotypes of okra during *kharif* season for their suitability in the alluvial ago climatic zone of West Bengal for twelve characters related to flowering pattern, yield and fruit quality. The highest yield was recorded in the cultivars Sagun, Arka Anamika, HR Selection, Sungrow Selection and Varsha Uphar. Bankim Selection-2, Nandini, Sungrow Selection and Selection-5 showed earliness in flowering.

Sindhumole *et al.* (2006) reported significant variation among 101 genotypes of okra for YVM resistance and yield traits. The study revealed that most of the traits including yield and its major components exhibited high phenotypic and genotypic coefficients of variation. Maximum values of both PCV and GCV were recorded for fruit yield and protein content in fruits. Most of the traits possessed high heritability, the highest for fruits per plant followed by fruit yield and ridges per fruit. Protein content and fruit yield exhibited high genetic advance. Incidence of yellow vein mosaic also had high PCV and GCV.

Singh *et al*. (2006) reported significant variation among fifteen okra genotypes for all the quantitative traits. GCV and GCV were high for number of fruits per plant, number of seeds per pod, internodal length, number of branches per plant and fruit yield per plant. Moreover, the characters such as internodal length, branches per plant, seeds per pod, fruits per plant, fruit yield per plant, plant height and 100-seed weight showed high heritability and genetic advance which indicated that there are more number of additive factors and further improvement is possible by selection.

A considerable amount of genetic variation was reported in bhindi for branches per plant, plant height, fruit yield per plant and fruit length (Singh and Singh, 2006). The heritability was high for days to first flowering and length of the first fruiting node.

Sood (2006) observed GCV, PCV and heritability for various characters in 43 okra lines of diverse origin. GCV and PCV were high for fruit yield per plant, node of first fruit set and plant height in market crop. The days to marketable maturity had low heritability, while ridges per pod had high heritability.

According to Singh *et al.* (2007), genotypic and phenotypic coefficients of variation were high for plant height, number of branches, plant height, number of fruits and fruit yield

in okra. GCV was found to be lower than the corresponding PCV. Moreover, most of the characters recorded high values of heritability coupled with high genetic gain. High magnitude of the genetic advance was observed for number of branches, plant height, number of fruits, fruit yield, fruit length, fruit girth and internodal length.

One hundred and one genotypes of okra were evaluated and high GCV as well as PCV for primary branches per plant, plant height, internodes per plant and fruit yield were reported by Saifullah and Rabbani (2009). High heritability and moderate genetic advance were noticed for days to first flowering, fruits per plant and seeds per fruit, while heritability and genetic advance were low for fruit length.

Prakash and Pitchaimuthu (2010) conducted an experiment on genetic variability of yield contributing characters in 40 genotypes of okra and observed high GCV and PCV values for plant height, length of internode, height of first flowering node, first flowering node, average fruit weight as well as the number of seeds per fruit. The highest value of heritability was noticed for hundred seed weight (93.93 %), while stem girth had the least value (56.98 %). Heritability was high for average fruit weight, seeds per fruit and days to 50 per cent flowering.

According to Rohit *et al*. (2011), no parallelism existed between genetic and geographic divergence in 53 okra germplasm. Kumar *et al*. (2016) assessed 30 okra genotypes for yield and yellow mosaic virus incidence. The character coefficient of disease infection alone contributed the highest percentage (51%) toward divergence, followed by branches per plant (24%) and percentage disease incidence (12%).

An investigation of the morphological distinctiveness among varieties and between species of okra was carried out by Ogwu *et al.* (2018). The study utilised five okra accessions obtained from the National Centre for Genetic Resources and Biotechnology, Nigeria, including two *Abelmoschus esculentus* (NO/OA/03/12/157 and NO/OA/05/12/159) and three *Abelmoschus caillei* (NG/OA/03/12/158, NG/SA/DEC/07/0475, and NG/SA/DEC/07/0482) species. Significant differences were observed among all the five accessions for stem length, petiole length and leaf node. This study suggested that morphological variations existed

among the accessions. The characteristics could distinguish the *Abelmoschus* accessions into *Abelmoschus caillei* and *Abelmoschus esculentus* and provide credence to the use of morphological traits to characterise plant genetic resources.

Thirty six okra genotypes were evaluated along with three checks for 27 quantitative characters by Mohammed *et al.* (2020). Significant variation was noticed for all quantitative traits. For the majority of the characters, the checks had low mean performance as compared to genotypes. GCV, PCV, H^2 and GAM were high for all the traits, except days to 90% maturity, hundred seed weight. Ridges per fruit and hundred seed weight showed moderate heritability. Moreover, ridges per fruit, days to 90 per cent maturity and percentage of mucilage content had moderate genetic advance whereas it was low for hundred seed weight.

2.4 Correlation

Yield has been considered as a complex character governed by polygenic system. It is also known to be highly influenced by environmental fluctuations. Hence, plant selection on the basis of yield only would be unreliable in many cases. The information on nature and extent of association between pair of characters would strengthen the selection programme, aiming at the improvement in crop yield. Better understanding of yield components can be highly supported by correlation studies and also helps the plant breeder during selection (Johnson *et al.,* 1955).

Reddy *et al.* (1985) noticed that fruit yield per plant in okra was positively correlated with other traits such as plant height, number of branches, days to flower, fruit length, fruit width and fruits per plant. The work further revealed that all the traits registered positive significant correlation among them except first flowering node.

Kale *et al.* (1989) worked out the estimates for genetical parameters such as phenotypic and genotypic correlation in 36 genotypes of bhindi and found that moderate to high correlation existed for number of branches, internodal distance, number of nodes, plant height and number of pods per plant. Moderate to high heritability estimates were also found for plant height, number of branches, and number of nodes, internodal length and number of pods per plant. The study further observed that yield per plant was significant and can be

positively correlated with plant height, days to flowering, number of fruits per plant and leaf area.

Patel and Dalal (1992) conducted a correlation study and reported a positive correlation between the yield and all traits in okra. Magnitude of correlation was found to be higher between yield and pod weight, pod length, pod girth, number of pods per plant and plant height except days to flowering.

Characters including pods per plant, weight of edible pod, stem thickness and plant height were significantly and positively correlated with yield per plant in bhindi (Gondane *et al.,* 1995). Negative correlation was noticed for length of pod with leaves per plant, days to 50 per cent flowering, node of first pod and branches per plant.

While studying the correlation between characters, Deo (1996) observed that plant height, number of seeds, 100-seed weight and length of pod in bhindi had highly significant and positive correlation among themselves.

Yadav (1996) in an association analysis, reported that yield per plant in okra showed positive and significant correlation with plant height, number of pods per plant and number of node at first pod appearance.

Dash and Mishra (1998) carried out an association analysis in okra germplasm and revealed a positive correlation between fruit yield per plant with branches per plant, fruit length, fruit girth, fruit weight, seeds per fruit and seed weight per fruit.

Dhankhar and Dhankar (2002) also conducted a correlation study between the yield and yield attributes for 15 lines of okra. This study concluded that crop yield showed significant positive association with number of fruits and branches per plant, while first fruit node on the stem and number of days to 50 per cent flowering showed positive association with yield. Negative association with yield was noticed for plant height and days to 50 per cent flowering. Positive relationship existed for fruits per plant with days to 50 per cent flowering, branches per plant and first fruiting node on the stem. Highest direct effects on fruit yield were attributed to fruits per plant and days to 50 per cent flowering.

Sindhumole (2003) reported higher genotypic correlation coefficients than phenotypic correlation coefficients for most of the characters in okra genotypes. The fruit yield manifested positive genotypic association with fruits per plant, leaf area, average fruit weight, fruit length, seeds per fruit, fruit girth, plant duration and protein content, while negative correlation with days to first flower, pollen sterility, YVMD and incidence of fruit and shoot borer.

Inverse relationship between growth and earliness, and strong association between growth and yield characters in okra was reported by Jaiprakashnarayan and Mulge (2004). Per plant fruit yield was positively and significantly correlated with fruits per plant, nodes on main stem, average fruit weight, fruit length, plant height at 60 and 100 days after sowing and number of leaves at 45 and 100 DAS.

In another correlation study by Alcinyele and Osekita (2006) in okra, seed yield per plant showed significant positive correlation with pods per plant, height at flowering, pod width and weight of hundred seeds.

Amoatey *et al*. (2015) worked to find out the correlation coefficients in 29 local and exotic lines of okra and concluded that seven pairs of quantitative traits had significant positive correlation, the highest being between days to 50 per cent flowering and number of days to 50 per cent fruiting.

Adaxial and abaxial pubescence density and the number of whitefly adults throughout the growth stages of plant had negative significant correlation (Jamir *et al*., 2020). Negative significant correlation was also proved between leaf morphological parameters and YVMV disease severity.

Materials and methods

3.MATERIALS AND METHODS

This chapter contains the details about the materials used and the methods adopted during the course of present investigation entitled **'Assessment of genetic variability for YVM resistance in okra (*Abelmoschus esculentus* (L.) Moench)'** carried out in *Rabi* season during November 2019 to February 2020.

3.1 Experimental site

The present experiment was laid out in the experimental field of Department of Plant Breeding and Genetics, College of Horticulture, Kerala Agricultural University, Vellanikkara (Plates 1 and 2).

3.2 Experimental design

The experiment was conducted using thirty okra accessions and four check varieties in augmented design (Table 1).

Table 1. Detailed information of experiment

Particulars	Details
Season	*Rabi*, 2019-20
Date of sowing	11.11.2019
Design	Augmented
Block	2
Treatment	34 genotypes (30 accessions + four checks)
Spacing	60 cm x 45 cm
Total number of plants per line	10

Germination

Earthing up and weed control

Plate 1. Land preparation

Plate 2. General view of experiment field

3.3 Field preparation and sowing

Seedbed was prepared and the field was laid out with ridges taken at 60 cm apart and at 15 cm height. Each entry was sown in a single row with a spacing of 60 cm x 45 cm. For each genotype, 10 plants were raised and the package of practices were followed as per the recommendation of KAU (2017).

3.4 MATERIALS

A total of 34 okra accessions including four checks *viz*., Parbhani Kranthi and Varsha Uphar (resistant checks) and Salkeerthi and Pusa Sawani (susceptible checks) were collected from NBPGR and KAU (Kerala Agricultural University). Details of accessions and checks are presented in Table 2.

Table 2. Details of genotypes used in the study

S.No	TCR No	Accession No	S.No	TCR No	Accession No
1	TCR-30	IC 033323	18	TCR-2626	IC 375805
2	TCR-32	IC 033329	19	TCR-2627	IC 375806
3	TCR-1648	IC 008991	20	TCR-2628	IC 375807
4	TCR-1652	IC 9856A	21	TCR-2631	IC410504
5	TCR-1653	IC 9856B	22	TCR-2632	IC410620
6	TCR-1774	IC 034100B	23	TCR-2634	IC415584
7	TCR-1775	IC 034124A	24	TCR-2710	IC 526547
8	TCR-1785	IC 039134	25	TCR-2744	IC427560
9	TCR-1797	IC 042456	26	TCR-2832	EC762245
10	TCR-1806	IC 042484B	27	TCR-2833	EC762250
11	TCR-2391	IC 034132	28	TCR-2839	EC762256
12	TCR-2392	IC 034190B	29	TCR-2847	EC762231
13	TCR-2393	IC 034912A	30	TCR-2869	EC762276
14	TCR-2568	IC 369302	C1	Parbhani Kranti	
15	TCR-2610	IC419639	C2	Pusa Sawani	
16	TCR-2618	IC383132	C3	Salkeerthi	
17	TCR-2621	IC394398	C4	Varsha Uphar	

3.5 METHODS

3.5.1 Recording Observations

Observation on fifteen quantitative and five qualitative characters were made at various growth stages of the crop from five randomly selected plants for each accession. The descriptor list developed at ICAR-NBPGR, New Delhi (NBPGR, 2001) was used for recording the observations.

3.5.1.1 Date of flowering

Number of days taken from the date of sowing to date of first flowering of the plants was recorded.

3.5.1.2 Leaf blade length (cm)

Measurement of length of leaf blade from the point of the attachment of leaf blade to the tip of middle leaf length was carried out from randomly selected three leaves of each genotype with the help of measurement tape and recorded in cm.

3.5.1.3 Leaf blade width (cm)

The width of leaf blade was measured from randomly selected three leaves of each accession with the help of measurement tape from one side of the leaf to another side of the leaf and recorded in cm.

3.5.1.4 Leaf area (cm^2)

Three leaves were randomly collected from each treatment and their area was determined graphically, average was taken and recorded in square centimeters (Plate 3).

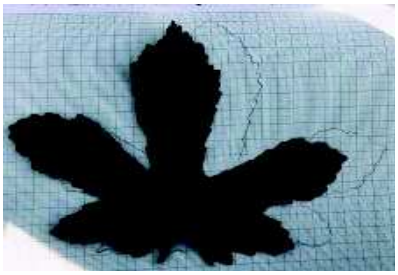


Plate 3. Graph paper method to record leaf area

3.5.1.5 Plant height (cm)

Height of the plant was recorded in centimeters using a meter scale from the ground level to the tip during last harvest and the mean value was recorded for each genotype.

3.5.1.6 Branches per plant

The number of branches of each observational plant was counted and recorded during final harvest.

3.5.1.7 Petal colour

The petal colour of the genotypes was recorded as per given below:

Petal colour	Score
Yellow	1
Cream	2
Purple	3

3.5.1.8 Petal base colour (purple)

The petal base colour (purple) of the genotypes was recorded as given below.

Petal base colour (Purple)	Score
Both side	1
Only inside	2

3.5.1.9 Fruits per plant

Fresh marketable fruits were picked from the selected plants separately throughout the harvesting period at an interval of 2-3 days, their number was recorded and finally the total number of fruits per plant was calculated for each genotype.

3.5.1.10 Fruit colour

Fruit colour was scored as per descriptor given below.

Fruit colour	Score
Yellowish green	1
Green	2
Green with red patches	3
Dark green	4
Dark red	5
Others	99

3.5.1.11 Fruit length

The length of fruit from the base to the tip was measured during harvest and the mean was expressed in centimeters Plate 4.

Plate 4. Measuring the fruit length

3.5.1.12 Fruit diameter (cm)

Fruit diameter was recorded at the mid portion of three fruits from five observational plants with the help of measurement tape and the mean was expressed in centimeters.

3.5.1.13 Fruit pubescence

The pubescence of sample fruits was recorded at marketable stage under the following categories as given below.

Fruit pubescence	Score
Downy	3
Slightly rough	5
Prickly	7
Others	99

3.5.1.14 Ridges per fruit

The number of ridges of sample fruits of each genotype was counted and recorded.

Ridges per fruit	Score
5-7	1
8- 10	2
More than 10	3
Others	99

3.5.1.15 Seeds per fruit

Three fruits were sampled randomly and their seeds were counted and average was recorded.

3.5.1.16 Seed hairiness

The presence of seed hairiness was noted on dried mature fruit samples after harvesting and was classified under the following categories.

Seed hairiness	Score
Smooth	1
Hairs present	2

3.5.1.17 Fruit weight (g)

The average of fruit weight was computed from the total fruit weight of the five randomly selected plants and expressed in grams.

3.5.1.18 Fruit yield per plant (g)

Fresh marketable fruits were picked from the selected plants separately throughout the harvesting period at an interval of 2-3 days and their weight was recorded. After final harvest, the total yield per plant of observation plants was calculated and the average per plant yield was calculated for each genotype.

3.5.1.19 Vector population on young leaves

The total population of whitefly (*Bemisia tabaci*) on first, third and fifth leaves of the plant in the morning and evening during 30, 50, 65 and 75 DAS of the crop were recorded. Observations were made on the lower side of the leaves in each plant and the total number of white flies was counted and means were computed.

3.5.1.20 Scoring for YVM disease

Scoring for disease incidence was done as per the rating scale by Arumugam *et al.* (1975) as furnished in Table 3.

Table 3. YVM disease rating scale in okra

Symptom	Severity grade	Reaction
Visible Symptoms were not observed	1	HR
Very Mild symptoms	2	R
Veins and veinlets completely turned to yellow	3	MR
leaf lamina turn yellow up to 50 per cent and fruits exhibit slight yellowing	4	S
The fruits color turns to yellow and the leaves start drying from the leave margin.	5	HS

3.5.1.20.1 Disease assessment

The disease incidence (PDI) was calculated as per cent using the following formula:

$$\textbf{PDI} = \frac{\text{Number of infected plants}}{\text{Number of plants observed}} \text{x} 100$$

Percentage of diseases severity (PDS) was calculated using the formula given below:

$$\mathbf{PDS} = \frac{\text{Sum of all numerical ratings}}{\text{Number of plants observed}} x \frac{100}{\text{maximum grade}}$$

The coefficient of YVM infection calculated based on the per cent disease incidence and severity (Dater and Mayee, 1981) (Table 4).

$$\mathbf{CI} = \frac{\text{PDI x PDS}}{100}$$

Table 4. Categories based on coefficient of infection (CI)

CI	Category
0-4	Highly Resistant (HR)
4.1-9	Resistant (R)
9.1-19	Moderately Resistant (MR)
19.1-39	Moderately Susceptible (MS)
39.1-69	Susceptible (S)
69.1-100	Highly Susceptible (HS)

3.6 Statistical analysis

3.6.1 Analysis of variance (ANOVA)

Analysis of variance, estimation of genetic parameters and correlation studies were done by using the software Windostat version 9.2.

3.6.2 Estimation of genetic parameters

A. Genetic components of variance

For each quantitative character, PCV and GCV were assessed by associating the value of expected mean squares to the respective variance components (Jain, 1982). The components of variance were estimated as follows:

i. Genotypic variance (VG)

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

ii. Environmental variance (VE)

$$VE = MSE$$

iii. Phenotypic variance (VP)

$$VP = VG + VE$$

B. Coefficients of variation

PCV and GCV were worked out for each trait using the estimates of VG and VP expressed in percentage (Burton, 1952).

Phenotypic coefficient of variation (PCV)

$$\mathbf{PCV} = \frac{\sqrt{Vp}}{\bar{\bar{x}}} \text{ x}100$$

Genotypic coefficient of variation (GCV)

$$\mathbf{GCV} = \frac{\sqrt{V_G}}{\bar{\bar{x}}} \text{ x}100$$

$\overline{X}$ is the mean of each character estimated over all the treatments

The coefficients of variation are categorised as:

According Burton (1952), PCV and GCV were classified as low (<10%), moderate (10-20%) and high (>20%).

C. Heritability

The heritability (H^2) of each trait (in broad sense) was calculated as the ratio of genotypic variance to phenotypic variance. The value obtained is expressed as a percentage (Lush, 1937).

$$\textbf{Heritability } (\mathbf{H^2}) = \frac{V_G}{V_p} x100$$

According to Robinson *et al*. (1949), heritability was categorized as low (< 30%), moderate (31-60%) and high (>60%).

D. Genetic Advance

Genetic advance was seen (Allard, 1960) as the measure of genetic gain under selection which depends upon standardized selection differential, heritability and phenotypic standard deviation.

$$\text{GA as percentage of mean} = k.\, H^2 \sqrt{V_p}$$

Here k is the standardized selection differential (2.06 at 5% selection).

According to Robinson *et al*. (1949), genetic advance as percentage of mean is categorized as low (< 10%), moderate (11-20%) and high (>20%).

3.6.3 Correlation analysis

Variances and covariances of the quantitative traits were used to determine the phenotypic correlation coefficients and such variances were observed to show significant change in the ANOVA.

$$\text{Phenotypic correlation coefficients, } r_{PXY} = \frac{COVp(X,Y)}{\sqrt{Vp(X).Vp(Y)}}$$

Where, CoVp (x, y) denotes the phenotypic covariance between the two traits x and y, Vp (x) is the phenotypic variance for x and Vp (y) is the phenotypic variance for y.

Results and discussion

4. RESULTS AND DISCUSSION

The present investigation entitled '**Assessment of genetic variability for YVM resistance in okra (*Abelmoschus esculentus* (L.) Moench)**' was conducted at the experimental field of Department of Plant Breeding and Genetics, College of Horticulture, Kerala Agricultural University, Vellanikkara, during November 2019 to February 2020.The experimental results are described under the following headings:

4.1 Evaluation of qualitative characters
4.2 Evaluation of quantitative characters
4.3 Genetic variability parameters
4.4 Correlation analysis
4.5 Disease response of okra genotypes

4.1 Evaluation of qualitative characters

Variability among genotypes for characters such as petal colour, petal base colour, fruit colour, fruit pubescence and seed hairiness were observed visually and the results are furnished below

4.1.1 Fruit colour

The classification of genotypes based on fruit colour is presented in Table 5. Observations recorded for fruit colour in 34 genotypes indicated that twelve genotypes had fruits with light green, eleven with green, five with dark green, one with yellowish green, three red, one dark red and one green with purple blend Plate 5. Fruit colour can be used as a distinguishing feature to identify these specific genotypes. Similar results on fruit colour stable over the environment and contributing more variations in different okra genotypes were reported by earlier researchers AdeOluwa and Kehinde (2011), Osawaru *et al*. (2013) Gangopadhyay *et al*.(2017) and Samim (2018). Kaur *et al*. (2018) reported variability among various genotypes (including wild species) with respect to fruit colour and grouped as yellowish green, green and dark green

Table 5. Classification of okra genotypes on the basis of fruit colour

Fruit colour	Code	Genotypes	Number of genotypes	Per cent
Yellowish green	1	TCR-2833	1	2.94
Green	2	TCR-1653, TCR-1797, TCR-1806, TCR-2391, TCR-2392, TCR-2393, TCR-2634, TCR-2710, TCR-2832, TCR-2847 and Parbhani Kranti	11	32.35
Dark green	4	TCR-1648, TCR-2618, TCR-2627, Pusa Sawani and Varsha Uphar	5	14.71
Dark red	5	TCR-2632	1	2.94
Light green	99	TCR-30, TCR-32, TCR-1652, TCR-1774,TCR-1775, TCR-2568, TCR-2610, TCR-2621, TCR-2631, TCR-2744, TCR-2839 and Salkeerthi	12	35.29
Red	99	TCR-2626, TCR-2628, TCR-2869	3	8.82
Green with purple blend	99	TCR-1785	1	2.94

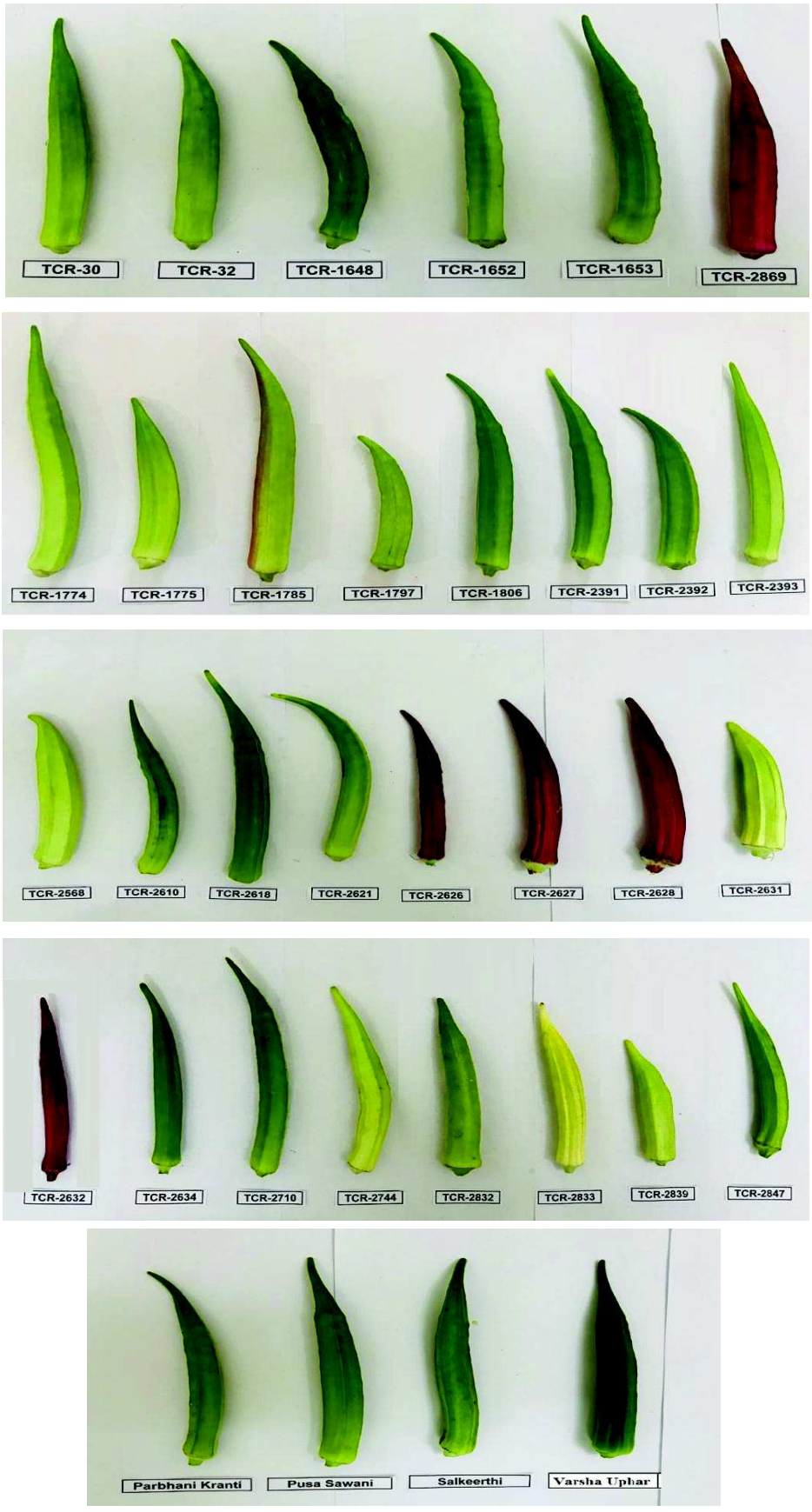


Plate 5. Variability in okra fruits

4.1.1 Fruit pubescence

Pubescence on surface of fruits was downy in 27 genotypes, slightly rough in five genotypes and strong in two genotypes (Table 6). Gangopadhyay *et al.* (2017) reported variability for fruit pubescence among eighteen *A. caillei* genotypes; two as weak, fourteen as medium and two as strong. As per the reports of Singh *et al*. (2015), hairs on fruits were absent in 2, weak in 12, medium in 14 and strong in 8 okra genotypes.

Table 6. Classification of okra genotypes based on fruit pubescence

Fruit pubescence	Code	Genotypes	Number of genotypes	Per cent
Downy	3	TCR-1806, TCR-2626, TCR-2627, TCR-2628, TCR-2869, TCR-30, TCR-32, TCR-1648, TCR-1774, TCR-1775, TCR-1797, TCR-2391, TCR-2392, TCR-2568, TCR-2610, TCR-2618, TCR-2621, TCR-2631, TCR-2632, TCR-2634, TCR-2710, TCR-2832, TCR-2847, Parbhani Kranti, Pusa Sawani, Salkeerthi and Varsha Uphar	27	79.41
Slightly rough	5	TCR-1653, TCR-1785, TCR-2393, TCR-2833 and TCR-2839	5	14.71
Strong	7	TCR-1652 and TCR-2744	2	5.88

4.1.2 Petal colour

Petal colour was yellow in fourteen, cream in fifteen and purple in five genotypes (Table 7). This trait can also be useful for identifying specific genotypes. Similar investigation was carried out in okra by Singh *et al*. (2015) and reported yellow petals in 32 genotypes and cream petals in four genotypes.

Table 7. Classification of okra genotypes based on petal colour

Petal colour	Code	Genotypes	Number of genotypes	Per cent
Yellow	1	TCR-1652, TCR-1653, TCR-1774, TCR-2391, TCR-2392, TCR-2621, TCR-2710, TCR-2744, TCR-2833, TCR-2847, Parbhani Kranti, Pusa Sawani ,Salkeerthi and Varsha Uphar	14	41.18
Cream	2	TCR-30, TCR-32, TCR-1648, TCR-1775, TCR-1785, TCR-1797, TCR-1806, TCR-2393, TCR-2568, TCR-2610, TCR-2618, TCR-2631, TCR-2634, TCR-2832 and TCR-2839	15	44.12
Purple	3	TCR-2626, TCR-2627, TCR-2628, TCR-2632 and TCR-2869	5	14.71

4.1.3 Petal base colour (purple)

Out of the 34 genotypes screened, twenty nine genotypes were with purple colour on both sides at the base of petal, while five genotypes were with purple colour at base of petal inside only (Table 8). Similar to this finding, Singh *et al*. (2015) reported variability in petal base colour (purple) as inside only in eight genotypes and on both sides in 28 genotypes. Gangopadhyay *et al.* (2017) observed this trait as inside only in 13 genotypes of *A. manihot* and 3 in *A. tuberculatus* genoytpes whereas, on both sides in sixteen *A. manihot* and two *A. tuberculatus* genotypes.

Table 8. Classification of okra genotypes based on petal base colour

Petal base colour (purple)	Code	Genotypes	Number of genotypes	Per cent
Both sides	1	TCR-30,TCR-32,TCR-1648,TCR-1775, TCR-1797,TCR-1806,TCR-2393,TCR-2568, TCR-2610,TCR-2618,TCR-2631,TCR-2634, TCR-2832,TCR-1652,TCR-1653,TCR-1774, TCR-2391,TCR-2392,TCR-2621,TCR-2710, TCR-2744,TCR-2833,TCR-2847, Pusa Sawani, Varsha Uphar,TCR-2626,TCR-2627, TCR-2632 and TCR-2869	29	85.29
Inside only	2	TCR-1785, TCR-2628, TCR-2839, Parbhani Kranti and Salkeerthi	5	14.71

4.1.5 Seed Hairiness

All the thirty four okra genotypes examined were without hairs on their seeds. In contrary, Singh *et al*. (2015) reported that among the thirty six genotypes, twenty eight were without seed hairs while eight were with seed hairs.

4.2 Evaluation of quantitative characters

Data on statistical analysis of 15 quantitative characters of okra genotypes in augmented design is presented in Table 9 and their mean performance for various traits presented in Table 10.

4.2.1 Days to first flowering

Significant variation was noticed among thirty accessions for days to first flowering with over all mean value of 44.64 days. TCR-1797(39.40) was the earliest flowering genotype and TCR-2628 (56.20) took maximum days to flowering. Among the check varieties, it ranged from 38.89 days in Parbhani Kranti to 48.73 days in Salkeerthi with a mean of 44.24 days. Eight accessions such as TCR-2628, TCR-2833, TCR-2631, TCR-2568, TCR-2627, TCR-1775, TCR-2869 and TCR-2632 were late in flowering while, eleven accessions *viz.,*TCR-2392, TCR-1648, TCR-1797, TCR-32, TCR-30, TCR-2839, TCR-2391, TCR-2621, TCR-1774, TCR-2710 and TCR-1652 were early to flower compared to the check mean.

The variation in first flowering among different genotypes might be due to their varying adaptability to the climatic conditions and genetic variation of the accessions as suggested by Haider *et al*. (2017). The results are in accordance with the findings of Sonia (1999) and Mann *et al*. (2009). According to Mohammed *et al*. (2020), days to first flowering varied from 44.33 to 71.00 in different okra genotypes and significant delay was noticed in some of the genotypes. In the present study, days to first flower opening was very much delayed in TCR-2628, nearly two weeks, which may sometimes be due to the effect of environment as reported by Ossom and Kunene (2011) and Elhag and Ahmed (2014). However, Silva *et al.* (2020) suggested that late flowering may be mostly contributed by the genetic variation.

Table 9. Mean sum of squares for quantitative traits in okra germplasm

Source	Mean sum of squares														
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
	DF	LL	LW	LA	PH	BP	FL	FD	RF	SF	FP	FW	FY	CI	VP
Genotypes	22.75	8.98	23.27	9156.94	342.75	0.88	10.57	0.46	1.43	102.11	6.50	14.72	4979.12	259.82	5.70
Checks	37.56	0.85	0.086	614.65	271.27	0.98	39.76	0.39	0.01	6.73	19.98	33.87	16167.09	856.63	4.05
Error	0.38	1.09	10.39	21.65	3.96	0.06	0.09	0.01	0.01	0.75	0.57	2.19	117.67	2.44	5.15

1- DF - Days to first flowering
2- LL - Leaf blade length (cm)
3- LW - Leaf blade width (cm)
4- LA - Leaf area (cm^2)
5- PH - Plant height (cm)
6- BP - Branches per plant
7- FL - Fruits length (cm)
8- FD -Fruit diameter (cm)
9- RF - Ridge per fruit
10- SF - Seeds per fruit
11- FP - Fruits per plant
12- FW - Fruit weight (g)
13- FY - Fruit yield per plant (g)
14- CI - Coefficient of YVM Infection (%)
15- VP - Vector population

Table 10. Mean performance of okra genotypes for quantitative traits

Tr. No.	Genotype	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
		DF	LL	LW	LA	PH	BP	FL	FD	RF	SF	FP	FW	FY	CI	VP
1	TCR-30	40.30	15.42	23.30	111.00	58.80	3.40	15.25	1.80	5.00	45.00	7.50	17.85	137.60	0.00	3.80
2	TCR-32	40.00	12.80	18.80	109.25	71.60	2.10	13.85	2.10	5.00	43.33	6.60	14.38	95.90	25.08	5.80
3	TCR-1648	39.60	21.90	22.85	125.25	70.90	2.60	17.70	2.00	5.00	58.00	6.50	15.17	101.20	39.44	6.80
4	TCR-1652	41.50	12.50	16.50	94.33	41.50	3.30	12.40	2.14	4.70	58.00	6.70	13.80	91.40	11.68	8.90
5	TCR-1653	41.60	19.10	24.30	130.67	39.80	3.20	13.00	1.70	5.00	38.33	6.80	14.56	99.00	48.24	9.10
6	TCR-1774	41.40	20.40	22.40	165.67	77.00	3.10	18.90	1.80	5.00	46.67	14.90	18.32	274.70	45.60	9.70
7	TCR-1775	50.20	15.10	20.30	109.33	92.00	2.70	11.80	2.10	5.00	44.00	8.80	16.96	153.10	57.44	9.10
8	TCR-1785	43.70	15.40	20.40	131.00	102.50	2.00	16.50	1.90	5.00	60.00	6.60	18.06	122.30	53.36	8.50
9	TCR-1797	39.90	16.20	22.60	156.33	98.50	2.70	17.90	2.20	5.20	49.67	10.90	17.39	190.00	52.40	4.70
10	TCR-1806	42.00	18.30	15.48	128.33	64.70	3.40	12.10	1.90	5.00	52.00	7.30	17.69	129.60	47.60	9.70
11	TCR-2391	41.00	14.70	24.00	120.00	73.50	2.00	17.70	1.70	5.00	41.33	6.00	14.35	89.00	55.20	8.50
12	TCR-2392	39.40	17.90	23.30	86.33	50.70	1.17	12.10	1.80	5.00	48.00	5.90	18.46	107.90	30.04	6.00
13	TCR-2393	43.33	16.56	22.89	207.33	57.56	3.56	18.44	1.90	5.00	42.00	6.89	19.12	131.56	25.60	7.30
14	TCR-2568	52.50	14.62	19.40	118.83	73.15	3.00	15.95	1.95	6.10	50.00	7.60	15.65	118.70	37.96	4.70
15	TCR-2510	46.00	9.05	10.90	43.00	31.10	2.90	11.30	1.35	5.00	28.00	5.10	14.17	74.20	29.00	6.60
16	TCR-2618	42.80	16.15	21.49	111.00	50.60	3.10	18.35	1.90	5.00	42.67	6.40	14.74	95.00	29.80	8.30
17	TCR-2621	41.30	9.95	14.30	100.33	60.30	3.10	18.05	1.80	5.00	41.00	7.40	13.95	103.30	31.36	7.80
18	TCR-2626	45.70	20.85	28.90	438.00	89.70	1.00	16.06	1.85	5.70	60.75	7.60	17.46	186.90	56.00	8.00
19	TCR-2627	52.50	18.69	29.15	399.67	97.90	2.40	15.58	2.00	6.80	48.25	8.10	23.14	186.90	61.16	9.20
20	TCR-2628	56.20	18.07	26.30	395.00	90.50	1.10	15.20	2.14	6.80	79.60	6.60	22.76	146.00	51.84	7.00
21	TCR-2631	52.70	18.28	30.20	251.33	80.40	3.60	14.73	2.62	6.90	71.00	7.30	30.97	224.70	41.60	9.50
22	TCR-2632	48.10	12.60	15.76	67.33	56.10	4.50	14.20	1.80	5.00	51.00	5.90	19.47	118.00	38.40	7.30
23	TCR-2634	42.70	15.70	22.30	86.85	60.10	3.30	16.35	2.10	5.00	50.33	6.10	17.13	104.10	49.96	9.60

		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
24	TCR-2710	41.50	13.40	18.05	59.30	55.70	2.90	16.83	1.90	5.00	49.33	7.60	17.46	134.20	52.60	8.00
25	TCR-2744	42.20	13.80	15.77	59.33	39.49	2.70	13.09	2.20	7.10	44.00	3.70	15.76	58.30	51.16	16.20
26	TCR-2832	45.00	10.50	12.65	142.33	74.65	3.80	16.41	1.90	0.00	36.00	7.90	22.80	179.00	68.64	11.90
27	TCR-2833	54.90	16.90	29.00	370.67	81.80	3.20	13.70	1.70	6.50	71.33	6.20	20.94	117.50	74.04	10.00
28	TCR-2839	40.80	14.08	20.24	156.67	53.20	3.40	9.71	1.80	6.10	41.00	5.90	18.75	109.90	66.24	10.80
29	TCR-2847	41.70	18.68	23.60	147.00	73.80	4.20	10.30	2.20	7.50	49.67	7.20	17.52	128.40	52.80	5.90
30	TCR-2869	48.60	14.00	20.80	115.50	55.25	5.30	15.48	1.95	5.00	58.67	6.10	19.05	115.90	30.32	5.70
C1	Varsha Uphar	42.50	17.20	29.00	153.33	77.50	3.40	18.30	2.10	5.00	51.33	11.75	24.71	292.25	2.44	9.30
C2	Pusa sawani	46.83	16.85	24.69	117.89	55.63	2.89	11.33	1.85	5.00	48.73	5.70	15.69	90.43	53.64	9.60
C3	Parbhani Kranti	38.89	16.27	23.89	146.73	71.83	3.00	18.83	2.10	5.00	49.44	11.39	21.41	248.85	3.52	4.10
C4	Salkeerthi	48.73	16.87	24.69	114.89	82.69	4.49	21.89	1.95	5.00	47.18	12.83	22.26	294.22	40.84	7.20
Grand mean		44.64	15.72	21.20	157.90	67.43	2.96	15.03	1.94	5.31	49.96	7.14	17.93	130.81	43.81	8.15
Minimum		39.40	9.05	10.90	43.00	31.10	1.00	9.71	1.35	0.00	28.00	3.70	13.80	58.30	0.00	3.80
Maximum		56.20	21.90	30.20	438.00	102.50	5.30	19.65	2.62	7.50	79.60	14.90	30.97	274.70	74.04	16.20
Mean of check vars		44.24	16.80	25.57	133.21	71.91	3.45	17.59	2.00	5.00	49.17	10.42	21.02	231.44	25.11	7.55
CD		2.69	4.55	14.05	20.27	8.68	1.03	1.37	0.51	0.46	3.76	3.30	6.45	47.27	6.81	9.89

1- DF - Days to first flowering
2- LL - Leaf blade length (cm)
3- LW - Leaf blade width (cm)
4- LA - Leaf area (cm^2)
5- PH - Plant height (cm)
6- BP - Branches per plant
7- FL - Fruits length (cm)
8- FD - Fruit diameter (cm)
9- RF – Ridge per fruit
10- SF - Seeds per fruit
11- FP - Fruits per plant
12- FW - Fruit weight (g)
13- FY - Fruit yield per plant (g)
14- CI - Coefficient of YVM Infection (%)
15- VP - Vector population

4.2.2 Leaf blade length (cm)

The leaf length showed variability among the accessions. It ranged between 9.05 cm (TCR-2510) to 21.90 cm (TCR-1648) with a mean value of 15.72 cm. Among the check varieties, it ranged from 16.27 cm (Parbhani Kranti) to 17.20 cm (Varsha Uphar) with a mean value of 16.80 cm. Only one accession, TCR-1648 (21.90 cm) had significantly longer leaf in comparison with the mean of check varieties. Accessions TCR-2832, TCR-2621 and TCR-2510 had shorter leaf blade. Osawaru *et al.* (2013) reported 11.5 cm of leaf blade length in accession NGAE-96-0064C of *A. esculentus*. Kaur (2018) reported that the wild parent *A. moschatus* had average leaf blade length of 19.70 cm.

4.2.3 Leaf blade width (cm)

Observation on leaf width varied from 10.90 cm (TCR-2510) to 30.20 cm (TCR-2631) with a mean value of 21.20 cm. Among the check varieties, it ranged from 23.89 cm in Parbhani Kranti to 29.00 cm in Varsha Uphar with a mean 25.57 cm. Osawaru *et al.* (2013), reported 7.3 cm of leaf blade width in accession B= NGAE-96-011B of *A. esculentus.*

4.2.4 Leaf area (cm^2)

Leaf area ranged from 43 cm^2 (TCR-2510) to 438 cm^2 (TCR-2626) with an overall mean of 157.90 cm^2 indicating high variability among the accessions for the trait. The genotype TCR-2626 with an increased leaf area might be having high photosynthetic efficiency compared to those accessions with small leaves.

Among the check varieties, leaf area ranged from 114.89 cm^2 (Salkeerthi) to 153.33 cm^2 (Varsha Uphar) with a mean value of 133.21 cm^2. The accessions *viz.,* TCR-2626, TCR-2627, TCR-2628, TCR-2833, TCR-2631, TCR-2393, TCR-1774, TCR-2839 and TCR-1797 had high leaf area than the check varieties, while TCR-2869, TCR-30, TCR-2618, TCR-1775, TCR-32, TCR-2621, TCR-1652, TCR-2634, TCR-2392, TCR-2632, TCR-2744, TCR-2710 and TCR-2510 recorded less leaf area than the check varieties. Sindhumole (2003) reported maximum leaf area of 325.63 cm^2 and minimum

of 61 cm^2 among 101 okra genotypes. The findings of this research are similar to those of AdeOluwa and Kehinde, 2011and Akotkar *et al*. 2010 who reported significant variation in leaf area of various okra cultivars. The variation in leaf area might be due to more adaptability, genetic compositions and suitability with environmental conditions of the study area of some cultivars more than others (Haider *et al*., 2017).

4.2.5 Plant height (cm)

Plant height ranged from 31.10 cm in accession TCR-2510 to 102.5 cm in accession TCR-1785 with an overall mean of 67.43 cm indicating wide variability between the accessions for the trait. Plant height of the check varieties ranged from 55.63 cm (Pusa sawani) to 82.69 cm (Salkeerthi) with a mean value of 71.91 cm. Seven accessions *viz*., TCR-1785, TCR-1797, TCR-2627, TCR-1775, TCR-2628, TCR-2626 and TCR-2833 were significantly taller than the check varieties while, TCR-1806, TCR-2621, TCR-2634, TCR-30 , TCR-2393, TCR-2632, TCR-2710, TCR-2869, TCR-2839, TCR-2392, TCR-2618, TCR-1652, TCR-1653, TCR-2744 and TCR-2510 were shorter than the check varieties. The present results are similar to the findings of Mihretu *et al.* (2014a) who reported significant difference for plant height among 25 accessions. Makhdoomi *et al*. (2018) and Vishnu and Priyanka *et al.* (2018) also reported that genotypes were significantly different for plant height.

4.2.6 Branches per plant

Among the okra accessions, branches per plant ranged from 1(TCR-2628) to 5.30 (TCR-2392) with an average of 2.96. In check varieties, it ranged from 2.89 (Pusa Sawani) to 4.49 (Salkeerthi) with a mean value of 3.45. Only two accessions *viz*., TCR-2847, TCR-2869 and TCR-2632 had significantly higher number of branches per plant compared to check varieties, while, TCR-2626,TCR-2628, TCR-2392, TCR-2391, TCR-1785, TCR-32 and TCR-2627 had less number of branches than check varieties. Mihretu *et al.* (2014b) also reported variability for branch number among twenty five accessions. According to Singla *et al.* (2018), branch number per plant varied from 1.90 to 5.56 in various okra genotypes.

4.2.7. Fruit length (cm)

Fruit length is an important character contributing to yield. Among the accessions evaluated, it ranged from 9.71 cm (TCR-2839) to 19.65 cm (TCR-1774) with mean of 15.03 cm. In check varieties, fruit length ranged between 11.33 cm (Pusa Sawani) to 21.89 cm (Salkeerthi) and the mean value was 17.59 cm. Two accessions *viz*., TCR-1774 and TCR-2393 were having longer fruit length compared to check mean while, TCR-2839, TCR-2847, TCR-2510, TCR-1775, TCR-2392, TCR-1806, TCR-1652, TCR-1653, TCR-2744, TCR-2833, TCR-32, TCR-2632, TCR-2631, TCR-2628, TCR-30, TCR-2869, TCR-2627, TCR-2568 and TCR-2626 had short fruit length compared to check varieties (Plate 4). Significant variation among okra genotypes for fruit length was reported by Ramanjinappa *et al*. (2011), Karri and Acharyya(2012), Mihretu *et al.* (2014), Kerure *et al*.(2017) and Samim(2018).

4.2.8 Fruit diameter (cm)

Among the accessions, fruit diameter ranged from 1.35 cm (TCR-1785) to 2.62 cm (TCR-2626) and the overall mean was 1.94 cm. The check varieties varied from 1.95 cm (Pusa Sawani) to 2.10 cm (Varsha Uphar and Parbhani Kranti) with a mean of 1.98 cm. TCR-2626 exhibited higher fruit diameter compared to check varieties. Significant variation for fruit length was reported by many previous researchers Mallesh *et al.* (2015), Choudhary (2016), Kerure *et al*., (2017), Makhdoomi *et al.* (2018), Samim (2018) and Jamir *et al.* (2020). Fruit diameter in okra determines the shape of fruits, which is an important commercial aspect.

4.2.9. Ridges per fruit

The ridge per fruit among okra accessions showed wide variation (Plate 6) with an overall mean of 5.31. Interestingly, the accession TCR-2832 had fruits without ridges, but it had five compartments inside each fruit, representing the locules of its ovary. Hence it can be used as a distinguishing feature for identifying this genotype. The highest number of ridges (7.5) was noticed in the fruits of TCR-2847. All the check

varieties had five ridges per fruit. Nine accessions *viz*., TCR-2847, TCR-2744, TCR-2631, TCR-2627, TCR-2628, TCR-2833, TCR-2568, TCR-2839 and TCR-2626 had significantly more ridges per fruit compared to the check varieties. Significant variation for this trait was observed by previous researchers (Chandra *et al*., 2014; Khajuria *et al*., 2015; Bagwale *et al*., 2016; Badiger *et al*., 2017; Thulasiram *et al*., 2017; Samim, 2018). However, Kaur *et al*. (2019) reported five ridges per fruit in all the evaluated genotypes of three species *viz., A. moschatus, A. tuberculatus,* and *A.esculentus*), their F_1 hybrids and backcross progenies.

4.2.10. Seeds per fruit

Seeds per fruit exhibited significant variation among the accessions and this result is in accordance with the findings of Moniruzzaman and Quamruzzaman (2009) and Mohammadi *et al.* (2015). The number of seeds per fruit among the accessions ranged from 28.00 in TCR-2510 to 79.60 in TCR-2628 with a mean value of 49.96. In check varieties, it ranged from 47.18 (Salkeerthi) to 51.33(Varsha Uphar) with a mean value of 49.17. Accessions TCR-2628, TCR-2833, TCR-2631, TCR-2626, TCR-1785, TCR-2869, TCR-1648 and TCR-1652 had more number of seeds per fruit compared to check varieties while, TCR-2510, TCR-2832, TCR-1653, TCR-2839, TCR-2621, TCR-2391, TCR-2393, TCR-2618, TCR-32, TCR-2744, TCR-1775 and TCR-30 had registered less seeds than the check varieties (Plate 7). The seeds of okra are a potential source of oil with concentrations varying from 20 per cent to 40 per cent, which contains linoleic acid up to 47.4 per cent, a polyunsaturated fatty acid, essential for human nutrition (Gemede *et al*., 2015).

4.2.11 Fruits per plant

Number of fruits per plant in okra is an important trait contributing directly to yield. This trait was showing high variability in the thirty accessions evaluated. It ranged from 3.70 numbers in accession TCR-2744 to 14.90 in accession TCR-1774 with a mean value of 7.14. Among the check varieties, it ranged from 5.70 in Pusa Sawani to 12.83

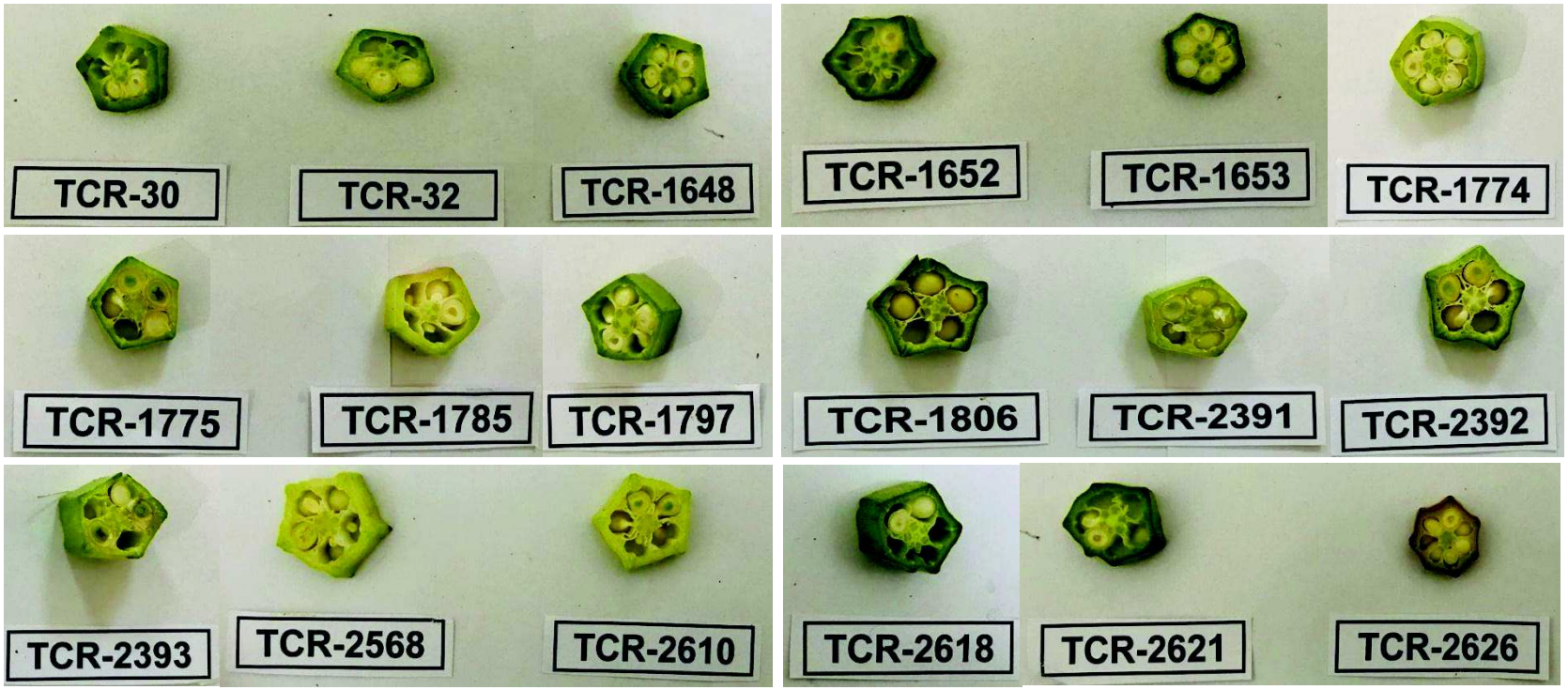
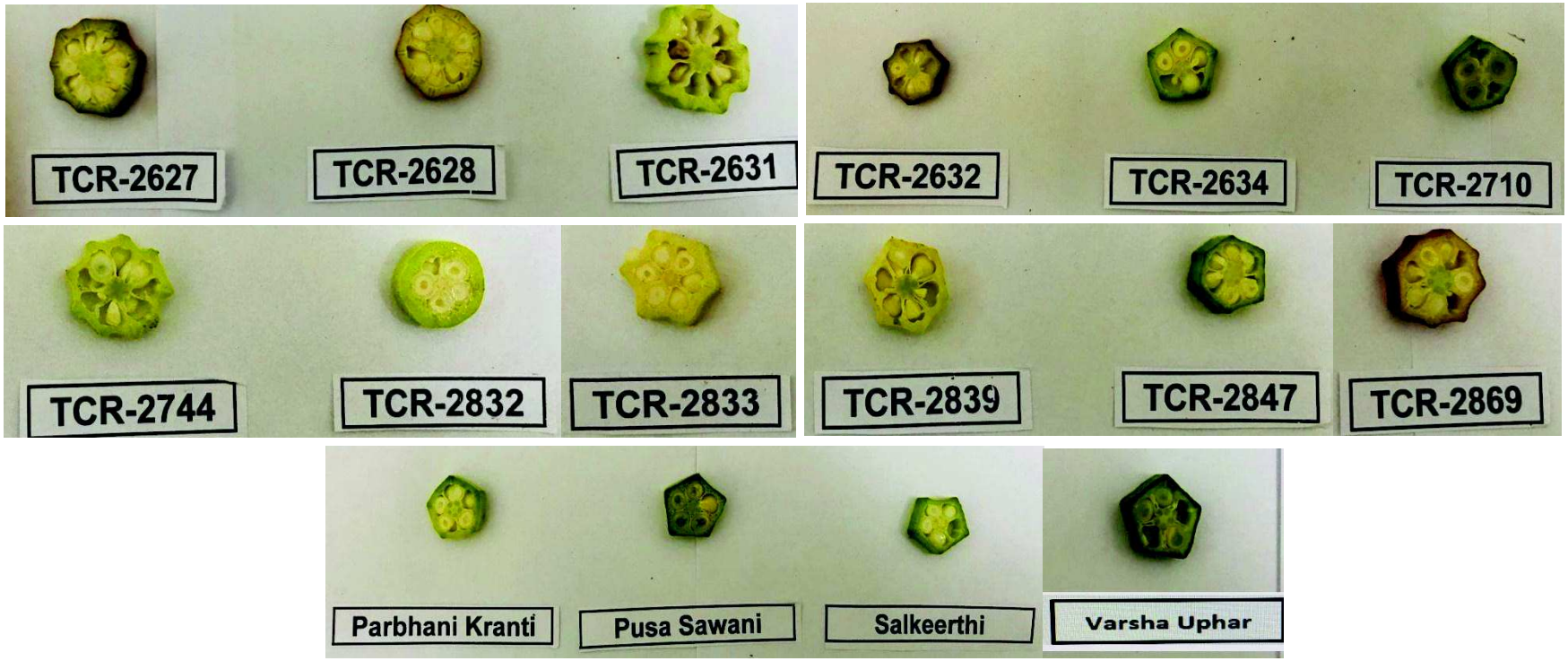


Plate 6. Ridge variability in okra fruits

Contd..


TCR-2627
TCR-2628
TCR-2631
TCR-2632
TCR-2634
TCR-2710
TCR-2744
TCR-2832
TCR-2833
TCR-2839
TCR-2847
TCR-2869
Parbhani Kranti
Pusa Sawani
Salkeerthi
Varsha Uphar

in Salkeerthi with a mean value of 10.42. Only TCR-1774 had more number of fruits than check varieties while, TCR-2744, TCR-2510, TCR-2839, TCR-2632, TCR-2392, TCR-2391, TCR-2869, TCR-2634, TCR-2833, TCR-2618, TCR-1648, TCR-2628, TCR-1785, TCR-32, TCR-1652, TCR-1653 and TCR-2393 had low number of fruit per plant compared to check varieties. Similar findings were recorded by many researchers (Reddy *et al*., 2012; Ramanjinappa *et al*., 2011; Choudhary, 2016; Kerure *et al*., 2017; Makhdoomi *et al*., 2018) in okra.

4.2.12 Fruit weight (g)

Among the accessions, fruit weight ranged from 13.80 g (TCR-1652) to 30.97 g (TCR-2631) with a mean value of 17.93 g. Among the check varieties, value varied from 15.69 g in Pusa sawani to 24.71 g in Varsha Uphar with a mean value of 21.02 g. Only one accession (TCR-2631) was significantly different compared to check varieties while, TCR-1652, TCR-2621, TCR-2510, TCR-2391, TCR-32 and TCR-1653 had less weight than the check varieties. These results are similar with the findings of scientists Mallesh *et al.* (2015), Badiger *et al.* (2017), Kerure *et al*. (2017) and Samim, 2018) in okra. Jamir (2020) reported similar fruit weight in Pusa Sawani (15.83 g) and low weight (9.55 g) in genotype IC- 029119-A. Fruit quality plays an important role for increasing total yield per plant which is mainly related to the weight of fruit (Olivera *et al*., 2012).

4.2.13 Fruit yield per plant (g)

Variability was noticed for fruit yield per plant among the accessions, which ranged from 58.30 g (TCR-2744) to 274.70 g (TCR-1774) with a mean value of 130.81 g. Among the check varieties, it ranged from 90.43 g (Pusa Sawani) to 294.22g (Salkeerthi) with a mean value of 231.44g. None of the accessions showed higher yield than the check varieties. These resuslts are in conformity with the findings of Khajuria *et al.* (2016). Sonia (1999), Chandra *et al.* (2014) and Jamir *et al*. (2020).

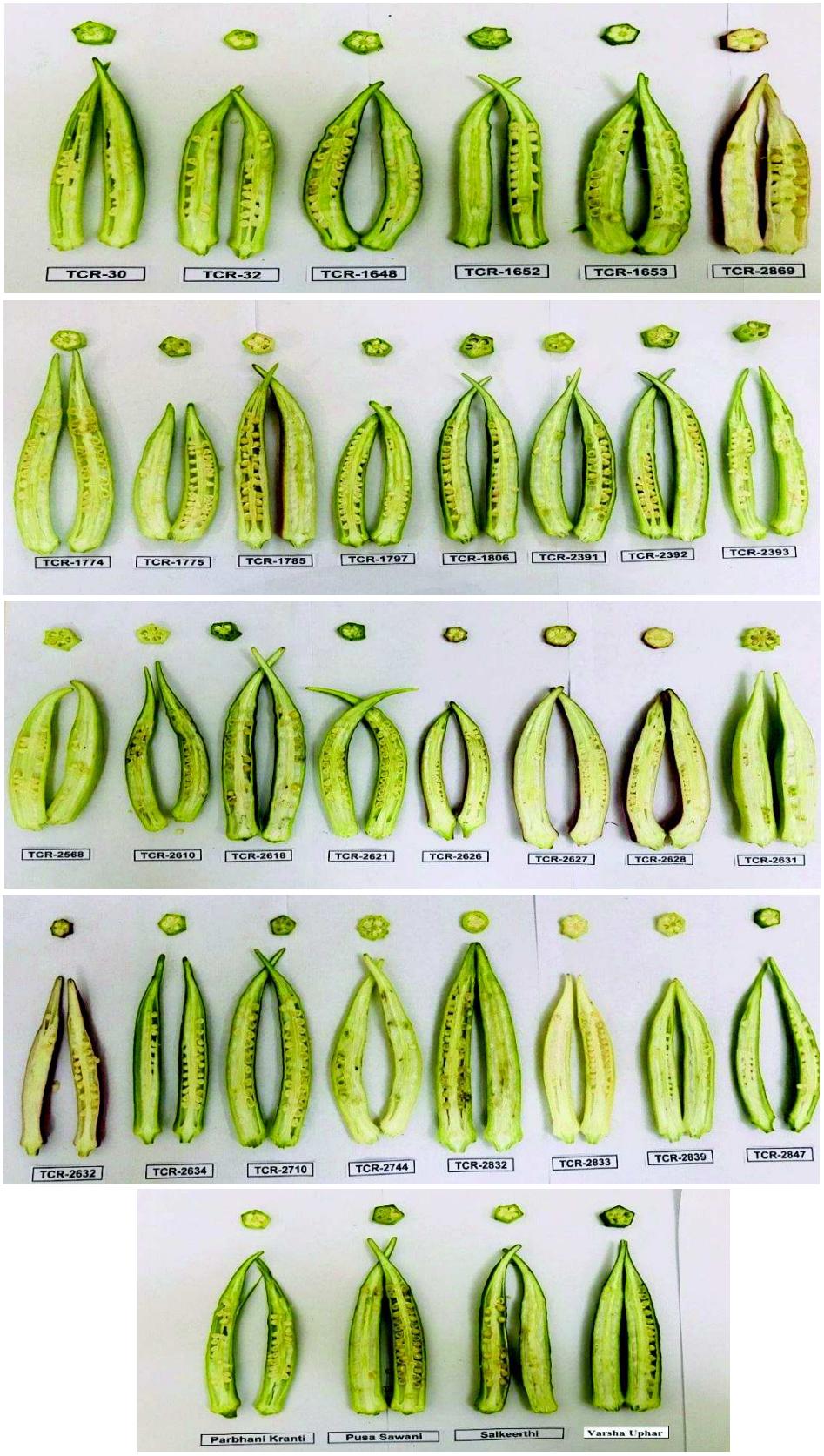


Plate 7. Seed variability in okra fruits

4.2.14. Coefficient of YVM infection (%)

The variability was noticed among the accessions for YVMD coefficient of YVM infection (%) compared to check varieties and ranged from minimum of CI = 0 in TCR-30 to the maximum CI= 74.04 in TCR-2833 with a mean value of 43.81 per cent. Among the resistant check varieties, it ranged from 2.44 per cent in Varsha Uphar to 3.90 per cent in Parbhani Kranti with a mean value of 2.50 per cent. Only one accession TCR-30 had less CI than the check varieties. Singh *et al*. (2002) reported Parbhani Kranti as susceptible to YVMV (51.2%) whereas, Arka Anamika as moderately resistant to YVMV (32.2%). Prakash *et al*. (2017) screened sixty genotypes Pusa Sawani as susceptible check variety along with sixty okra genotypes for YVMV and reported seven genotypes as resistant against YVMV.

4.2.15 White fly population

Significant variation was observed among the 30 accessions under study for the number of white flies on leaves at 30 DAS, 50 DAS, 65 DAS and 75 DAS. The lowest number of white flies(3.80) was observed in TCR-30 and the highest number was found in TCR-2744 (16.20) with a mean number of 8.15. In the check varieties, value ranged from 4.10 (Varsha Uphar) to 9.60 (Parbhani Kranti) with a mean value of 6.85. The occurrence of YVMDand whitefly in South India was the highest in the month of March to June (Sanwal *et al.,* 2016). Cooler weather with high relative humidity and rainfall were harmful to the whitefly multiplication and hence whitefly population decreased with increase in relative humidity whereas, YVMV incidence increased with the rise in minimum temperature (Prabu *et al*., 2008).

4.3 Genetic variability parameters

In the present investigation, an attempt was made to study the genetic parameters such as phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), broad sense heritability (H^2) and genetic advance as per cent of mean (GA) for thirty okra accessions along with four checks for fifteen parameters. The results are presented in Table 11 and Figures 1 and 2.

4.3.1 Days to first flowering

Low PCV and GCV values with a narrow difference between them (10% and 9.90%, respectively) coupled with high heritability (98.08%) and high genetic advance (20.21%) were evident for this trait.

4.3.2 Leaf blade length (cm)

A moderate PCV (18.37%) and GCV (17.13%) estimates with high broad sense heritability (H^2) and high genetic advance (86.92% and 32.89%, respectively) were observed.

4.3.3 Leaf blade width (cm)

For this character, high PCV (21.78%), moderate GCV (15.59%) as well as heritability (51.23%) and high genetic advance as percent mean (22.98%) were noticed.

4.3.4 Leaf area (cm^2)

Greater variability was evident for leaf area with a wide range (43cm^2 to 438 cm^2) and very high values of all the genetic parameters *viz*., PCV, GCV, heritability and genetic advance (60.24 %, 60.17%, 99.76 % and 123.81 %, respectively).

4.3.5 Plant height (cm)

PCV (25.25%) and GCV (25.08%) were high for plant height,. Heritability (98.63%) was very high coupled with high genetic advance (51.32%) for this trait.

4.3.6 Branches per plant

A high PCV and GCV (28.72% and 27.58%, respectively) along with very high heritability (92.23%) and high genetic advance (54.57%) were observed for branches per plant.

4.3.7 Fruit length (cm)

The PCV (15.44%) and GCV (15.30%) values were moderate for fruit length, whereas very high heritability (98.15) and high genetic advance (31.22%) were recorded.

4.3.8 Fruit diameter (cm)

Moderate PCV and GCV (10.99% and 10.91%, respectively), very high heritability (98.54%) and high genetic advance (22.31%) were observed for this character.

4.3.9 Ridges per fruit

High PCV and GCV (21.17% and 21.68%, respectively), very high heritability and high genetic advance (99.16% and 44.47%, respectively) were recorded for this character.

4.3.10 Seeds per fruit

The PCV (19.82%) and GCV (19.75%) values were moderate while, a very high heritability (99.24%) and high genetic advance (40.53%) were recorded for seeds per fruit.

4.3.11 Fruits per plant

High PCV and GCV (24.56% and 22.15%, respectively) with high heritability (81.33%) as well as high genetic advance (41.16%) were registered for fruits per plant.

4.3.12 Fruit weight (g)

Though PCV (18.33%) and GCV (16.36%) were moderate, high values of heritability as well as genetic advance (79.70% and 30.09, respectively) were recorded for this trait.

4.3.13 Fruit yield per plant (g)

High variability was observed for fruit yield per plant (93.24%) . Also, the estimates of PCV and GCV (31.88% and 30.78% respectively) and genetic advance estimates were very high (61.23%) for this yield trait.

4.3.14 Coefficient of YVM infection

Very high PCV, GCV, heritability and genetic advance (45.46%, 45.16%, 98.70%, and 92.43% respectively) were observed for coefficient of YVM infection.

4.3.15 Vector population

PCV (29.57%) was high for this trait. However, low values were observed for GCV, heritability and genetic advance (9.93%, 11.29%, and 6.87%, respectively).

Out of the fifteen characters studied, phenotypic coefficient of variation was very high for two characters *viz*., leaf area (60.24%), coefficient of YVM Infection (45.46%); high in seven characters *viz*., fruit yield per plant (31.88%), vector population (29.57%), branches per plant (28.72%), plant height (25.25%), fruits per plant (24.56%), leaf blade width (21.78%) and ridge per fruit (21.17%). Moderate PCV was observed for the remaining six characters *viz*., seeds per fruit (19.82%), Leaf blade length (18.37%), fruit weight (18.33%), fruit length (15.44%) fruit diameter (10.99%) and days to first flowering (10%). These results are in agreement with the previous reports of Mehta *et al*. (2006) Mallesh *et al*. (2015), Badiger *et al*. (2017) and Makhdoomi *et al*. (2018). Pravinaben (2017) and Samim (2018) reported moderate PCV for plant height, number of fruits per plant and fruit yield per plant.

Genotypic coefficient of variation (GCV) was very high for two characters *viz*., leaf area (60.17%) and coefficient of YVM Infection (45.16%); high in five characters *viz*., fruit yield per plant (30.78%), branches per plant (27.58%), plant height (25.08%), fruits per plant (22.15%) and ridges per fruit (21.68%). Moderate PCV was observed for six characters *viz*., seeds per fruit (19.75%), leaf blade length (17.13%), fruit weight

(16.36%), leaf blade width (15.59%), fruit length (15.30%) and fruit diameter (10.91%). Low GCV was observed for two characters *viz*., vector population (9.93%) and days to first flowering (9.9 %). Similar observations were reported by Mallesh *et al.* (2015). Pravinaben (2017) and Samim (2018) had noticed moderate GCV for plant height, number of fruits per plant and fruit yield per plant.

Phenotypic and genotypic coefficients of variation (PCV and GCV) were very high in leaf area and coefficient of YVM infection, and high in five characters *viz*., fruit yield per plant, branches per plant, plant height, fruits per plant and ridges per fruit. In general, GCV was slightly lower than PCV for most of the traits, indicating a small environmental effect in their expression.

Broad sense heritability (H^2) was very high for three characters *viz*., leaf area (99.76%), seeds per fruit (99.24%) and ridge per fruit (99.16%); high in ten traits *viz.,* coefficient of YVM Infection (98.70%), plant height (98.63%), fruit diameter (98.54%), fruits length (98.15%), days to first flowering (98.08%), fruit yield per plant (93.24), branches per plant (92.23), leaf blade length (86.92%), fruits per plant (81.33%) and fruit weight (79.7%); moderate in leaf blade width (51.23%) and low in vector population (11.29%). Similar results were obtained by earlier researchers in case of fruit yield per plant (Chandramouli *et al.* (2016); fruits per plant (Kerure *et al*.(2017), plant height (Sawant *et al.,* 2014; Kerure *et al.,* 2017), fruit length (Karri and Acharyya, 2012; Kerure *et al.,* 2017) and fruit diameter (Karri and Acharyya, 2012).According to Samim (2018), high heritability was observed for fruit yield per plant and fruits per plant in okra.

Among the fifteen quantitative characters studied, genetic advance was very high for two traits *viz*., leaf area (123.81%) and coefficient of YVM Infection (92.43%); high in seven characters *viz*., fruit yield per plant (61.23%), branches per plant (54.57%), plant height (51.32%), ridges per fruit (44.47%), fruits per plant (41.16%), seeds per fruit (40.53%), leaf blade length (32.89%), fruit length (31.22%), fruit weight (30.09%), leaf blade width (22.98%) fruit diameter (22.31%) and days to first flowering (20.21%). Low Genetic was observed only one character *viz.,* vector population (6.87%).

The results are in accordance to the findings of earlier researchers *viz.,* Patel *et al*. (2014), Saryam *et al*. (2015a), Rao *et al*. (2015), Shivaramegowda *et al*. (2016) and Kerure *et al*. (2017). High genetic advance was observed for plant height by Kumar *et al*. (2018) and for fruit yield per plant and fruits per plant by Samim (2018).

High H^2 and GA were noticed for most of the traits including number, length, diameter, weight and yield of fruits. Coefficient of YVM infection also exhibited high H^2 as well as GA. This indicates that these characters can be improved to a great extent by selection.

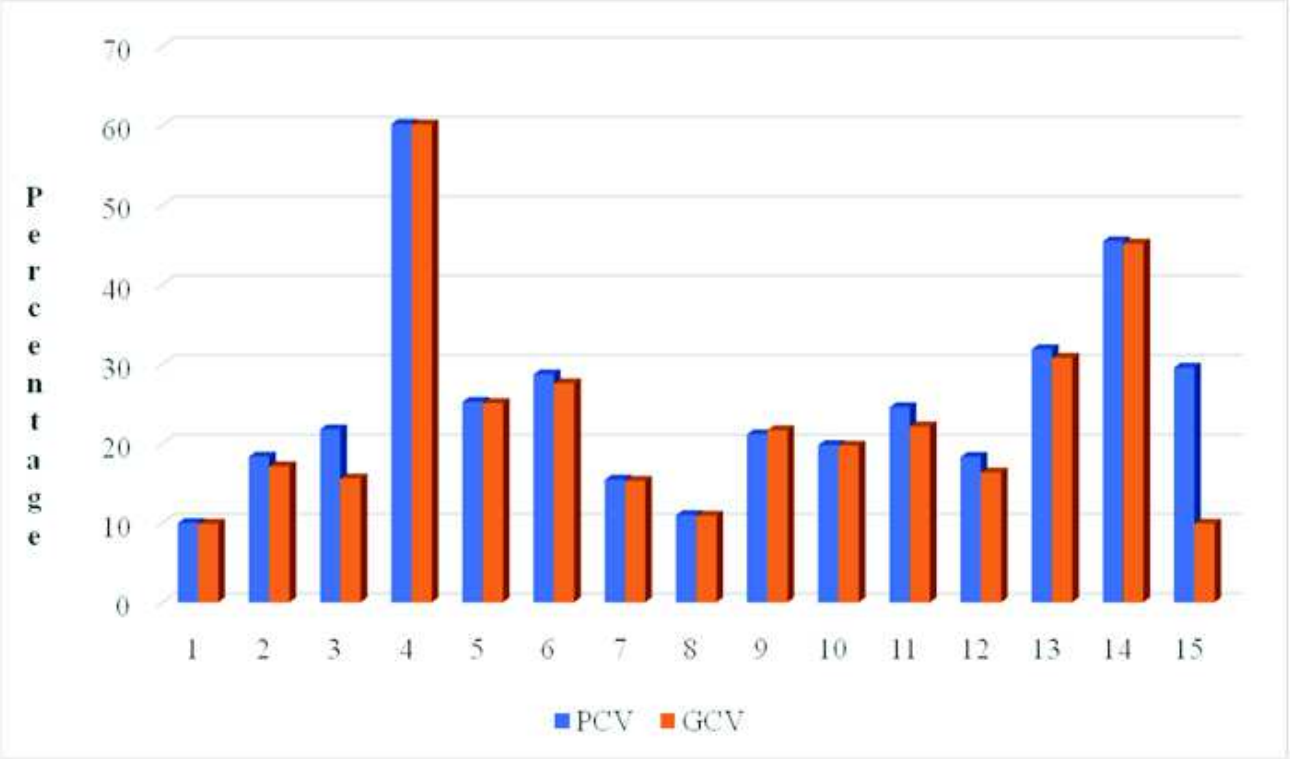
4.4 Correlation analysis

The correlation coefficients were estimated among the quantitative characters under phenotypic level and the results are presented in Table 12.

Table 11. Estimates of variability parameters for various characters of okra genotypes

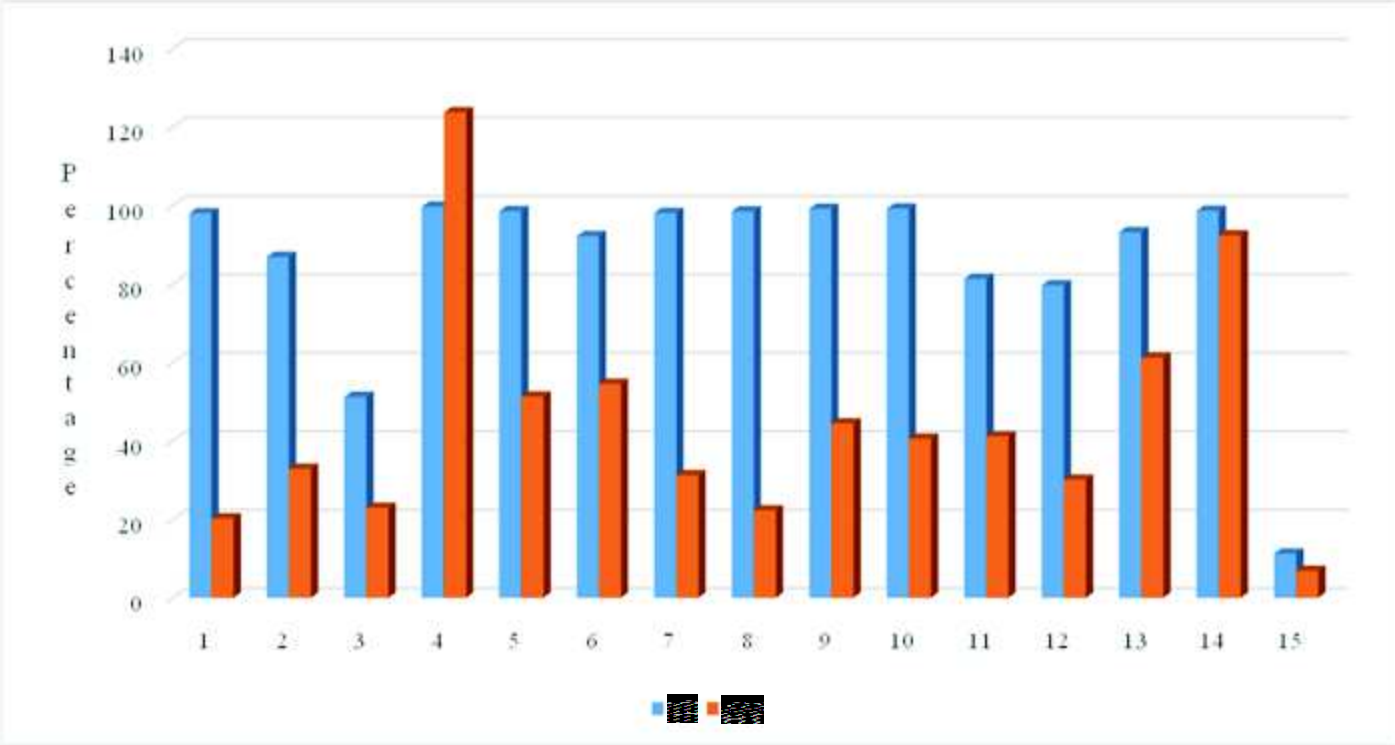
Characters	Mean	Range	PCV (%)	GCV (%)	H^2 (%)	GA as % Mean
		Min- Max				
Days to first flowering	44.64	39.40-56.20	10.00	9.90	98.08	20.21
Leaf blade length (cm)	15.72	9.05-21.90	18.37	17.13	86.92	32.89
Leaf blade width (cm)	21.71	10.90-30.20	21.78	15.59	51.23	22.98
Leaf area (cm^2)	157.90	43-438	60.24	60.17	99.76	123.81
Plant height (cm)	67.43	31.1-102.5	25.25	25.08	98.63	51.32
Branches per plant	2.96	1-5.30	28.72	27.58	92.23	54.57
Fruits length (cm)	15.03	9.71-19.65	15.44	15.30	98.15	31.22
Fruit diameter (cm)	1.94	1.35-2.62	10.99	10.91	98.54	22.31
Ridge per fruit	5.31	0-7.50	21.17	21.68	99.16	44.47
Seeds per fruit	49.96	28 -79.6	19.82	19.75	99.24	40.53
Fruits per plant	7.14	3.7-14.9	24.56	22.15	81.33	41.16
Fruit weight (g)	17.93	13.80 -30.97	18.33	16.36	79.70	30.09
Fruit yield per plant (g)	130.81	58.3-274.7	31.88	30.78	93.24	61.23
Coefficient of YVM infection	30.10	0.00- 74.04	45.46	45.16	98.70	92.43
Vector population	8.15	3.80 -16.20	29.57	9.93	11.29	6.87

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



1- Days to first flowering
2- Leaf blade length (cm)
3- Leaf blade width (cm)
4- Leaf area (cm^2)
5- Plant height (cm)
6- Branches per plant
7- Fruits length (cm)
8- Fruit diameter (cm)
9- Ridge per fruit
10- Seeds per fruit
11- Fruits per plant
12- Fruit weight (g)
13- Fruit yield per plant (g)
14- Coefficient of YVM Infection
15- Vector population

Fig. 2 Heritability (%) and Genetic Advance (%) for various characters of okra genotypes



1- Days to first flowering
2- Leaf blade length (cm)
3- Leaf blade width (cm)
4- Leaf area (cm^2)
5- Plant height (cm)
6- Branches per plant
7- Fruits length (cm)
8- Fruit diameter (cm)
9- Ridge per fruit
10- Seeds per fruit
11- Fruits per plant
12- Fruit weight (g)
13- Fruit yield per plant (g)
14- Coefficient of YVM infection
15- Vector population

Table 12. Phenotypic correlation coefficients between the quantitative characters in okra

	DF	LL	LW	LA	PH	BP	FL	FD	RF	SF	FP	FW	FY	CI	VP
	1	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**	**12**	**13**	**14**	**15**
DF	**1.00**														
LL	0.06	**1.00**													
LW	0.33	0.76**	**1.00**												
LA	0.55**	0.51**	0.69**	**1.00**											
PH	0.38*	0.37*	0.49**	0.58**	**1.00**										
BP	0.03	-0.28	-0.26	-0.36*	-0.27	**1.00**									
FL	-0.03	0.07	0.15	0.07	0.35*	0.07	**1.00**								
FD	0.27	0.07	0.13	-0.05	-0.08	0.26	0.02	**1.00**							
RF	0.20	0.39*	0.49**	0.35*	0.11	-0.16	-0.24	0.23	**1.00**						
SP	0.51**	0.45**	0.54**	0.59**	0.45**	-0.17	0.01	0.22	0.42*	**1.00**					
FP	0.15	0.29	0.35	0.32	0.55	0.16	0.52	-0.01	-0.06	0.15	**1.00**				
FW	-0.03	0.24	0.18	0.10	0.47**	0.16	0.58**	-0.12	-0.14	-0.04	0.87	**1.00**			
FY	0.43*	0.18	0.40*	0.45**	0.41*	0.20	0.16	0.21	0.09	0.43**	0.67	0.27	**1.00**		
CI	0.45**	0.13	0.21	0.48**	0.31	-0.22	-0.19	0.04	0.07	0.17	-0.08	-0.14	0.03	**1.00**	
VP	0.06	-0.04	-0.13	0.06	-0.15	-0.06	-0.22	0.03	-0.02	-0.04	-0.20	-0.25	-0.02	0.55**	**1.00**

Positive and highly significant correlation at 1 % level
Positive and significant correlation at 5 % level
Negative significant correlation

1- Days to first flowering
2- Leaf blade length (cm)
3- Leaf blade width (cm)
4- Leaf area (cm^2)
5- Plant height (cm)
6- Branches per plant
7- Fruits length (cm)
8- Fruit diameter (cm)
9- Ridge per fruit
10- Seeds per fruit
11- Fruits per plant
12- Fruit weight (g)
13- Fruit yield per plant (g)
14- Coefficient of YVM Infection (%)
15- Vector population

4.4.1 Days to first flowering

Days to first flowering had a positive and highly significant correlation with leaf area, seeds per fruit and coefficient of YVM infection. This trait also had positive and significant correlation with plant height and fruit yield per plant. Many previous researchers had reported significant negative correlation for days to first flowering with plant height Adiger *et al*. (2011), Kumar *et al*. (2012), Balai *et al*. (2014), Saryam *et al*. (2015a) and Rashwan (2011). Rajat *et al*. (2018) also observed positive and non-significant association of days to first flowering with yield per plant.

4.4.2 Leaf blade length (cm)

Positive and highly significant association was observed for leaf blade length with leaf blade width, leaf area and seeds per fruit. It also showed significant association with plant height and ridges per fruit. Saryam *et al*. (2015a) reported that yield per plant had highly significant positive phenotypic association with leaf blade length, fruit diameter, fruit length, number of seeds fruit, days to maturity, fruit weight, seed weight, flower diameter, fruiting span, petiole length and stem diameter in okra.

4.4.3 Leaf blade width (cm)

Leaf blade width showed positive and highly significant correlation with leaf blade length, leaf area, plant height, ridge per fruit, and seeds per fruit. It also had significant positive correlation with fruit yield per plant. Mohammed *et al.* (2020) recently reported positive and significant association of leaf blade width with fruit length and seeds per fruit.

4.4.4 Leaf area (cm^2)

Leaf area exhibited highly significant and positive association with days to first flowering, leaf blade length, leaf blade width, plant height, seeds per fruit, fruit yield per plant and coefficient of YVM infection and also positive and significant correlation with ridges per fruit. Significant negative association existed between leaf area and branches

per plant. According to Magagula and Ossom (2011), leaf area in different okra genotypes had positive and significant association with plant height, petiole length, number of leaves and seedling emergence.

4.4.5 Plant height (cm)

Correlation studies between plant height and other traits showed a positive and highly significant association with leaf blade width, leaf area, seeds per fruit and fruit weight. It had positive and significant correlation with days to first flowering, leaf blade length, fruit length and fruit yield per plant. Similar highly significant positive association of plant height with fruit length and yield per plant was reported by Raval *et al*. (2019). Patel and Dhruve (2018) reported highly significant association of plant height with leaf area. Reddy *et al*. (2012) reported significant positive correlation for this trait- with fruit length but significant negative correlation with days to 50% flowering.

4.4.6 Branches per plant

Branches per plant had negative and significant correlation with leaf area and no positive association with any other traits. In a study of 36 okra genotypes, Rashwan (2011) observed positive correlation of branches per plant with number of fruits per plant and fruit diameter.

4.4.7 Fruit length (cm)

Fruit length showed positive and highly significant with fruit weight and significant positive correlation with plant height. This finding is in agreement with the earlier findings of Reddy *et al*. (2012). Saryam *et al*. (2015b) reported that yield per plant had highly significant positive phenotypic correlation with fruit length, number of seeds fruit, days to maturity and fruit weight.

4.4.8 Fruit diameter (cm)

Fruit diameter had no association with any of the other traits studied. However, Mihretu *et al*. (2014) and Saryam *et al*. (2015b) reported that fruit diameter had positive and significant genotypic correlation with fruit yield.

4.4.9 Ridges per fruit

Ridges per fruit had highly significant positive correlation with leaf blade width and significant positive association with leaf blade length, leaf area and seeds per fruit. Kerure *et al*. (2017) observed that number of ridges per fruit had highly significant positive correlation with stem girth, number of locules per fruit and highly significant negative correlation with 100 seeds per weight.

4.4.10 Seeds per fruit

Positive highly significant association was observed for seeds per fruit with days to first flowering, leaf blade length, leaf blade width, leaf area, plant height and fruit yield per plant. Pithiya *et al*. (2017) reported that number of seeds per fruit and number of fruits per plant showed the highest positive and significant correlation with yield per hectare followed by 100-seed weight and plant height. Mohammed *et al.* (2020) reported positive and significant correlation of seeds per plant with plant height.

4.4.11 Fruits per plant

Fruits per plant had no correlation with any of the other traits studied. According to Reddy *et al.* (2012), fruits per plant had significant positive correlation with plant height, fruit length and fruit weight. Contrary to this, Pithiya *et al*. (2017), reported high positive and high significant association of number of fruits per plant swith yield per hectare.

4.4.12 Fruit weight (g)

Fruit weight had positive and highly significant correlation with plant height and fruit length. Reddy *et al*. (2012) and Raval *et al*. (2019) found positive significant correlation of fruit weight with fruit length. Saryam *et al*. (2015b) reported that fruit weight had highly significant positive phenotypic correlation with yield per plant.

4.4.13 Fruit yield per plant (g)

Fruit yield per plant had positive and highly significant correlation with leaf area and seeds per fruit. It had positive and significant association with days to first flowering, leaf blade width and plant height. Similar finding was reported by Reddy *et al.*(2012) and Niraja *et al.* (2018). Singh *et al*. (2017) and Raval *et al*. (2019) reported significant and positive correlation of fruit yield per plant with seeds per fruit and plant height. A study by Saryam *et al*. (2015b) showed that yield per plant had highly significant positive association with fruit diameter, fruit length, number of seeds fruit, days to maturity, fruit weight, seed weight, flower diameter, petiole length and stem diameter.

4.4.14 Coefficient of YVM infection

Positive and highly significant association was observed for coefficient of YVM infection with days to first flowering, leaf area and vector population. Highly negative non-significant association was observed for incidence of YVMV,days to 50 per cent flowering and first flower appearance by Saryam *et al*. (2015b). A similar report by Seth *et al*. (2016), described that YVMV disease incidence was positively and significantly correlated with whitefly population.

4.4.15 Vector population

Vector population had highly significant positive association with coefficient of YVM infection. Shahid *et al*. (2019) found positive and highly significant correlation of vector population with disease development.

4.5 Disease response of okra genotypes

The genotypes varied significantly for YVM incidence during all the crop stages except at 30 DAS and 50 DAS stages and the response of genotypes varied greatly regarding their level of resistance and susceptibility (Table 13) and okra YVM rating scale Plant 8.

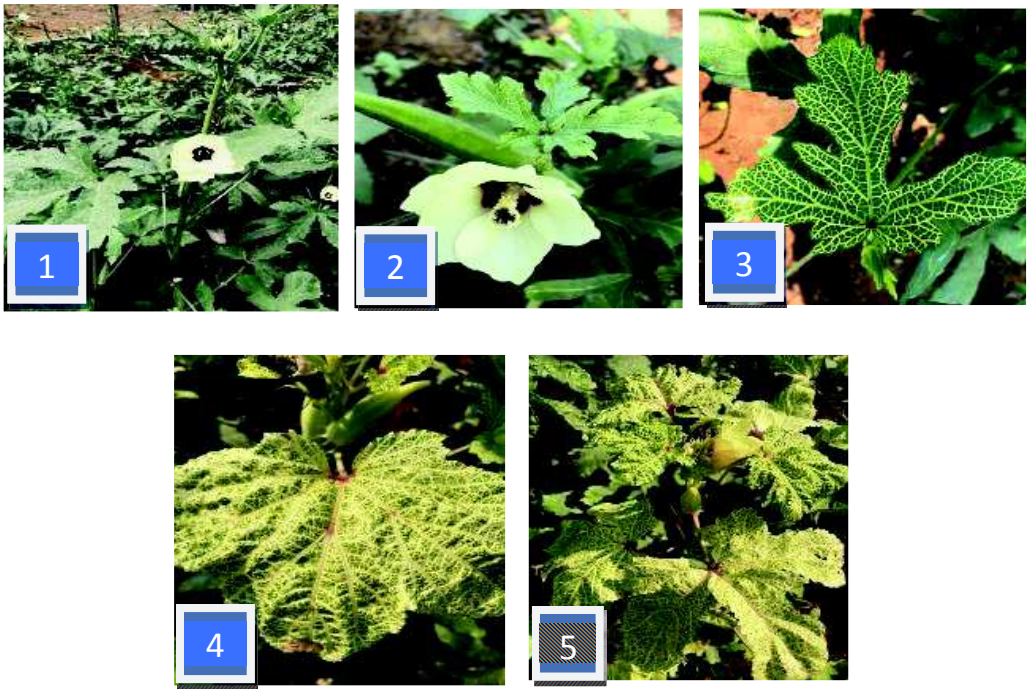


Plate 8. Okra YVM rating scale (1-5)

Among the thirty genotypes and four check varieties screened, one accession *viz*., TCR-30and two checks *viz.,* Varsha Uphar and Parbhani Kranti were graded as highly resistant to YVM disease (Plate 9). Only one accession viz., TCR-1652 was found as moderately resistant (Plate 10), TCR-32, TCR-1648, TCR-2392, TCR-2393, TCR-2568, TCR-2610, TCR-2618, TCR-2621, TCR-2632 and TCR-2869 as moderately susceptible (Plate 11), TCR-1653, TCR-1774, TCR-1775, TCR-1785, TCR-1797, TCR-1806,TCR-2391,TCR-2626,TCR-2627,TCR-2628,TCR-2631,TCR-2634, TCR-2710, TCR-2744,TCR-2832,TCR-2839,TCR-2847,Pusa Sawani and Salkeerthi as susceptible (Plate 12) and TCR-2833 as highly susceptible symptoms of YVM in different accessions . Seth *et al.* (2018) reported the highest disease severity in Arka Anamika (75.00%)

followed by Pusa Sawani (70.00%) and VRO-6 (65.00%), at 60 DAS. Deo *et al*. (2000) reported that Parbhani Kranti and its hybrid Parbhani Kranti x HRB-9-2 were highly resistant to YVMV. Vinutha (2015) reported that Parbahni Kranthi as YVMV resistant with low PDI, PDS and CI (40%,16% and 4.6%, respectively) and Salkeerthi as YVMV highly susceptiblewith high PDI, PDS and CI (100%,99.67% and 99.67%, respectively). Niraja *et al*. (2018) reported that various okra genotypes showed significant tolerance to YVMV up to 30 to 45 DAS of incidence. According to Jamir *et al.* (2020), the first disease appearance was observed at 16 DAS after sowing among 565 okra genotypes and PDI was (87.5%). In a contradictory report by Naim *et al*.(2019), Varsha uphar and Parbhani kranti were observed as moderately resistant to YVMV.

4.6 Selection of the best okra genotypes

4.6.1 Okra genotypes highly resistant to YVM

Based on the disease resistance to YVM exhibited, three genotypes are selected which exhibited high resistance during the present study. They are the two check varieties *viz*., Varhsa Uphar and Parbhani Kranti, and one accession collected from NBPGR *viz*., TCR- 30 (IC 033323). Among these, Varhsa Uphar, and Parbhani Kranti are well known varieties, for their high yield coupled with YVM resistance. In the present study also, they exhibited superiority in fruit yield (292.25 and 248.85 g/plant respectively) as well as yield components *viz*., fruit number/plant, fruit length, fruit diameter, and fruit weight. Varsha Uphar had 11.75 fruits/plant, fruit length 18.3 cm, fruit diameter 2.1 cm and fruit weight 24.71 g, whereas Parbhani Kranti had 11.39 fruits/plant, fruit length 18.83 cm, fruit diameter 2.1 cm and fruit weight 21.41 g. Though TCR-30 was not a high yielding genotype, it had a consistent high resistance (0.00 CI) to YVM throughout the crop period. Moreover, the lowest number of white flies (3.80) was observed in this genotype which empasises its resistance mechanism. Hence it can be selected as a donor for imparting YVM resistance in crossing programmes.

4.6.2 High yielding okra genotypes susceptible to YVM

In the high yielding susceptible category, six best okra genotypes selected are Salkeerthi, TCR- 1774, TCR-1797, TCR- 2631, TCR-2627 and TCR-2626. Salkeerthi, a variety released from KAU had the highest fruit yield per plant (294.22 g) among all the genotypes evaluated during the present study, with superior yield components *viz*., 12.83 fruits/plant, fruit length of 21.89 cm, fruit diameter of 1.95 cm and fruit weight of 22.26 g.

All the other selected genotypes were collected from NBPGR. The second best genotype was TCR- 1774 which had a fruit yield of 274.7 g/plant, 14.90 fruits/plant, fruit length of 18.90 cm, fruit diameter of 1.80 cm and fruit weight of 18.32 g. Moreover, it had the lowest coefficient of YVM infection (45.60) among the selected six high yielding susceptible genotypes. TCR-1797, the third best genotype in the susceptible high yielding category had 190 g fruit yield/plant only. But, it had 10.9 fruits/plant, fruit length of 17.9 cm, fruit diameter of 2.2 cm and fruit weight of 17.39 g. The fourth best high yielding susceptible genotype was TCR- 2631, fruit yield 224.7 g/plant better than TCR-1797 (third rank). However, it produced only 7.3 fruits/plant with a length of 14.73 cm. But it had more fruit diameter *i.e*, 2.62 cm. And, the major contributing trait for its high yield was the high fruit weight, *i.e*, 30.97 g, which is the highest among all the accessions. TCR-2627 and TCR-2626 were ranked as the fifth and sixth high yielding susceptible okra genotypes of this study, both with the equal fruit yield of 186.9 g/plant. Fruit number (8.10), fruit weight (23.14 g) and fruit diameter (2 cm) were higher, but less fruit length (15.58 cm) in TCR-2627. TCR-2626 had 7.6 fruits/plant with fruit length of 16.06 cm, fruit weight of 17.46 g and fruit diameter (1.85 cm).

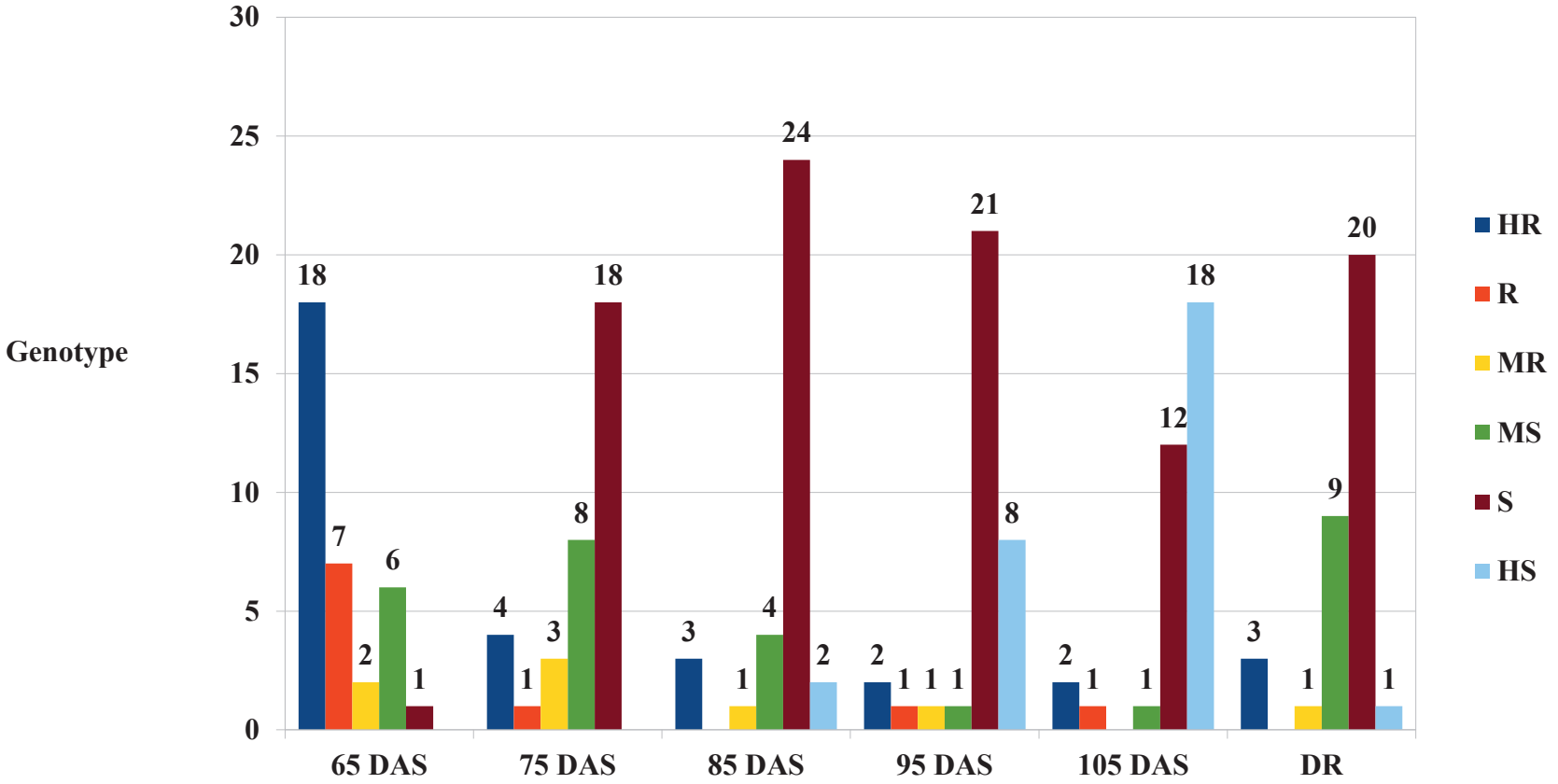
Table 13. Response of okra genotypes to yellow vein mosaic virus

Tr. No.	Genotype	65 DAS				75 DAS				85 DAS				95 DAS				105 DAS				AVE DR	AVE (CI)
		PDI	PDS	CI	DR	PDI	PDS	CI	DR	PDI	PDS	CI	DR	PDI	PDS	CI	DR	PDI	PDS	CI	DR		
1	TCR-30	0	20	0	HR	0	20	0	HR	0	20	0	HR	0	20	0	HR	0	20	0	HR	0	HR
2	TCR-32	0	20	0	HR	20	24	4.8	R	90	38	34.2	MS	90	44	39.6	S	90	52	46.8	S	25.08	MS
3	TCR-1648	0	20	0	HR	60	32	19.2	MS	100	46	46	S	100	60	60	S	100	72	72	HS	39.44	MS
4	TCR-1652	0	20	0	HR	0	20	0	HR	60	30	18	MR	60	30	18	MR	70	32	22.4	MS	11.68	MR
5	TCR-1653	40	28	11.2	R	100	44	44	S	100	54	54	S	100	62	62	S	100	70	70	HS	48.24	S
6	TCR-1774	0	20	0	HR	100	44	44	S	100	54	54	S	100	64	64	S	100	66	66	S	45.6	S
7	TCR-1775	40	28	11.2	R	100	52	52	S	100	60	60	S	100	78	78	HS	100	86	86	HS	57.44	S
8	TCR-1785	20	24	4.8	R	100	44	44	S	100	52	52	S	100	80	80	HS	100	86	86	HS	53.36	S
9	TCR-1797	0	20	0	HR	100	52	52	S	100	56	56	S	100	68	68	S	100	86	86	HS	52.4	S
10	TCR-1806	0	20	0	HR	100	46	46	MS	100	58	58	S	100	62	62	S	100	72	72	HS	47.6	S
11	TCR-2391	0	20	0	HR	100	48	48	S	100	62	62	S	100	80	80	HS	100	86	86	HS	55.2	S
12	TCR-2392	0	20	0	HR	100	36	36	MS	90	38	34.2	MS	100	40	40	S	100	40	40	S	30.04	MS
13	TCR-2393	10	20	2	HR	50	28	14	MR	100	34	34	MS	100	38	38	MS	100	40	40	S	25.6	MS
14	TCR-2568	70	34	23.8	MS	100	40	40	S	100	40	40	S	100	42	42	S	100	44	44	S	37.96	MS
15	TCR-2610	0	20	0	HR	50	30	15	MR	100	40	40	S	100	42	42	S	100	48	48	S	29	MS
16	TCR-2618	0	20	0	HR	50	30	15	MR	100	42	42	S	100	44	44	S	100	48	48	S	29.8	MS
17	TCR-2621	0	22	0	HR	80	36	28.8	MS	100	42	42	S	100	42	42	S	100	44	44	S	31.36	MS
18	TCR-2626	100	40	40	S	100	44	44	S	100	52	52	S	100	66	66	S	100	78	78	HS	56	S
19	TCR-2627	70	34	23.8	MS	100	60	60	S	100	66	66	S	100	70	70	HS	100	86	86	HS	61.16	S
20	TCR-2628	40	28	11.2	R	100	54	54	S	100	56	56	S	100	64	64	S	100	74	74	HS	51.84	S
21	TCR-2631	0	20	0	HR	90	40	36	MS	100	46	46	S	100	58	58	S	100	68	68	S	41.6	S
22	TCR-2632	30	26	7.8	R	90	38	34.2	MS	100	40	40	S	100	52	52	S	100	58	58	S	38.4	MS
23	TCR-2634	30	26	7.8	R	100	44	44	S	100	56	56	S	100	64	64	S	100	78	78	HS	49.96	S

24	TCR-2710	50	30	15	MR	100	44	44	S	100	58	58	S	100	64	64	S	100	82	82	HS	52.6	S
25	TCR-2744	30	26	7.8	R	100	44	44	S	100	58	58	S	100	64	64	S	100	82	82	HS	51.16	S
26	TCR-2832	60	32	19.2	MS	100	58	58	S	100	72	72	HS	100	94	94	HS	100	100	100	HS	68.64	S
27	TCR-2833	90	38	34.2	MS	100	62	62	S	100	84	84	HS	100	90	90	HS	100	100	100	HS	74.04	HS
28	TCR-2839	60	32	19.2	MS	100	58	58	S	100	68	68	S	100	86	86	HS	100	100	100	HS	66.24	S
29	TCR-2847	0	20	0	HR	100	48	48	S	100	54	54	S	100	74	74	HS	100	88	88	HS	52.8	S
30	TCR-2869	0	20	0	HR	70	34	23.8	MS	90	42	37.8	MS	100	44	44	S	100	46	46	S	30.32	MS
31	Parbhani Kranti	0	20	0	HR	10	22	2.2	HR	10	22	2.2	HR	20	24	4.8	R	30	28	8.4	R	3.52	HR
32	Pusa Sawani	50	30	15	MR	90	48	43.2	S	100	64	64	S	100	68	68	S	100	78	78	HS	53.64	S
33	Salkeerthi	50	30	15	MS	60	44	26.4	MS	80	56	44.8	S	100	56	56	S	100	62	62	S	40.84	S
34	Varsha Uphar	0	20	0	HR	0	20	0	HR	10	22	2.2	HR	20	24	4.8	HR	20	26	5.2	HR	2.44	HR

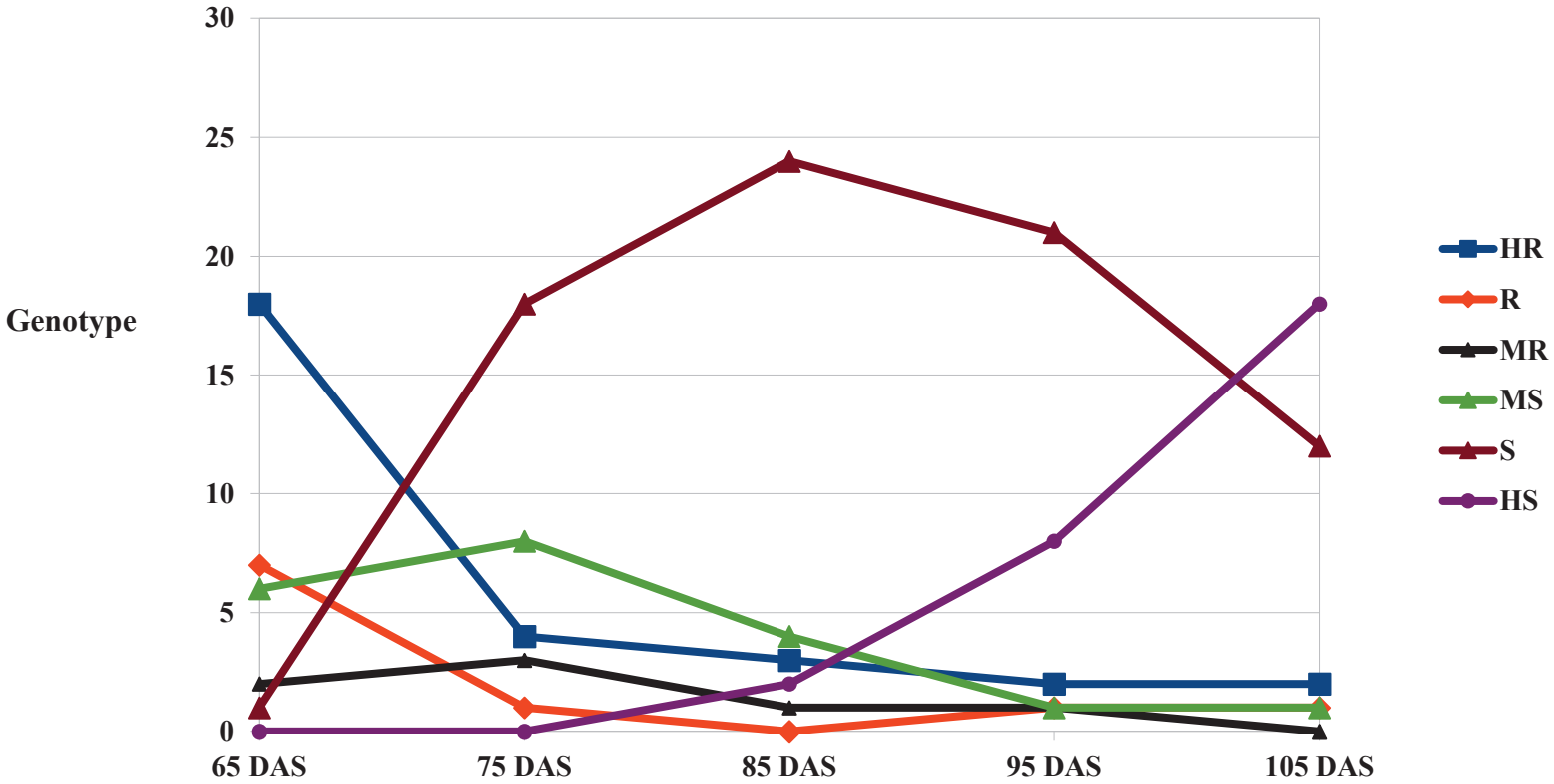
PDI : Per cent disease incidence
CI : Coefficient of YVM infection
PDS: Per cent of disease severity
HR : Highly resistant
MR: Moderately resistant
MS: Moderately susceptible
S: Susceptible
HR: Highly susceptible
DR: Disease reaction
AVE-DR: Average disease reaction
AVE-CI: Average coefficient of infection

Fig.3 Response of okra genotypes to YVM in different stages



Contd….

Fig.4 Response of okra genotypes to YVM in different stages



TCR -30

Varsha Uphar

Parbhani Karnti

Plate 9. Highly resistant genotypes

TCR -1652

Plate 10. Moderately resistant genotype

TCR -32

TCR -2393

TCR -2610

TCR -2618

TCR -2392

TCR -2869

TCR -2621

TCR -2568

TCR -2632

Plate 11. Moderately susceptible genotypes

TCR -1648

Salkeerthi

TCR -2631

TCR -1774

TCR -1806

TCR -1653

TCR -2634

TCR -2744

TCR -2628

TCR -1797

Plate 12. Susceptible genotypes

Contd…

Susceptible genotypes

TCR -2710

TCR -2847

TCR -1785

Pusa Sawani

TCR -2391

TCR -2626

TCR -1775

TCR -2627

TCR -2839

TCR -2832

TCR -2833

Plate 13. Highly susceptible

Summary

5. SUMMARY

The summary of the present study entitled **'Assessment of genetic variability for YVM resistance in okra (*Abelmoschus esculentus* (L.) Moench)**' are furnished as below:

- Thirty four genotypes were classified based on five qualitative characters *viz.*, fruit colour, fruit pubescence, petal colour, petal base colour and seed hairiness. Fruit colour was multimorphic - twelve genotypes had fruits with light green, eleven with green, five with dark green, one with yellowish green, three red, one dark red and one green with purple blend. Fruit pubescence was trimorphic- twenty seven were downy, five slightly rough and two strong. Petal colour was trimorphic - yellow in fourteen, cream in fifteen and purple in five. Petal base colour was dimorphic - twenty nine were with purple colour on both sides at the base of petal, five genotypes were with purple colour at base of petal inside only. Seed hairiness was monomorphic - all the thirty four okra genotypes were without hairs on their seeds.
- Analysis of variance showed significant variation among the okra accessions, TCR-1797 (39.40) was the earliest flowering genotype and TCR-2628 took maximum days to produce flowering.
- One accession (TCR-1648) had significantly longer leaf blade whereas, three TCR-2832, TCR-2621 and TCR-2510 were having shorter leaf blade, compared to checks.
- None of the genotypes had significantly broader leaves compared to the check varieties. Nine accessions had high leaf area while, thirteen accessions had less leaf area, compared to check varieties.
- Eight accessions were significantly taller than the check varieties while, fifteen accessions were shorter compared to check varieties.
- Only two accessions had significantly higher number of branches per plant compared to check varieties, while, seven accessions had less number of branches.

- Two accessions *viz*., TCR-1774 and TCR-2393were having longer fruit length compared to check varieties while, nineteen had short fruit length, compared to the check varieties.
- Only one accession (TCR-2626) exhibited higher fruit diameter compared to check varieties.
- . The highest number of ridges was noticed in the fruits of TCR-2847. All the check varieties had five ridges per fruit and the accession TCR-2832 had fruits without ridges. Nine had significantly more ridges per fruit, compared to check varieties.
- Eight accessions *viz.,* TCR-2628, TCR-2833, TCR-2631, TCR-2626, TCR-1785, TCR-2869, TCR-1648 and TCR-1652 had more number of seeds per fruit while, twelve accessions had showed less seeds, compared to check varieties.
- Only TCR-1774 among accessions had more number of fruits while, seventeen accessions had low number of fruit per plant, compared to check varieties.
- Only one accession (TCR-2631) was significantly different while, six accessions had less weight, compared to check varieties.
- None of the accessions showed higher yield while, twenty five accessions had lower fruit yield per plant, compared to check varieties.
- Significant variability was noticed among the accessions for coefficient of YVM infection (%), which varied from minimum CI = 0 in TCR-30 to the maximum CI= 74.04 in TCR-2833. Twenty-five accessions showed higher CI while, TCR-30 and TCR-1652 had less CI than the check varieties.
- Significant variation was observed for white fly population on young leaves. The lowest number of white flies was observed in TCR-30 (3.80) and the highest number was found in TCR-2744 (16.20).
- Phenotypic and genotypic coefficient of variation were very high for leaf area and coefficient of YVM Infection and high for five characters *viz*., fruit yield per plant, branches per plant, plant height, fruits per plant and ridges per fruit. In general, GCV was slightly lower than PCV for most of the traits.
- Broad sense heritability (H^2) was very high for three traits (leaf area, seeds per fruit

and ridges per fruit), while genetic advance as % of mean (GA) was very high in two traits (leaf area and coefficient of YVM Infection). High H^2 and GA were noticed in most of the traits including number, length, diameter, weight and yield of fruits. Coefficient of YVM Infection exhibited high H^2 as well as GA.

- Fruit yield per plant had highly significant positive correlation with leaf area and seeds per fruit and significant positive association with days to first flowering, leaf blade width and plant height. Positive and highly significant association was observed for coefficient of YVM infection with days to first flowering, leaf area and vector population.
- Six best okra genotypes were selected under high yielding susceptible category *viz.,* Salkeerthi, TCR- 1774, TCR-1797, TCR- 2631, TCR-2627 and TCR-2626. Salkeerthi had the highest fruit yield per plant (294.22 g) and superior yield components *viz*., 12.83 fruits per plant, fruit length of 21.89 cm, fruit diameter of 1.95 cm and fruit weight of 22.26 g.
- Three genotypes *viz*., Varhsa Uphar, Parbhani Kranti and TCR- 30 exhibited high resistance. Varhsa Uphar and Parbhani Kranti (two resistant checks) exhibited superiority in fruit yield (292.25 and 248.85 g per plant respectively) as well as other yield components *viz*., fruit number per plant, fruit length, fruit diameter, and fruit weight. TCR- 30 exhibited consistent high resistance (0.00 CI) to YVM throughout the crop period, with the lowest number of white flies.

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ASSESSMENT OF GENETIC VARIABILITY FOR YVM RESISTANCE IN OKRA (*Abelmoschus esculentus* (L.) Moench)

by

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ABSTRACT

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ABSTRACT

Okra (*Abelmoschus esculentus* (L.) Moench) is an important vegetable crop which is widely grown in tropical, temperate and subtropical regions of the world. The present investigation on 'Assessment of genetic variability for YVM resistance in okra (*Abelmoschus esculentus* (L.) Moench)' was conducted at the Department of Plant Breeding and Genetics, College of Horticulture, Vellanikkara, Thrissur during November 2019 to February 2020. The experiment was laid out in augmented design using thirty four okra accessions including two resistant check varieties (Parbhani Kranti and Varsha Uphar) and two susceptible check varieties (Salkeerthi and Pusa Sawani) collected from NBPGR and KAU. Ten plants of each accession were sown on ridges in a row with 60 cm x 45 cm spacing and the crop was managed as per package of practices recommendations of KAU (2017). Observations on five qualitative characters and fifteen quantitative characters were recorded from five randomly selected plants for each accession, as per the NBPGR descriptors. Scoring for YVM disease incidence was done as per the rating scale given by Arumugam *et al*. (1975).

The genotypes were classified based on five qualitative characters *viz*., fruit colour (multimorphic), fruit pubescence and petal colour (trimorphic), petal base colour (dimorphic) and seed hairiness (monomorphic). ANOVA for fifteen quantitative characters showed significant variation for days to flowering, leaf blade length , leaf area), plant height, branches per plant, fruit length, fruit diameter, ridges per fruit, seeds per fruit, number of fruits per plant, fruit weight, fruit yield per plant, coefficient of YVM incidence and vector population on young leaves. This indicated high variability in the okra germplasm which can be utilised in breeding programmes.

Phenotypic and genotypic coefficients of variation (PCV and GCV) were very high for leaf area and coefficient of YVM infection and high for five characters *viz*., fruit yield per plant, branches per plant, plant height, fruits per plant and ridges per fruit. In general, GCV was slightly lower than PCV for most of the traits indicating a small environmental effect in their expression.

Broad sense heritability (H^2) was very high in three traits (leaf area, seeds per fruit and ridges per fruit) while genetic advance as % of mean (GA) was very high in two traits (leaf area and coefficient of YVM Infection). High H^2 and GA were noticed in most of the traits including number, length, diameter, weight and yield of fruits. Coefficient of YVM infection also exhibited high H^2 as well as GA. This indicates that these characters can be improved to a great extent by selection.

Fruit yield per plant had highly significant positive correlation with leaf area and seeds per fruit and significant positive correlation with days to first flowering, leaf blade width and plant height. Positive and highly significant correlation was observed for coefficient of YVM infection with days to first flowering, leaf area and vector population.

In the high yielding YVM susceptible category, the six best okra genotypes selected were Salkeerthi, TCR- 1774, TCR-1797, TCR- 2631, TCR-2627 and TCR-2626. Salkeerthi (KAU variety) in spite of being susceptible to YVM, had the highest fruit yield per plant (294.22 g) among all the genotypes evaluated in the present study. Besides, it had superior yield components *viz*., fruitsper plant, fruit length, fruit diameter and fruit weight. All the other selected genotypes (collected from NBPGR) were also superior in fruit yield per plant and other major yield components. These selected NBPGR accessions may further be evaluated for confirming their superiority in yield and yield traits.

Three genotypes *viz*., TCR- 30, Varhsa Uphar and Parbhani Kranti showed high resistance during the present study. Varhsa Uphar and Parbhani Kranti (two resistant checks) exhibited superiority in fruit yield as well as yield components *viz*., fruit number/plant, fruit length, fruit diameter and fruit weight. Even though a low yielder, TCR- 30 exhibited consistent high resistance to YVM disease throughout the crop period with the lowest number of white flies emphasising its resistance mechanism. Hence it can be recommended as a donor for imparting YVM resistance in breeding programmes.