EVALUATION OF PROMISING DISTANT HYBRIDIZATION DERIVATIVES OF OKRA (*A. esculentus* (L.) Moench)

By

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THESIS

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DECLARATION

I hereby declare that this thesis entitled **"Evaluation of promising distant hybridization derivatives of 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 this thesis entitled **"Evaluation of promising distant hybridization derivatives of okra (*A. esculentus* (L.) Moench)"** is a record of research work done independently by **Ms. Yamuna Mogili** under my guidance and supervision and that it has not previously formed the basis for the award of any degree, diploma or fellowship to her.

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INTRODUCTION

INTRODUCTION

Okra (*Abelmoschus esculentus* (L.) Moench) is one of the important warm season fruit vegetables grown in the tropical and sub tropical parts of the world. It is a potential export earner and provides high returns to the farmers. Okra is grown for its tender green fruits, rich in vitamin A (86.67 µg/100 g), riboflavin (0.10µg / 100g), vitamin C (18µg / 100g) and minerals like calcium (66mg/100g), phosphorus, iodine, iron and potassium (Gopalan *et al.*, 2007).

Okra requires a long, warm and humid growing period. Thus it can be successfully grown in hot humid areas. It is sensitive to frost and extremely low temperatures. Okra has a prominent position among vegetables due to its multiple virtues like high nutritive and medicinal value, ease of cultivation, wide adaptability, year round cultivation, good portability and bountiful returns. Early bearing, extended period of harvest coupled with short life span of this crop are some other plus points for vegetable growers.

Eight *Abelmoschus* species occur in India. Out of these, *A. esculentus* is the only known cultivated species. *A. moschatus* occur as semi wild species and is also cultivated for its aromatic seed oil, while the rest six are truly wild types. Species resistant to Yellow Vein Mosaic Virus (YVMV) are *A. caillei, A. manihot, A. tetraphyllus* and *A. crinitus.* Wild species have not been fully utilized in breeding programmes due to crossing barriers. Resistance to YVMV is not stable in the cultivated species and frequent breakdown of resistance has been observed in developed varieties. There is an urgent need to adopt appropriate method of breeding programmes for the development of lines resistant to YVMV.

Yellow vein mosaic (YVM)) is the most destructive viral disease of okra and has become a major limiting factor in the successful cultivation of this crop. It infects all stages of the crop and severely reduces plant growth and yield. The virus produces

typical vein yellowing and thickening of leaves forming a network of mottled veins and vein lets in the infected leaves. Initially, the leaves exhibit only mild yellow colored veins but under the severe infection, the leaves become completely chlorotic and turn yellow. There is reduction of leaf chlorophyll and the infected plants give a stunted look and produce small-sized pale yellow fruits (Gupta and Paul, 2001). The virus is neither sap nor seed transmissible. In nature the virus transmission occurs through the insect vector white fly (*Bemisia tabaci*). The production losses due to YVMV have been reported to range from 50-94 per cent (Sastry and Singh, 1974).

As the casual organism is virus the only control measure is the control of vectors using pesticides. But the disease cannot be controlled properly by chemical means. The escalating cost of pesticides and the chemical residues which cause the health hazards warrant alternative methods. Uprooting of infected plants is not practical and economical because of heavy infection rate in the field. So the only practical solution for this problem is to develop resistant varieties (Horvath, 1984). Unfortunately, many of the existing released varieties of okra are showing the signs of susceptibility to YVMV. Several varieties exhibited tolerance / resistance to this virus at the time of release, but this tolerance / resistance have broken down with time. Since, there is no source of resisistance to YVMV in *A. esculentus,* interspecific hybridization for YVMV resistance followed by selection in the segregating generations is an effective method for obtaining desirable recombinants. Several wild species of cultivated okra showed high degree of resistance to YVMV. However resistant varieties developed by various research organizations by interspecific hybridization have also started showing signs of susceptibility probably due to the arrival of new virus strains. Hence it is imperative to find diverse sources of resistance to YVMV and evolve YVMV resistant varieties in a continuous manner by suitable gene introgression programmes.

In this context a semi cultivated okra species *Abelmoschus caillei* (A. Cher.) Steveis deserves importance. It adorns many remarkable traits such as resistance to YVMV, adaptability and long fruiting period (Charrier, 1984; Chacko, 1996). This species is a complex polyploid considered to be originated by contributing genomes of *A.esculentus* and *A. manihot* (Siemonsuma, 1982).

In *A. caillei*, a variety 'Susthira' has been developed in the Department of Olericulture, College of Horticulture, Kerala Agricultural University, Vellanikkara by selection from the existing variability expressed by this species (Sureshbabu *et al*., 2004). Although Susthira is highly resistant to YVMV and high yielding, it is more suitable for kitchen garden due to its perennial nature, late bearing habit and less attractive pods. At the same time a popular *A. esculentus* variety 'Salkeerthi' developed by the same Department has a wide range of acceptability owing to its early bearing habit, excellent fruit quality, attractive light green pods and high yield, but it is susceptible to YVMV. Hence it cannot be grown during summer when the disease is more prevalent. In this regard it would be a viable proposal to transfer YVMV resistance from 'Susthira' (*A. caillei*) to 'Salkeerthi' (*A. esculentus*). Accordingly interspecific hybridization between *A. caillei* and *A. esculentus* was done and the generations were advanced up to F_8 (Sureshbabu *et al*., 2009). Thus in order to continue the breeding programme the F_8 generation has to be advanced further to stable F_9 generation along with proper selection for YVMV resistance and other desirable traits.

In the distant hybridization programmes, genetically diverse parents are involved hence in the segregating generations there are more scope for the selection of desirable recombinants. Assessing the genetic divergence among the stabilized F_9 generation selections in comparison with parents will show their extent of possession of divergent genes. Thus the proposed study will pave a way for the final selection of lines having resistance to YVMV combined with other desirable traits.

The major objectives of the present study are:

- To evaluate 12 okra selections of the F_9 generation of the cross *Abelmoschus caillei* var. Susthira x *Abelmoschus esculentus* var. Salkeerthi to study the extent of variability.
- To study the genetic diversity among the selections along with parental lines and a standard check variety Arka Anamika.
- To select promising selections having high level of resistance to yellow vein mosaic virus combined with desirable traits.

REVIEW OF LITERATURE

2. REVIEW OF LITERATURE

Okra is one of the important vegetable crops grown chiefly for its tender green fruits. It has high nutritive value and also possesses export potential. But the susceptibility of most of the okra varieties to YVMV is a major problem limiting the production of this crop. There is no source of resistance to this disease in *A. esculentus*. Therefore, there is a need to develop new okra varieties with improved resistance to YVMV by transferring resistant genes from diverse wild species by interspecific hybridization followed by selection of promising lines. The pertinent literature on this aspect is reviewed under the following heads citing the research works in okra and other vegetable crops.

2.1 Origin and cytogenetics

Okra belongs to the genus *Abelmoschus* which was established by Medikus (1787). The genus is believed to be of Asiatic origin whereas centre of origin of the major cultivated species *A. esculentus* is controversial- the species is believed to have originated in India (Masters, 1875); Ethiopia (Candolle, 1883); West Africa (Chevalier, 1940) and Tropical Asia (Grubben, 1977). Index kewensis lists over 30 species of *Abelmoschus* in the old world, four in the new world and four in Australia. Waalkes (1966) has a more conservative point of view retaining only six species. These are *A. moschatus* Medikus, *A. manihot* (L.) Medikus, *A. esculentus* (L.) Moench, *A. ficulneus* (L.) Wt and Art. ex Wt, *A. crinitus* Wall. and *A. angulosus* Wall ex Wt and Art. The former three species consisted of wild and cultivated forms and the latter three species consisted of wild forms only. Bates (1968) suggested some additional modifications like inclusion of *A. tuberculatus* and the grouping of all subspecies and varieties of *A. manihot.* The genus became more complex by discovery of an African cultivated species by Siemonsuma (1982) and described it as *A. caillei* (A. Cher.) Stevies. Based on the available cytogenetical evidence, the International Okra Workshop (1990)

adopted a classification in which nine species were included in the genus *Abelmoschus*. This classification also included the new cultivated species, *Abelmoschus caillei* which was wrongly identified earlier as *A. manihot* ssp. *manihot.*

Joshi and Hardas (1956) proposed a polyphyletic origin for the species. They reported an allopolyploid genome for cultivated okra. The chromosome polymorphism has been reported in okra that is chromosome count within a species exhibit a wide range of variation. The somatic chromosome number reported for *A. esculentus* varied greatly from 2n=72 to 144. However, the most frequently observed chromosome number was 2n=130 (Siemonsuma, 1982). Dutta and Nang (1968) proposed that the 2n numbers, 2n=72,108,120, 132 and 144 were an indication of a regular polyploid series with x=12.

2.2 Yellow Vein Mosaic Virus (YVMV)

Yellow Vein Mosaic Virus (YVMV) is a most devastating viral disease transmitted through whitefly (*Bemisia tabaci*) in okra (Padda, 1968). In India, the occurrence of this disease was first reported by Kulkarni (1924) in Bombay province. Later it was studied by Uppal *et al.* (1940) and Kapoor and Varma (1950). Infection of 100 per cent plants in a field is very usual and yield losses ranges from 50 to 94 per cent depending on the stage of crop growth at which infection occurs (Sastry & Singh, 1974). This disease adversely affects the quantity and quality of the fruits.

2.2.1 Incidence of YVMV

Sangar (1997) revealed that Arka Anamika was highly resistant, Arka Abhay resistant and Parbhani Kranti and V-6 were moderately resistant to YVMV during rainy and summer seasons in his experiment.

Nath *et al.* (1999) noticed minimum disease incidence (4.44%) in Parbhani Kranti and Arka Abhay at 90 days after sowing.

Pun and Doraisami (1999) revealed effect of age of plants on susceptibility to YVMV. The greatest loss in the yield of fresh fruit was highest (95.7%) when virus inoculated at one week old plants.

Anonymous (2010) noticed maximum YVMV disease incidence in summer months (15.2 to 48.9%). The high incidence of disease has been attributed to higher activities of whiteflies population and their active dispersal in summer.

Fajinmi and Fajinmi (2010a) studied degree of okra mosaic virus at different growth stages of plants. Virus infection was severe at growth stages earlier than four weeks. Late infection of Yellow Vein Mosaic Virus had little or no effect on performance of okra, but early infection had a significant effect on growth and yield Fajinmi and Fajinmi (2010b).

2.2.2 Screening for resistance to YVMV

Raghupathy *et al.* (2000) conducted screening experiment among 12 okra cultivars, including highly susceptible Pusa Sawani and MDU-1. The disease was absent in the highly resistant cultivars BO-1 and HRB-55. Resistant cultivars were KS-404, HRB 9-2, HY-8, P-7, Parbhani Kranti, Sel-10 and Sel-4 with a disease incidence of 0.5, 0.82, 1.26, 1.68, 2.87, 3.63 and 8.69 per cent respectively. BO-2 was susceptible (19.55%) and MDU-1 and Pusa Sawani recorded 90.83 and 91.53 per cent respectively.

Singh *et al.* (2000) revealed performance of different varieties to YVMV. Out of the twelve cultivars screened, disease incidence varied from 0.7 per cent (Arka Abhay) to 57.4 per cent (Chhindwala Local).

Ravisankar (2002) conducted screening experiment by grafting and vector transmission studies. He reported line AE-238 was free from YVMV. AE-265 x AE-190 also did not show disease symptoms in the field screening.

Rashid *et al.* (2002) screened twelve okra cultivars for YVMV resistance. Lines OK-285 and OK-292 were identified as resistant and OK-315, OK-316, OK-317 were found tolerant.

During field screening trials, *Abelmoschus esculentus* variety Salkeerthi was highly susceptible to YVMV (CI=70.7), whereas *A. caillei* variety Susthira was highly resistant (CI=0.1) (Kousalya, 2005). The interspecific F_1s were moderately resistant to YVMV (CI=18.9) and all the F_2 generation plants were resistant to YVMV.

Singh *et al.* (2007) reported that among thirty five genotypes screened, three genotypes Cos-05-25, Arka Anamika and Punjab-7 were found highly resistant.

Bhattiprolu and Rahman (2008) observed that the mean disease incidence was ranged from 3.63 per cent (VRO-4) to 75.09 per cent (Pusa Sawani). No disease was recorded in KS-410 and Arka Abhaya in three years of trails.

Jaseena (2008) done field screening for resistance to YVMV revealed that *Abelmoschus esculentus* variety Salkeethi was highly susceptible, *A. caillei* variety Susthira was highly resistant in both F_4 and F_5 generations. F_4 segregants were completely free of YVMV and F_5 segregants showed CI of 0.87 to 14.01.

Prasanth *et al.* (2008) revealed that out of fifty five screened genotypes, five were highly resistant, thirteen were resistant, seventeen were moderately resistant, thirteen were moderately susceptible, five were susceptible and two were highly susceptible based on coefficient of infection.

Tripathy *et al.* (2008) conducted screening experiment during summer and kharif season under reduced level of chemical fertilizers supplemented with organic manures. YVMV disease incidence was ranged from 22.48 per cent (Arka Anamika) to 43.96 per cent (Sansar selection).

Padvibulya *et al.* (2009) in his experiment, two okra varieties (Annie and Okura) were subjected to irradiation. Screening for YVMV resistance was conducted for M_3 and M_4 plants. One M_4 plant of Okura (B-21) was found highly resistant, but none of Annie. Ten resistant lines obtained by screening for YVMV resistance up to the M_7 generation were selected for yield trial observations. Only a small portion of the plants of the mutant lines appeared to be resistant throughout the whole growth duration.

Phad *et al.* (2009) screened ten okra hybrids along with two checks i.e, Parbhani Kranti and Pusa Sawani. He reported all hybrids were resistant and the disease incidence was less in Mahabeej-333 and Pusa Sawani.

Breeding for resistance to YVMV

2.2.2.1 Selection

Joshi *et al.* (1960) used treatment line IC 1542 from West Bengal for developing the resistant varieties.

AE-286 (*A. caillei*)), an YVMV resistant edible perennial okra line developed through single plant selection (Sureshbabu *et al.,* 2002).

2.2.2.2 Hybridization and Selection

Singh *et al.* (1962) developed "Pusa Sawani" from the cross between IC-1542 and Pusa Makhmali. Dhankar *et al*. (1996) bred YVMV resistant okra "Varsha Uphar" out of the cross between Lam Selection 1 x Parbhani Kranti.

Deo *et al.* (2000) reported that Parbhani Kranti and its hybrid Parbhani Kranti x HRB-9-2 were highly resistant to YVMV. Rattan and Bindal (2000) in their experiment to develop okra hybrids resistant to YVMV found that lines 407, 409, 417, 430 were completely resistant. The F_1 hybrids between the resistant lines were resistant, and that of susceptible parents susceptible. The studies indicated that resistance to disease is monogenic and dominant. Maximum number of fruits and yield per plant was recorded

by hybrid 410 x 407 followed by 409 x 421 and 409 x 408 involving resistant x resistant and resistant x susceptible crosses, respectively.

Ravisankar (2002) crossed fifteen lines with two testers, AE-285 and AE-190 (Parbhani Kranti) in a line x tester mating design to produce 30 hybrids. Among them a parent AE-238 and two hybrids were free from YVMV.

Jaseena (2008) found that six promising lines selected from F_5 generation of the corss *A. caillei* x *A. esculentus* were highly resistant to YVMV.

Sureshbabu *et al*. (2009) reported high degree of variability in the F_6 generation of the cross *A. caillei* x *A. esculentus* and selected six promising lines expressing high levels of resistance to YVMV.

2.2.2.3 Interspecific Hybridization

Interspecific hybridization followed by selection in the segregating generations is an effective method for obtaining YVMV resistant recombinants.

Arumugham and Muthukrishnan (1978) developed four YVMV resistant F_1s by crossing two resistant forms of *A. manihot* with susceptible okra cultivars, Pusa Sawani and CO 1.

Mamidwar *et al.* (1980) found that fruit set was higher when *A. esculentus* was used as female parent with 8.33 as the near value for per cent fruit set while studying crosses between cultivars of *A. esculentus* and *A. manihot*.

Jambhale and Nerkar (1981) in his experiment, two *Abelmoschus* species, viz., *A. manihot* (L.) Medik and *A. manihot* (L.) Medik ssp. *manihot*, resistant to yellow vein mosaic (YVM) were crossed with *A.esculentus* cv. 'Pusa Sawani', a susceptible culture. The hybrids were resistant and partially fertile. Segregation pattern for disease reaction in F_2, BC_1 and subsequent generations of the two crosses revealed that resistance to YVM is controlled by a single dominant gene in each species.

Nirmaladevi (1982) revealed that *A. manihot* was crossable with *A. esculentus*. The interspecific F_1 hybrid exhibited resistance to YVMV. She observed significant genetic distance between *A. esculentus* and *A. manihot.*

Jambhale and Nerkar (1983) observed resistance to YVMV in plants which were obtained from backcrosses of *A. esculentus* and *A. manihot* to *A. esculentus* cv. Pusa Sawani. Seed fertility in the plants was 58 to 88 per cent.

Pillai (1984) developed interspecific hybrids from *A. manihot* and YVMV susceptible *A. esculentus* cultivars. The hybrids were found to be resistant to the YVMV disease. A decrease in percentage of pollen fertility in the hybrids (28.7-57.4) as against the parents (98-99) is presumably the reason for scanty hybrid seed recovery.

Sharma and Sharma (1984) used *A. manihot* as a male parent in hybridization with Pusa Sawani for developing resistant 'Punjab Padmini'.

Nerkar and Jambhale (1985) used the YVMV resistant Ghana line *A. manihot* ssp. *manihot* in their hybridization programme which resulted in the variety 'Parbhani Kranti'.

Mathews (1986) observed preponderance of low yielding YVM resistant plants similar to semi-wild parent among the F_2 population of the interspecific hybrids between the YVM susceptible cultivars of *A. esculentus* and YVM resistant semi wild species of *A. manihot*. Varying degrees of sterility were observed in the F_2 progenies. He also reported high phenotypic and genotypic coefficients of variation for weight of fruits per plant, number of leaves per plant and height of plants.

Prabha (1986) made cross between the YVMV disease susceptible varieties of *A. esculentus* and resistant semi wild species *A. manihot*. The first generation hybrids though did not produce viable

seeds profusely were not totally sterile. The scanty viable seed recovery from the hybrids against the parents was suspected to be due to chromosomal differentiation that could have taken place during speciation in the genus.

Sureshbabu (1987) produced vigorous F_1 hybrid between *A. esculentus* and *A. manihot* ssp. *tetraphyllus* var. *tetraphyllus.* Sterility in the hybrid was attributed to the failure of development of female gamete.

Reciprocal crosses between *A. manihot* ssp. *manihot* and *A. tetraphyllus* and also between *A. manihot* ssp. *manihot* and induced amphidiploid of (1) *A. esculentus* x *A. tetraphyllus* and (2) *A. esculentus* x *A. manihot* revealed that *A. manihot* ssp. *manihot* (hexaploid) contained two genomes from *A. tetraphyllus* and a third from *A. manihot* (Kondaiah *et al*., 1990).

Sureshbabu and Dutta (1990) produced heterotic hybrids from crosses of *A. esculentus* with *A. tetraphyllus.* Meiosis was abnormal in hybrids leading to hybrid sterility. They produced fully fertile amphidiploid *A. esculentus* x *A. tetraphyllus* by colchicine treatment, resembling the F_1 plants with YVMV resistance and larger fruits. They also reported that progenies from the back cross of the amphidiploid of the cross between *A. esculentus* and *A. tetraphyllus* with the cultivated parent was readily feasible and they combined the YVMV resistance of the wild species and the desirable fruit characters of the cultivated species with high level of pollen fertility.

Dutta (1991) developed the okra lines having high yield, quality and resistance to YVMV by interspecific hybridization between *A. esculentus* and YVMV resistant wild species *A. manihot ssp. tetraphyllus.*

Nerkar (1991) noticed the importance of wild okra with resistance to okra YVMV, powdery mildew (*Erysiphae cichoracearum*), Jassids (*Empoasca* spp.) in breeding programmes to develop pest and disease resistant varieties.

Chandran *et al.* (1996) reported that transplantable seedlings could be obtained by embryo rescue technique through culturing twelve and fifteen days old embryos of the cross between *A. esculentus* x *A. moschatus*. This suggested the potential of tissue culture methods to overcome the post zygotic incompatibility barriers in interspecific crosses.

Interspecific hybridization between *A. esculentus* and *A. manihot* was successful when *A. manihot* was used as the female parent (Chacko, 1996).

Chandran and Rajamony (1997) reported that when cultivated types were used as the female parent in hybridization using wild donors, maximum fruit set was obtained in crosses where *A. manihot* used as pollen source. The percentage of viable seeds obtained was also maximum in crosses involving *A. manihot.*

John (1997) estimated the extent of variability in the F_2M_2 and F_3M_3 generations as a result of hybridization and irradiation of the interspecific hybrids between *A. esculentus* and *A. manihot.* In the F_2M_2 generation, the irradiated treatments were late flowering and had more number of leaves, flowers and fruits. Irradiation increased pollen sterility and was maximum at 10 kR. Seed set was lower in the irradiated treatments.

Dhankar *et al*. (2005) reported the nature of inheritance for resistance to YVMV in inter specific cross of 'Hissar Unnat' *A. esculentus* × *A. manihot subsp. Manihot.* The resistance showed Mendelian segregation as per the condition governed by two complimentary dominant genes.

Crossability studies between *A.esculentus* and *A.caillei* revealed that crosses were more successful when *A.caillei* was used as female parent (Kousalya, 2005). The F_1 hybrid was also secured in the cross *A.esculentus* x *A.caillei* but crossability index was less (15.3%). The cross *A.caillei* x *A.esculentus* was more successful , probably due

to the higher ploidy level of female parent *A.caillei* which provided better embryo endosperm balance.

Pitchaimuthu *et al.* (2009) reported that interspecific crosses involving *A. tetraphyllus, A. tuberculatus*, IIHR-223 (Red Bhendi) and Arka Anamika were found to be promising with least Per cent Disease Incidence (PDI) of YVMV.

2.2.2.3.1 Interspecific Hybrid Sterility

Teshima (1933) observed that *A. esculentus* and *A. manihot* crossed only when the former was used as female parent. He also studied this cross and reported that the F_1 hybrids were partially fertile. The interspecific hybrid sterility may be genic or chromosomal (Stebbins, 1950). Genetic sterility is typically due to the genetic constitution of the organism and so is diplontic (Dobzhansky, 1951).

Pal *et al.* (1952) made interspecific crosses between five species of *Abelmoschus* viz., *A. esculentus, A. tuberculatus, A. ficulneus, A. manihot* and *A. manihot* var. pungens and reported that the crosses mostly resulted in shriveled or empty seeds. The various F_1 hybrids studied were sterile.

Arumugham *et al.* (1975) reported about 90 per cent sterility in interspecific hybrid between *A. esculentus* x *A. manihot.* In interspecific hybridization between different *Abelmoschus* spp. viable seeds could be obtained only in cross between *A. ficulneus* (2n=72) and *A. tuberculatus* (2n=58), resulting plants were sterile (Siemonsuma, 1982). Partial seed fertility of 5.9 and 7.1 per cent were obtained in crosses *A. esculentus* x *A. manihot and A. esculentus* x *A. manihot* ssp. *manihot* respectively by Jambhale and Nerkar (1985).

Chacko (1996) reported that in the interspecific hybrid of *A. esculentus* x *A. manihot* pollen stainability was only 18.26 per cent. The mean diameter of sterile pollen grains was 0.03 µm where as fertile pollen grain was 0.062 µm.

Kousalya (2005) observed that in the cross *A.caillei* x *A.esculentus* the F_1 hybrid was partially sterile. This can be attributed to the cytological irregularities including the presence of lagging chromosomes, occurrence of micronuclei and multipolar spindle formation.

2.2.2.3.2 Segregating progenies

Mathews (1986) evaluated the F_2 population of interspecific cross of *A. manihot* x *A. esculentus* along with the parents and F_1s. A preponderance of low yielding yellow vein mosaic resistant plants similar to the semi-wild parents was observed among the F_2 populations, suggesting the presence of powerful genetic mechanisms which restrict free recombination.

Gill *et al.* (1983) successfully transferred Yellow Mosaic Virus resistance from black gram (*Phaseolus mungo*) to mung bean (*Phaseolus aureus*) by advancing the segregating generations and subsequent selections. YVMV resistant mung bean lines were recovered in advanced generations of interspecific cross involving the mosaic susceptible mung bean line SML32 and the resistant black gram variety Saradhu, without backcrossing (Pal *et al.*, 1991).

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

Singh *et al*. (2000) noticed that when ten okra genotypes and five F_1s derived from them were screened for resistance to yellow vein mosaic virus, HRB-55 x Arka Anamika, Prabhani Kranti x HRB-9-2 and BO-1 x P-7 were highly resistant to the virus, while BO-1 x Pusa Sawani was susceptible.

The interspecific hybridization between *A. esculentus* x *A. caillei* showed that F_1 and F_2 generations were partially fertile, Kousalya (2005). She also observed that the F_2 plants were free of YVMV infection.

Jaseena *et al*. (2008) evaluated F_4 and F_5 generations of the cross *A. caillei* x *A. esculentus* and reported high levels of variability and resistance to YVMV in the segregating population. F_5 generation plants exhibited high degree of pollen fertility.

2.3 Achievements in breeding for resistance to YVMV

Since some of the tolerant varieties as well as inter varietal hybrid derivatives of okra lost their resistance to YVMV disease in due course, attempts have been made to incorporate the resistant genes from wild species to susceptible commercial types of okra through interspecific breeding programmes.

Pusa Sawani, once most widely cultivated variety of okra developed from a cross between 1C-1542, an indigenous stock with symptom less carrier type of resistance and Pusa Makhmali, a high yielding, adapted but susceptible variety of *A. esculentus* (Singh *et al.*, 1962). However the initial resistance was given way to high susceptibility due to genetic and environmental factors.

Sharma (1982) made interspecific hybridization between *A. esculentus and A. manihot* ssp. *manihot* and the segregating generations were advanced upto F_8 followed by selection to develop Punjab Padmini, an YVMV resistant variety.

The Maharashtra state seed Committee in 1985, released an YVMV resistant variety Parbhani Kranti developed from cross of *A. esculentus* cv Pusa Sawani x *A. manihot* (Jambhale and Nerkar, 1986).

P-7, an YVMV resistant variety was evolved from the cross between *Abelmoschus esculentus* cv. Pusa Sawani and *A. manihot* ssp. *manihot*. The F_1 was backcrossed to the cultivated parent for four generations and selection was followed in the selfing generations up to F_8 (Thakur and Arora, 1988).

Selections from IIHR, Bangalore, Viz., Selection-4, Selection-7, Selection-9, Selection-10 and Selection-12 possessed YVM diseases resistance and these were derived from the cross of *A. esculentus* x *A. manihot* var. *tetraphyllus* (Markose and Peter, 1990).

Arka Anamika, high yielding YVMV resistant variety obtained by interspecific hybridization between *A. esculentus and A. manihot* ssp *tetraphyllus* was released by IIHR Bangalore for National level cultivation. Arka Abhay, another high yielding and resistant line derived from the same cross was released for state level cultivation (Dutta, 1991).

Tamilnadu Agricultural University, Coimbatore developed one okra variety, MDU-1 in 1978. It is an induced mutant isolated from Pusa Sawani and had been notified by the Central Seed Committee in 1985 (Ram, 1998).

Varsha Uphar (HRB 9-2), an YVMV resistant variety had been developed by Haryana Agricultural University, Hisar from the cross, Lam Selection-1 x Parbhani Kranti following pedigree selection method. It was released in 1992 and notified in 1995 by the Central Sub- Committee on Crop Standards (Ram, 1998).

Pusa A4 has been released by IARI in 1994 as a substitute for Pusa Sawani. It is also resistant to YVMV (Ram, 1998).

Hisar Unnat (HRB 55), an YVMV resistant variety developed by Haryana Agricultural University, Hisar from the cross, Sel-2 x Parbhani Kranti had been released by the Central Variety Release Committee and notified in 1996 (Ram, 1998).

EMS-8 (Punjab-8) had been developed by PAU, Ludhiana in 1989. It is an induced mutant derived from Pusa Sawani treated with one per cent EMS. The final selection was made in the M_8 generation. It has field resistance to YVMV (Ram, 1998).

A. caillei variety Susthira had been developed in the Department of Olericulture, College of Horticulture, Kerala Agricultural University, Vellanikkara by selection (Sureshbabu *et al.,* 2004).

KAU had released two yellow vein mosaic resistant varieties, 'Manjima' of the cross Goreesapattom local x NBPGR/ TCR- 874 and 'Anjitha' by interspecific hybridization followed by mutation breeding and selection (KAU, 2007).

Several YVMV resistant varieties like Kashi Vibhuti, Kashi Pragati, Kashi Satdhari, Kashi Bhirav, Kashi Mahima had been released by IIVR, Varanasi (Pradeepkumar *et al.,* 2008).

2.4 Genetic variability in okra

Variability may be defined as the amount of variation present among the members of a population or species for one or more characters at genotypic or phenotypic levels. Presence of variability among genotypes is a prerequisite for any crop improvement programme.

Considerable genetic variation for YVMV infection, fruit yield and number of fruits per plant in okra was reported by Kaul *et al.* (1979).

Twenty eight accessions of okra varied for plant height, node of first fruit set, fruits and yield per plant and the highest yielder was Pusa Selection 6-2 (Korla and Sharma, 1987).

When the performance of seven okra varieties was studied, Bhubaneswari had the credit of being the best yielder with the highest fresh pod weight while AE-180 was the earliest bearer and Pusa Sawani was the tallest with maximum pods (Nandi, 1990). Jeyapandi and Balakrishnan (1992) observed the highest variability for yield per plant followed by plant height.

During a comparison of eight genotypes and their 28 hybrids, considerable variation was observed for the characters under study (Kumbhani *et al*., 1993). Among the six YVM resistant / tolerant okra varieties from various regions of India compared with Pusa Sawani, during various seasons AROH-1 had the highest mean yield followed by Arka Anamika and Sel-4 (Mathews *et al*, 1993).

In an evaluation of 30 genotypes across four environments, Pusa Sawani and Strain 6316 were the most stable genotypes with respect to days to 50 per cent flower while White Velvet Strain 7116 had the highest stability for days to first flower and plant height respectively (Mandal and Dana, 1994). Sheela (1994) reported good genetic diversity in okra germplasm which consisted of 56 accessions for all the characters under investigation except, YVM incidence.

Variability was observed for all the characters studied in F_2M_2 and F_3M_3 families by John (1997) and John *et al*. (1999) and in F_4M_4 and F_5 M_5 families by Philip (1998). Out of the twelve okra varieties evaluated, Panchsira was the best with maximum yield (15.4 t/ha) as well as fruits per plant (35.1) while Pusa Sawani also performed well (Dutta, 1999).

Hazra and Basu (2000) observed wide variation for plant height, days to flower, fruits per plant and yield among twenty two okra genotypes. Variation was moderate for fruit length and primary branches whereas low for node of first flower and ridges per fruit.

Philip *et al*. (2000) assessed the variability in F_4 generation of irradiated interspecific hybrids in okra and observed significant variation for branches and fruits per plant, yield and incidence of YVMV.

Amjad *et al*. (2001) conducted an experiment involving four Indian cultivars viz., Pusa Sawani, Parbhani Kranti, Hybrid Bhindi Sakshi and Krisma-51, a local cultivar Sabz Pari tested for earliness and yield of green pods. Green pod length was maximum in Hybrid Bhindi Sakshi (12-18 cm) which was on par with Sabz Pari (12-15 cm).

The study conducted by Gandhi *et al*. (2001) involving 44 okra genotypes collected from NBPGR shown significant variability for all the thirteen traits under investigation including plant height, internodal length, fruits and branches per plant, length and girth of fruits and yield per plant.

Dhankar and Dhankar (2002) observed broad range of variation and high mean values for fruit yield and plant height in both rainy and spring- summer seasons.

Sharma and Mishra (2007) evaluated the induced genetic variation in okra cv. Ankur-40 under gamma radiation treatment. Nine characters were evaluated in the M_2 population. Variation was observed for days to flower bud initiation, fruit length, fruit yield, seed number and seed yield. Maximum range of statistical and genetic variation was observed for fruit yield per plant.

2.5 Coefficient of variation

In okra high genotypic coefficient of variation coupled with high estimates of heritability and genetic advance for yield and yield components were observed by Rao (1972).

High magnitude of genotypic coefficient of variation for characters like yield per plant, number of fruits and weight of fruits per plant were noticed by (Majumdar *et al.,* 1974).

High estimates of PCV and GCV were observed for plant height and fruit weight per plant by Mathews (1986). Estimates of GCV were high for plant height and yield per plant but moderate for number and length of pods noticed by Yadav (1986). As per reports of Balakrishnan and Balakrishnan (1990), fruits and yield per plant had high PCV and GCV.

In the F_4 generation of interspecific hybrid between, *A. esculentus* and *A. manihot,* evaluated by Alex (1988) the genotypic coefficient of variation was maximum for number of branches per plant and minimum for first fruiting node.

Philip (1998) noticed high GCV and PCV for flower number and YVM disease. GCV was the highest for number of primary branches where as moderate for plant height, fruits and yield per plant (Hazra and Basu, 2000).

John *et al.* (2001) evaluated the extent of genetic variability in the F_2 population of irradiated interspecific hybrids of okra. Selfed seeds obtained from two parents, *A. esculentus cv. Kiran* and *A. manihot*, their F_1M_1 was used to raise the F_2M_2 generation. High genotypic coefficient of variation was observed for number of branches per plant and number of seeds per fruit. High GCV was noticed in the treatment 20 kR for number of leaves per plant, number of flowers per plant and number of fruits per plant. Very low GCV was noticed for yellow vein mosaic disease incidence in all treatments.

High PCV and GCV were observed for branches per plant, fruits per plant and plant height in both rainy and spring-summer seasons (Dhankar and Dhankar, 2002). For fruit yield and plant height, values of PCV and GCV were almost equal indicating the environment had little effect but days to first flower and fruits and branches per

plant had some influence by environment. Moreover, PCV and GCV were higher for all the traits during rainy season than spring summer.

Sindhumole (2003) observed high PCV and GCV for most of the traits including yield and its major components. However GCV was moderate for fruit girth, ridges and seeds per fruit and leaf axil bearing first flower but low for plant duration and YVM incidence at 30 days after sowing.

Singh *et al*. (2009) reported high GCV for Plant height and fruit yield per plant and this finding had been supported by Gandhi *et al.* (2001).

Guddamath *et al.* (2010) revealed that PCV and GCV values were higher for the characters like plant height, nuber of branches per plant, number of fruits per plant, average fruit weight and fruit yield per plant.

Jindal *et al*. (2010) reported high genotypic and phenotypic coefficients of variation for number of primary branches per plant indicating maximum variability among the different genotypes.

Adiger *et al*. (2011) reported that GCV values were higher for plant height, fruit yield per plant, fruit weight and days to 50 per cent flowering. The Fruit yield has significantly positive correlation with plant height, number of branches per plant, inter nodal length, fruit length, fruit weight and number of fruits per plant at both genotypic and phenotypic level, indicating mutual association of these traits.

Chaukhande *et al.* (2011) revealed that highest genotypic coefficient of variation (GCV) as well as phenotypic coefficient of variation (PCV) was observed for incidence of yellow vein mosaic virus. The maximum difference between GCV and PCV was noted for inter nodal length.

2.6 Heritability and Genetic advance

Genetic advance was maximum for plant height followed by fruit number, days to first flower and yield (Murthy and Bavaji, 1980). Moreover, maximum heritability (narrow sense) was recorded for days to flower followed by plant height and fruits per plant.

Variability studies by Balakrishnan and Balakrishnan (1990) revealed high heritability and genetic advance for fruit yield per plant. This suggested the efficiency of taking number of fruits per plant and fruit weight as reliable indices for improving yield in okra.

High heritability for branches per plant was recorded by Ariyo (1990) while Vijay and Manohar (1990) opined that plant height, branches per plant and ridges per pod had maximum high heritability and genetic advance over mean. High heritability and genetic advance were observed for number, length and weight of pods as well as yield per plant (Jeyapandi and Balakrishnan, 1992). Days to first flower and branches per plant were highly influenced by environment as reported by (Patel and Dalal, 1992).

Bindhu *et al.* (1997) reported that fruit length, fruit weight per plant and plant height established high heritability coupled with moderately high genetic advance. Moderate heritability and low genetic advance were noticed for fruit girth. High heritability and genetic advance were noticed for branches per plant in F_2M_2 generation and for fruits and fruit weight per plant in F_3M_3 generation of irradiated interspecific hybrids (John, 1997).

Yield per plant had high estimates of heritability and genetic advance (Rajani and Manju, 1997). High heritability but low genetic advance was observed for branches and first fruiting node. Estimates of heritability were moderate to high for yield per plant, plant height and YVM incidence and low for fruits per plant.

Philip (1998) noticed maximum GCV and PCV for flowers per plant followed by YVM incidence and branches per plant where as maximum for days to first flower in F_4M_4 generation. The highest GCV and PCV were observed for YVM incidence while the lowest value was for plant duration followed by fruit girth and days to first flower.

Gandhi *et al.* (2001) observed medium to high heritability for all characters of which fruit length (64.4 %) and fruit girth (43.60 %) were the highest. However, these traits were coupled with varied genetic advance i.e, high, medium and low respectively suggesting the complexity of genetic mechanism in the expression of these characters.

High heritability coupled with genetic advance was displayed by all the characters except days to 50 per cent flower in spring summer season (Dhankar and Dhankar, 2002).

Dhall *et al*. (2003) studied genetic variability, heritability and genetic advance in 48 advanced F_8 generations of okra, developed through inter varietal crosses involving 6 parents. Fruit length, plant height, number of fruits per plant and virus incidence exhibited high heritability and high genetic advance.

More or less equal influence of genetic and environmental factors in the case of pollen sterility, plant duration and YVM incidence was evident from their moderate heritability (Sindhumole, 2003).

Sindhumole (2003) also observed high values of heritability in the characters studied including yield and its major components viz., days to first flower, leaf area, fruits per plant, average fruit weight, fruit length, fruit girth, fruit colour, fruit pubescence and ridges per pod indicating the prominence of genetic component and low environmental influence on these characters. She observed high genetic advance for fruit yield per plant which clearly indicates the additive gene action involved in this trait which makes the selection highly effective.

Yadav (2002) studied genetic parameters for yield and yield components in okra cultivars. High heritability accompanied with high genetic advance was observed for yield per plant and plant height. Moderate to high heritability coupled with low to moderate genetic advance was observed for number of days to flowering, number of branches per plant, number of nodes per plant, fruit length, fruit width, tapering length of fruit, and number of fruits per plant, indicating the prevalence of the non-additive type of gene action for these traits.

Indurani (2005) studied heritability and genetic advance for eight characters in okra. High heritability coupled with high genetic advance was recorded for plant height at first flower bud appearance, number of fruits per plant, fruit weight and yield per plant. These characters had importance in selection programmes.

2.7 Correlation analysis in okra

Several studies had been conducted in the past to identify the effect of yield contributing characters towards the yield.

Number of branches and fruit traits viz., number, length and width could be considered as the primary yield determining components in okra (Elangovan *et al.*, 1980).

Fruit yield was highly correlated with number and length of fruits but only to a lower degree with plant height and days to flower (Arumugham and Muthukrishnan, 1981). Prathap *et al.* (1982) observed a direct positive contribution of fruit number towards yield. Vashista *et al.* (1982) noticed that yield in bhindi depended primarily on plant height, fruit number and fruit length.

In all the three generations studied, major contributing yield traits were plant height, earliness, flowers and fruits (Mathews, 1986). She reported that up to F_2 generation of interspecific hybrids of *Abelmoschus,* number of fruits per plant, number

of flowers per plant, plant height and earliness to flower were the major yield components. Significant positive association of YVM disease intensity with number of branches per plant and length of fruits were revealed in the study. Negative association was reported between the intensity of mosaic incidence and days to flowering.

Sheela (1986) revealed that fruit length and girth were the important contributing characters towards yield.

Alex (1988) observed positive correlation for yield with number, length and weight of fruits per plant.

The directly influencing compounds of yield were plant height, branches, fruit length and fruits per plant (Kale *et al.*, 1989).

Sheela (1994) revealed that branches per plant and fruit girth were major characters contributing to yield in okra. Fruit number displayed maximum positive and negative direct effects on yield were as with regard to YVM incidence, maximum positive and negative direct effects were recorded for branch number and single fruit weight respectively. Selection of early flowering types with increased fruit weight was suggested for enhancing the level of YVM resistance.

Lakshmi *et al.* (1996) observed positive association of yield with nodes, branches and fruits per plant. Moreover high direct effects were exerted by nodes, pods and pod weight on yield.

According to Philip (1998), fruit yield per plant displayed positive association with plant height, branches and fruits per plant in both F_4M_4 and F_5M_5 generations of irradiated interspecific hybrids between *A. esculentus* and *A. manihot.*

Indurani (1999) reported a strong positive association between number and yield of fruits per plant in F_1 hybrids of okra. Marketable yield per plant, fruit weight, fruit

length, fruits per plant and plant height exhibited positively significant correlation as well as high direct effect with total yield per plant (Dhall *et al.* 2000).

Correlation studies involving 62 inbred lines during rainy and spring-summer seasons revealed that during both seasons, fruit yield was associated positively with fruits and branches per plant and plant height while fruits per plant was correlated positively with branches per plant and negatively with days to 50 per cent flower (Dhankar and Dhankar, 2002). Maximum direct effect on yield was contributed by plant height and branches per plant. The researchers suggested the selection of plants with high fruits, branches and medium plant height for improving the yield.

Correlation analysis of nineteen traits in the F_5M_5 generation of interspecific hybrids of okra revealed the positively significant correlation of yield per plant with branches, fruits per plant, average fruit weight and plant height (Philip and Manju, 2002).

Fruit yield displayed positive genotypic association with fruits per plant, average fruit weight, fruit length, fruit girth and plant duration and negative correlation with days to first flower, pollen sterility and incidence of YVM (Sindhumole, 2003).

Jaiprakashnarayan and Mulge (2004) showed that total yield per plant was positively and significantly correlated with number of fruits per plant, average fruit weight, number of nodes on main stem, fruit length, plant height at 60 and 100 days after sowing and number of leaves on 45 and 100 days after sowing, where as total yield per plant had negative and significant association with number of locules per fruit, number of nodes at first flowering and first fruiting.

Fruit yield per plant had highly positive association with fruit length, tapering length, plant height, fruits per plant, width of the fruit whereas days to first flower and first fruiting node were negatively correlated with fruit yield per plant (Singh and Singh,

2006). Therefore, the positively associated characters could be used for increased yield by selecting early flowering types.

For increasing yield in okra emphasis should be given to number of fruits, number of internodes, plant height and fruit length (Dakahe *et al.,* 2007). All these characters had high heritability and highly significant positive association with fruit yield, which can be increased through selection in okra.

Balakrishnan and Sreenivasan (2010) reported that fruit yield was positively associated with number of fruits, number of internodes, fruit weight and fruit length.

2.8 Genetic divergence

It is reasonable to expect the genetic divergence to be associated with geographic diversity. This may be true for land races, but in applied plant breeding where the origin of lines is not always known, selection of parents based on geographic diversity alone is not always relevant.

Statistical techniques such as Mahalanobis D^2, which quantify the differences among several quantitative traits is an efficient method to gauge the extent of diversity among genotypes. The concept of Mahalanobis D^2 statistic is based on the technique of utilizing the measurements of potential parents under study with respect to aggregate of characters.

Ariyo (1987) employed various multivariate techniques to determine the relative contribution of various plant characters in okra germplasm.

Seventy genotypes when subjected to D^2 analysis using 14 economic characters, six clusters formed was not associated with geographical origin of the genotypes (Bindu *et al.*, 1994).

Patil (1995) observed that weight of good fruits per plant and weight of borer affected fruits per plant were the major contributors for nine divergent clusters formed when 171 accessions of okra with 10 characters were subjected to D^2 statistics.

Patil *et al.* (1996) evaluated genetic divergence for quantitative characters in 171 okra genotypes. Plant characters like nodal length, number and weight of pods/plant and plant height were shown maximum divergence.

Plant height, days to first flowering, nodes per plant and seeds per fruit were the major contributors for six clusters formed when 12 characters of 27 okra cultivars subjected to Mahalanobis D^2 analysis (Dash and Mishra, 1998).

Twenty two genotypes of okra were evaluated by Hazra *et al*. (2002) for 13 fruit characters to determine their genetic divergence. Most of the genotypes were not much divergent based on character constellation but were highly variable for individual character. Genotypes (MDO-10, LORM-1, KS-410 and MDO-6) were shown highest genetic divergence.

Genetic divergence was studied by Patro and Ravisankar (2004) for 17 characters in 41 genotypes of okra. D^2 values ranged from 205.03 to 32666.9. The cluster means revealed that plant height, yield per plant and germination percentage contributed towards divergence.

Kumari and Choudhury (2006) revealed that maximum divergence was contributed by fruit length followed by fruit yield per plant in rainy season. In summer season it was found maximum for fruit yield per plant followed by number of primary branches.

Patel *et al.* (2006) estimated the genetic distance for 26 genotypes of okra by using D^2 statistics. More than 86 per cent of total divergence was contributed by five

traits *viz*., fruit yield, day to 50 per cent flowering, fruit girth, fruit length and length of internode.

The genetic diversity among 30 genotypes of okra was reported by Bendale *et al.* (2008). Cluster I indicated the highest intra cluster value for divergence, followed by cluster IV, cluster III and cluster II. Arka Anamika from cluster V had superior performance.

Paul *et al.* (2008) attempted to assess genetic divergence in thirty nine okra genotypes using Mahanalobis D^2 statistics. The population was grouped into eight clusters. The characters namely number of seeds per fruit, fruit width, average fruit weight, plant height, node at which 1st flower appears, number of fruits per plant and fruit length contributed maximum divergence.

The nature and magnitude of genetic divergence in 35 okra genotypes for ten characters were assessed by Ramya and Senthil kumar (2009) using Mahalanobis D^2 statistics. Pod yield, plant height and length of edible pod were the major characters contributing towards divergence. Cluster VII and X (83.25) were the most divergent followed by cluster V and X (74.05).

Highest genetic divergence was reported for plant height by Akotkar *et al.* (2010). Among the fifty genotypes, IC-332454 showed the highest cluster mean for fruit yield per plant and number of pods per plant.

Prakash and Pitchaimuthu (2010) were attempted to evaluate the genetic diversity in forty four genotypes of okra collected from the IIHR, Bangalore. The intra cluster distance was maximum in cluster XII (28.14), while inter-cluster distance was maximum between cluster VI and VIII (35.57) followed by I and IX (35.31). The characters namely days to 50% flowering (35.62%), 100 seed weight (28.44%), number of seeds per fruit (17.23%) and average fruit weight (8.14%) directly contributed towards maximum divergence.

Garg *et al*. (2011) successfully evaluated fifty three germplasm lines of okra for genetic divergence by using Mahalanobis D^2 statistics. Considering extent of diversity among genotypes and cluster means for various characters, crosses among genotypes of clusters XI, X, VI, VII and I results in heterotic hybrids and wide spectrum of variability in subsequent segregating generations. The genotypes POS-16, JOL-2K-19, POS-8, POS-18, VRO-10, VRO-22, POS-27, Hissar Unnat and Punjab-8 were observed as promising lines.

Genetic divergence among hundred genotypes of okra was reported by Reddy *et al.* (2012) using Mahalanobis D^2 statistics. Genotypes with high inter cluster distance (cluster VI and X, VI and IX and VII and XI) are useful in high heterosis and throw desirable transgressive segregants. The genotypes of six solitary clusters IC043279 (cluster VI), IC033350 (cluster VI), IC90210 (cluster VII), IC26375 (cluster IX), IC018530 (cluster X) and IC043751-B (cluster XI) being divergent from others serve as potential parents for breeding programmes.

2.9 Mucilage extraction studies

Wolfe *et al.* (1977) reported that a typical Ghanian okra soup was contain approximately 0.2-0.3 per cent mucilage.

Thampi and Indira (2000) evaluated 20 genotypes of thamara venda along the Pusa Sawani for nutritive value and organoleptic qualities. The mucilage content of thamara venda genotypes was higher than the control variety Pusa Sawani.

Girase *et al*. (2003) observed a marked genetic variation for cortex mucilage contents (1.02 to 1.51%) in 15 okra cultivars including four wild species. The fresh cortex tissue was contained more mucilage (1.49%) than green mature fruits (0.57%) and green leaves (0.05%).

Kadlag *et al*. (2005) studied the influence of integrated plant nutrient supply on yield, quality and nutrient uptake of okra. He reported that application of inorganic fertilizers increased the mucilage content of fruits.

Chavan *et al*. (2007) obtained mucilage powder from fresh stems of okra plants. The mucilage content was about four per cent.

Girase *et al*. (2008) studied the cortex mucilage content at various growth stages of okra. Mucilage content was maximum (0.94%) at 90 days growth stage compared to 45, 60, 75 days growth stage.

MATERIALS& METHODS

3. MATERIALS AND METHODS

This research work on "Evaluation of promising distant hybridization derivatives of okra (*Abelmoschus esculentus* (L.) Moench)" was carried out in the Department of Olericulture, College of Horticulture, KAU, Vellanikkara, Thrissur during 2011-12.

3.1 SITE, SOIL AND CLIMATE

The experiment was carried out in the Department of Olericulture, College of Horticulture, Vellanikkara. The experimental site is located at an altitude of 22.5m above MSL. The experimental site has a sandy loam soil, which is acidic in reaction (pH 5.3). The area lies in tropical monsoon climatic region, with more than 80 per cent of the rainfall getting distributed through southwest and northeast monsoon showers. Data on temperature, rainfall, relative humidity, number of rainy days and sunshine hours during the entire cropping period were collected from meteorological observatory of College of Horticulture, Vellanikkara (Appendix 1).

3.2 SEASON OF EXPERIMENT

The experiment was conducted during June - October 2011 and consisted of the following aspects:

- Evaluation of the F_9 generation plants for the selection of desirable lines.
- Screening for resistance to YVMV.
- Genetic divergence among the selections to be tested.

3.3 EXPERIMENTAL MATERIAL

The present study was carried out in the Department of Olericulture, College of Horticulture, Kerala Agricultural University, Vellanikkara, which accomplished an interspecific hybridization between *Abelmoschus caillei* variety Susthira (a semi wild yellow vein mosaic resistant species) (Plate1) and *Abelmoschus esculentus* variety Salkeerthi (a high yielding, widely adapted, but YVMV susceptible variety) (Plate 2). The generations out of this cross had been advanced up to F_8 generation.

The seeds of selected stabilizing superior F_8 population generated the F_9 population needed for the present study. Superior selections from the F_8 generation were selected based on the plant morphology, fruit characters, fruit yield, pollen fertility and field resistance to yellow vein mosaic virus disease. These plants were genetically evaluated along with the parents and a standard variety Arka Anamika. The source of materials used in the study is given in the Table 1.

3.4 EXPERIMENTAL METHOD

3.4.1 Design and layout

Design - Randomised Block Design

Replication - 2

Plot size - 4.5 × 1.8 m

Spacing - 60 × 45cm

Treatments - 15

Plate 1. *Abelmoschus caillei* variety Susthira

Plate 2. *Abelmoschus esculentus* variety Salkeerthi

3.4.2 Evaluation of the genotypes

Twelve F_9 generation selections along with their parents and Arka Anamika were evaluated during June to October (2011) in a Randomized Block Design (RBD) with two replications (Plate 3). Thirty plants were raised in each treatment in each replication. Highly susceptible okra line *A. esculentus* variety Salkeerthi was planted all around the field. The treatments received timely management and care as per the package of practice recommendation of KAU 2010. Ten plants selected at random from each treatment were used to take observations. No plant protection measures were taken up as it would reduce the vector population and thereby hinder the natural epiphytotic condition for Yellow Vein Mosaic Disease.

Plate 3. View of the experimental plot

Table 1. Source of materials used for the study

Sl. No	Variety/selection used	Species/others	Mode of evolution /parents	Reaction to YVMV	Evolved from
1	F_9 -1 (T1)	Interspecific hybrid derivative	Susthira x Salkeerthi	To be tested	Department of Olericulture, COH, Vellanikkara
2	F_9 -2 (T2)	Interspecific hybrid derivative	Susthira x Salkeerthi	To be tested	,,
3	F_9 -3 (T3)	Interspecific hybrid derivative	Susthira x Salkeerthi	To be tested	,,
4	F_9-4 (T4)	Interspecific hybrid derivative	Susthira x Salkeerthi	To be tested	,,
5	F_9 -5 (T5)	Interspecific hybrid derivative	Susthira x Salkeerthi	To be tested	,,
6	F_9 -6 (T6)	Interspecific hybrid derivative	Susthira x Salkeerthi	To be tested	,,
7	F_9 -7 (T7)	Interspecific hybrid derivative	Susthira x Salkeerthi	To be tested	,,
8	F_9 -8 (T8)	Interspecific hybrid derivative	Susthira x Salkeerthi	To be tested	,,
9	F_9 -9 (T9)	Interspecific hybrid derivative	Susthira x Salkeerthi	To be tested	,,
10	F_9 -10 (T10)	Interspecific hybrid derivative	Susthira x Salkeerthi	To be tested	,,
11	F_9 -11 (T11)	Interspecific hybrid derivative	Susthira x Salkeerthi	To be tested	,,
12	F_9 -12 (T12)	Interspecific hybrid derivative	Susthira x Salkeerthi	To be tested	,,
13	Salkeerthi (P2)* (T14)	*A. esculentus*	Pure line Selection	Susceptible	,,
14	Susthira (P1)* (T15)	*A. caillei*	Pure line Selection	Resistant	,,
15	Arka Anamika (T13)	Interspecific hybrid derivative	*A.esculentus* x *A. tetraphyllus*	Resistant	IIHR, Bangalore

P1* - Female parent

P2* - Male parent

3.5 Biometrical observations recorded

All the observation plants were tagged individually in each replication and their morphological characters were noted. The following observations were recorded and analyzed statistically.

3.5.1 Qualitative characters:

1. Plant characters
    a. Plant habit : Branched or unbranched
2. Leaf characters
    a. Leaf lobing : Deeply lobed/narrowly lobed/serrated
    b. Colour of leaf base : Green /green with red tinge/red with green tinge
    c. Colour of leaf vein : Green/whitish green
3. Flower characters
    a. Flower colour : Yellow/golden yellow
    b. Flower size : Small/medium/large
    c. Nature of corolla : Red throat/purple throat
4. Fruit characters
    a. Colour of fruit : Green/dark green/yellowish green/red/ deep red / others
    b. Pod pubescence : Smooth/less pubescent/highly pubescent

Leaf characters like leaf lobing, colour of leaf base and the colour of the leaf vein were recorded from seventh leaf of each observation plant. Flower characters such as flower colour, flower size and nature of corolla were noted at the time of anthesis. Fruit characters such as fruit colour and fruit pubescence were recorded at the time of harvest.

3.5.2 Quantitative characters

1. Plant height (cm)

   The height of the plant was measured from the base of the plant to tip at 100 days after sowing.

2. Internodal length (cm)

   The length of the internode between sixth and seventh node of the plant was measured at 100 days after sowing.

3. Number of primary branches

   The number of primary branches was counted at 60 days after sowing .

4. Length of epicalyx segment

   Length of epicalyx segment of the ripe flower bud was recorded at 60 days after sowing.

5. Width of epicalyx segment

   Width of epicalyx segment of the ripe flower bud was recorded at 60 days after sowing.

6. Petiole length (cm)

Length of petiole of the seventh leaf was recorded at 60 days after sowing.

7. Days to flower

In each observation plant, date of opening of the first flower was recorded and the number of days from sowing to flowering was worked out.

8. Days to first harvest

The number of days taken to harvest the first fruit was noted and expressed in numbers.

9. First fruiting node

The node at which first fruit was formed was noted and expressed in numbers.

10. Length of fruit (cm)

Three fruits were harvested from each observation plant at six days after flowering and the fruit length was measured from basal cap to the tip of the fruit

11. Girth of fruit (cm)

Three fruits were harvested from each observation plant at six days after flowering and the circumference of the fruit was recorded at the point of maximum bulging.

12. Locules per pod

Three fruits were harvested from each observation plant at six days after flowering and the number of locules per pod was recorded by taking cross section of the pod.

13. Number of ridges per pod

The number of ridges per pod of each plant was noted.

14. Number of fruits per plant

Total number of fruits borne on the observation plants was recorded

15. Number of harvests

Total number of harvests was recorded from first to final harvest.

16. Crop duration

Time taken for last harvest from sowing was done separately.

17. Yield per plant

Weight of fruits harvested from the observation plants in each treatment was taken and their average was taken to get yield per plant.

18. Incidence of other pests and diseases

Incidence of other pests and diseases such as shoot and fruit borer, *Cercospora* leaf spot, jassids etc., was recorded.

3.6 Statistical analysis

The observations taken from the experimental plants were tabulated and subjected to statistical analysis.

3.6.1 Analysis of variance

Analysis of variance for RBD was carried out for comparison among different treatments and replications and to estimate variance components.

3.6.2 Estimation of variability components

The phenotypic and genotypic components of variance for each character were estimated by equating the expected value of mean squares (MS) to the respective variance components (Jain, 1982).

3.6.2.1 Phenotypic variance ($V_{(P)}$)

$$V_{(P)} = V_{(G)} + V_{(E)}$$

Where $V_{(G)}$ = Genotypic variance

$V_{(E)}$ = Environmental variance estimated as mean square due to error

3.6.2.2 Genotypic variance ($V_{(G)}$)

$$V_{(G)} = \frac{\text{Mean square (treatment) - Mean square (error)}}{\text{Number of replications}}$$

The phenotypic and genotypic coefficients of variation were worked out for each character by making use of the estimates of $V_{(P)}$ and $V_{(G)}$ and were expressed in percentage.

3.6.2.3 Phenotypic coefficient of variance (PCV)

$$PCV = \frac{\sqrt{V_{(P)}}}{\text{Mean}} \times 100$$

3.6.2.4 Genotypic coefficient of variance (GCV)

$$GCV = \frac{\sqrt{V_{(G)}}}{\text{Mean}} \times 100$$

In all cases, the mean of a character was calculated over all the treatments.

3.6.3 Estimation of heritability

The heritability (in broad sense) for each character was worked out as the ratio of genotypic variance to the phenotypic variance and was expressed as percentage (Jain, 1982).

$$\text{Heritability (h2)} = \frac{V_{(G)}}{V_{(P)}} \times 100$$

3.6.4 Estimation of genetic advance

The expected genetic improvement by selection was proportional to the product of heritability and phenotypic standard deviation (Allard, 1960).

$$\text{Genetic advance (GA)} = k.h^2 \sqrt{V_{(P)}}$$

Where, 'k' is the standardized selection differential, usually taken as 2.06 (at 5 per cent selection) in large samples.

3.6.5 Correlation

The analysis of covariance was done between each pair of observations and the correlations were computed. The phenotypic correlation coefficient between two characters x and y was estimated as γp (x,y)

$$\gamma p\,(x,y) = \frac{Cov(p)\,(x,y)}{\sqrt{V_{(P)}\,x \times V_{(P)}\,y}}$$

Where $Cov_{(P)}$ (x,y) denotes the phenotypic covariance between the characters x and y estimated by taking the respective expected values of mean sum of products.

$V_{(P)}$ x and $V_{(P)}$ y indicate the estimated phenotypic variances for x and y respectively.

The genotypic correlation coefficient between the characters x and y was estimated in the similar manner, replacing the phenotypic covariance by the genotypic covariance between the two characters and the phenotypic variances by the genotypic variances.

$$\gamma_G (x,y) = \frac{Cov_{(G)} (x,y)}{\sqrt{V_{(G)} x \times V_{(G)} y}}$$

3.7 Genetic divergence

The genetic divergence was calculated according to the method suggested by Mahalanobis (1928). Clustering of genotypes was done using Tocher's method (Rao, 1952).

3.8 Screening for resistance to YVMV

The parental species, F_9 generation selections and Arka Anamika were subjected to standard screening techniques to assess their reaction to YVMV.

3.8.1 Field Screening

The treatment plants were selected for testing resistance to YVMV by providing sufficient amount of virus inoculum by planting highly susceptible variety 'Salkeerthi' in boarder rows.

Observations on disease incidence and disease severity were recorded as per the standard methods. Disease severity was scored using 0-5 scale as suggested by Deo *et al*. (2000).

Grade	**Per cent leaves infected**
0	No symptom
1	< 25
2	25-50
3	51-75
4	76-90
5	> 90

Per cent Disease Incidence (PDI) was calculated using the formula given below,

$$PDI = \frac{\text{Number of plants infected}}{\text{Total number of plants observed}} \times 100$$

Per cent Disease Severity (PDS) was calculated using the formula given below,

$$PDS = \frac{\text{Sum of all numerical ratings}}{\text{Total number of leaves observed} \times \text{Maximum disease grade}} \times 100$$

Based on the per cent disease incidence and severity, coefficient of infection (CI) was calculated as suggested by Datar and Mayee (1981)

$$CI = \frac{\text{Per cent disease incidence} \times \text{Per cent disease severity}}{100}$$

Based on the CI the genotypes were categorized into six categories as shown below,

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)

3.8.2 Artificial inoculation of virus

3.8.2a Whitefly transmission

The promising F_9 selections which were found to be resistant in the field screening were selected for this study along with the susceptible variety Salkeerthi. Whitefly (*Bemisia tabaci*), the vector of YVMV was used for artificial inoculation. Whiteflies were subjected to pre-acquisition fasting for half an hour and then for acquisition access for 24 h on YVMV infected plants followed by 24 h inoculation

access period. Inoculated seedlings were kept under net house conditions for symptom expression. Healthy plants without inoculation served as control.

3.8.2b Graft transmission technique

Artificial inoculation of YVMV was done through grafting techniques. The method suggested by Kapoor and Varma (1950) was followed to confirm the level of resistance to YVMV in the selected treatment plants.

The promising F_9 generation lines which were found to be resistant in the field screening and whitefly tranmission were again subjected to artificial inoculation by grafting. In this method one month old healthy resistant lines were grafted with same old highly disease susceptible variety 'Salkeerthi' raised in polybags by approach grafting.

The grafted portions were tied with polythene tape and covered with moistened cotton. The complete graft union occurred within a month. The daily observations were taken for about a month for symptom expression in resistant genotypes.

3.9 Pollen fertility studies

For studying the pollen fertility in the treatment plants pollen grains were collected from flowers within one hour after anthesis. Pollen grains were dusted on a clean slide using a camel hair brush and a drop of one per cent acetocarmine stain was added to it. It was kept for five minutes for staining and then covered with a cover slip and observed under a microscope at different fields. In each field, the numbers of stained and unstained pollen grains were noted. The pollen fertility per cent was assessed by calculating the mean stained and unstained pollen grains.

4.0 Extraction of mucilage

The mucilage content of the edible stage fruits was estimated by extracting the mucilage with ethyl alcohol (Thampi, 1998).

Twenty five grams of fresh fruit sample was taken, with that 100 ml of distilled water was added and kept for 24 h. Thus it was filtered through a muslin cloth into a flask. Fifty ml of alcohol was added to the flask and then it was filtered through a pre weighed filter paper. The filtrate along with the filter paper was dried and weighed. The percentage of the mucilage content was calculated by the formula given below.

$$\text{Percentage of mucilage} = \frac{B-A}{\text{Weight of sample taken}} \times 100$$

B - Weight of the filter paper with mucilage

A - Weight of the filter paper alone

RESULTS

4. RESULTS

The data collected for the evaluation of 12 F_9 generation selections along with the parental varieties and Arka Anamika was tabulated and subjected to statistical analysis. The results obtained from the experiments are presented under following heads.

4.1 Evaluation of genotypes

4.1.1 Qualitative characters

Leaf margin was deeply fid in *A. esculentus* and Arka Anamika, but that in *A. caillei* it was narrowly fid. In F_9 lines it was varied from narrowly fid to deeply fid. Flower colour was yellow in the parents, F_9 lines and Arka Anamika. Flower size was medium in both the parental species and Arka Anamika where as advanced generation selections had large, medium and small sized flowers. Parents, Arka Anamika and F_9 selections had purple throat at base of corolla in the inside and colour of leaf vein was green with purple tinge. Colour of leaf base was red with green tinge in the parents, selections and Arka Anamika. Colour of fruit was light green in *A. esculentus* whereas that in *A. caillei* and Arka Anamika it was green. The F_9 selections produced green, light green and dark green fruits. Pod pubescence was absent in both the parents and Arka Anamika but the F_9 lines were slightly pubescent (Table 2). The variability expressed by the genotypes in epicalyx segment, fruit and leaf is shown in the Plate 4.

4.1.2 Quantitative characters

Mean values for the 20 characters relating to different treatments are given in Table 3. Analysis of variance for different quantitative characters is given in Table 4.

Height of the plant varied significantly among the treatments. The mean values ranged from 127.44 cm in T14 to 153.35 cm in T11.

4a. Variability in epicalyx segment

4b. Variability in fruit shape and size

4c. Variability in leaf shape and size

Plate 4. Variability in epicalyx segment, fruit and leaf

Table 2. Comparison of qualitative characters of parental species, Arka Anamika and F_9 selections

Sl. No	Characters	*A. esculentus*	*A. caillei*	F_9 selections	Arka Anamika
1	Leaf margin	Deeply fid	Narrowly fid	Deeply/Narrowly fid	Deeply fid
2	Flower colour	Yellow	Yellow	Yellow	Yellow
3	Flower size	Medium	Medium	Large, medium and Small	Medium
4	Purple throat at base of corolla	Present inside	Present inside	Present inside	Present inside
5	Colour of leaf vein	Green with purple tinge	Green with purple tinge	Green with purple tinge	Green with purple tinge
6	Colour of leaf base	Red with Green tinge	Red with Green tinge	Red with Green tinge	Red with Green tinge
7	Colour of fruit	Light green	Green	Green, Light green and Dark green	Green
8	Pod pubescence	Absent	Absent	Slightly pubescent	Absent

Table 3. Mean values for different quantitative characters

Treatments	Plant Height (cm)	Internodal length (cm)	No. of primary branches	Length of epicalyx segment (cm)	Width of epicalyx segment (cm)	Petiole length (cm)	Days to flower	Days to first harvest	Number of harvests	First fruiting node
	1	2	3	4	5	6	7	8	9	10
T1	139.42	8.38	2.79	1.83	0.63	34.70	53.53	59.53	12.01	6.00
T2	152.83	10.70	3.09	1.81	0.59	36.56	53.14	58.63	11.87	5.87
T3	150.86	9.95	3.35	2.19	0.63	35.12	53.35	58.84	11.33	5.66
T4	148.62	10.18	3.16	2.15	0.92	35.31	54.20	59.70	10.68	6.05
T5	137.97	9.36	2.89	1.84	0.74	36.17	53.09	59.09	10.99	6.01
T6	145.77	9.77	3.05	2.3	0.58	34.74	53.63	59.63	10.59	5.85
T7	151.04	10.51	3.03	2.17	0.65	35.82	52.38	58.38	10.98	6.02
T8	150.97	10.11	3.15	2.40	0.66	36.33	51.79	57.79	11.56	6.00
T9	151.96	9.98	3.51	2.07	0.61	36.72	53.55	59.10	10.42	5.69
T10	142.55	9.34	3.18	2.37	0.87	34.98	52.51	58.51	9.84	5.89
T11	153.55	9.95	3.05	1.69	0.96	35.46	53.15	58.65	10.12	5.66
T12	152.90	8.72	3.15	2.15	0.51	35.93	52.51	58.51	12.03	6.04
T13	150.96	10.17	3.34	2.08	0.62	34.96	47.00	52.00	11.15	5.07
T14 (P2)*	127.44	12.27	3.24	2.28	0.52	30.27	39.28	44.29	14.73	4.65
T15 (P1)*	143.78	7.82	3.08	1.32	1.15	34.06	47.15	52.65	11.95	4.68
CD	2.08	0.39	0.08	0.15	0.02	1.63	1.51	1.90	0.72	0.24
SE	0.68	0.13	0.02	0.04	0.009	0.54	0.49	0.62	0.23	0.07

*P1: Parent 1 (*A. caillei*) *P2: Parent 2 (*A. esculentus*)

T1-T12: F_9-1 to F_9-12 selections T13: Arka Anamika

Table 3. Continued

Treatments	Length of fruit (cm)	Girth of fruit (cm)	Locules per pod	No. of fruits per plant	No. of ridges per pod	Crop duration (days)	Yield per plant (g)	Pollen sterility (%)	Mucilage content (g/100g)	Coefficient of infection
	11	12	13	14	15	16	17	18	19	20
T1	19.93	8.2	5.96	12.10	5.96	166.24	179.54	2.32	0.47	23.63
T2	16.78	8.11	6.05	11.93	6.02	166.68	176.54	3.54	0.32	10.18
T3	16.81	8.06	6.09	11.52	6.09	166.48	176.21	4.22	0.32	10.77
T4	19.98	8.08	6.09	10.70	6.02	164.31	178.92	1.25	0.28	0.00
T5	17.70	7.93	5.85	11.00	5.85	165.51	176.44	1.46	0.27	0.00
T6	17.96	8.07	5.89	11.07	5.88	165.75	177.93	2.11	0.59	0.00
T7	20.69	8.09	5.97	11.71	5.97	166.12	180.56	5.82	0.32	28.37
T8	14.23	7.76	5.96	11.21	5.88	165.83	169.93	2.48	0.49	0.00
T9	18.81	7.81	6.03	11.22	6.03	165.22	177.31	1.55	0.53	0.00
T10	12.75	7.64	6.07	9.80	5.96	161.06	166.52	1.67	0.38	0.00
T11	19.84	7.68	5.94	10.63	5.95	162.44	178.92	1.93	0.61	9.67
T12	20.07	8.17	5.89	12.50	5.89	167.59	186.30	2.32	0.62	12.53
T13	17.80	7.57	6.00	14.55	6.09	165.96	178.01	3.43	0.33	24.96
T14	27.91	7.48	5.05	15.07	5.05	171.88	191.43	0.1	0.25	69.21
T15	16.86	8.43	6.16	12.06	6.01	171.61	177.34	0.5	1.12	1.4
CD	0.50	0.09	0.16	0.48	0.03	1.64	2.26	0.78	0.06	8.99
SE	0.16	0.03	0.05	0.15	0.11	0.54	0.74	0.26	0.02	2.97

Table 4: ANOVA (mean squares) for different quantitative characters

SI. No	Characters	Treatments	Replications	Error
1	Plant height (cm)	107.26**	1.51	0.94
2	Internodal length (cm)	2.19**	0.02	0.03
3	Number of primary branches	0.06**	0.00	0.00
4	Length of epicalyx segment (cm)	0.17**	0.00	0.00
5	Width of epicalyx segment (cm)	0.06**	0.00**	0.00
6	Petiole length (cm)	4.66**	0.98	0.58
7	Days to flower	31.80**	1.42	0.49
8	Days to first harvest	35.81**	0.70	0.79
9	Number of harvests	3.13**	0.35	0.11
10	First fruiting node	0.46**	0.00	0.01
11	Length of fruit (cm)	34.73**	0.01	0.05
12	Girth of fruit (cm)	0.14**	0.00	0.00
13	Locules per pod	0.13**	0.00	0.00
14	Number of fruits per plant	3.91**	0.00	0.05
15	Number of ridges per pod	0.12**	0.00	0.00
16	Crop duration (days)	10.03**	0.64	0.58
17	Yield per plant (g)	66.47**	1.72	1.11
18	Pollen sterility (%)	4.28**	0.006	0.001
19	Mucilage content (g/100g)	0.10**	0.01**	0.00
20	Coefficient of infection	550.34**	0.02	0.03

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

Significant differences were observed for internodal length. The mean values for the character ranged from 7.82 cm in T15 to 12.27 cm in T14.

Significant differences were observed for number of primary branches among the treatments. The mean values for the character ranged from 2.79 (T1) to 3.51 (T9).

Length of epicalyx segement revealed significant differences among the treatments. The maximum and minimum values for the character were recorded in T8 (2.4) and T15 (1.32) respectively.

Width of epicalyx segement varied significantly among the genotypes. The means ranged from 0.51 in T12 to 1.15 in T15.

Petiole length revealed high significant differences among the treatments. The mean values for the character ranged from 30.27 cm in T14 to 36.72 cm in T9.

High significant differences were present among the treatments for days to first flowering. The mean values for the character ranged from 39.28 in T14 to 54.2 in T4.

Days to first harvest revealed significant differences among the treatments. The maximum and minimum mean values for the character were recorded in T4 (59.7) and T14 (44.29) respectively.

Number of harvests revealed significant differences among the genotypes. The means ranged from 9.84 (T10) to 14.73 (T14).

Significant differences were noticed for first fruiting node among the genotypes. The mean values ranged from 4.65 (T14) to 6.05 (T4).

Length of fruit varied significantly among the treatments. The means ranged from 12.75 cm in T10 to 27.91 cm in TI4.

Girth of fruit revealed significant differences among the treatments. The maximum and minimum values for the character were recorded in T15 (8.43) and T14 (7.48).

Significant differences were observed for number of locules per pod. The mean values ranged from 5.06 in T14 to 6.16 in T15.

Number of fruits per plant varied significantly among the genotypes. The maximum and minimum values for the character were recorded as 15.07 in T14 and 9.8 in T10 respectively.

Number of ridges per pod varied significantly among the treatments. The means ranged from 5.05 (T14) to 6.09 (T3).

Significant differences were observed for duration of the crop among the treatments. The mean values ranged from 162.44 days in T11 to 171.88 days in T14.

Yield per plant exhibited high significant differences among the treatments. Yield was maximum for T14 (191.43 g) and minimum for T10 (166.52 g).

The differences in pollen sterility (%) among the treatments were highly significant with both the parents. The mean values for pollen sterility ranged from 0.1 in T14 to 5.82 in T7. Parent P1(T15) was on par with parent P2 (T14) in pollen sterility**.**

Highly significant differences were observed among the treatments for mucilage content (g/100g). The mean values were ranged from 0.25 (T14) to 1.12 (T15).

4.2 Genetic parameters

The genetic parameters, viz., the phenotypic and genotypic coefficients of variation, heritability and genetic advance for each character under study were estimated and presented in Table 5.

Table 5. Genetic parameters for different quantitative characters

Sl. No	Characters	PCV	GCV	Heritability	Genetic advance
1	Plant height (cm)	5.01	4.97	98.2	14.89
2	Internodal length (cm)	10.76	10.59	96.9	2.11
3	Number of primary branches	5.76	5.61	94.9	0.35
4	Length of epicalyx segment (cm)	14.59	14.18	94.5	0.58
5	Width of epicalyx segment (cm)	25.64	25.58	99.5	0.37
6	Petiole length (cm)	4.60	4.06	77.8	2.60
7	Days to flower	7.83	7.70	96.9	8.02
8	Days to first harvest	7.5	7.34	95.7	8.43
9	Number of harvests	11.10	10.70	92.9	2.44
10	First fruiting node	8.59	8.36	94.7	0.95
11	Length of fruit (cm)	23	22.97	99.7	8.56
12	Girth of fruit (cm)	3.42	3.37	97.3	0.54
13	Locules per pod	4.45	4.27	91.9	0.5
14	Number of fruits per plant	11.93	11.78	97.5	2.83
15	Number of ridges per pod	4.25	4.16	95.7	0.5
16	Crop duration (days)	1.39	1.31	88.9	4.22
17	Yield per plant (g)	3.26	3.21	96.7	11.58
18	Pollen sterility (%)	63.16	63.16	99.9	3.01
19	Mucilage content (g/100g)	48.29	47.85	98.2	0.45
20	Coefficient of infection (CI)	135.93	135.92	99.9	34.17

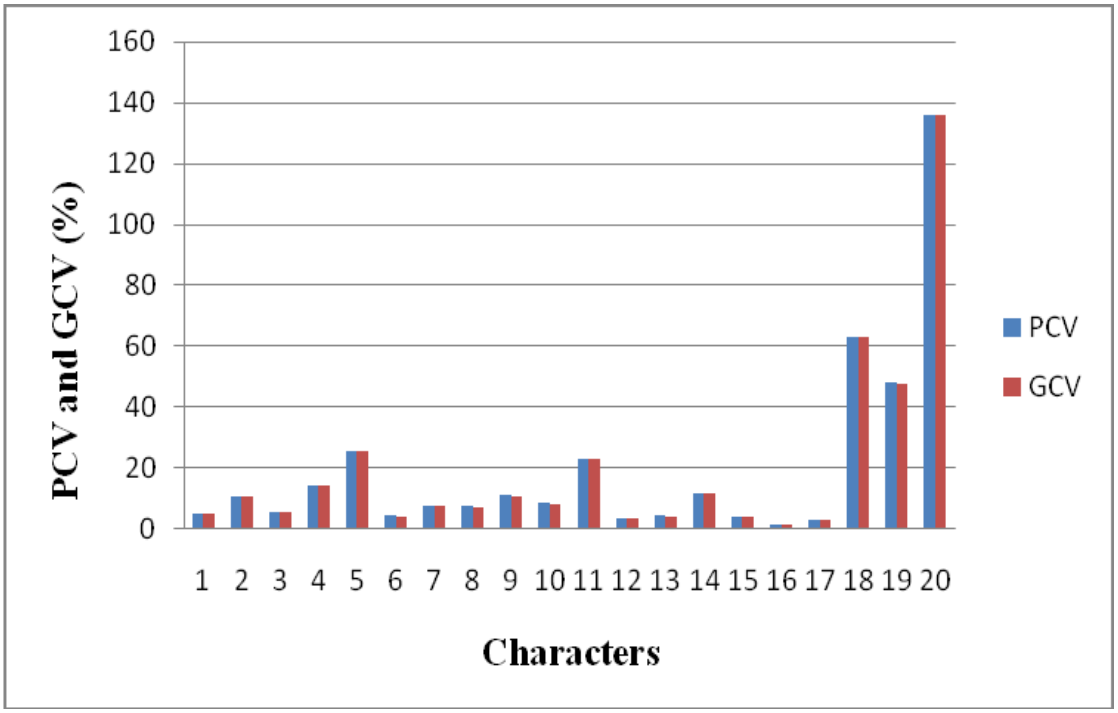


Fig.1. Phenotypic and Genotypic coefficients of variation for characters in the genotypes

1. Plant height
2. Inter nodal length
3. No. of primary branches
4. Length of epicalyx segment (cm)
5. Width of epicalyx segment (cm)
6. Petiole length (cm)
7 Days to flower
8. Days to first harvest
9. Number of harvests
10. First fruiting node
11. Length of fruit (cm)
12. Girth of fruit (cm)
13. Locules per pod
14. Number of fruits per plant
15. Number of ridges perpod
16. Crop duration (days)
17. Yield per plant (g)
18. Pollen sterility (%)
19. Mucilage content (g/100g)
20. Coefficient of infection

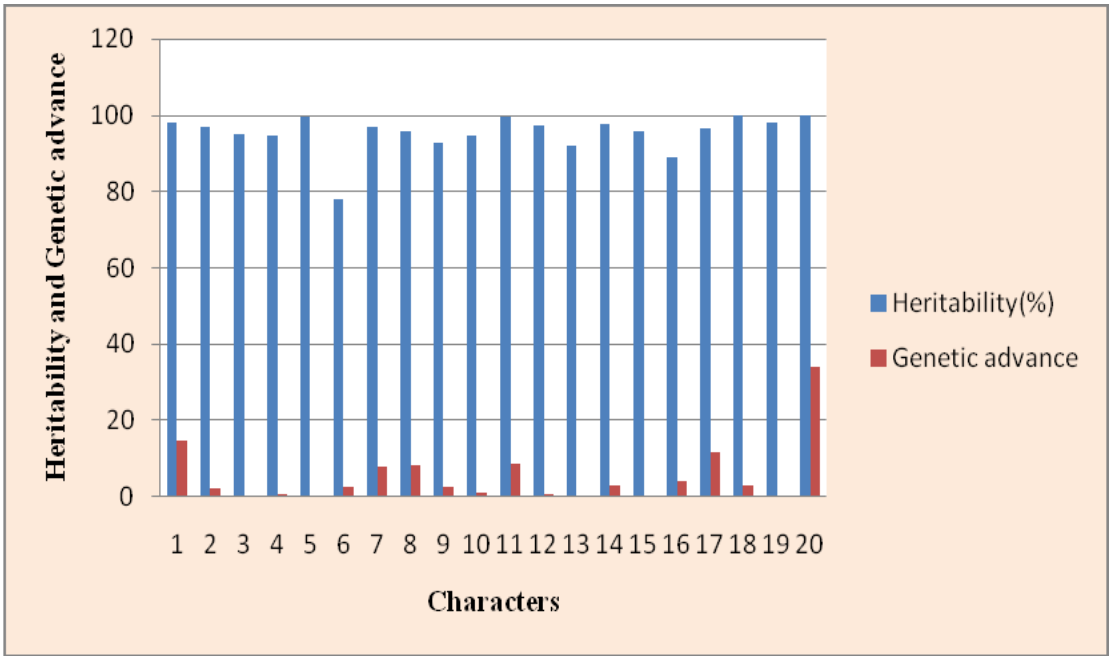


Fig.2. Heritability and Genetic advance for characters in the genotypes

1. Plant height
2. Inter nodal length
3. No. of primary branches
4. Length of epicalyx segment (cm)
5. Width of epicalyx segment (cm)
6. Petiole length (cm)
7 Days to flower
8. Days to first harvest
9. Number of harvests
10. First fruiting node
11. Length of fruit (cm)
12. Girth of fruit (cm)
13. Locules per pod
14. Number of fruits per plant
15. Number of ridges per pod
16. Crop duration (days)
17. Yield per plant (g)
18. Pollen sterility (%)
19. Mucilage content (g/100g)
20. Coefficient of variation

4.2.1 Phenotypic and genotypic coefficients of variation

The maximum value for phenotypic and genotypic coefficient of variation was recorded for coefficient of infection of YVMV (135.93 and 135.92 respectively) followed by pollen sterility (63.16 and 63.16 respectively) (Fig 1).

The phenotypic coefficient of variation was minimum for duration of crop (1.39) followed by yield per plant (3.26), girth of fruit (3.42) and number of ridges per pod (4.25).

The genotypic coefficient of variation was minimum for duration of crop (1.31) followed by yield per plant (3.21), girth of fruit (3.37) and petiole length (4.06).

4.2.1 Heritability and genetic advance

All the characters exhibited very high heritability. The heritability value was maximum (99.9) for coefficient of infection and pollen sterility closely followed by fruit length (99.7) (Fig 2).

Maximum genetic advance was exhibited by coefficient of infection (34.17) followed by plant height (14.89) and yield per plant (11.58). Most of the characters exhibited low genetic advance values and the minimum value expressed for the character, number of primary branches (0.35) followed by width of epicalyx segment (0.37) and mucilage content (0.45).

4.3 Correlation studies

The data relating to the characters studied was subjected to correlation analysis and the results are presented in Table 6.

4.3.1 Phenotypic correlation

First fruiting node had significant positive phenotypic correlation with pollen sterility, petiole length and days to flower and significant negative correlation with number of fruits per plant and number of harvests per plant.

Length of fruit had significant positive phenotypic correlation with yield per plant and highly significant negative correlation with locules per pod. Girth of fruit showed highly significant negative correlation with internodal length.

Significant positive correlation was noticed for locules per pod with girth of fruit, number of ridges per pod, petiole length, days to flower and days to first first harvest and highly significant negative correlation with length of fruit, yield per plant and number of harvests per plant.

Number of fruits per plant showed significant positive phenotypic correlation with length of fruit and number of harvests per plant while the correlation was negative and significant with first fruiting node, locules per pod, yield per plant, days to flower and days to first harvest.

Number of ridges per pod recorded highly significant positive phenotypic correlation with first fruiting node, girth of fruit, locules per pod, petiole length, days to flower and days to first harvest and highly significant negative correlation with length of fruit, number of fruits per plant and number of harvests per plant.

Crop duration showed high positive phenotypic correlation with girth of fruit and number of fruits per plant and highly significant negative correlation with fruiting node and number of ridges per pod.

Yield per plant showed high positive phenotypic correlation with length of fruit, number of fruits per plant, crop duration and number of harvests per plant and highly significant negative correlation with locules per pod and number of ridges per pod.

Pollen sterility exhibited high positive phenotypic correlation with first fruiting node, locules per pod, number of ridges per pod, days to flower and days to first harvest. Plant height showed positive phenotypic correlation with pollen sterility.

Internodal length had high positive phenotypic correlation with plant height and significant negative correlation with girth of fruit, locules per pod, number of ridges per pod and mucilage content.

Number of primary branches had high positive phenotypic correlation with plant height and internodal length.

Length of epicalyx segment showed significant positive phenotypic correlation with plant height, internodal length and number of primary branches and significant negative phenotypic correlation was presented for girth of fruit and duration of crop.

Significant negative correlation was observed for width of epicalyx segment with number of fruits per plant, plant height, internodal length and length of epicalyx segment.

Petiole length had high positive phenotypic correlation with first fruiting node, locules per pod, number of ridges per pod, pollen sterility, days to flower and days to first harvest and significant negative correlation with length of fruit, number of fruits per plant, yield per plant and number of harvests per plant.

Days to flower exhibited high positive phenotypic correlation with first fruiting node, locules per pod, number of ridges per pod, pollen sterility, petiole length and days to first harvest and significant negative correlation with length of fruit, number of fruits per plant, yield per plant and number of harvests per plant.

Days to first harvest was having high positive phenotypic correlation with first fruiting node, locules per pod, number of ridges per pod, pollen sterility, petiole length and days to flower and significant negative correlation with length of fruit, number of fruits per plant and yield per plant.

Number of harvests per plant recorded highly significant positive phenotypic correlation with length of fruit, number of fruits per plant, duration of crop and yield and significant negative correlation with fruiting node, locules per

Table 6. Genotypic and phenotypic correlation coefficients for 19 characters in the genotypes

	1	2	3	4	5	6	7	8	9	10
1. First fruiting node		0.368	0.239	0.379	-0.684**	0.446*	-0.551**	-0.372	0.646**	0.414
2. Length of fruit (cm)	-0.360		-0.039	-0.684**	0.615**	-0.598**	0.353	0.959**	-0.345	0.045
3. Girth of fruit (cm)	0.224	-0.038		0.477*	-0.252	0.448*	0.584**	0.027	0.198	-0.034
4. Locules per pod	0.380	-0.660*	0.450		-0.572**	0.994**	-0.094	-0.708**	0.462*	0.039
5. No. of fruits per plant	-0.661*	0.606	-0.262	-0.546		-0.533**	0.516*	0.692**	-0.360	-0.008
6. No. of ridges per pod	0.434	-0.587	0.434	0.970*	-0.519		-0.116**	-0.616**	0.548**	0.147
7. Crop duration (days)	-0.518	0.331	0.526	-0.110	0.507	-0.144		0.460*	-0.365	-0.432
8.Yield per plant (g)	-0.363	0.943*	0.022	-0.647*	-0.67 8*	-0.598	0.449		-0.366	0.07
9. Pollen sterility (%)	0.630*	-0.344	0.191	0.441	-0.354	0.537	-0.344	-0.359		0.434*
10. Plant height (cm)	0.403	0.045	-0.341	0.039	-0.004	0.147	-0.404	0.064	0.431	
11. Internodal length (cm)	-0.173	0.409	-0.632*	-0.593	0.384	-0.560	-0.220	0.321	-0.144	0.508
12. No. of primary branches	-0.320	-0.024	-0.393	0.023	0.200	0.030	-0.080	-0.012	-0.036	0.424
13. Length of epicalyx segment (cm)	0.306	-0.120	-0.466	-0.266	0.002	-0.247	-0481	0.076	0.191	0.488
14. Width of epicalyx segment (cm)	0.198	-0.285	0.213	0.409	-0.440	0.296	0.015	-0.363	-0.403	-0.513
15. Petiloe length (cm)	0.634*	-0.548	0.333	0.737*	-0.585	0.769*	-0.178	-0.534	0.482	0.307
16. Days to flower (days)	0.852*	-0.475	0.414	0.667*	-0.813*	0.731*	-0.421	-0.518	0.712*	0.293
17. Days to first harvest (days)	0.867*	-0.485	0.423	0.648*	-0.817*	0.715*	-0.416	-0.524	0.697*	0.265
18. No. of harvest per plant	-0.624*	0.542	-0.194	-0.625*	0.936*	-0.622*	0.543	0.620*	-0.375	-0.125
19. Mucilage content (g/100g)	-0.320	-0.148	0.481	0.284	-0.125	0.218	0.530	-0.057	-0.259	-0.466

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

Table 6. Continued

	11	12	13	14	15	16	17	18	19
1. First fruiting node	-0.177	-0.342	0.323	-0.206	0.738**	0.895**	0.908**	-0.675**	-0.33
2. Length of fruit (cm)	0.418	-0.027	-0.117	-0.286	-0.615**	-0.485*	-0.497*	0.565**	-0.150
3. Girth of fruit (cm)	-0.634**	-0.424	-0.489*	0.216	0.357	0.409	0.421	-0.195	0.496*
4. Locules per pod	-0.632**	0.022	-0.300	0.424	0.846**	0.723**	0.710**	-0.629**	0.317
5. No. of fruits per plant	0.374	0.226	0.009	-0.442*	-0.651**	-0.814**	-0.828**	0.970**	-0.126
6. No. of ridges per pod	-0.581**	0.025	-0.270	0.301	0.882**	0.761**	0.738**	-0.632**	0.218
7. Crop duration (days)	-0.253	-0.047	-0.540**	0.020	-0.221	-0.426	-0.421	0.578**	0.571**
8.Yield per plant (g)	0.324	-0.000	-0.078	-0.368	-0.601**	-0.519**	-0.519**	0.666**	-0.043
9. Pollen sterility (%)	-0.145	-0.036	0.198	-0.405	0.549**	0.724**	0.712**	-0.391	-0.264
10. Plant height (cm)	0.518**	0.436*	0.511*	-0.520**	0.352	0.300	0.277	-0.126	-0.476*
11. Internodal length (cm)		0.386**	0.514*	-0.445*	-0.433	-0.410	-0.431	-0.369	-0.679**
12. No. of primary branches	0.355		0.354**	-0.188	-0.029	-0.238	-0.275	0.098	-0.095
13. Length of epicalyx segment (cm)	0.488	0.353		-0.585**	-0.158	-0.004	0.012	0.005	-0.600**
14. Width of epicalyx segment (cm)	-0.443	-0.178	-0.566		0.092	0.068	0.063	-0.408	0.527**
15. Petiloe length (cm)	-0.382	-0.035	-0.117	0.074		0.885**	0.877**	-0.691**	0.107
16. Days to flower (days)	-0.418	-0.202	0.011	0.072	0.783*		1.002**	-0.859**	-0.029
17. Days to first harvest (days)	-0.434	-0.233	0.030	0.064	0.779*	0.993*		-0.867**	-0.021
18. No. of harvest per plant	0.356	0.094	0.001	-.0.394	-0.657*	-0.818*	-0.813*		-0.135
19. Mucilage content (g/100g)	-0.668*	-0.090	-0.575	0.522	0.837	-0.021	-0.006	-0.117	

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

pod, number of ridges per pod, petiole length, days to flower and days to first harvest.

Mucilage content had high positive phenotypic correlation with girth of fruit, duration of crop and width of epicalyx segment and significant negative correlation with plant height, internodal length and length of epicalyx segment.

4.3.2 Genotypic correlation

First fruiting node had significant positive genotypic correlation with number of ridges per pod, pollen sterility, petiole length, days to first flowering, days to first harvest, and significant negative correlation with number of fruits per plant and duration of crop and number of harvests per plant.

Length of fruit had significant positive genotypic correlation with number of fruits per plant and yield per plant and number of harvests per plant and highly significant negative correlation with locules per pod, number of ridges per pod, petiole length, days to flowering and days to first harvest.

Girth of fruit showed high positive genotypic correlation with locules per pod, number of ridges per pod, duration of crop and mucilage content and significant negative correlation with internodal length and length of epicalyx segment.

Significant positive correlation was noticed for locules per pod with nu mber of ridges per pod, pollen sterility, petiole length, days to flower and days to first harvest and highly significant negative correlation with length of fruit, number of fruits per plant, yield, internodal length and number of harvests per plant.

Number of fruits per plant showed significant positive genotypic correlation with crop duration, yield and number of harvests per plant while the correlation was negative and significant with first fruiting node, number of ridges per pod, width of epicalyx segment, petiole length, days to flower and days to first harvest.

Number of ridges per pod recorded highly significant positive genotypic correlation with locules per pod, pollen sterility, petiole length, days to flower and days to first harvest and highly significant negative correlation with duration of crop and yield per plant, internodal length and number of harvests per plant.

Duration of crop showed high positive genotypic correlation with yield per plant, number of harvests per plant and mucilage content and highly significant negative correlation with length of epicalyx segment.

Yield per plant showed high positive genotypic correlation with length of fruit and number of harvests per plant and highly significant negative correlation with locules per pod, number of fruits per plant, petiole length, days to flower and days to first harvest.

Pollen sterility exhibited high positive genotypic correlation with first fruiting node, plant height, petiole length, days to first flowering, days to first harvest.

Plant height had high positive genotypic correlation with internodal length, number of primary branches and length of epicalyx segment and significant negative correlation with width of epicalyx segment and mucilage content.

Internodal length had high positive genotypic correlation with number of primary branches, length of epicalyx segment and plant height and significant negative correlation with girth of fruit, width of epicalyx segment and mucilage content.

Number of primary branches had significant negative genotypic correlation with length of epicalyx segment.

Length of epicalyx segment showed significant negative genotypic correlation with width of epicalyx segment and mucilage content. Width of epicalyx segment had significant positive correlation with mucilage content.

Petiole length had high positive genotypic correlation with first fruiting node, locules per pod, number of ridges per pod, days to first flowering and days to first harvest and significant negative correlation with number of harvests per plant.

Days to flower had high positive genotypic correlation with first fruiting node, locules per pod, number of ridges per pod, pollen sterility, petiole length and days to first harvest and significant negative correlation with number of fruits per plant and number of harvests per plant.

Days to first harvest showed significant positive genotypic correlation with first fruiting node, locules per pod, number of ridges per pod, pollen sterility, petiole length and days to first flowering and significant negative correlation with number of fruits per plant and number of harvests per plant.

Number of harvests per plant had high positive genotypic correlation with number of fruits per plant and yield and significant negative correlation with first fruiting node, locules per pod, number of ridges per pod, petiole length and days to first flowering and days to first harvest. Mucilage content had high significant negative correlation with internodal length.

4.4 Genetic divergence

Fifteen genotypes were grouped into five clusters using Mahalanobis D^2 statistics. The clustering pattern and the variable means of clusters are presented in Tables 7 and 8.

Among the five clusters, cluster numbers I and III had maximum number of genotypes (4), cluster II and cluster IV had 3 genotypes and cluster V had single genotype.

Genotypes included in cluster I were F_9-2, F_9-6, F_9-11 and *A. caillei*. This cluster recorded highest mean value for width of epicalyx segment (0.82) and mucilage content (0.66). The lowest mean value for number of fruits per plant (11.42) and intermodal length (9.56).

Table 7: List of genotypes in each cluster

Cluster Number	No. of genotypes in each cluster	Genotypes
I	4	F_9-2, F_9-6, F_9-11, *A. caillei*
II	3	F_9-3, F_9-8, F_9-12
III	4	F_9-1, F_9-5, F_9-10, *A. esculentus*
IV	3	F_9-4, F_9-9, Arka Anamika
V	1	F_9-7

Table 8: Means of variables for five clusters

Clusters	Girth of fruit (cm)	Number of fruits per plant	Number of ridges per pod	Plant height (cm)	Internodal length (cm)	Width of epicalyx segment (cm)	Days to first flowering	Mucilage content (g/100g)
I	8.07	11.42	5.96	144.54	9.56	0.82	51.76	0.66
II	8	11.74	5.95	151.57	9.59	0.6	52.55	0.47
III	7.81	11.99	5.7	140.93	9.83	0.69	49.6	0.34
IV	7.82	12.15	6.05	150.51	10.11	0.72	51.5	0.34
V	8.09	11.71	5.97	151.04	10.51	0.65	52.38	0.32

Table 9: Inter and Intra cluster D^2 values among five clusters

Clusters	I	II	III	IV	V
I	**4.72**				
II	30.10	**5.39**			
III	16.48	34.03	**4.47**		
IV	32.75	21.47	23.31	**5.44**	
V	13.34	11.27	26.79	29.02	**0.00**

The values printed in bold indicates intra cluster D^2 values

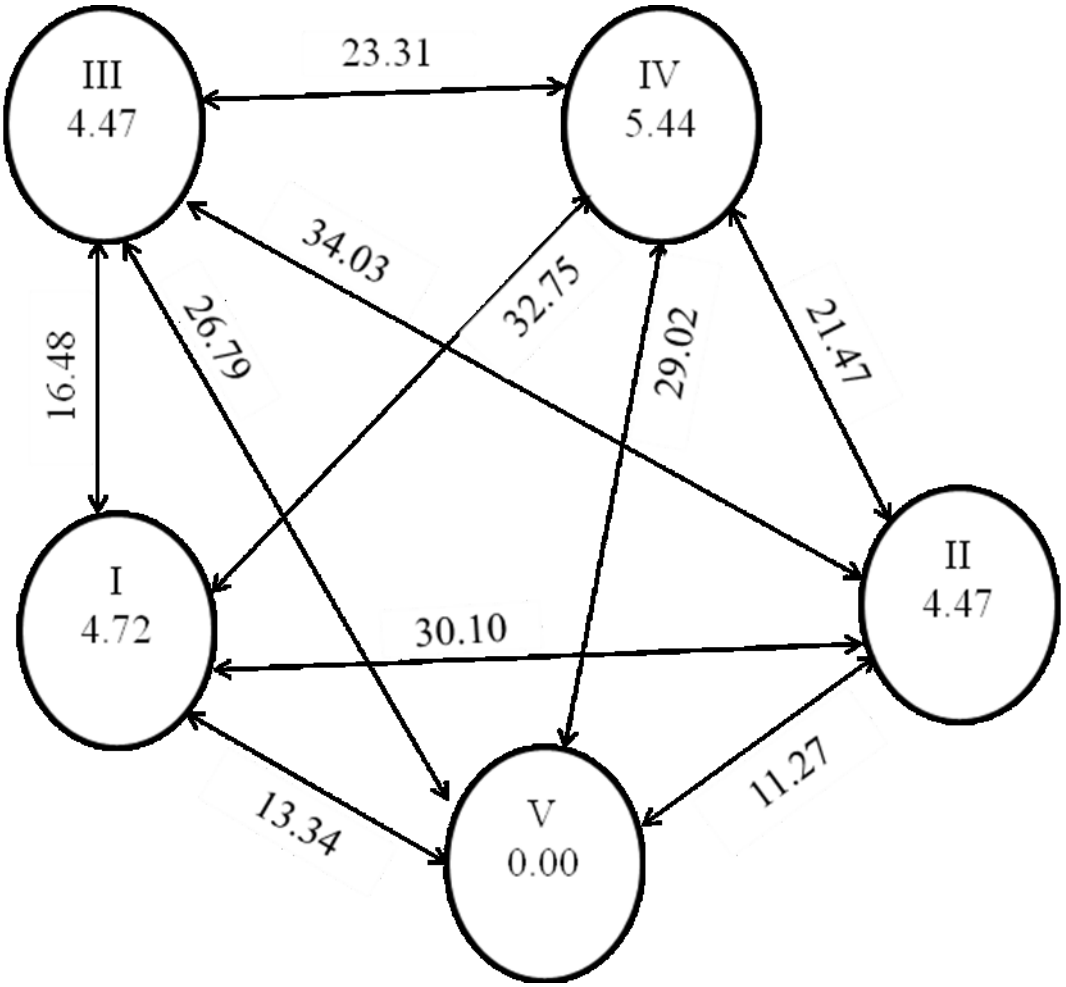


Fig. 3. Diagrammatic representation of clustering of 15 genotypes

Cluster II included the genotypes F_9-3, F_9-8 and F_9-12 and they had the highest mean value for plant height (151.57) and days to first flowering (52.55). The lowest mean value for width of epicalyx segment (0.6).

The genotypes F_9-1, F_9-5, F_9-10 and *A. esculentus* were included in cluster III which had the lowest mean value for girth of fruit (7.8), number of ridges per pod (5.70), plant height (140.93) and days to first flowering (49.60).

Three genotypes were in cluster IV which included F_9-4, F_9-9 and Arka Anamika. They had the highest mean value for number of fruits per plant (12.15) and number of ridges per pod (6.05).

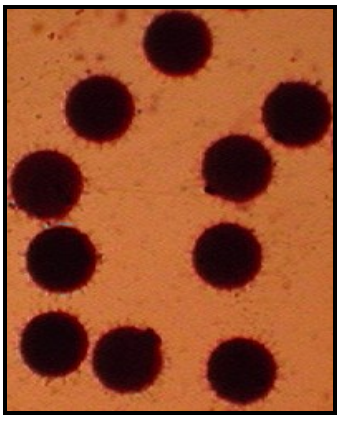
Cluster V included the single genotype F_9-7. It had highest mean value for girth of fruit (8.09) and internodal length (10.51) and the lowest mean value for mucilage content (0.32). Inter and intra cluster D^2 values among the five clusters were given in Table 9.

Cluster IV had the maximum intra cluster value (5.44). Cluster V comprised only one genotype hence value of intra cluster distance for this cluster was zero. Out of the clusters comprising more than one genotype, the minimum intra cluster distance was recorded for the cluster III (4.47) followed by cluster I (4.72) and cluster II (5.39).

The maximum statistical distance was found between cluster II and cluster III (34.03) followed by cluster I and cluster IV (32.75). The distance between the cluster II and cluster V displayed the lowest degree of divergence (11.27). A diagrammatic representation of clustering of genotypes is shown in Fig. 3.

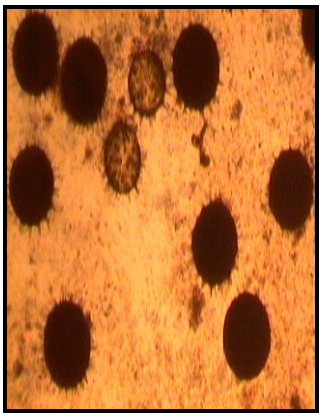
4.5 Pollen fertility studies

The pollen fertility of parental lines, Arka Anamika and F_9 selections was studied by staining with one per cent acetocarmine. Pollen fertility in the parental species *A. esculentus* variety Salkeerthi was as high as 99.9 per cent (Plate 5a) and *A. caillei* variety Susthira recorded 99.5 per cent pollen stainability (Plate 5b). Variety Arka Anamika recorded 96.56 per cent pollen stainability (Plate 5c). In



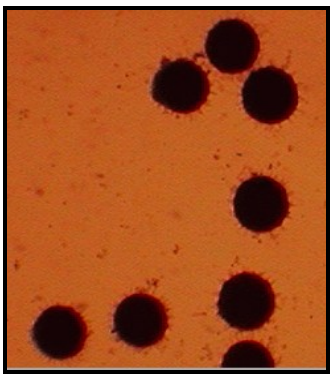
5a. *A. esculentus* (400x)

5b. *A. caillei* (400x)

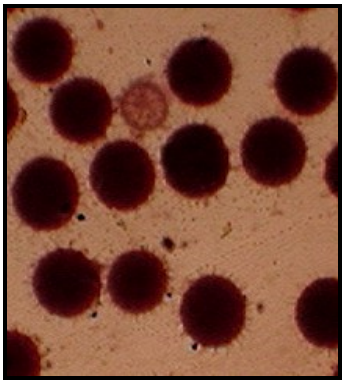


5c. Arka Anamika (400x)

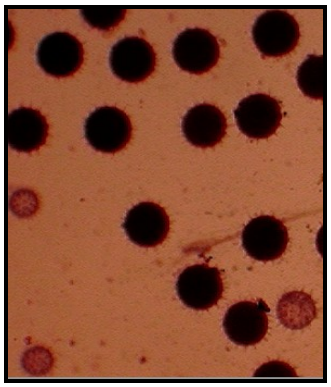
5d. Pollen grains of promising F_9 selections



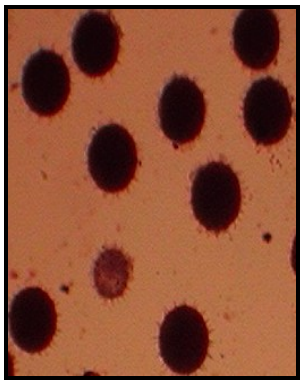
5d (1). F_9-5-5



5d (2). F_9-6-8 (400X)



5d (3). F_9-8-14 (400X)



5d (4). F_9-9-23 (400X)

Plate 5. Pollen grains of parents, Arka Anamika and promising F_9 selections showing fertile and sterile pollen grains

the F_9 generation selections, it ranged from 94.18 to 98.75 per cent. The highly YVMV resistant and high yielding plants selected out of F_9 selections viz., F_9-5-5, F_9-6-8, F_9-8-14 and F_9-9-23 expressed high levels of pollen fertility in the range of 97.52 to 98.54 (Plate 5d).

4.6 Reaction to YVMV

4.6.1 Field screening

Field screening trial for resistance to YVMV showed that the parent *A. esculentus* as highly susceptible (CI=69.21) whereas the other parental species *A. caillei* and six F_9 selections (F_9-4, F_9-5, F_9-6, F_9-8, F_9-9 and F_9-10) were completely free from YVMV. Variety Arka Anamika expressed coefficient of infection value of 24.96 (Moderately Susceptible). The other F_9 lines showed CI values ranging from 9.67 to 28.37 (Moderately resistant to moderately susceptible). Reaction of the parental species, Arka Anamika and F_9 selections to YVMV in the field screening studies is given in Table 10.

4.6.2 Screening by whitefly transmission

For the confirmation of disease resistance, whitefly transmission studies were carried out. Six genotypes (F_9-4, F_9-5, F_9-6, F_9-8, F_9-9, F_9-10) which found as highly resistant in the field screening were inoculated by viruliferous whiteflies carrying YVMV. Variety Salkeerthi served as control. Tested plants reaction to YVMV is given in Table 10. All six genotypes remained resistant and did not show any disease symptoms even after 40 days of inoculation (Plate 6a), whereas *A. esculentus* var. Salkeerthi showed typical symptoms of YVMV within 30 days of inoculation (Plate 6b).

4.6.3 Screening by graft transmission

Six genotypes (F_9-4, F_9-5, F_9-6, F_9-8, F_9-9, F_9-10) identified highly resistant to YVMV in the field screening as well as white fly transmission studies were artificially inoculated by approach grafting. Their reaction to YVMV is given in Table 10. Only four selections (F_9-5, F_9-6, F_9-8 and F_9-9) remained

6a. Absence of YVMV symptoms in F_9 selections by whitefly transmission

F_9-4

F_9-5

F_9-6

F_9-8

F_9-9

F_9-10

6b. *A. esculentus* showing symptoms of YVMV by whitefly transmission

Plate 6. Artificial inoculation of YVMV by whitefly transmission

7a. F_9-5 grafted with *A. esculentus*

7b. F_9-6 grafted with *A. esculentus*

7c. F_9-8 grafted with *A. esculentus*

7d. F_9-9 grafted with *A. esculentus*

Plate 7. Absence of YVMV symptoms in F_9 selections in the graft combination with diseased *A. esculentus*

Table 10. Reaction of genotypes to YVMV in the field screening, graft transmission and whitefly transmission studies

Sl. No	Field screening			Whitefly transmission		Graft transmission	
	Genotypes	CI	Disease reaction	Genotypes	Disease reaction	Genotypes	Disease reaction
1	F_9-1	23.63	MS	F_9-4	HR	F_9-4	S
2	F_9-2	10.18	MR	F_9-5	HR	F_9-5	HR
3	F_9-3	10.77	MR	F_9-6	HR	F_9-6	HR
4	F_9-4	0	HR	F_9-8	HR	F_9-8	HR
5	F_9-5	0	HR	F_9-9	HR	F_9-9	HR
6	F_9-6	0	HR	F_9-10	HR	F_9-10	S
7	F_9-7	28.37	MS				
8	F_9-8	0	HR				
9	F_9-9	0	HR				
10	F_9-10	0	HR				
11	F_9-11	9.67	MR				
12	F_9-12	12.53	MR				
13	Arka Anamika	24.96	MS				
14	*A. esculentus*	69.21	HS				
15	*A. caillei*	0	HR				

HR - Highly Resistant R - Resistant

MR- Moderately Resistant HS - Highly Susceptible

F_9-5-5

F_9-6-8

F_9-8-14

F_9-9-23

Plate 8. Promising selections from F_9 generation

Table 11. Details of the quantitative and qualitative characters expressed by the promising selections in the F_9 generation in comparison with parents and Arka Anamika

		(F_9-5-5)	(F_9-6-8)	(F_9-8-14)	(F_9-9-23)	*A.c**(P1)	*A.e** (P2)	*Arka Anamika*
I	**Quantitative characters**							
1	Plant Height (cm)	100.23	120	97	105	143.7	123	140
2	Internodal length (cm)	4	8	6	8	7.8	12.2	10
3	No. of primary branches	3	4	3	3	3	3	3.3
4	Length of epicalyx segment (cm)	1.7	2.1	2.2	2.0	1.3	2.2	2.0
5	Width of epicalyx segment (cm)	0.5	0.6	0.8	0.5	1.1	0.5	0.6
6	Petiole length (cm)	31	25	29	27	34	30.2	34
7	Days to flower	42	47	52	46	47	39.2	47
8	Days to first harvest	48	52	58	51	52.6	44.2	52
9	No. of harvests	8	9	8	6	11	14	11
10	First fruiting node	4	5	5	4	4.6	4	5
11	Length of fruit (cm)	18	22	19	22	16.8	27.9	18
12	Girth of fruit (cm)	6.4	5.9	6.5	5.8	8.4	7.4	7.5
13	Locules per pod	5	5	5	5	6	5	6
14	No. of fruits per plant	25	24	17	20	12	15	15
15	No.of ridges per pod	5	5	5	5	6	5	5
16	Crop duration (days)	149	154	153	155	171.6	167.3	145
17	Yield per plant (g)	278	285	192	210	177.3	191.4	178.01
18	Pollen fertility (%)	98.54	97.89	97.52	98.45	99.9	99.5	96.57
19	Mucilage content (g/100g)	0.27	0.59	0.49	0.53	1.12	0.25	0.33
20	YVMV reaction	HR	HR	HR	HR	HR	HS	MS
II	**Qualitative characters**							
1	Pod pubescence	NP	NP	NP	NP	NP	NP	NP
2	Leaf margin	DF	NF	DF	NF	NF	DF	DF
3	Flower colour	Yellow	Yellow	Yellow	Yellow	Yellow	Yellow	Yellow
4	Flower size	Medium	Large	Large	Large	Medium	Medium	Medium
5	Purple throat at base of corolla	Present	Present	Present	Present	Present	Present	Present
6	Colour of leaf vein	GWPT	GWPT	GWPT	GWPT	GWPT	GWPT	GWPT
7	Colour of leaf base	RWGT	RWGT	RWGT	RWGT	RWGT	RWGT	RWGT
8	Colour of fruit	DG	G	G	DG	G	LG	G

G-Green DG- Dark Green LG- Light Green

HR- Highly Resistant GWPT- Green with purple tinge DF-Deeply fid

NP- Not pubescent LP- Less pubescent NF- Narrowly fid

HS-Highly susceptible *A.c * - A. caillei* *A.e * - A. esculentus*

highly resistant in graft transmission also (Plate 7). The other two genotypes (F_9-4, F_9-10) showed symptoms of YVMV.

4.7 Selection of desirable promising lines from F_9 generation

The F_9 generation plants showed considerably good amount of variability with respect to plant, leaf, flower and fruit characters. The F_9 generation lines were morphologically more similar to parent, *A. esculentus*. Four selections (F_9-5, F_9-6, F_9-8 and F_9-9) remained highly resistant to YVMV in screening trials. The pods of these lines also have less mucilage content. Out of these F_9 generation selections individual plant selections viz., F_9-5-5, F_9-6-8, F_9-8-14 and F_9-9-23 were made (Plate 8). These selections have attractive fruit colour, desirable number of ridges per fruit, high yield and less mucilage content considerably good amount of pollen fertility and high level of resistance to YVMV (Table 11).

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DISCUSSION

5. DISCUSSION

The present study was aimed at the evaluation of the genetic variability in the F_9 generation selections out of the cross *A. caillei* var. Susthira x *A. esculentus* var. Salkeerthi and also to identify YVMV resistant high yielding lines from these advanced generation selections. In interspecific hybridization programmes, progenies developed from the crosses are expected to exhibit a broad spectrum of genetic variability, there by offering great scope for isolating desirable selections in the advanced generations. The salient results gathered in the light of the present investigation are discussed here under.

5.1 Evaluation of genotypes

Most of the characters exhibited significant variation among the treatments (Table 3). The *A. esculentus* parent had the lowest mean value for first fruiting node. Many of the F_9 selections resembled the wild parent with respect to this character. This result is in accordance with the findings of Sheela (1994) and John (1997).

The promising F_9 lines (F_9-5-5, F_9-6-8, F_9-8-14 and F_9-9-23) showed characters similar to the cultivated species *A. esculentus* line Salkeerthi such as longer fruit length, less number of ridges per pod, reduced width of epicalyx segment etc (Table 11). This shows the transfer of desirable genes from cultivated parent to F_9 generation lines.

5.2 Genetic parameters in the genotypes evaluated

5.2.1. Variability

An estimate of the magnitude of variability present in a population is of great importance as it provides basis for effective selection. The observed variability in a population is the total variation arising due to the genotypic and environmental effects. But only the genotypic component of total variability contributes to gain

under selection. So knowledge of the nature and magnitude of genetic variation governing inheritance of quantitative characters like yield and its components is essential (Allard, 1960). In okra great variability in qualitative and quantitative characters had been observed by many workers like Vashista *et al.* (1982); Hamon and Charrier (1983) and Ariyo (1993).

In the present study, length of fruit, number of fruits per plant, plant height, petiole length, days to flower, days to first harvest, crop duration, yield per plant and pollen sterility exhibited considerable variability. Murthy and Bavaji (1980) also reported considerable variability for length and number of fruits and yield per plant. Vashista *et al.* (1982) observed significant difference for yield and agronomic characters. Jeyapandi and Balakrishnan (1992) observed highest variability for yield per plant followed by plant height. Significant variation among six parental strains and their 30 F_1 hybrids was reported by Rajani and Manju (1997) for days to flower, fruits per plant, length of fruit, yield per plant and plant height. Yassin and Anbu (1997) observed wide variability for plant height, fruits and yield per plant but not for girth of fruits.

Twenty two okra genotypes exhibited wide variation for plant height, days to first flower, fruits per plant and yield (Hazra and Basu, 2000). Philip *et al.* (2000) observed significant variation for fruits per plant. Gandhi *et al.* (2001) observed significant variability for plant height, fruits per plant, length of fruits and yield per plant. Highest variability for average fruit length and number of fruits per plant was observed by Jindal *et al*. (2010).

Adiger *et al*. (2011) observed highest variability for fruit yield per plant, followed by plant height and number of fruits per plant. Chaukhande *et al.* (2011) reported wide range of variation for most of the traits including fruit length, days to first flower, plant height and fruit weight per plant

5.2.2 Coefficient of variation

Variability is also expressed as the coefficient of variation. Phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) are better indices for comparison of characters with different units of measurements. The GCV provides a valid basis for comparing and assessing the range of genetic diversity for quantitative characters and PCV measures the extent of total variation. GCV is a better tool to understand useful variability as it is free from the environmental component affecting variability. In the present study GCV and PCV for all characters are presented in Fig 1.

The magnitude of PCV was higher than GCV for all the treatments suggesting the role of environmental variance. Similar results were observed by Adiger *et al.* (2011) and Chaukhande *et al*. (2011).

High GCV and PCV values were exhibited by incidence of YVMV. Same results were obtained by Chaukhande *et al*. (2011), but Mathews (1986) and John (1977) reported low phenotypic and genotypic coefficient of variation for YVMV incidence.

Duration of the crop and girth of fruit exhibited low phenotypic and genotypic coefficient of variation. John (1997) also observed low genotypic and phenotypic coefficients of variation for these characters. The low variability noticed for these characters indicate the difficulty in improving these characters by selection.

5.2.3 Heritability and Genetic Advance

While evaluating more than one character, their interrelations also have to be worked out. The parameters like heritability and genetic advance are unavoidable. The phenotypic variance which is due to genotypic variance is expressed in heritability. The magnitude of improvement through selection programme is detected

by genetic advance. High heritability together with high genetic advance is an important requirement for selection programme.

Selection acts on genetic differences and gains from selection for a specific character depend largely on the heritability of the character (Allard, 1960). Heritable variation may be efficiently used with greater degree of accuracy when heritability is studied on conjunction with genetic advance (Majumdar *et al.,* 1974).

High heritability was observed for all the 20 characters under study which indicates that the environment plays a little role on inheriting these traits to progenies.

High heritability coupled with high genetic advance was shown by incidence of YVMV. This indicates the presence of additive genes and shows that these characters can be improved by selection. Chaukhande *et al*. (2011) reported high genetic advance for above character.

High heritability along with moderate genetic advance was shown by Plant height and yield per plant. It is in accordance with findings of Bindu *et al.* (1997), but Reddy *et al* (1985); Balakrishnan and Balakrishnan (1990); Yadav (2002) and Indurani (2005) were observed high heritability along with high genetic advance for above characters.

High heritability coupled with low genetic advance was observed for first fruiting node, number of primary branches. Same results were observed by Rajani and Manju (1997); Yadav (2002).

5.2.4 Correlation studies

Information regarding association of characters like growth, earliness, yield and its component characters is very useful for plant breeder in developing commercial variety or hybrid. Many of these characters are interrelated in desirable and undesirable direction. Correlation studies measure the mutual relationships

between various characters and help in determining the component characters on which selection can be based. The efficiency of selection mainly depends upon the direction and magnitude of correlation between the different characters studied. Correlation analysis provides reliable information on nature, extent and direction of selection.

The magnitude and direction of association among the 19 characters studied in the genotypes were assessed by means of correlation analysis (Table 6).

Number of fruits per plant was positively correlated with yield. The same result was also obtained by Arumugham and Muthukrishnan (1981). Mishra and Singh (1985) suggested the importance of fruit number per fruit as a selection criterion for increasing yield. Ariyo (1992) and Sheela (1994) also observed strong positive association between number of fruits per plant and weight of fruits per plant. Singh and Singh (2006) reported the same with fruit yield and girth of fruit.

Days to first flowering was negatively correlated with number of fruits per plant and yield per plant. This is in agreement with findings of Alex (1988) and Adiger *et al*. (2011).

Significant positive phenotypic and genotypic correlation with yield was shown by fruit length and fruits per plant indicating that an improvement of these characters will produce a simultaneous improvement in yield. This had also been reported by Chacko (1996); Antur (1999) and Bhalekar *et al*. (2005) and Balakrishnan and Sreenivasan (2010). Significant positive association of fruit yield per plant with number of fruits per plant has been reported by several workers (Mahajan and Sharma, 1979; Elangovan *et al.* 1980; Vashista *et al.* 1982; Mathews 1986; Alex, 1988; Ariyo, 1992; Sheela, 1994 and John, 1997).

Total yield had negative and significant association with number of locules per fruit as observed by Sood *et al*. (1995) and days to flowering according to Majumdar *et al*. (1974) and Adiger *et al*. (2011) in okra.

Nodes at first flowering had positive and significant correlation with days to first flowering. This result is in accordance with the findings of Parthap *et al.* (1979) and Singh and Singh (2006).

5.3 Genetic divergence

Mahalanobis D^2 statistics is a valuable multivariate analytical tool used for obtaining quantitative estimates of divergence between biological populations. Genetically divergent parents are essential to generate new variability and desired recombinants. In the present study, 15 genotypes were grouped into five clusters, indicating considerable genetic diversity prevailing among them. The distribution of genotypes into five clusters was not according to their places of origin showing that the genotypes forming one group were genetically diverse, while genotypes obtained from the same region were genetically different. This is in agreement with the findings of Ramya and Senthilkumar (2009); Prakash and Pitchaimuthu (2010). Therefore, selection of cultivars for breeding programme should be based on genetic diversity rather than geographical diversity.

Analysis of inter cluster distance revealed that the genetic divergence was maximum between cluster II and cluster III (34.03) followed by cluster I and cluster IV (32.75) suggesting thereby that the genotypes belonging to cluster II and III and I and IV were more divergent than the rest of the clusters, can be undertaken in a hybridization programme for evolving good hybrids.

The inter cluster distance between cluster II and cluster V was low (11.27) suggesting less genetic divergence among them compared to other clusters.

High intra cluster distance within a cluster indicates the high degree of variability within that cluster offering scope for improvement by various selection methods. The maximum intra cluster distance was shown by cluster IV (5.44) followed by cluster II (5.39), cluster I (4.72) there by indicating highest degree of variability in cluster IV.

Cluster V comprised only one genotype hence value of intra cluster distance for this cluster was zero. Out of the clusters comprising more than one genotype, the minimum intra cluster distance was recorded for the cluster III (4.47) followed by cluster I (4.72). Thus, the hybridization between genotypes from distant clusters may result in heterotic hybrids and trasgressive segregants.

Cluster IV recorded maximum number of fruits per plant followed by cluster III. Cluster II recorded maximum number of days to flowering while cluster III had the minimum. Cluster V recorded lowest mean value for mucilage content whereas cluster I had maximum.

Three F_9 selections viz., F_9-1, F_9-5, F_9-10 were grouped along with *A. esculentus* and F_9-4 and F_9-9 were grouped along with Arka Anamika. This clearly shows that in advanced generation lines desirable *A. esculentus* characters has been recovered by eliminating the undesirable characters of *A. caillei*.

This information regarding genetic divergence studies will provide to adopt appropriate breeding methods for improvement of okra as done by workers Patel *et al*. (2006); Prakash and Pitchimuthu (2010) and Garg *et al.* (2011).

5.4 Mucilage content

Okra pods are especially characteristic for their mucilage content. The mucilage content of edible stage fruits was estimated by extracting the mucilage with ethyl alcohol. This method was followed by many researchers like Thampi (1998); Ravisankar (2002) and kadlag *et al*. (2005). Presence of less mucilage content in okra

fruits is a desirable character. Mucilage content in the parental species *A. esculentus* variety Salkeerthi was as low as 0.25 g/100g and *A. caillei* variety Susthira recorded 1.12 g/100g which is very high among all the genotypes under study. Similar results were obtained by Thampi (1998) and Ravisankar (2002). In the F_9 generation lines, it ranged from 0.27-0.62 g/100g. Variety Arka Anamika recorded 0.33 g/100g. The desirable promising F_9 selections were showed mucilage content in the range of 0.27-0.59 g/100g which was on par with Arka Anamika.

5.5 Pollen fertility studies

The pollen fertility in *A. esculentus* and *A. caillei* were 99.9 and 99.5 per cent respectively due to their regular chromosome behavior during meiosis. Similar results were reported by Jaseena *et al*. (2008). Pollen stainability in the F_9 lines varied from 94.18 to 98.75 per cent. In case of standard check variety Arka Anamika pollen fertility was 96.57 per cent. The promising lines selected from F_9 generation viz., F_9-5-5, F_9-6-8, F_9-8-14 and F_9-9-23 showed pollen fertility in the range of 97.52 to 98.54 per cent.

Pollen fertility studies shows that high amount of pollen fertility exists in F_9 generation lines on par with Arka Anamika. The promising lines selected from F_9 generation selections showed pollen fertility even more than Arka Anamika. Jaseena *et al.* (2008) reported 12.47 per cent pollen sterility in the F5 generation of the cross *A. caillei* x *A. esculentus.* The present study indicated that the degree of sterility was decreasing in the succeeding generation and provided scope for securing highly fertile advanced generation lines combined with desirable traits. Similar line of work has been reported by Jambhale and Nerkar (1983); Sureshbabu and Dutta (1990).

5.6 Screening for YVMV resistance

5.6.1 Field screening

In the field screening trials the *A. esculentus* var. Salkeerthi was highly susceptible to YVMV (CI=69.21) whereas *A. caillei* var. Susthira was highly resistant (CI=0). This observation is in accordance with the findings of Sureshbabu *et al*. (2002).

Even though Arka Anamika, a highly popular okra variety was reported by earlier researchers as highly reisistant one, it was found to be moderately susceptible (CI=24.96) during the present study. Sindhumole (2003) and Prashanth *et al*. (2008) also reported this variety as highly susceptible and moderately resistant one respectively. In F_9 lines, six were highly resistant (F_9-4, F_9-5, F_9-6, F_9-8, F_9-9, F_9-10) and remaining were moderately susceptible (CI=28.37) to YVMV. This result is in agreement with Cheriyan (1986) and Philip (1998).

5.6.2 Artificial inoculation

Artificial inoculation studies were carried out in order to ascertain the nature of resistance, since the resistant reaction expressed consequent to virus inoculation can be either due to escape or due to true resistance.

YVM disease resistance identified in the F_9 selections was further confirmed by conducting following methods:

5.6.2a Whitefly transmission

All six selections highly resistant in field screening were found highly resistant to YVMV on whitefly transmission also and only susceptible check Salkeerthi showed symptoms of the disease. Ravisankar (2002) and Kousalya (2005) have adopted whitefly transmission for artificial screening of okra genotypes against YVMV.

5.6.2b Graft transmission method

Out of the six selections tested, only two selections showed symptoms and other four selections (F_9-5, F_9-6, F_9-8 and F_9-9) were completely free of YVMV in graft transmission confirming the true resistance of these genotypes. Similar graft transmission technique for confirming the YVM resistance in okra was performed previously by Ali *et al*. (2000); Ravisankar (2002) and Jaseena (2008). The present study also showed that graft transmission technique is more effective method for screening of YVMV in okra.

5.6.3 Stable YVMV resistant F_9 selections

As evidenced in the above mentioned confirmation tests, the highly YVMV resistant selections (F_9-5, F_9-6, F_9-8 and F_9-9) possessed true and stable resistance which could be utilised for future breeding programmes to develop new YVM resistant okra varieties.

The occurrence of highly YVMV resistant advanced F_9 generation lines clearly shows that the flow of desirable YVMV resistant genes from the semi-wild species *A. caillei* to the cultivated species *A. esculentus* had been successful. Thaker *et al*. (1981); Jambhale and Nerkar (1983); Sureshbabu and Dutta (1990) and Philip (1998) have reported similar type of gene introgression in okra.

5.7 Selection of desirable promising lines in F_9 generation

Out of the F_9 generation, four individual plant selections viz., F_9-5-5, F_9-6-8, F_9-8-14 and F_9-9-23 were made. The prominent features of these F_9 selections were that they expressed high level of resistance to YVMV (CI=0), earliness, yield per plant, high pollen fertility (97.52 to 98.54 per cent), less mucilage content (0.27-0.59 g/100g) and prominent morphological characters of *A. esculentus*. This clearly shows that breeding programme of developing YVMV resistant okra genotypes with desirable qualitative and quantitative traits had proceeded in the right direction.

Further advancing these lines made from the F_9 generation will be able to develop high yielding and YVMV resistant okra varieties in the near future as reported by Thakur (1976); Jambhale and Nerkar (1983) and Sureshbabu and Dutta (1990).

SUMMARY

6. SUMMARY

Okra has captured a prominent position among the vegetables due to its year round cultivation, export potential and high nutritive value. However many of the okra cultivars now in vogue are highly susceptible to YVMV disease which reduces the yield considerably. Hence it is essential to evolve varieties resistant to YVMV disease. The present investigation was undertaken in the Department of Olericulture, College of Horticulture, Thrissur, during 2011-2012. The main objective of the study was to identify the promising lines in F_9 generation of the cross *Abelmoschus caillei* var. Susthira x *Abelmoschus esculentus* var. Salkeerthi and select the high yielding YVMV resistant lines from this population and also to study the variability and genetic divergence among the genotypes.

The F_9 generation plants were raised in the field along with their parents and variety Arka Anamika. The morphological traits of genotypes were compared. The genotypes were screened for YVMV resistance.

Evaluation of genotypes

All the genotypes exhibited significant variation for the different characters studied.

Less mucilage content and high level of pollen fertility were noted in the selected desirable F_9 lines. Incidence of YVM disease was much lower in the selected lines compared with the cultivated parent.

The PCV and GCV were maximum for incidence of YVMV disease whereas duration of the crop exhibited low variation. High heritability and genetic advance were noted for coefficient of infection of YVMV. This indicates the presence of additive genes. High heritability coupled with low genetic advance was observed for first fruiting node, number of primary branches.

Fruit yield per plant recorded significant positive correlation with number of fruits per plant and crop duration thereby indicating the plant and fruit characters that should be considered while selection for yield improvement.

Genetic divergence

The 15 genotypes were grouped into five clusters based on genetic distance. There was no parallelism between geographical distribution and genetic diversity. Intra cluster distances were much lesser than inter cluster distances, suggesting homogeneity and heterogeneity of the genotypes within and between the clusters respectively.

Mucilage content

Presence of less mucilage content in okra fruits is a desirable character. Mucilage content in the parental species *A. esculentus* variety Salkeerthi was as low as 0.25 g/100g and *A. caillei* variety Susthira recorded 1.12 g/100g which is very high among all the genotypes under study. In the F_9 generation lines, it ranged from 0.27-0.62 g/100g. Variety Arka Anamika recorded 0.33 g/100g. The desirable F_9 lines (F_9-5-5, F_9-6-8, F_9-8-14 and F_9-9-23) were showing less amounts of mucilage content compared to wild parent.

Pollen fertility studies

The pollen fertility studies revealed that the parents *Abelmoschus caillei* var. Susthira and *A. esculentus* var. Salkeerthi, standard check variety Arka Anamika and all advanced F_9 generation lines had higher pollen fertility. The pollen fertility in the genotypes ranged from 94.18 to 99.9 per cent. The F_9 lines were on par with parental lines and Arka Anamika in pollen fertility. The high level of pollen fertility in the parents must be attributed to their regular chromosome pairing during meiosis.

Screening for resistance to YVMV

All the genotypes under study were screened for YVMV resistance. Field screening trial for resistance to YVMV showed that the parent *A. esculentus* as highly susceptible (CI=69.21), while the other parental species *A. caillei* was completely free of YVMV. Standard check variety Arka Anamika was moderately susceptible (CI=24.96). The F_9 lines were ranged from highly resistant to moderately susceptible (CI=0 to 28.37).

All six F_9 selections highly resistant in field screening were found highly resistant to YVMV in whitefly transmission studies. However, in artificial inoculation of YVMV by grafting method; out of the six resistant F_9 lines only four genotypes (F_9-5, F_9-6, F_9-8 and F_9-9) remained highly resistant and the other two genotypes showed symptoms of YVMV.

Selection of promising lines from the F_9 population

Four advanced generation selections viz., F_9-5-5, F_9-6-8, F_9-8-14 and F_9-9-23 showed characters such as less number of ridges per pod, longer fruit length, reduced width of epicalyx segment etc morphologically similar to the cultivated species *A. esculentus* var. Salkeerthi. Their fruits were having green pods with five ribs and less mucilage content. They were also having more number of fruits per plant and high yield. These selections also showed high level of pollen fertility and resistance to YVMV.

Suggested future line of work

The four F_9 selections viz., F_9-5-5, F_9-6-8, F_9-8-14 and F_9-9-23 made from this study can be advanced to further generations to obtain more stability of the characters, so that the resultant lines can be developed as high yielding YVMV disease resistant varieties and work out the genetics of resistance to YVMV.

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APPENDICES

Appendix I. Mean monthly meteorological data

Months	Max. Temp.(°C)	Min. Temp. (°C)	Rainfall (mm)	RH(%)	No. of rainy days	Sunshine (hr.)	Wind Speed (Km/hr)
June	29.3	23.6	26.7	88.95	0.9	2.5	2.8
July	29.1	22.9	19	87.8	0.8	1.6	2.2
August	29.4	22.9	23	87.05	0.8	2.2	3.0
September	30	23.1	14.5	84.45	0.5	4.4	2.6
October	32.1	23.5	6.1	77.9	0.3	6.1	2.8
November	31.4	22.9	8	68.1	0.3	6.3	3.0

Source: Department of Agricultural Meteorology, KAU, Vellanikkara

EVALUATION OF PROMISING DISTANT HYBRIDIZATION DERIVATIVES OF OKRA (*A. esculentus* (L.) Moench)

By

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ABSTRACT OF THESIS

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ABSTRACT

Yellow Vein Mosaic (YVM) is a devastating disease infecting okra (*Abelmoschus esculentus* (L.) Moench), at all stages of crop growth, causing 50 to 94 per cent crop loss. The best way to tackle this disease is the use of resistant varieties developed by interspecific hybridization. Hence a study was undertaken in the Department of Olericulture, College of Horticulture, Kerala Agricultural University, Vellanikkara during 2011-2012 for the evaluation of F_9 selections of the cross between *Abelmoschus caillei* var. Susthira (YVMV resistant variety) and *Abelmoschus esculentus* var. Salkeerthi (high yielding, widely adapted but YVMV susceptible variety), with the objective of identifying promising lines having high level of resistance to YVMV.

Okra genotypes consisting of 12 F_9 selections along with their parents and Arka Anamika were evaluated for qualitative, quantitative characters, pollenfertility and YVMV resistance in RBD with two replications. Variability, correlation and genetic divergence were also worked out. The screening for YVMV resistance was done by field evaluation creating artificial epiphytotic conditions, white fly transmission studies and graft transmission techniques. Four F_9 generation selections (F_9-5-5, F_9-6-8, F_9-8-14 and F_9-9-23) exhibited high level of resistance to YVMV.

During the evaluation of quantitative characters in the F_9 generation selections, significant variation among the genotypes was observed for the traits such as, plant height, petiole length, days to first flowering, days to first harvest, length of fruit, number of fruits per plant, crop duration and yield per plant.

The maximum values for both PCV and GCV were noticed for coefficient of infection of YVMV, pollen sterility and mucilage content. Most of the traits possessed high heritability especially for the coefficient of infection of YVMV and pollen sterility. High genetic advance could be noticed for coefficient of infection of YVMV and plant height. Correlation analysis indicated that fruit yield displayed

positive genotypic association with length of fruit, number of fruits per plant and crop duration. The 15 genotypes were grouped into five clusters and no parallelism between geographical distribution and genetic diversity was observed.

Pollen fertility studies indicated that high level of pollen fertility was present in F_9 generation lines also. Mucilage extraction analysis revealed that only low amount of mucilage was present in F_9 generation lines compared to the wild parent *A. caillei* var. Susthira.

Four F_9 selections showed characters such as lower number of ridges per pod, longer fruit length, reduced width of epicalyx segment and less mucilage content similar to the cultivated species *A. esculentus* var. Salkeerthi. Based on its promising fruit characters tending towards *A. esculentus,* selections such as F_9-5-5, F_9-6-8, F_9-8-14 and F_9-9-23 were identified. These selections expressed good amount of pollen fertility and high yield. Hence these selections can be further advanced to develop YVMV resistant varieties with desirable plant and fruit characters.