BREEDING FOR RESISTANCE TO FRUIT FLY (*Zeugodacus* spp.) IN ORIENTAL PICKLING MELON (*Cucumis melo* (L.) var. *conomon* Mak.)

by

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(2015-22-007)

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THESIS

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KERALA, INDIA

2020

DECLARATION

I, hereby declare that the thesis entitled **"BREEDING FOR RESISTANCE TO FRUIT FLY (*Zeugodacus* spp.) IN ORIENTAL PICKLING MELON (*Cucumis melo* (L.) var. *conomon* Mak.)"** is a bonafide record of research work done by me during the course of research and the thesis 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.

Vellanikkara **SILPA RAMACHANDRAN**

Date: (2015-22-007)

CERTIFICATE

Certified that this thesis entitled **"BREEDING FOR RESISTANCE TO FRUIT FLY (*Zeugodacus* spp.) IN ORIENTAL PICKLING MELON (*Cucumis melo* (L.) var. *conomon* Mak.)"** is a record of research work done independently by **Ms. Silpa Ramachandran (2015-22-007)** under my guidance and supervision and that it has not previously formed the basis for the award of any degree, diploma, fellowship or associate ship to her.

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We, the undersigned members of the advisory committee of **Ms. Silpa Ramachandran (2015-22-007)**, a candidate for the degree of Doctor of Philosophy in Horticulture with major field in Vegetable Science, agree that the thesis entitled "**BREEDING FOR RESISTANCE TO FRUIT FLY (*Zeugodacus* spp.) IN ORIENTAL PICKLING MELON (*Cucumis melo* (L.) var. *conomon* Mak.)"** may be submitted by Ms. Silpa Ramachandran (2015-22-007), in partial fulfillment of the requirement for the degree.

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SILPA RAMACHANDRAN

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Introduction

1. INTRODUCTION

Cucurbits are a group of vegetables belonging to the family Cucurbitaceae. Oriental pickling melon (*Cucumis melo* var. *conomon* Mak.) is one of the common vegetable of the melon group of the family Cucurbitaceae, with the chromosome number 2n=24. It is highly cross pollinated and usually andromonoecious in nature, preferring warm weather and bright sunlight for its better growth and development. Fruits are varying in size, small to medium and big fruits with smooth tender skin, white flesh usually with low sweetness and odour (Munshi and Alvarez, 2005). It is popularly called as golden melon or culinary melon in English. In Kerala, it is called by local names as *Sambar Vellari*, *Vellari* or *Kanivellari*; it occupies a predominant place in the summer rice fallows of Kerala. Its fruit is kept as a symbol of prosperity during the festival of '*Vishu*'.

Oriental pickling melon plants are characterized by compact plant type, high creeping vines, earliness of harvest and high yielding ability. The crop performs well in rain fed, irrigated and in rice fallows during summer seasons. The fruits are large, botanically known as pepo and have long storage life under ambient conditions. It is an ideal summer vegetable crop chiefly grown for use as a fresh vegetable as well as for pickling. The fruit contains moderate amount of vitamins and minerals and are used in the preparation of array of traditional vegetarian dishes like chutney, curry, *sambar* and pickles. The fruits possess cooling properties and are used as a skin moisturizer and as a digestive agent. 100 g pulp of fruit contains 285 mg phosphorus, 150 mg calcium and 100 mg of iron. Oriental pickling melons are commonly grown in Far East Asia. Kerala, South Karnataka, Andhra Pradesh and Tamil Nadu are the major oriental pickling melon growing states in India (Lakshmi *et al*., 2017). In India, it is grown in an area of 109 thousand ha with annual production of 1.696 m t (National Horticulture Board, 2018).

The fruit fly, *Zeugodacus cucurbitae* Coq. is one of the most serious insect pest of cucurbitaceous crops in India. This causes tremendous economic losses to fruit and vegetable growers by reducing the yield qualitatively and quantitatively. In India, it causes severe damage in 28 species of fruits and vegetables and approximately 50 per cent of the

cucurbits are partially or completely damaged by melon fly (Kapoor, 1993). The attack is severe during high humidity especially after rains (Ingoley *et al*., 2005). The infested fruits can be identified by the presence of brown resinous juice which oozes out of the punctures made by the flies for oviposition. The distinct life cycle of the fruit flies renders them less amenable for conventional pest management measures. The female fruit fly lays eggs beneath the fruit skin about 3 to 5mm deep inside using its long ovipositor. Developing maggots are seen inside the fruit. The mature maggots nearing pupation has a habit of jumping up and moving away from the surrounding host plant. As a result, pupae are very much scattered in their habitat and found inside the soil at depth of 0.5 to 15cm and consequently escaping from the management practices. Besides, adult flies spend most of their life span on non-host plants and visit the host plant mainly for oviposition. Thus, fruit flies have several adaptation factors favouring their infestation potential and survival.

Depending upon the season and prevailing climatic conditions, loss of 32-100 per cent can be caused in cucurbits by melon fruit fly. It can be managed in the farmer's field by suppressing rather than eradicating the flies. As a result of the efforts made by Environmental Protection Agency to reduce the use of harmful insecticides in vegetable crops, the trend has now changed towards Integrated Pest Management (IPM) for control of fruit flies. The development of varieties resistant to fruit fly is an important component of IPM for this pest. Cultivation of fruit fly resistant oriental pickling melon cultivars is limited due to lack of adequate information on the genetic variability and source of resistance (Dhillon *et al*., 2005b).

Therefore, taking into account the importance of the crop in Kerala, severity of damage caused by fruit fly and non-availability of resistant varieties, the present study was undertaken to evaluate oriental pickling melon germplasm for identifying source of resistance for fruit fly, to attempt hybridization to incorporate genes for resistance to fruit fly from wild species to high yielding genotypes and to work out the mechanisms of inheritance of fruit fly resistance. The specific objectives of this study were

1. Selection of superior genotypes with resistance to melon fruit fly in oriental pickling melon
2. Incorporation of resistant genes to melon fruit fly in high yielding genotypes through hybridization.
3. Study the genetics of inheritance of qualitative, quantitative characters and melon fruit fly resistance.

Review of Literature

2. REVIEW OF LITERATURE

Commonly known as cucurbits or gourds, the botanical family Cucurbitaceae includes a number of cultivated species of global or local economical importance. Melons *Cucumis melo* L., are a familiar crop of the gourd family Cucurbitaceae. Melon plants are procumbent vines that thrive on heat and sunshine and are grown in field and gardens throughout the warmer and sunnier part of the world. Available literatures related to "Breeding for resistance to fruit fly (*Zeugodacus* spp.) in oriental pickling melon (*Cucumis melo* var. *conomon* Mak.)" are reviewed in this chapter.

2.1. Species and genetic diversity in melons

The biological variation and technical issues associated with the assessment of diversity in melon, (*Cucumis melo* L.) typify the problems inherent in the germplasm management of cucurbits. Cultivated melon (x=n=12) is horticulturally important, morphologically diverse, out crossing species that belongs to the Cucurbitaceae. As melons differ widely in leaf, vine, plant and fruit characters, *Cucumis melo* is subdivided into *Cucumis melo* subsp. *agrestis* and *Cucumis melo* subsp. *melo*. Truly, wild forms of *Cucumis melo* are found in South of Saharas; only in Eastern tropical Africa (Whitaker and Davis, 1962). Based on different agro ecological regions, climatic patterns, extensive variation in cultivated melon types, its polymorphism in leaf, flower, fruit shape and colour, melons are classified into seven groups (Kirkbride, 1993).

1. *Cucumis melo* var. *cantaloupensis* Naud. - Netted Muskmelon

2. *Cucucmis melo* var. *reticulatus* Ser. – Muskmelon

3. *Cucumis melo* var. *saccharinus* Naud. - Cantaloupe

4. *Cucumis melo* var. *inodorus* Naud. – Winter melon

5. *Cucumis melo* var. *flexuosus* Naud. – Snake melon

6. *Cucumis melo* var. *conomon* Mak. - Oriental pickling melon

7. *Cucumis melo* var. *dudaim* Naud. – Mangomelon

The high polymorphism of fruits in cultivated melon has led botanist to propose different intra specific classification. An excellent, updated and completed study on *Cucumis* genus was undertaken by Kirkbride, Jr. (1993) from the book " Biosystematic Monograph of the genus *Cucumis* (Cucurbitaceae)". It is the corner stone in melon classification. *Cucumis melo* L. is an important horticultural crop across wide areas of the world and their use is extremely diverse depending on the type of fruits (Akashi *et al*., 2002).

India is likely to be a center of origin and center of diversity of melons. Several Indian melon accessions are maintained in major gene banks like USDA and VIR collected during the explorations in India. Among 2276 *Cucumis melo* accessions curated at National Plant Germplasm System (NPGS), 716 (33 per cent) are from India (Roy *et al*., 2012).

2.1.1. Diversity of *Cucumis* species grown in Kerala

Melon (*Cucumis melo* L.) is an important summer vegetable crop in Kerala especially in rice fallows. Melons exhibit variability in fruit, flesh and skin characters, seed cavity space, shelf life and reaction towards pest and disease incidence.

Oriental pickling melon (*Cucumis melo* var. *conomon* Mak.) is one of the melon group in the family Cucurbitaceae. The fruits are small to big in size, smooth surface and white flesh. It is popularly called as golden melon or culinary melon. Its fruit is kept as a symbol of prosperity during the festival of '*Vishu*'. It is an ideal summer vegetable crop chiefly grown for use as fresh vegetable as well as for pickling. It is highly cross pollinated and usually andromonoecious in nature, preferring warm weather and bright sunlight for its better growth and development. Three varieties released from Kerala Agricultural University in oriental pickling melon are Mudicode Local, Arunima, and Saubhagya (Lakshmi *et al.*, 2017).

Snap melon (*Cucumis melo* var. *momordica*) is another melon group in the family Cucurbitaceae. The fruit is flat to round to elongated, fruit skin is smooth and thin, slightly

ribbed. In Kerala snap melon is called as "*Pottu Vellari*" because the skin cracks at the fruit maturity. The flesh is white at maturity with low aroma and flesh is mealy. The sex type is monoecious in nature (Ram, 2014).

Cucumber melon or Acidulus melon (*Cucumis melo* var. *acidulus*) fruits are oval or elliptical, smooth with a green or orange skin colour, uniform or with spots. The flesh is white, very firm and crisp. The plants are monoecious and found mainly in Southern parts of India and Kerala. Vishal is the variety released from Kerala Agricultural University in cucumber melon (Ram, 2014).

2.1.2. Variability and genetic diversity in *Cucumis melo* var. *conomon*.

High heritability accompanied by high genetic advance in oriental pickling melon was reported for first female flowering node, number of fruits per vine, average fruit weight, fruit flesh thickness and total yield per vine (Krishnaprasad *et al*., 2004a). Narrow sense heritability was lower for days to anthesis and number of primary branches in melon (Zalapa *et al*., 2006).

Lakshmi *et al*. (2017) reported significant difference among PCV and GCV in oriental pickling melon for all characters except fruit length, fruit diameter and vine length. Moderate PCV and GCV coupled with moderate heritability and genetic advance over percent of mean was recorded in vine length, fruit length and fruit diameter. Fifteen genotypes were group into five clusters based on relative magnitude of D^2 values.

Sakulphrom *et al*. (2018) reported significant positive correlations among four traits. Fruit width gave the highest correlation with fruit thickness followed by fruit weight and fruit weight with fruit thickness respectively.

2.1.3. The species *Cucumis melo* subsp. *callosus*

Cucumis species is an important genus of cucurbitaceous vegetable crop and is widely grown for their fresh fruits at various stages. *Kachri* non dessert forms of *Cucucmis melo* var. *callosus* is an underexploited drought hardy cucurbit vegetable of Indian Thar

Dessert. *Kachri* is Hindi name; it is also called as Mango melon. This species is widely found as rainy season crop in arid and semi-arid regions of India (Samadia and Pareek, 2000).

Cucumis callosus can be distinguished from other species of the genus by its tuberous tap root, deeply lobed, upward curved strong yellowish green coloured leaf lamina, drooping branches, visibly white long hairy tomentose ovary, U shaped curved pedicel of female flowers brilliant greenish yellow coloured corolla, round or obovoid fruit with ten prominent white longitudinal stripes and thick shining epicarp. It has potential for tolerance to extreme drought, growing and reproducing for many months and resistance to fruit fly and fusarium wilt (John *et al*., 2013).

2.1.4. The species *Cucumis melo* var. *agrestis*

Kirkbride (1993) reported *agrestis* and *melo* as two sub species of *Cucumis melo*. The cultivated subsp *melo* and subsp. *agrestis* a wild form are morphologically closer to each other except for plant and fruit size. *Cucumis melo* subsp. *agrestis* has wild traits like bitterness, small fruit size, long maturity periods, hard flush and has resistance to biotic an abiotic stress (John *et al*., 2013).

2.2. Cross compatibility among *Cucumis melo* species

Cucumis melo ssp. *callosus* and *Cucumis melo* var. *agrestis* are resistant to fruit fly, but there is not much information on transfer of resistant genes from wild species to cultivated melons. For effective gene transfer through conventional breeding, prior knowledge on crossability between wild and cultivated melons is imperative hence their aspects are reviewed here under.

2.2.1. Cross compatibility of *Cucumis melo* with *Cucumis callosus* and *Cucumis agrestis*

Cucumis melo crossed with *Cucumis callosus* as direct cross resulted in 14.73 per cent fruit set and filled with viable seeds. The cross of *Cucumis callosus* and other taxa of

Indian melons resulted in 195 crosses and cross compatibility was observed only in the cross involving different taxa of *Cucumis melo*. Fruit set without viable seeds was observed when *Cucumis callosus* was used as pollen parent with different taxa of *Cucumis sativus*. *Cucumis callosus* falls in the primary gene pool of *Cucumis melo*. However, even with hand pollination at optimum stigma receptivity, direct crosses yielded only 15 per cent fruit set and reciprocal cross with 6 per cent as compared to 65 per cent in case of selfing. Reciprocal crosses with *Cucumis melo* var. *conomon*, *Cucumis melo* var. *momordica* and *Cucumis melo* var. *cantaloupensis* failed to set fruits but *Cucumis melo* var. *maltensis* produced fully developed mature fruits with 232 healthy seeds. No natural hybrids of *Cucumis melo* x *Cucumis callosus* and vice versa were produced when both were grown side by side.

Cross compatibility studies indicated in the primary gene pool of *Cucumis melo* under the broader biological species concept of *Cucumis melo*. F_1 and BC_1 of *Cucumis melo* var. *conomon* and *Cucumis callosus* were found to be fully fertile, the F_1 being intermediate between parents for quantitative traits. *Cucumis melo* when crossed with *Cucumis melo* var. *agrestis* as direct cross, fruit set was 28.21 per cent and filled with viable seeds, while reciprocal cross resulted in 37.24 per cent fruit set and filled with viable seeds (John *et al*., 2013).

2.3. Fruit fly of melons

The dipteran family Tephritidae consists of 4000 species of which 250 species are of economic important and are distributed widely in temperate, subtropical, tropical regions of the world (Christenson and Foote, 1960).

The melon fruit fly is distributed all over the world, but India is considered as its native home. Forty three species have been described under the genius *Zeugodacus*. Among this *Zeugodacus cucurbitae* is major threat to Cucurbits. *Zeugodacus* causes heavy damage to fruits and vegetables in Asia (Nagappan *et al*., 1971).

2.3.1. Nature and extent of damage caused by fruit fly

Melon fruit fly damages over 81 plant species. Based on the extensive surveys carried out in Asia, plants belonging to the family Cucurbitaceae is most preferred by melon fruit fly. The female flies lay the eggs in soft tender fruit tissues of various cucurbits by piercing them with ovipositor. Emerging larvae known as maggots, feed inside the fruits, flowers and stems. Psuedo puntures have also been observed on the skin of fruit which reduces market value of the produce (Doharey, 1983).

The extent of losses varies between 30 to 100 per cent depending on the cucurbit species and the season. Fruit infestation by melon fruit fly in bitter gourd has been reported to vary from 41 to 89 per cent (Rabindranath and Pillai, 1986).

Miyatake *et al*. (1993) studied the extent of damage of melon fruit fly and reported that less than 1 per cent damage by pseudo punctures by the sterile female in cucumber, sponge gourd and bitter gourd. The melon fruit fly has been reported to infest 95 per cent bitter gourd fruits in New Guinea and 90 per cent in snake gourd and 50 to 80 per cent damage in pumpkin fruits in Solomon Islands (Hollingsworth *et al*., 1997).

Singh *et al*. (2000) studied the nature and extent of damage caused by melon flies and reported 31.27 per cent percentage of infestation in bitter gourd and 28.55 per cent in watermelon in India.

2.4. Resistance to melon fruit fly

2.4.1 Resistance in germplasm lines and commercial varieties

Nath, (1966) observed high resistance in bottle gourd genotypes like NB29, moderate resistance genotypes like NB22, NB25 and N28. NS-14 sponge gourd genotype has moderate resistance to fruit fly and pumpkin accessions like IHR35, IHR40, IHR79-2, IHR83 and IIHR86 has high resistance against melon fruit fly.

Pal *et al*. (1984) studied bitter gourd genotypes to melon fruit fly infestation and observed that IHR-89 and IHR-213 are resistant genotypes against melon fruit fly.

Arka Suryamukhi is a resistant source of melon fruit flies infestation and used in the breeding program for pumpkin. Ridge gourd genotypes like NR-2, NR-5 and NR-7 has moderate resistance whereas, Arka Tinda, a round melon variety developed by IIHR showed resistance to melon fruit fly (Mahajan *et al*., 1997).

Ingoley *et al*. (2005) screened 20 cucumber genotypes for fruit fly infestation and reported that genotypes AAUC-2 showed lowest fruit infestation (35.08 per cent) and Sel-75-1-10 recorded highest fruit infestation (81.05 per cent) compared to other genotypes by melon fruit fly.

Gogi *et al*. (2010) screened 13 varieties of bitter gourd for fruit fly infestation and noticed that Col-II (18.70 per cent) and FSD Long (19.30 per cent) showed lowest infestation and categorized as more resistant than other eleven genotypes.

Haldhar *et al*. (2013) studied allelochemical resistance traits of muskmelon to the fruit flies. Eleven genotypes of muskmelon were studied in relation to allelochemical resistance to fruit fly under field condition. They observed significant difference among genotypes for fruit infestation and larval density per fruit. AHMM/BR-1, RM-50 and AHMM/BR-8 were the most resistant, MHY-5, Durgapura Madhu and Pusa Sarbati were moderately resistant, Pusa Madhuras and Arka Jeet were susceptible whereas, Arka Rajhans and GMM-3 were highly susceptible to fruit fly infestation.

Fifteen genotypes of watermelon were studied for various antixenotic and allelochemical traits against *Bactrocera cucurbitae* under field conditions in India. The genotypes Asahi Yamato (12.73 per cent), AHW/BR-16 (15.10 per cent) and Thar Manak (18.27 per cent) were found to be resistant. Durgapura Lal (23.03 per cent), Sugar Baby (26.67 per cent), Arka Manik (34.15 per cent), Charleston Gray (38.70 per cent), AHW-65 (35.80 per cent) and AHW-19 (48.97 per cent) were moderately resistant to fruit fly infestation (Haldhar *et al*., 2015a).

Haldhar *et al*. (2015b) screened 15 genotypes of ridge gourd against melon fruit fly infestation during summer season and observed that AHRG-57, Pusa Nasdar and AHRG-

29 were resistant, AHRG-35, Arka Sujata, AHRG-41, AHRG-36 were moderately resistant.

Twenty four genotypes of oriental pickling melon were screened against melon fruit fly infestation. The lowest infestation was recorded in Sirsi Local (40.00 per cent) followed by BCMCO-01 (41.30 per cent), BCMCO-02 and BCMCO-03 (41.75 per cent) showed moderate resistance to melon fruit fly (Gondi *et al*., 2016).

Nath *et al*. (2017) screened seventy four genotypes of bitter gourd against fruit fly infestation. The lowest fruit fly infestation was recorded in the genotypes IC-248282, Kerala Collection-1, VRBT-4, DRAR-1 and IC-68314 and were categorized in resistant genotypes while 61 genotypes as moderately resistant, five as susceptible and 3 as highly susceptible genotypes.

Haldhar *et al*. (2018) studied 43 snap melon accessions against melon fruit fly infestation. The study was conducted into two stages as preliminary and final screening in summer and rainy seasons. The accessions IC-430190 (11.21 per cent), DKS-AHS 2011/4 (14.97 per cent) and DKS-AHS 2011/3 (18.57 per cent) were found to be resistant genotypes.

2.4.2. Resistance in F_1 hybrids and advanced breeding lines

Sivaprasad, (2013) studied comparative performance of different muskmelon hybrids to fruit fly infestation. Out of eight hybrids studied, the least fruit fly infestation was noticed in the MS-910 (10.60 per cent) and highest in Arka Jeet (25.41 per cent).

Twenty five F_1 hybrids of oriental pickling melon were evaluated against pest and disease. The F_1 hybrids CMC GKVK-2 X CMC GKVK-4, CMC GKVK-3 X CMC GKVK-11 and CMC GKVK-5 X CMC GKVK-13 were moderately resistant to fruit fly infestation (Thyagaraj *et al*., 2013).

Shivaji, (2014) evaluated ten F_1 hybrids of cucumber and their nutrient management under Konkan agro climatic condition. The hybrid Malini, Snow White and Nandini showed resistance and found effective against fruit fly infestation.

Sharma *et al*. (2016) has evaluated fifty five F_1 progenies of cucumber at Palampur and Bajaura locations along with sixteen parents and two standard checks, Pusa Sanyog and Solan Khira Hybrid -1 during summer season. The cross combination, G-1 X K-75 showed resistance to fruit fly infestation at Palampur followed by EC5082 X EC 17393, EC 5082 X K-75 and G-1 X DPC-1 were moderately resistant. Plp X K-pap, G-1 x K-75 and G-3 X K-pap were moderately resistant progenies at Bajaura locations. Progenies of G-3 X Sel-75-2-10 recorded moderate resistance to fruit fly infestation at two locations taken together.

2.4.3. Resistance in wild and semi wild melons

Parthasarathy and Sambandam (1989) reported that *Cucumis melo* ssp. *callosus* is a feral species and wild species to melon, which possesses resistance to fruit fly and leaf eating caterpillers.

Cucumis melo var. *agrestis* is a wild species having resistance to fruit fly, white fly and Melon Yellow Virus (Nuez *et al*., 1999).

Dhillon *et al*. (2005a) revealed high resistance to fruit fly in wild accessions of bitter gourd. The accessions are IC256185, IC 248256, IC213311, IC 248282, and IC 256110. IC 248254, IC 248281 and IC 248292.

2.4.4. Biochemical basis of resistance

Dhillon *et al*. (2005b) reported that ascorbic acid, nitrogen, phosphorus, potassium, protein, reducing sugars, non-reducing sugars and total sugars were negatively correlated while moisture content showed a positive association with fruit fly infestation and larval density per fruit in bitter gourd.

Gogi *et al*. (2010) studied allelochemical compounds in the bitter gourd fruit as resistance to fruit fly infestation. Total chlorophyll and p^H were lowest in resistant and highest in susceptible genotypes. Tannin, flavanol, phenol, ash and silica content were highest in resistant and lowest in susceptible genotypes. Tannin and flavanol content was 96.50 per cent of the total variation in fruit fly infestation and 97.70 per cent of the total variation in larval density per fruit.

The larval density per fruit in muskmelon increased with an increase in percent fruit infestation. Total sugar, non-reducing, reducing sugar and p^H were lowest in resistant in genotypes and highest in susceptible genotypes whereas tannin, phenols, alkaloid and flavonoids content were highest in resistant genotypes and lowest in susceptible (Haldhar *et al*., 2013).

Haldhar *et al*. (2015a) studied antixenotic and allelochemical resistance of watermelon against fruit fly infestation and observed that maximum variation in fruit infestation and larval density was due to length of ovary pubescence (83.60 per cent) followed by fruit length and rind thickness respectively. Phenols, tannins, total alkaloids and flavanoids were highest in resistant and lowest in susceptible genotypes. Flavonoids (88.40 per cent) and total alkaloid contents (92.00 per cent) of the total variation in fruit fly infestation and in larval density per fruit.

The free amino acids (3.36 to 5.77 mg/g) was significantly lower in the resistant and higher in susceptible genotypes. Flavonoids, tannin, phenols, and ascorbic acid were higher in resistant and lower in susceptible genotypes. The free amino acids showed significant positive correlations whereas, flavonoids, phenol, tannin and ascorbic acid had a significant negative correlation to fruit fly infestation in ridge gourd genotypes (Haldhar *et al*., 2015b).

The nitrogen, phosphorus, potassium and protein content showed significant negative correlations with fruit fly infestation. The non-reducing, reducing, total sugars, total phenols, silica and ash content had significant impact on fruit damage and have negative correlations with fruit fly infestation (Nath *et al*., 2017).

Haldhar *et al*. (2017) studied bottom up effect of *Cucumis melo* var. *callosus* against melon fruit fly and reported that the phenols (r= -0.90), tannin (r= -0.88), total alkaloid (r= -0.80) and flavonoids (r=-0.96) had significant negative correlations with percent of fruit fly infestation.

Haldhar *et al*. (2018) reported bottom up effect of snap melon and observed that allelochemical compounds like free amino acid and total soluble solids (TSS) was positive correlations with percent fruit infestation whereas phenols, tannin, total alkaloid and flavonoids content has significant negative correlations with percent fruit infestation.

2.4.5. Biophysical basis of resistance

Fruit length, fruit diameter, number of longitudinal ribs and number of small ridges had significant positive correlations whereas, fruit toughness, depth of small ridges, height of longitudinal ribs and pericarp thickness has negative correlations with percentage of fruit fly infestation and larval density in bitter gourd genotypes (Gogi *et al*., 2009).

Haldhar *et al*. (2015a) reported a negative correlation with length of ovary pubescence, rind hardness (r= -0.86) and rind thickness (r = -0.77) to fruit fly infestation and larval density per fruit in watermelon.

The percentage of fruit infestation and larval density had significant positive correlations with fruit length and diameter and negative correlations with length of ovary pubescence, rind thickness and rind hardness in ridge gourd (Haldhar *et al*., 2015b)

Nath *et al*. (2017) reported that the moisture content had significant positive effect on the fruit damage and number of larvae per fruit. Maximum variation in fruit infestation and larval density was by the length of ovary pubescence (89.50 per cent) followed by rind hardness (4.30 per cent) in *Cucumis melo* var. *callosus* (Haldhar *et al*., 2017a).

The percentage of fruit infestation and larval density of fruit showed positive correlations with the length of ovary pubescence, rind hardness at immature stage, rind hardness at mature stage, pericarp thickness in snap melon genotypes (Haldhar *et al*., 2018).

2.4.6. Anatomical basis of resistance

Am *et al*. (2017) studied varying infestation of fruit fly in different cucurbit crops and reported that fruit fly infestation was more in low tissue firmness in 5 days old snake gourd and lowest infestation was observed in high tissue firmness in 5 days old bottle gourd. More hairs were present in bottle gourd skin compared to snake gourd skin. The fruit fly highly preferred skin hairs and low tissue firmness snake gourd than the bottle gourd fruit.

2.5. Gene action

2.5.1 Gene action for yield attributes.

Zalapa *et al*. (2006) studied generation mean analysis for yield attributes and found that addictive gene effects was most important factor in number of primary branches and number of fruits per plant while dominance and epistatic genetic effect was observed in days to anthesis, fruit weight per plant and average weight per fruit in melons.

The components of gene effects for character related to earliness in sponge gourd were studied based on generation mean analysis for eight diverse genotypes. Non allelic interactions were preponderant for all the characters in majority of the crosses. Earliness in flowering, fruiting as well as number of pickings was governed by dominance and dominance x dominance gene effects and hence these characters can be improved through heterosis breeding (Sanandia *et al*., 2008).

A generation mean analysis study was designed to determine the types of gene action and to estimate the heritability for resistance to downy mildew in four selected crosses of muskmelon. Generation mean analysis revealed that genetic dominance may be of greater importance for expression of resistance to downy mildew in both green house and field experiments in all crosses. High mid parent heterosis in all the crosses indicated strong dominance effects for resistance to downy mildew. Resistance to downy mildew appeared to be controlled mainly by dominance effects and the inbred lines IIHR 122 and IIHR 122 could be used strategically to exploit heterotic effects (Shashikumar *et al*., 2010)

Kumar and Wehner (2013) studied quantitative inheritance in water melon for fruit characters. Multiple genetic factors were involved in controlling fruit yield and fruit size. Additive effects were moderate for fruit yield and fruit size in water melons.

The genetic control of fruit shape, sex expressions, gelatinous sheath around the seeds, sutures, number of placenta and white flush in musk melons were determined by recessive genes (Pitrat, 2013a).

An experiment was carried out to study the nature and magnitude of gene effects for yield and yield attributing traits in bitter gourd by generation mean analysis. The results revealed the presence of additive x dominance gene effects and epistatic interactions for all the characters except for vine length in cross IC-470550 x IC-470558. The greater magnitude of dominance gene effects as compared to additive effect for the traits suggested that the heterosis breeding may be more useful. Bi-parental mating which could exploit both additive and non-additive gene effects were appropriate for the improvement of bitter gourd traits (Rani *et al*., 2013).

The mechanism of inheritance of yield and fruit fly resistance studied by various author Patil *et al*. (2014). The magnitude of dominance effects was high in all crosses for traits *viz*., number of female flowers, days required for first harvest of fruits, number of fruits per vine, yield per vine and weight of fruit.

Chlorophyll *b* content in bitter gourd was governed by additive gene for the trait fruit color (Huang and Hsieh, 2017).

A study was done to determine the types and magnitude of gene effects and heritability for yield and physiological traits in melon (*Cucumis melo* L.). The results indicated that additive gene effects were significant for fruit length, seed length and TSS. The significant additive and dominance effects were observed in fruit diameter, fruit length/diameter ratio, flesh and skin thickness. Additive x additive gene effects were significant for all the characters while dominance x dominance significant effects were observed for flesh thickness, skin thickness and TSS (Javanmard *et al*., 2018)

Sakulphrom *et al*. (2018) studied genetic effects of fruit characters in musk melon. The results showed that both additive and dominance effects governed fruit weight, fruit length, fruit width and fruit thickness.

Generation mean analysis was carried out in infra-specific cross combinations of muskmelon x snap melon using five generations. Profound influence of dominance effects were observed in traits like polar circumference of fruit, flesh thickness, pedicel length and fruit weight, while additive effect was prevalent in equatorial circumference of fruit, TSS, number of fruits per plant and yield per plant. Among the interactions, dominance x dominance was predominant over additive x additive for all traits. Fruit flesh colour showed dominant and external striped epicarp showed recessive inheritance (Singh *et al*., 2018).

2.5.2. Gene action for fruit fly resistance

Khandelwal and Nath (2011) studied inheritance of resistance to fruit fly in watermelon and revealed that fruit fly resistance was controlled by single dominant gene.

Kumar *et al*. (2018) reported non additive gene action governing all of the traits except fruit fly incidence in cucumber.

Thakur *et al*. (2019) studied gene action in cucumber for different biotic stress. Studies indicated that biotic stresses were governed by additive gene action.

Materials and Methods

3. MATERIALS AND METHODS

The present study entitled "Breeding for resistance to fruit fly (*Zeugodacus* spp.) in oriental pickling melon (*Cucumis melo* (L.) var. *conomon* Mak.)" was carried out at the Department of Vegetable Science, College of Horticulture, Vellanikkara from 2015 to 2018. The experimental area was located at 10° 32' N latitude and 76°16 'E longitude and an altitude of 23m above M. S. L. The site experienced a typical warm humid tropical climate, received an average rainfall of 2663 mm per year. The soil was laterite with sandy clay loam texture and acidic in nature.

3.1. EXPERIMENTAL MATERIALS

The experimental materials comprised of 56 genotypes in which 53 accessions of oriental pickling melon collected from the farmers' field, three released varieties of KAU and three wild species of *Cucumis* resistant to fruit fly *viz, Cucumis melo* spp. *callosus, Cucumis melo* var. *agrestis* (W-10) and *Cucumis melo* var. *agrestis* (W-51) (Table.1)

Table 1. Sources of oriental pickling melon genotypes

Sl.No.	Name of Genotype/Accessions	Source
1	CM001	Peruvayal, Kozhikode, Kerala
2	CM002	Koyilandi, Kozhikode, Kerala
3	CM003	Velliparambu, Kozhikode, Kerala
4	CM004	Peruvayal, Kozhikode, Kerala
5	CM005	Koyilandi, Kozhikode, Kerala
6	CM006	Panagad, Kozhikode, Kerala
7	CM007	Peruvayal, Kozhikode, Kerala
8	CM008	Peruvayal, Kozhikode, Kerala
9	CM009	Peruvayal, Kozhikode, Kerala
10	CM010	Kuttikatoor, Kozhikode, Kerala
11	CM011	Peruvayal, Kozhikode, Kerala

12	CM012	Panagad, Kozhikode, Kerala
13	CM014	Peruvayal, Kozhikode, Kerala
14	CM015	Panagad, Kozhikode, Kerala
15	CM016	Peruvayal, Kozhikode, Kerala
16	CM017	Koyilandi, Kozhikode, Kerala
17	CM018	Perambra, Kozhikode, Kerala
18	CM019	Eravattor, Kozhikode, Kerala
19	CM020	Eravattor, Kozhikode, Kerala
20	CM022	Vatakara, Kozhikode, Kerala
21	CM023	Cheruvannur, Kozhikode, Kerala
22	CM024	Cheruvannur, Kozhikode, Kerala
23	CM025	Cheruvannur, Kozhikode, Kerala
24	CM028	Cheruvannur, Kozhikode, Kerala
25	CM032	Bangalore, Karnataka
26	CM033	Bangalore, Karnataka
27	CM034	Thrissur, Kerala
28	CM035	Indosum Cucumber Yellow Round
29	CM036	Indosum cucumber RNSM-1
30	CM037	Perambra, Kozhikode,Kerala
31	CM038	Cheruvannur, Kozhikode,Kerala
32	CM039	Cheruvannur, Kozhikode,Kerala
33	CM040	Cheruvannur, Kozhikode,Kerala
34	CM042	Perambra Kozhikode,Kerala
35	CM043	Paithoth, Kozhikode,Kerala
36	CM044	Paithoth, Kozhikode,Kerala
37	CM045	Perambra, Kozhikode,Kerala
38	CM046	Perambra, Kozhikode,Kerala
39	CM047	Perambra, Kozhikode,Kerala

40	CM048	Thrissur, Kerala
41	CM049	Thrissur, Kerala
42	CM050	Thrissur, Kerala
43	CM051	Thrissur, Kerala
44	CM052	Thrissur, Kerala
45	CM053	Thrissur, Kerala
46	CM055	Thrissur, Kerala
47	CM056	Thrissur, Kerala
48	CM057	Thrissur, Kerala
49	CM058	Thrissur, Kerala
50	CM059	Thrissur, Kerala
51	CM060	Arunima- KAU Variety
52	CM061	Mudicode local –KAU Variety
53	CM062	Saubhagya- KAU Variety
54	*Cucumis melo* spp. *callosus*	NBPGR, Thrissur
55	*Cucumis melo* var. *agrestis* (W-10)	NBPGR, Thrissur
56	*Cucumis melo* var. *agrestis* (W-51)	NBPGR, Thrissur

3.2. Cataloguing of oriental pickling melon accessions:

Fifty three accessions of oriental pickling melon and three species of *Cucumis* were catalogued based on Minimal Descriptor of Vegetable Crops- *Cucumis melo* (L.), NBPGR (2000) as shown in Table.2.

Table 2. Cataloguing of oriental pickling melon accessions

Sl.No.	Characters	Description
1	Flower colour	White/Cream/Yellow
2	Stem hairiness	Absent/Present
3	Fruit shape	Globular/Flattened/ Oblate/ Elliptical/ Pyriform /Ovate /Elongate
4	Fruit colour at maturity	Yellow/Orange
5	Skin surface	Smooth/ Cracked
6	Skin hardness	Soft/ Intermediate/ Hard
7	Skin texture	Plain/Striped/ Dotted
8	Taste of fruit	Sour/ Sweet/ Bitter
9	Flesh colour	White/ Green/ Light orange/ Greenish orange/ Orange
10	Flesh texture	Crispy/ Intermediate/ Soft
11	Flesh flavor	Mild/Moderate/ Strong
12	Seed colour	White/Cream/ Light brown

3.3. METHODOLOGY

3.3.1. Field experiments

The investigations in the present study were divided into two experiments namely Experiment 1 and Experiment 2.

Experiment 1 consisted of evaluation of oriental pickling melon accessions based on divergence analysis for qualitative and quantitative characters, bitterness, resistance to melon fruit fly and selection of high yielding and melon fruit fly resistant genotypes for hybridization.

Experiment 2 consisted of incorporation of resistance to melon fruit fly into high yielding accessions through hybridization; generation of six generations and evaluation of six generations to elucidate inheritance of characters.

3.3.1.1 Experiment1: Field screening of oriental pickling melon accessions to identify resistance source(s) for *Zeugodacus* spp.

Evaluation of 53 oriental pickling melon accessions was done based on divergence analysis for qualitative and quantitative characters, bitterness and resistance to melon fruit fly during March 2016 - May 2016 to select high yielding, non-bitter, as well as melon fruit fly resistant genotypes for hybridization. Fifty three oriental pickling melon accessions were raised in the field in two replications in Randomized Complete Block Design (RBD) at a spacing of 2.0 m x1.5 m in a plot size of 24.0 m. sq maintaining nine plants per plot (Plate1). All crop management practices were undertaken as per the Package of Practices Recommendations–Crops, KAU, (2016). No plant protection practices were undertaken during the crop period. The crop was left for natural infestation by melon fruit fly. Observations were recorded from five plants per replication in each accession. Qualitative and quantitative data were recorded as per the Minimal Descriptor of Vegetable Crops-*Cucumis melo* (L.), NBPGR (2000). Observations on melon fruit fly infestation was recorded as detailed by Nath (1966).

3.3.1.2. Confirmation of field resistance to melon fruit fly in oriental pickling melon accessions

Evaluation of 53 oriental pickling melon accession were done in two more seasons to confirm the field resistance of accessions to melon fruit fly infestation. Fifty three oriental pickling melon accessions were raised in the field using two replications in Randomized Complete Block Design (RCBD) at a spacing of 2.0 m x1.5 m in a plot size of 24.0 m sq. maintaining nine plants per plot during September 2016 - November 2016 and March 2017- May 2017. All crop management practices were undertaken as per the Package of Practices Recommendations–Crops, KAU, (2016). No plant protection practices were undertaken during the crop period. The crop was left for natural infestation

Plate.1. Field view of oriental pickling melon accession

by melon fruit fly and fruits were allowed to remain on the plant till ripening to allow prolonged exposure to fruit fly infestation. Data on infestation of melon fruit fly was recorded (Nath, 1966). The pooled mean data of three seasons were considered for statistical analysis to find out the seasonal variations in melon fruit fly infestation, to confirm field resistance to melon fruit fly infestation.

3.3.1.3: Experiment 2: Hybridization to incorporate melon fruit fly resistance into high yielding accessions

Eight high yielding accessions (CM022, CM033, CM045, CM047, CM051, CM060, CM061 and CM062) from experiment 1 were selected as female parents for hybridization programme. Three wild species of *Cucumis* (*Cucumis melo* ssp. *callosus, Cucumis melo* var. *agrestis* (W-10) *Cucumis melo* var. *agrestis* (W-51) which were known sources of resistance to melon fruit fly and one accession CM033 which was found resistant to melon fruit fly from the Experiment 1 were selected as male parents for hybridization programme (Table 3).

Table 3. Female and male parents used in hybridization

Sl. No.	**Female parents**	**Status**	**Remarks**
1	CM022	Cultivated	High yielding
2	CM033	Cultivated	Resistant to fruit fly
3	CM045	Cultivated	High yielding
4	CM047	Cultivated	High yielding
5	CM051	Cultivated	High yielding
6	CM060	Cultivated	KAU variety
7	CM061	Cultivated	KAU variety
8	CM062	Cultivated	KAU variety
	Male parents	**Status**	**Remarks**
1	CM033	Cultivated	Resistant to fruit fly
2	*Cucumis melo* var. *agrestis* (W-51)	Wild species	Resistant to fruit fly
3	*Cucumis melo* var. *agrestis* (W-10)	Wild species	Resistant to fruit fly
4	*Cucumis melo* ssp. *callosus*	Wild species	Resistant to fruit fly

3.3.1.4. Evaluation of F_1's and generation of F_2, B_1 and B_2

Forty three genotypes (31 F_1's and 12 parents) were raised in the field during September - November 2017 in a Randomized Complete Block Design (RCBD) with three replications at a spacing of 2.0 m x1.5 m in a plot size of 24.0 m. sq. maintaining nine plants per plot. All the crop management practices were done as per the Package of Practices Recommendations-Crops, KAU (2016) (Plate 2). No plant protection practices were undertaken during the crop period. The crop was left for natural infestation by melon fruit fly. Five plants per replication in each genotype were tagged for recording observations. Number of fruits, fruit yield, bitterness and melon fruit fly infestation were recorded from entire plant population. Qualitative and quantitative data were recorded as per the Minimal Descriptor of Vegetable Crops- *Cucumis melo* (L.), NBPGR (2000) from all the F_1's. Based on the mean performance of F_1's , four high yielding F_1's with resistance to fruit fly and absence of bitterness were selfed as well as backcrossed to their respective female parent (P_1) and male parent (P_2) to generate F_2, B_1 and B_2 generations.

3.3.1.5. Evaluation of P_1, P_2, F_1, F_2, B_1, and B_2, generations

Six generations of four high yielding F_1's (Table 4) were raised during September 2018- December 2018 in Randomized Complete Block Design with three replications as per Package of Practices Recommendations-Crops, KAU (2016) at a spacing of 2.0 mx1.5 m maintaining nine plants per plot in P_1, P_2, F_1,B_1 B_2, and 36 plants per plot in F_2 generation (Plate 3). No plant protection practices were undertaken during the crop period and the crop was left for natural infestation by melon fruit fly. Data on qualitative, quantitative characters, bitterness and melon fruit fly infestation were recorded from five randomly selected plants per replication of P_1, P_2, F_1's, B_1's, B_2's and from 20 plants of F_2's. The data was analyzed for significance of means to test the difference among six generations and generation mean analysis was executed to elucidate inheritance.

Plate 2. Field view of F_1 generations of oriental pickling melon

Plate 3. Field view of six generations of oriental pickling melon

Table 4. Selected F_1s for generation mean analysis

Sl. No.	Cross	Name of cross
1	CM045 X CM033	Cross I
2	CM061 X CM033	Cross II
3	CM051 X *Cucumis melo* ssp. *callosus*	Cross III
4	CM033 X *Cucumis melo* ssp. *callosus*	Cross IV

3.3.2. Laboratory and Screen house studies for confirmation of resistance to melon fruit fly

3.3.2.1. Mass rearing of *Zeugodacus cucurbitae* in the laboratory

Mass rearing of melon fruit fly was done in the Pesticide Residue Testing Laboratory of Department of Agricultural Entomology, College of Horticulture, Vellanikkara for identification of different species of fruit fly infesting oriental pickling melon and for confirmation of melon fruit fly resistance. Melon fruit fly infested ten fruits of oriental pickling melon were collected randomly from the experimental field from all replications during the crop season. The infested fruits having live maggots inside were brought to the laboratory and kept inside the plastic bottles/ polythene bag containing a layer of clean and moist sand/soil at the bottom to facilitate pupation of mature maggots. The infested fruits were kept above the sand/ soil; plastic bottles/ polythene bag were covered with muslin cloth as applicable, tied tightly using twine (Plate 4). The bottles were regularly observed for emergence of melon fruit flies (Plate 5).

3.3.2.2. Identification of *Zeugodacus* spp.

After emergence, fruit flies were collected, preserved in the 10 per cent alcohol solution for identification at species level. The preserved fruit flies were sent to the ICAR

Plate 4. Mass rearing of melon fruit flies

Plate 5. Emergence of fruit flies

- National Bureau of Agricultural Insect Resources (NBAIR), Bengaluru for identification of different species of fruit fly infesting oriental pickling melon in the field (Plate 6).

3.3.2.3. No choice assay for confirmation of resistance to melon fruit fly

Resistance to melon fruit fly was confirmed by using no choice assay in cage condition in the Pesticide Residue Testing Laboratory, Department of Agricultural Entomology, College of Horticulture, Vellanikkara. Mature fruits of each resistant accession(s) having uniform size collected from the field were kept inside the cage having three sided wire mesh and a glass door (Plate 7). Five pairs of adult male and female melon fruit flies reared from infested fruits, fed with sugar and jaggary solution and allowed random mating were released inside the cage having fresh fruits. Adults were fed with yeast and jaggery solutions inside the cage and allowed for ovi-position. The adults were allowed to lay eggs till their life span is completed. The observations were recorded on number of fruit flies emerged from the caged fruits.

3.3.2.4. Biochemical studies for confirmation of resistance to melon fruit fly

Fruit samples of six generations of the selected four crosses (Cross I, Cross II, Cross III and Cross IV) were analyzed for total soluble solids (TSS), acidity, total sugars, total soluble sugars, crude protein, total phenols, tannin and silica at the Department of Soil Science and Agricultural Chemistry, College of Horticulture, Vellanikkara (Plate 8). Correlations were worked out to find out the biochemical basis of resistance to melon fruit fly.

3.3.2.5. Anatomical studies for confirmation of resistance to melon fruit fly

Anatomical studies were carried out at the Department of Forest Products and Utilization, College of Forestry, Kerala Agricultural University using Electron Microscope. Transverse sections of matured fruit skin of resistant and susceptible genotypes were stained. The stained sections were observed for skin thickness under Electron Microscope and were micro- photographed using a microscope attached with image analyzer.

Plate 6. Fruit flies preserved in alcohol solutions

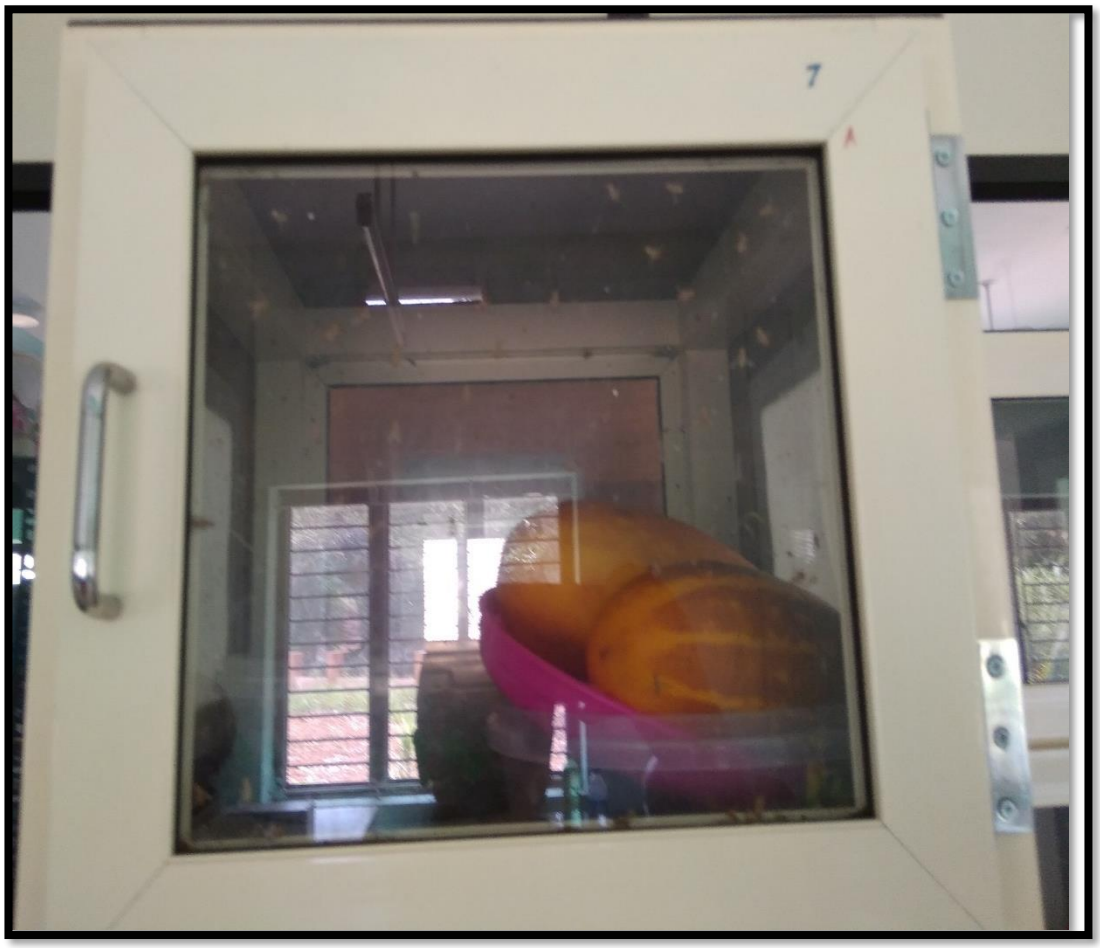


Plate 7. Confirmation study to fruit fly resistance

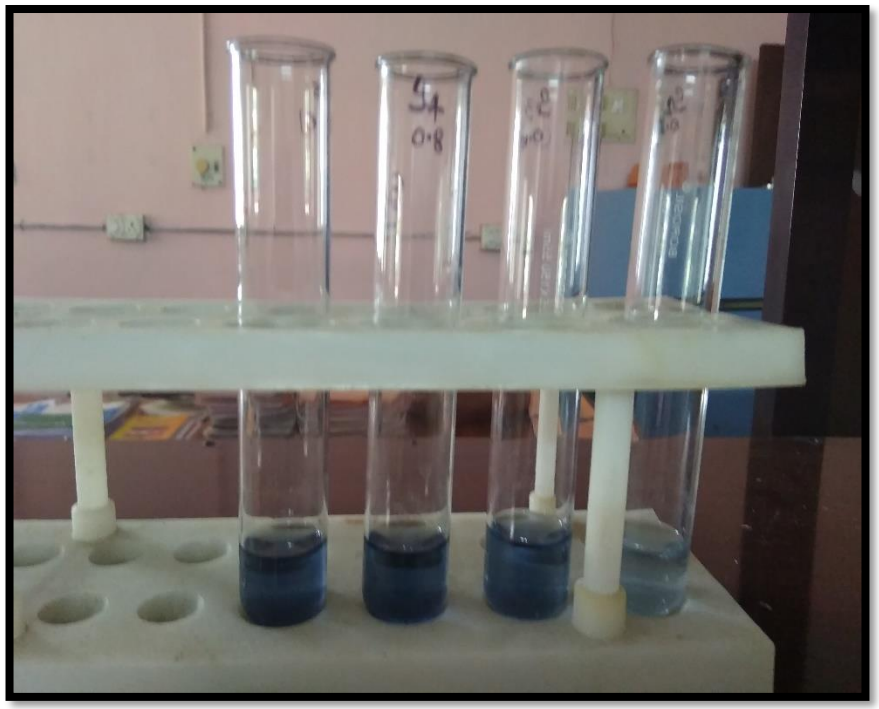


Plate 8. Biochemical analysis

3.4. COLLECTION OF EXPERIMENTAL DATA

Morphological (qualitative, quantitative) and biochemical data of oriental pickling melon genotypes were collected for further analysis. Morphological data were recorded from field the experiments conducted at the Department of Vegetable Science, College of Horticulture, Vellanikkara as per Minimal Descriptor of Vegetable Crops- *Cucumis melo* (L.), NBPGR (2000). Biochemical data were recorded from laboratory studies conducted at the Department of Soil Science and Agricultural Chemistry, College of Horticulture, Vellanikkara.

3.4.1. Morphological characters

3.4.1.1. Days to first female flower production:

Number of days taken from planting to first female flower opening was counted and recorded as an average of five plants per replication.

3.4.1.2. Days to first male flower production:

Number of days from planting to first male flower opening was counted and recorded as an average of five plants per replication.

3.4.1.3. Node of first female flower:

Number of nodes were counted from the first one to the node at which the first female flower emerged and recorded as average of five plants per replication.

3.4.1.4. Node of first male flower:

Numbers of nodes were counted from the first one to the node at which the first male flower emerged and recorded as average of five plants per replication.

3.4.1.5. Vine length (cm):

Length of vine was measured from first cotyledonary node to the tip of the main vine at the phage end of the crop from randomly selected five plants using a tape and expressed in centimeters.

3.4.1.6. Inter nodal length (cm):

Inter nodal length is measured from tip, middle and bottom of five randomly selected plants during the final harvest and the average is expressed in centimeters.

3.4.1.7. Number of branches per plant:

Number of branches arising from the main stem were counted from five randomly selected plants per replication and average was recorded as number of branches.

3.4.1.8. Fruit diameter (cm)

Fruit diameter was recorded from the cross section of five fruits from five randomly selected plants per replication and mean value is expressed in centimeters.

3.4.1.9. Fruit girth (cm)

Fruit girth was recorded at the widest portion of five matured fruits from five randomly selected plants per replication and mean value was expressed in centimeters.

3.4.1.10. Fruit length (cm):

Length of fruits from the point of pedicel attachment to apex was measured from five fruits from five randomly plants per replication and the average was recorded in centimeters.

3.4.1.11. Fruit weight (g):

Fruit weight of five fruits from five randomly selected plants per replication was measured and the average was expressed in grams.

3.4.1.12. Fruit rind thickness (cm):

Fruit rind thickness was measured from the flesh to outer skin using scale from five fruits of five randomly selected plants per replication and the average value was expressed in centimeters.

3.4.1.13. Flesh thickness (cm):

Flesh thickness was measured from inner region of rind to the outer region of seed cavity using scale from five fruits of five randomly selected plants per replication and the average was expressed in centimeters.

3.4.1.14. Seed cavity length (cm):

Length of the seed cavity was measured from pedicel end to the stylar end from five fruits of randomly selected five plants per replication using a scale and the average was expressed in centimeters.

3.4.1.15. Seed cavity breadth (cm):

Width of the cavity was measured from five fruits of five randomly selected plants per replication using a scale and the average was expressed in centimeters.

3.4.1.16. Seed length (cm):

Length of the seed was measured from ten seeds of fruits from five randomly selected plants per replication from tip to end and the average was expressed in centimeters.

3.4.1.17. Number of seeds per fruit:

Number of healthy seeds present in five fruits randomly selected five plants of each replication was counted and the average was expressed as number.

3.4.1.18. Number of fruits per plants:

Number of fruits from five randomly selected plants per replication was recorded and average was recorded as cumulative number of fruits per plant.

3.4.1.19. Days taken for fruit maturity:

Ten flowers were randomly tagged on the day of anthesis, days taken to attain physiological maturity was counted. Days taken for fruit maturity was recorded as average number of days for ten fruits of randomly selected plants per replication and recorded as average number of days.

3.4.1.20. Days to first harvest:

Number of days from planting to first fruit harvest was counted for five fruits and recorded as average of five plants per replication.

3.4.1.21. Days to last harvest:

Number of days from planting to last fruit harvest was counted from five randomly selected plants per replication and recorded as average number of days.

3.4.1.22. Yield per plant (kg):

Total weight of fruits harvested from five plants of each accession per replication was computed as average and expressed in kilograms.

3.4.1.23. Marketable fruit yield (kg):

Weight of healthy fruits was divided by total weight of fruits (healthy + damaged) from five plants and expressed in kilogram

3.4.1.24. Days to fruit fly infestation after anthesis

Ten flowers were tagged on the day of anthesis. Days taken from fruit set to the initiation of fruit fly infestation on fruits of five plants were counted and expressed as average number of days.

3.4.1.25. Percentage of fruit fly infestation:

Percentage of fruit fly infestation was calculated by counting the total number of infested fruits to the total number of fruits from five randomly selected plants and expressed as percentage.

$$\text{Percentage of fruit fly infestation} = \frac{\text{Total number of infested fruits}}{\text{Total number of fruits}} \times 100$$

Reaction of oriental pickling melon accessions to fruit fly infestation was recorded from fruit set onwards. Incidence was recorded based on 1-6 scale for grading the percentage of fruit damage (Nath, 1966) as given in the Table 5.

Table. 5. Scales for grading the percentage of fruit damage

Scale	Fruit damage (per cent)	Rating
1	Nil	Immune
2	1-10	Highly resistant
3	11-20	Resistant
4	21-50	Moderately resistant
5	51-75	Susceptible
6	76-100	Highly susceptible

3.4.1.26. Incidence of pest and disease:

Observations on occurrence of pest and disease were recorded throughout the period of crop growth and expressed as percentage.

3.4.1.27. Incidence of different species of fruit fly:

Various species of fruit fly attacking oriental pickling melon were recorded by collecting infested fruits and melon fruit flies were reared under laboratory condition using infested fruits. The adults emerged were collected, stored in alcohol solution (10 per cent) and identified at species level at ICAR- NBAIR, Bengaluru

3.4.2. Sensory evaluation

Sensory attributes namely, colour, flavour, texture, taste, after taste and overall acceptability were recorded over a nine point hedonic scale (Amerine *et al*., 1965) from fresh mature and cooked fruits of six generations of selected four crosses. Sensory attributes were evaluated by a panel of 20 semi –trained judges and expressed as scores converted to ranks (Appendix 1).

3.4.3. Biochemical characters

Biochemical characters of six generations (P_1, P_2, F_1, F_2, B_1 and B_2) were analyzed from a composite sample made of three fruits from randomly selected three plants per replication in each generation**.**

3.4.3.1. Total Soluble Solids (TSS)

Total Soluble Solids constitutes 80-85 per cent of sugars. Juice from fruits were collected, mixed thoroughly, a representative sample is put on the prism of refractometer and TSS is read directly by noting the line that separated light and dark region on the scale of refractometer and represented as degree Brix (^{o} Brix).

3.4.3.2. Acidity

Acidity of oriental pickling melon samples were determined by acid titration method. A representative sample was made by grinding samples of three fruits collected from three plants per replication.

Reagents: Phenolphthalein, 0.1N sodium hydroxide solution.

Procedure: From the representative sample, 10 g of fruit pulp was weighed out, mixed with 100 ml distilled water, heated on a water bath to dissolve the pulp for 30 min. Cooled, filtered and transferred the aliquot into 250 ml standard flask, made up the volume. Pipetted out 30 ml of fruit sample into a conical flask, diluted with equal amount of distilled water. Added one or two drops of phenolphthalein indicator and titrated against 0.1N sodium hydroxide solution taken in a burette. Appearance of pink colour was taken as the end point and the titre value was noted by checking the lower meniscus level of sodium hydroxide solution in the burette. Acidity is expressed in percentage.

$$\text{Acidity} = \frac{\text{Titre value x Normality of alkali x Equivalent weight of acid x Volume made upto x100}}{\text{Weight of sample x volume pipetted out}}$$

3.4.3.3. Total sugar

Total sugars were estimated by Anthrone method suggested by Sadasivum and Manickam (2008).

Reagents: (1) 2.5 N HCl, (2) Anthrone reagent: Dissolved 200 mg anthrone in 100 ml of ice-cold 95 per cent H_2SO_4. Prepared fresh before use. (3) Standard glucose: Dissolved 100 mg standard glucose in 100 ml water to prepare stock solution. Prepared working standards by diluting 10 ml of stock solution to 100 ml with distilled water. Stored refrigerated after adding a few drops of toluene.

Procedure: Weighed out 100 mg of fruit sample into a boiling tube. To hydrolyze the fruit sample, added 5 ml of 2.5 N HCl, the sample was kept on a boiling water bath for three hours and then cooled to room temperature. Sample was neutralized with solid sodium carbonate until the effervescence ceased. Sample volume was made up to 100 ml and centrifuged. Supernatant was collected and 1.0 ml aliquot was used for analysis. Working standards were prepared by 0.0, 0.2, 0.4, 0.6, 0.8 and 1.0 ml of the working solution, 0 served as the blank. Volume of the working standards and sample test tubes were made up the volume to 1.0 ml by adding distilled water. To all test tubes 4.0 ml of anthrone reagent was added. Then standards and samples were placed on a boiling water bath for 8 minutes

until the dark green colour obtained. Cooled rapidly and absorbance was read at 630 nm in spectrophotometer. A standard graph was drawn to plot the sugar content in the sample by plotting the concentration of working standards on 'x' axis and the absorbance on the 'y' axis.

3.4.3.4. Total soluble sugar

Total sugars was estimated by Anthrone method suggested by Sadasivum and Manickam (2008).

The procedure, reagents and the calculation were the same as detailed in 3.4.3.3.

3.4.3.5. Crude protein

Crude protein was estimated by Lowry's method suggested by Sadasivum and Manickam (2008).

Reagent A:2 per cent Sodium carbonate in 0.1N Sodium hydroxide

Reagent B: 0.5 per cent Copper sulphate ($CuSO_4.5H_2O$) in 1.0 per cent Potassium sodium tartarate solution

Reagent C: Alkaline copper solution: Mixed 50.0 ml of reagent A and 1.0 ml reagent B prior to use.

Reagent D: Folin Ciocalteau reagent

Protein solution (Stock Standard): Weighed 50 mg of Bovine Serum Albumin (BSA)and dissolved in 0.1 N NaOH and made up the volume to 50 ml in a standard flask.

Working standard: Diluted 10 ml of BSA stock solution to 50 ml with 0.1N NaOH in a standard flask.

Oriental pickling melon fruit sample (0.5 g) was ground well using mortar and pestle with 5-10 ml of phosphate buffer. Centrifuged the sample at 1000 rpm for 10 min., the supernatant was collected for the protein estimation.

Working standards of bovine serum albumin (BSA) of 0.2, 0.4, 0.6, 0.8 and 1.0 ml were pipetted out in a series of test tubes. Sample extract (0.2 ml) was pipetted in another test tube and made up volume to 1.0 ml using distilled water. To all test tubes including blank, 5 ml of Reagent C was added. It was well mixed and made to stand for 10 min. After 10 min., added 0.5 ml of reagent D, mixed well and incubated at room temperature in the dark for 30 min. until the blue colour obtained. The absorbance was read at 660 nm in spectrophotometer. A standard graph was drawn to plot the protein content in the sample by plotting the concentration of working standards on 'x' axis and the absorbance on the 'y' axis.

3.4.3.6. Total phenols

Method suggested by Sadasivam and Manickam (2008) was used to estimate the content of total phenols in the fruit samples.

Reagents (1**)** Folin –Ciocalteau reagent (2) Sodium carbonates (20 per cent) Standard phenol: Dissolved 100 mg catechol in 100 ml water.

Working standard: 10 ml of stock solution diluted to 100 ml distilled water.

Phenols are highly soluble in water as well as in alcohol. Eighty percent (80 per cent) ethanol was employed for efficient extraction of phenols. The sample extract was prepared by blending 0.25 g of fresh fruit sample in 10 times volume of 80 per cent ethanol. The sample was centrifuged at 5000 rpm for 10min. The supernatant was collected and made the volume to 10 ml using distilled water.

Working standards of 0.2, 0.4, 0.6, 0.8, 1.0 ml and sample extract of 0.2 ml were pipetted in a series of test tubes. Each test tubes volume was made to 3 ml using distilled water and mixed it thoroughly. Then to each test tubes 0.5 ml of Folin –Ciocalteau reagent was added and kept for 5 min. After 5 min., 2.0 ml of 20 per cent sodium carbonate was added. All the test tubes were placed on a boiling water bath for one minute. Test tubes were cooled and absorbance was read at 660 nm after 30 min. To find out the phenol content in the

sample, a standard graph was drawn by plotting the concentration of standards on ‘x’ axis and absorbance on ‘y’ axis.

3.4.3.7. Tannins

Tannins content in the samples were estimated as per the method suggested by Sadasivam and Manickam (2008).

Reagents: (1) Folin-Denis Reagent: 100 g sodium tungstate, 20 g phosphomolybdic acid, 50 ml phosphoric acid and 750 ml distilled water. Allowed this mixture to reflux for 2 hour and made up to one litre and protected from exposure to light. (2) Sodium carbonate solution: dissolved 350 g sodium carbonate in one litre of water at 70-80ºC. Filtered through glass wool after allowing it to stand overnight. (3) Standard tannic acid solution: dissolved 100 mg of tannic acid in 100 ml of distilled water.

Working standard solution: Diluted 5 ml of stock solution to 100 ml with distilled water.

To extract tannins from fruit samples, 0.25 g of fresh fruit sample was weighed and transferred to 50 ml conical flask. Added 10 ml distilled water to the conical flask and heated gently for 30 min. Cooled the conical flask and transferred the contents to a centrifuge tube and centrifuged at 5000 r.p.m. for 20 min. Collected the supernatant and made up the volume to 10 ml using distilled water.

Working standards of 0.2, 0.4, 0.6, 0.8, 1.0 ml and 0.2 ml of fruit of samples were pipetted out in a series of test tubes and volume is made up to 8.5 ml using distilled water. Then added 0.5 ml of Folin-Denis reagent to all test tubes, 1.0 ml of sodium carbonate solution. Shaked well the test tubes and the absorbance was read at 700 nm after 30 min. To find out the tannins content in the sample a standard graph was drawn by plotting the concentration of standards on ‘x’ axis and absorbance on ‘y’ axis.

3.4.3.8. Silica

Silica content of fruit skin samples were determined as per the procedure suggested by Ma *et al*., (2002).

Reagents: (1) Concentrated Nitric acid (2) Concentrated Hydrogen peroxide (3) Concentrated Hydrogen fluoride (4) Boric acid 4 per cent (5) 0.1N Hydrochloric acid (6) Ammonium molybdate 20 (7) 20 per cent Tartaric acid (8) ANSA (1-amino -2-napthol-4-sulfonic acid).

Silicon standard: From 1000 ppm stock solution, 20 ppm of working standard solution was prepared. Silicon standards (0.2, 0.4, 0.8, 1.2 and 1.4 ml) were prepared and were added with the reagents.

Procedure: 0.25 g of fruit skin sample was weighed out and 10 ml of concentrated nitric acid was added to get fruit skin sample digested. After digestion samples were diluted and made up the volume to 100 ml using distilled water. For the estimation of silica, an aliquot of 0.25 ml fruit skin sample was taken in a centrifuge tube, 3.75 ml of 0.2 N hydrochloric acid was added. After that 0.5 ml of 10 per cent ammonium molybdate solution, 0.5 ml of 20 per cent tartaric acid was added to the sample. Then 0.5 ml of reducing agent ANSA (1-amino-2-napthol-4-sulfonic acid) was added. After adding all these reagents, the sample volume was made to 12.5 ml. After one hour, following the addition of reducing agent absorbance was measured at 600 nm using UV visible spectrophotometer. To find out the silica content in the fruit skin sample, a standard graph was drawn by plotting the concentration of standards on ‘x’ axis and absorbance on ‘y’ axis.

3.5. STATISTICAL ANALYSIS

3.5.1. Analysis of variance

Data on quantitative characters were analyzed for variance and significance of treatments. Statistical analysis was done using OPSTAT software and treatments were compared using C.D. value.

3.5.2. Variability and Heritability studies

3.5.2.1. Phenotypic and genotypic coefficients of variation

The phenotypic and genotypic co-efficient of variation were calculated as per the formula of Burton (1952).

$$\text{Phenotypic coefficient of variation (PCV)} = \frac{\text{Phenotypic standard deviation}}{\text{Grand mean}} \times 100$$

$$\text{Genotypic coefficient of variation (GCV)} = \frac{\text{Genotypic standard deviation}}{\text{Grand mean}} \times 100$$

The estimates of PCV and GCV were categorized based on the scale given by Sivasubramanian and Menon, (1973).

Less than per cent= Low

10 – 20 per cent = Moderate

More than 20 per cent= High

3.5.2.2. Heritability

Heritability in a broad sense was worked out based on the formula of Lush (1940) and expressed in percentage.

$$H^2 = \frac{\sigma^2 g}{\sigma^2 p}$$

$\sigma^2 g$ = Genotypic variance

$\sigma^2 p$ = Phenotypic variance

The range of heritability was categorized as suggested by Robinson *et al.* (1949) *i.e.,*

0 – 30 per cent=Low

31 – 60 per cent=Moderate

61-62 per cent and above =High

3.5.3. Genetic Advance and Genetic advance as per cent of mean

3.5.3.1. Genetic Advance

Genetic Advance for each character was worked out as given below based on the formula of Johnson *et al. (*1955*a) i.e.,*

Genetic advance $GA = \frac{\sigma^2 g}{\sigma p}$ x K

Where,

σ^2 g = Genotypic variance.

σ p = Phenotypic standard deviation.

K = 2.06, Selection differential at 5 per cent selection intensity (Falconer, 1967).

3.5.3.2. Genetic advance as per cent mean

Genetic advance as per cent mean is the percentage of genetic advance based on the mean of each character. The method for assessment of genetic advance as per cent of mean and range was suggested by Johnson *et al.* (1955a).

$$\text{Genetic Advance as percent of mean} = \frac{\text{Genetic Advance}}{\text{Grand mean}} \times 100$$

Less than 10 per cent= Low

10 – 20 per cent= Moderate

More than 20 per cent= High

3.5.4. Correlation Studies

Correlation coefficients for yield and other traits in all the 53 accessions were worked out as suggested by Johnson *et al*. (1955b).

(i) Genotypic correlation coefficient

$$rg(1.2) = \frac{\sigma g(12)}{\sigma g(1).\sigma g(2)}$$

Where,

r g 1.2 = Genotypic correlation coefficient between traits 1and 2.

$\sigma g(12)$ = Genotypic covariance between character 1 and 2.

$\sigma g(1)$ = Genotypic standard deviation of trait 1.

$\sigma g(2)$ = Genotypic standard deviation of trait 2

(ii) Phenotypic correlation coefficient

$$r_p(12) = \frac{\sigma_p(2)}{\sigma_p(1).\sigma_p(2)}$$

where,

r p 1.2 = Phenotypic correlation between characters 1 and 2.

$\sigma_p(2)$ = Phenotypic covariance between characters 1 and 2.

$\sigma_p(1)$ = Phenotypic standard deviation of trait 1.

$\sigma_p(2)$ = Phenotypic standard deviation of trait 2.

The significance of the phenotypic and genotypic correlation coefficients was tested by referring the standard table given by Snedecor (1961).

3.5.5. Path coefficient analysis

Path coefficient analysis as applied by Dewey and Lu (1959) was used to partition the genotypic correlation into components of direct and indirect effects. By keeping yield as dependent variable and the other traits as independent variables, simultaneous equations, which express the basic relationship between path coefficients were solved to estimate the direct and indirect effects. The direct and indirect effects were classified based on the scale given by Lenka and Mishra (1973).

Scale/ value	Rating
More than 1.0	Very high
0.30 – 0.99	High
0.20 – 0.29	Moderate
0.10 – 0.19	Low
0.00 – 0.09	Negligible.

3.5.6. Genetic divergence

3.5.6.1. D^2 analysis

The D^2 analysis suggested by Mahalanobis (1936) was used for estimating the genetic divergence among the 53 accessions. The inverse of the error variance - covariance matrix was used to set of equations by which the correlated variables (X_1 to X_n) were transformed into the uncorrelated set of variables (Y_1 to Y_n). This transformation was done by the pivotal condensation method of Rao (1952). All possible D^2 values n $(n-1)^{1/2}$ were worked out by taking the sum of squares of different pairs of corresponding 'Y' values taking two accessions at a time.

3.5.6.1.1. Determination of group consternations or clusters

Based on degree of divergence (D^2 values) between any two genotypes, grouping was done by using Tocher's method (Rao, 1952). The criterion of grouping was that any two populations belonging to the same cluster should at least, on the average, show a smaller D^2 then those belonging to the different cluster. Starting with two closely associated varieties, a third variety having the smallest average D^2 from the first two was added. Similarly, the fourth one was chosen to have the smallest average D^2 from the first three and so on. If at any stage, the average D^2 of a group appeared to be high from those already included, it was considered that the group did not fit in with the former cluster and hence taken outside the cluster. The group of the cluster was omitted and the rest treated in the same way.

3.5.6.1.2. Intra and inter cluster distance

After establishing the cluster, the intra cluster distance was worked out by taking average of the component genotypes in that cluster. The average inter cluster divergence was arrived at by taking into consideration of all the compound D^2 values possible among the members of two clusters. The square root of the average D^2 values gave the genetic distance D^2 between the clusters. Based on D^2 values (inter cluster distance) the following scale for rating of the distance was adopted (Rao, 1952).

Category	D^2 values
Less divergent (L)	99 and above
Moderately divergent (M)	Between 100 and 200
Highly divergent (H)	Above 200

3.5.7. Generation mean analysis

3.5.7.1. Detection of gene effects

Scaling test was used to detect digenic interaction components as per Mather (1949) and Hayman and Mather (1955). The estimates of gene effects were derived from the generation mean analysis joint scaling test (Cavalli, 1952) and perfect fit solution of Mather and Jinks (1971).

Before estimating the gene effects from the generation mean analysis, following assumptions were made.

a. Normal diploid segregation
b. Homozygous parents
c. Absence of reciprocal cross differences
d. Absence of multiple allelism
e. Absence of linkage
f. Equal viability of genotypes
g. Absence of genotype x environment interactions.

3.5.7.2. Scaling test

The scaling test was performed for judging whether simple additive dominance model was followed for those characters which exhibited significant difference among

generation means. The scaling test was suggested by Mather (1949) and Hayman and Mather (1955) gave the following effects.

$A=2B_1-P_1-F_1$

$B=2B_2-P_2-F_1$

$C=4F_2-2F_1-P_1-P_2$

$D=2F_2-B_1-B_2$

Where. P_1 = mean of the parent (First)

P_2 = mean of the parent (Second)

F_1 = mean of the F_1 generation

F_2 = mean of the F_2 generation

B_1 = mean of the backcross population with first parent

B_2 = mean of the backcross population with second parent

When the scale is adequate the value of A, B, C and D should be zero (A=B=C=D=0) within the limits of their respective standard error as

S.E. (A) = $(4\ VB_1 + VP_1 – VF_1)$ ½

S.E. (B) = $(4\ VB_2 + VP_2 – VF_1)$ ½

S.E. (C) = $(16\ VF_1 + 4VF_1 – VP_1 - 4VP_2)$ ½

S.E. (D) = $(4VF_1 + VP_1 - 4VB_1)$ ½

Where, VP_1, VP_2, VF_1, VF_2, VB_1 and VB_2 where the mean of variances of P_1, P_2, F_1, F_2, B_1 and B_2 respectively.

The significance of each scale whether deviate significantly or not from the expected values were tested by‘t’ test.

t(A)= A/ S.E. (A)

t(B)= B/ S.E. (B)

t(C) = C/ S.E. (C)

t(D)=D/ S.E. (D)

The calculated ‘t’ values were compared with the tabulated ‘t’ value at 5 per cent and 1 per cent level of significance. If any of the scale is found to be significant, additive dominance model is considered not adequate, indicating the presence of non-allelic (epistasis) interactions whereas, if not significant, the model is adequate and non-allelic (epistatic) interactions were absent.

3.5.7.3. Joint scaling test

Adequacy of the additive-dominance model was further tested by joint scaling test proposed by Cavalli (1952). It consisted of estimating the parameters (m), (d) and (h) from mean of the available generations followed by a comparison of the observed generation means with expected values derived from the estimates of three parameters. The adequacy of additive- dominance model was tested by chi-square test. The model is adequate when χ^2 was non-significant, if otherwise, inadequate. This test, thus provided the best possible estimates of all the parameters required to amount for difference among family means when the model is adequate.

3.5.7.4. Estimation of gene effects (non- allelic interaction in interacting crosses)

When simple additive- dominance model was inadequate i.e. in the presence of non –allelic interactions six parameter model of Hayman (1958) was fitted and various components accordingly where,

m = mean

d = additive

h = dominance

i = additive x additive

j = additive x dominance

l = dominance x dominance

All the above components were estimated from the population means of P_1, P_2, F_1, F_2, B_1 and B_2.

Where,

$m = F_2$

$d = B_1 – B_2$

$h = ½ P_1 - ½P_2 - F_1 - + 4F_2 + 2B_1 + 2B_2$

$i = 2B_1 + 2B_2 - 4F_2$

$j = B_1 - ½ P_1 - B_2 + ½P_2$

$l = P_1 + P_2 + 2 F_1 + 4 F_2 - 4 B_1 - 4 B_2$

The variance for the above gene effects were obtained as follows:

$Vm = VF_2$

$Vd = VB_1 – VB_2$

$Vh = ¼ (VP_1 – VP_2) + VF_1 + 16VF_2 + 4(VB_1 + VB_2)$

$Vi = 16 VF_2 + 4(VB_1 + VB_2)$

$V_j = ¼ (VP_1 – VP_1) + VB_1 + VB_2$

$V_l = VP_1 + VP_2 + 4F_1 + 16F_2 + 16\ VB_1 + 16\ VB_2$

The standard errors for each component were computed as follows:

S.E. (m) = √V (*m*)

S.E. (*d*) = √V (*d*)

S.E. (*h*) = √V (*h*)

S.E. (*i*) = √V (*i*)

S.E. (*j*) = √ V(*j*)

S.E. (*l*) = √ V(*l*)

The ‘ t ‘ values were calculated as follows

t(*m*) = m/ S.E.(*m*)

t(*d*) = d/ S.E.(*d*)

t(*h*) = h/ S.E.(*h*)

t(*i*) = i/ S.E. (*i*)

t(*j*) = j/S.E. (*j*)

t(*l*) = l/ S.E. (*l*)

The significant of each genetic effect was tested by comparing ‘t’ calculated with ‘t’ tabulated values at 5 per cent and 1 per cent levels of significance.

Results

4. RESULTS

Melon fruit fly (*Zeugodacus* spp.) is one of the major pests in cucurbits and it causes a loss of 32-100 per cent depending upon the season and prevailing climatic conditions. The development of resistant varieties either by selection from germplasm or through backcross breeding is an economical way to reduce the fruit loss due to melon fruit fly infestation. Hence, the present study was undertaken to study the variability for quality, yield attributes; to identify the sources of resistance to melon fruit fly from germplasm and to transfer genes responsible for melon fruit fly resistance from wild species to high yielding varieties. Experimental data recorded during the course of study were subjected to statistical analysis and the results obtained are presented under following headings.

- Variability studies in oriental pickling melon accessions
- Identification of resistance source(s) against melon fruit fly
- Incorporation of fruit fly resistance to high yielding varieties
- Generation mean analysis to elucidate the genetics of melon fruit fly resistance

4.1. Variability

Results of variability studies on quality traits viz; flower colour, stem hairiness, fruit shape, fruit colour at maturity, skin surface, skin hardness, skin texture, taste of fruit, flesh colour, flesh texture, flesh flavour, fruit bitterness and seed colour of 53 oriental pickling melon accessions are presented in Appendix II, (Plate 9). Estimates of variability *viz*; range, mean, genotypic variance (GV), phenotypic variance (PV), genotypic coefficient of variation (GCV), genotypic coefficient of variation (PCV), heritability in broad sense (H^2), genetic advance (GA) and genetic advance as percentage of mean (GAM) on yield contributing traits, yield and resistance to melon fruit fly were estimated and presented in Table.6.

4.1.1. Days to first female flower production

Days to first female flower production ranged from 27.50 days -34.20 days in oriental pickling melon accessions with a general mean of 29.91 days**.** The estimates of GV, PV were 2.63 and 2.88 respectively which indicated low variability. Estimates of

Table.6. Estimates of variability parameters for oriental pickling melon

Sl. No.	Characters	Range	Mean	GV	PV	GCV	PCV	H^2	GA	GAM
1	Days to first female flower production	27.50-34.20	29.91	2.63	2.88	6.02	6.96	74.79	3.02	10.72
2	Days to first male flower production	24.70-31.20	26.92	1.27	1.46	76.17	76.62	98.83	20.86	155.99
3	Node of first female flower	2.70-9.90	6.06	1.32	2.08	26.32	36.10	53.14	2.08	39.52
4	Node of first male flower	2.10-6.70	4.58	3.25	3.93	75.09	86.69	75.04	232.00	134.00
5	Vine length (cm)	93.70-414.20	263.29	5701.78	9356.83	129.29	135.44	91.14	247.53	254.28
6	Inter nodal length (cm)	5.67-12.35	8.78	1.53	1.76	50.86	52.93	92.36	5.45	100.70
7	Number of branches per plant	2.50-5.50	3.42	0.18	0.54	41.79	46.06	82.30	5.98	78.09
8	Fruit diameter (cm)	6.19-12.99	10.16	2.66	2.87	37.83	46.08	67.38	13.93	63.97
9	Fruit girth (cm)	12.47-42.55	28.57	42.21	54.54	19.92	32.44	37.71	6.21	25.20
10	Fruit length (cm)	7.97-32.51	21.06	34.16	37.50	65.87	106.93	37.96	529.09	83.60
11	Fruit weight (g)	245.00-3590.00	946.45	3254.91	3732.87	121.66	175.27	48.19	557.93	173.98
12	Fruit rind thickness (cm)	0.14-0.41	0.2	0.003	0.004	63.48	70.21	81.75	2.09	118.24
13	Flesh thickness (cm)	1.72-4.21	2.59	0.26	0.29	58.36	69.27	70.98	9.39	101.30
14	Seed cavity length (cm)	5.87-22.80	12.26	20.53	23.76	46.26	61.29	56.97	4.91	71.94

15	Seed cavity breadth (cm)	2.07-7.35	4.6	1.44	1.50	89.89	98.02	84.12	3.58	169.85
16	Seed length (cm)	0.56-0.79	0.71	0.002	0.003	79.34	103.65	58.59	273.67	125.11
17	Number of seeds per fruit	56.70-830.80	338.17	18712	39473	136.93	162.66	70.87	293.01	237.47
18	Number of fruits per plant	3.90-10.40	5.59	1.80	2.38	64.05	65.67	95.15	57.20	128.71
19	Days taken for fruit maturity	55.90-75.20	65.18	19.75	30.53	5.89	6.98	71.29	6.35	10.25
20	Days to first harvest	54.90-63.60	60.59	1.19	3.29	11.28	11.74	92.52	16.09	22.37
21	Days to last harvest	72.30-81.70	77.88	2.89	5.67	129.01	131.88	95.69	72.86	259.99
22	Marketable yield per plant (kg)	0.37-2.25	1.18	3.51	4.54	60.41	63.53	90.41	7.08	118.32
23	Days to fruit fly infestation after anthesis	5.20-11.80	8.44	1.99	2.31	61.95	68.29	82.28	57.07	115.76
24	Percentage of fruit fly infestation (per cent)	18.99-89.80	69.57	274.23	338.06	119.10	126.71	88.35	58.63	230.62
25	Yield per plant (kg)	1.23-9.75	3.38	31.39	44.15	61.92	64.59	91.87	24.60	122.26

Plate 9. Variability of fruit shape in oriental pickling melon

GCV, PCV were 6.02, 6.96 respectively which also indicated low variability and close association between genotype and phenotype or low influence of environmental factors on this trait. However, high heritability (74.79) along with low GA (3.02), and GAM (10.72) were observed.

4.1.2. Days to first male flower production

Days to first male flower ranged from 24.70 days -31.20 days in oriental pickling melon accessions with a mean of 26.92 days**.** GV (1.27), PV (1.46) were low which indicated low variability for this trait. However, high GCV (76.17), PCV (76.62) with high heritability (98.83) were observed. Days to first male flower showed moderate GA (20.86) with high GAM (155.99).

4.1.3. Node of first female flower

Node number of first female flower ranged from 2.70-9.90 in oriental pickling melon accessions with a general mean of 6.06. GV, PV were 1.32, 2.08 resepctively which showed low variability for this trait**.** However, close association and moderate estimates of GCV (26.32), PCV (36.10) with moderate heritability (53.14) was observed. GA (2.08) was low with moderate GAM (39.52).

4.1.4. Node of first male flower

Node number of first male flower ranged from 2.10-6.70 with a general mean of 4.58**.** Estimates of GV **(**1.32), PV (3.93) were very low which showed that low variability existed in the accessions. However**,** GCV (75.09), PCV (86.69), heritability (75.04), GA (232.00) and GAM (134.00) were high for this trait.

4.1.5. Vine length (cm)

Vine length ranged from 93.70 cm - 414.20 cm in oriental pickling melon accessions with a general mean of 263.29 cm. GV (5701.78), PV (9356.83), GCV (129.29), PCV (135.44), heritability (91.14), GA (247.53) and GAM (254.28) were very high which indicated considerable heritable variations existed for this trait.

4.1.6. Inter nodal length (cm)

Inter nodal length ranged from 5.67 cm-12.35 cm in oriental pickling melon accessions with a general mean of 8.78 cm. GV (1.53), PV (1.76) respectively were very

low for this trait which indicated low variability in the accessions. GCV (50.86), PCV (52.93) were moderate with close correspondence between them. High heritability (92.36), low GA (5.45) and moderate GAM (100.70) were observed.

4.1.7. Number of branches per plant

Number of branches per plant ranged from 2.50 - 5.50 in oriental pickling melon accessions with a general mean of 3.42. GV (0.18) and PV (0.54) were very low. GCV (41.79), PCV (46.07) were moderate. Heritability (82.30) was fairly high with low GA (5.98) and with fairly high GAM (78.09).

4.1.8. Fruit diameter (cm)

Fruit diameter ranged from 6.19 cm - 12.99 cm in oriental pickling melon accessions with a general mean of 10.16 cm. GV (2.66) and PV (2.87) were very low which indicated low variability in the accessions. GCV (37.83), PCV (46.08) were moderate with high heritability (67.38). However, GA (13.93) was low with intermediate GAM (63.97).

4.1.9. Fruit girth (cm)

Fruit girth ranged from 12.47 cm - 42.55 cm in oriental pickling melon accessions with a general mean of 28.57 cm. GV (42.21) and PV (54.54) were average which indicated moderate variability for the trait. GCV (19.92), PCV (32.44) and heritability (37.71) were moderate with low GA (6.21) and moderate GAM (25.20).

4.1.10. Fruit length (cm)

Fruit length ranged from 7.97 cm - 32.51 cm in oriental pickling melon accessions with a general mean of 21.06 cm. GV (34.16) and PV (37.50) were moderate which indicated moderate variability. GCV (65.87) was fairly high with high PCV (106.93) which indicated moderate influence of environment on the trait. Heritability (37.96) was moderate; GA (529.09) and GAM (83.60) were high.

4.1.11. Fruit weight (g)

Fruit weight ranged from 245.00 g - 3590.00 g in oriental pickling melon accessions with a general mean of 946.45 g. GV (325491), PV (373287) was very high which indicated high variability in the accessions. GCV (121.66), PCV (175.27) were high with moderate heritability (48.19), GA (557.93) and GAM (173.98) were very high.

4.1.12. Fruit rind thickness (cm)

Fruit rind thickness ranged from 0.14 cm-0.41 cm in oriental pickling melon accessions with a general mean of 0.20 cm. GV (0.003), PV (0.004) were very low which indicated very low variability for this trait. GCV (63.48), PCV (70.21), heritability (81.75) were high. However, GA (2.09) was very low with high GAM (118.24).

4.1.13. Flesh thickness (cm)

Flesh thickness ranged from 1.72 cm - 4.21 cm in oriental pickling melon accessions with a general mean of 2.59 cm. GV (0.26), PV (0.29) were very low which indicated very low variability for this trait. GCV (58.36), PCV (69.27) were moderately high, heritability (70.98) was fairly high. GA (9.39) was very low with high GAM (101.30).

4.1.14. Seed cavity length (cm)

Seed cavity length ranged from 5.87 cm - 22.80 cm in oriental pickling melon accessions with a general mean of 12.26 cm. GV (20.53), PV (23.76) were low which indicated low variability for this trait. GCV (46.26), PCV (61.29), heritability (56.97) were moderate. GA (4.91) was very low, with fairly high GAM (71.94).

4.1.15. Seed cavity breadth (cm)

Seed cavity breadth ranged from 2.07 cm - 7.35 cm in oriental pickling melon accessions with a general mean of 4.60 cm. GV (1.44), PV (1.50) were very low which indicated low variability. However, GCV (89.89), PCV (98.02) were high with high heritability (84.12). GA (3.58) was low, with high GAM (169.85).

4.1.16. Seed length (cm)

Seed length varied from 0.56 cm - 0.79 cm in oriental pickling melon accessions with a general mean of 0.71 cm. GV (0.002), PV (0.003) were low which indicated low variability. Estimates of GCV (79.34), PCV (103.65), GA (273.67) and GAM (125.11) were very high. However, moderate heritability (58.59) was observed.

4.1.17. Number of seeds per fruit

Number of seeds per plant ranged from 56.70-830.80 in oriental pickling melon accessions with a mean of 338.17. GV (18712), PV (39473) were very high which indicated high variability. Estimates of GCV (136.93), PCV (162.66), heritability (70.87), GA (293.01) and GAM (237.47) were very high.

4.1.18. Number of fruits per plant

Number of fruits per plant ranged from 3.90-10.40 in oriental pickling melon accessions with a mean of 5.59. GV (1.80), PV (2.38) were very low which indicated low variability. Estimates of GCV (64.05), PCV (65.66), heritability (95.15), GA (57.20) and GAM (128.71) were very high.

4.1.19. Days taken for fruit maturity

Days taken for fruit maturity varied from 55.90 days - 75.20 days in oriental pickling melon accessions with a general mean of 65.18. GV (19.75), PV (30.53) were moderate which indicated moderate variability. Estimates of GCV (5.89), PCV (6.98), GA (6.35) and GAM (10.25) were low whereas, heritability (71.29) was high.

4.1.20. Days to first harvest

Days to first harvest ranged from 54.90 days- 63.60 days in oriental pickling melon accessions with a general mean of 60.59. GV (1.19), PV (3.29) were low which indicated low variability, Estimates of GCV (11.28) and PCV (11.74) were low, GA (16.09) and GAM (22.37) were moderate. However, heritability (92.52) was very high.

4.1.21. Days to last harvest

Days to last harvest ranged from 72.30 days - 81.70 days in oriental pickling melon accessions with a general mean of 77.88. GV (2.89), PV (5.67) were low which indicated low variability. Estimates of GCV (129.01), PCV (131.88), heritability (95.69), GA (72.86) and GAM (259.99) were very high for this character.

4.1.22. Marketable yield per plant (kg)

Marketable yield per plant ranged from 0.37 kg - 2.25 kg in oriental pickling melon accessions with a general mean of 1.18 kg. GV (3.51), PV (4.54) were low which indicated

low variability. GCV (60.41), PCV (63.53) were high. High heritability (90.41) and GAM (118.32) were observed. However, GA (7.08) for this character was low.

4.1.23. Days to fruit fly infestation after anthesis

Days to fruit fly infestation after anthesis ranged from 5.20 days-11.80 days in op melon accessions with a mean of 8.44. GV (1.99), PV (2.31) were low which indicated low variability. Estimates of GCV (61.95), PCV (68.29), heritability (82.28), GA (57.07) and GAM (115.76) were high for this character.

4.1.24. Percentage of fruit fly infestation (per cent)

Percentage of fruit fly infestation varied from 18.99 per cent - 89.80 per cent in oriental pickling melon accessions with a mean of 69.57. GV (274.22), PV (338.06) were very high which indicated high variability. Estimates of GCV (119.10), PCV (126.71), heritability (88.35), and GAM (230.62) were very high for this character while, GA (58.63) was moderate (Fig.1.).

4.1.25. Yield per plant (kg)

Yield per plant ranged from 1.23 kg- 9.75 kg in oriental pickling melon accessions with a general mean of 3.38 kg. GV (31.39), PV (44.15) were moderate which indicated moderate variability. Estimates of GCV (61.92), PCV (64.59), heritability (91.87), and GAM (122.26) were very high for this character. GA (24.60) was moderate (Fig. 2.).

4.2.0. Genetic divergence

To access extent of genetic diversity among the accessions, data recorded on 25 quantitative traits from 53 accessions in experiment I was subjected to D^2 analysis. The results are presented below Table. 7, Table .8 and Table 9.

4.2.1. Clustering of accessions

The clustering was performed by treating the estimated D^2 values as the square of generalized distance. The resulted average D^2 value within (intra) and between (inter) clusters were given in Table.7. Fifty three accessions were formed into eight clusters. Maximum intra cluster distance was observed in VI cluster (649.02) followed by cluster V (541.54) . Minimum intra cluster distance of was observed in clusters I (277.42). Maximum inter cluster distance was observed between cluster VI and V (1337.80) followed by cluster

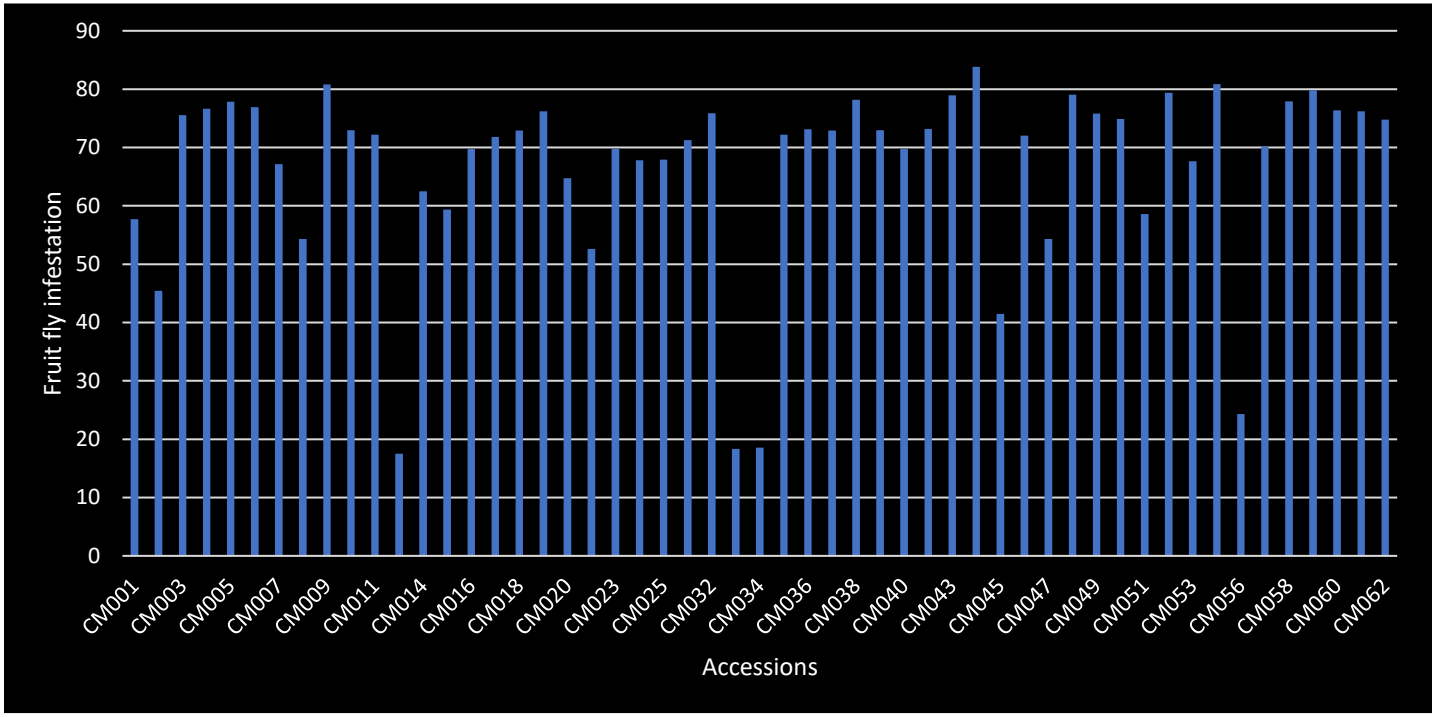


Fig. 1. Fruit fly infestation in oriental pickling melon accessions

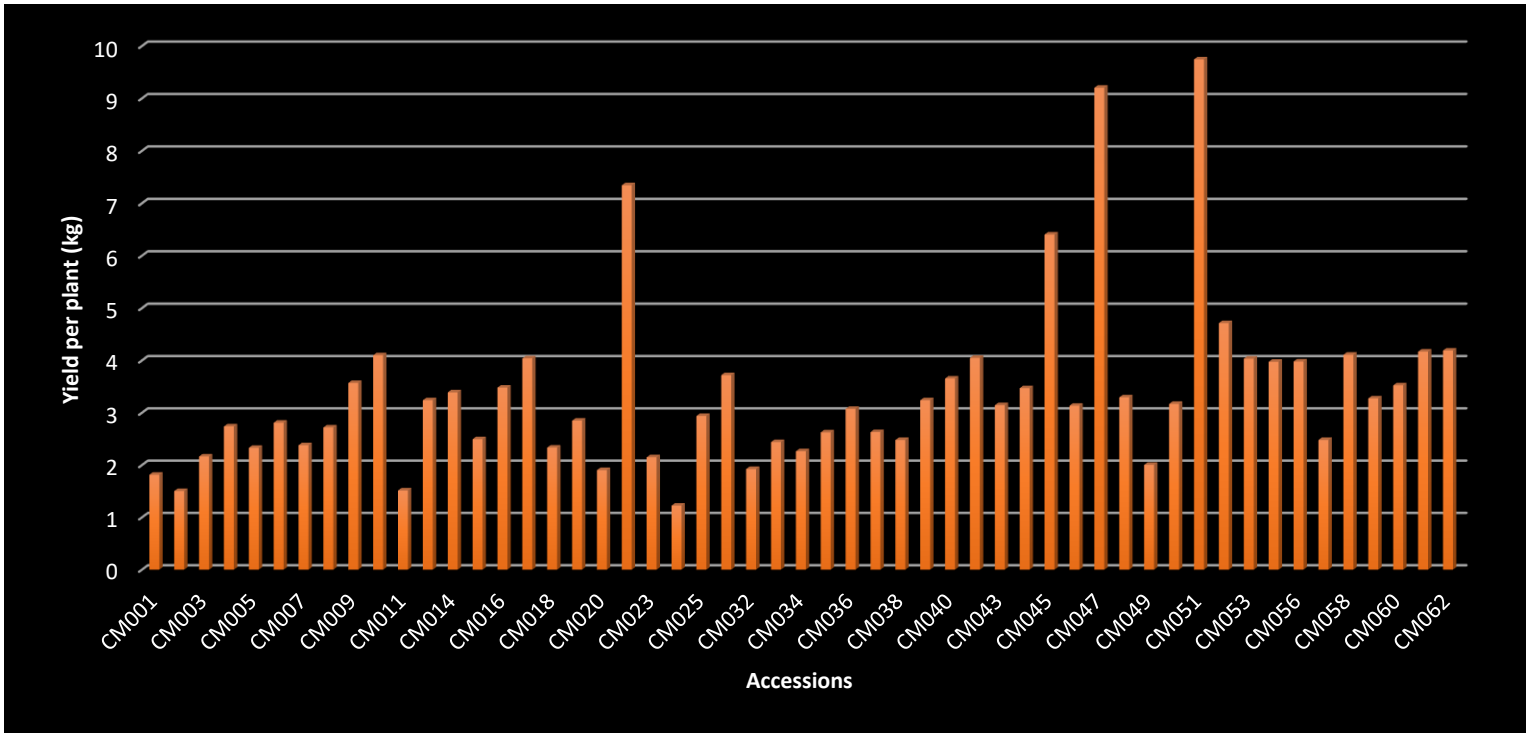


Fig.2. Yield of oriental pickling melon accessions

Table.7. Average inter and intra cluster D^2 values

	I	II	III	IV	V	VI	VII	VIII
I	277.42 (16.65)							
II	415.83 (20.39)	288.33 (16.98)						
III	482.94 (21.97)	736.92 (27.14)	349.09 (18.68)					
IV	636.11 (25.22)	700.69 (26.47)	784.86 (28.01)	361.75 (19.01)				
V	660.64 (25.70)	563.01 (23.72)	1067.83 (32.67)	982.42 (31.34)	541.54 (23.27)			
VI	656.81 (25.62)	915.94 (30.26)	740.98 (27.22)	1021.62 (31.96)	1337.80 (36.57)	649.02 (25.47)		
VII	646.04 (25.41)	582.85 (24.14)	1328.15 (36.44)	1019.01 (31.92)	905.58 (30.09)	1058.85 (32.53)	360.97 (18.99)	
VIII	441.45 (21.01)	539.67 (23.16)	589.84 (24.28)	595.02 (24.39)	791.94 (28.14)	782.18 (27.96)	917.90 (30.29)	353.53 (18.80)

Intra cluster distance: Diagonal values

Inter cluster distance: Off-diagonal values

D values : Values in parenthesis

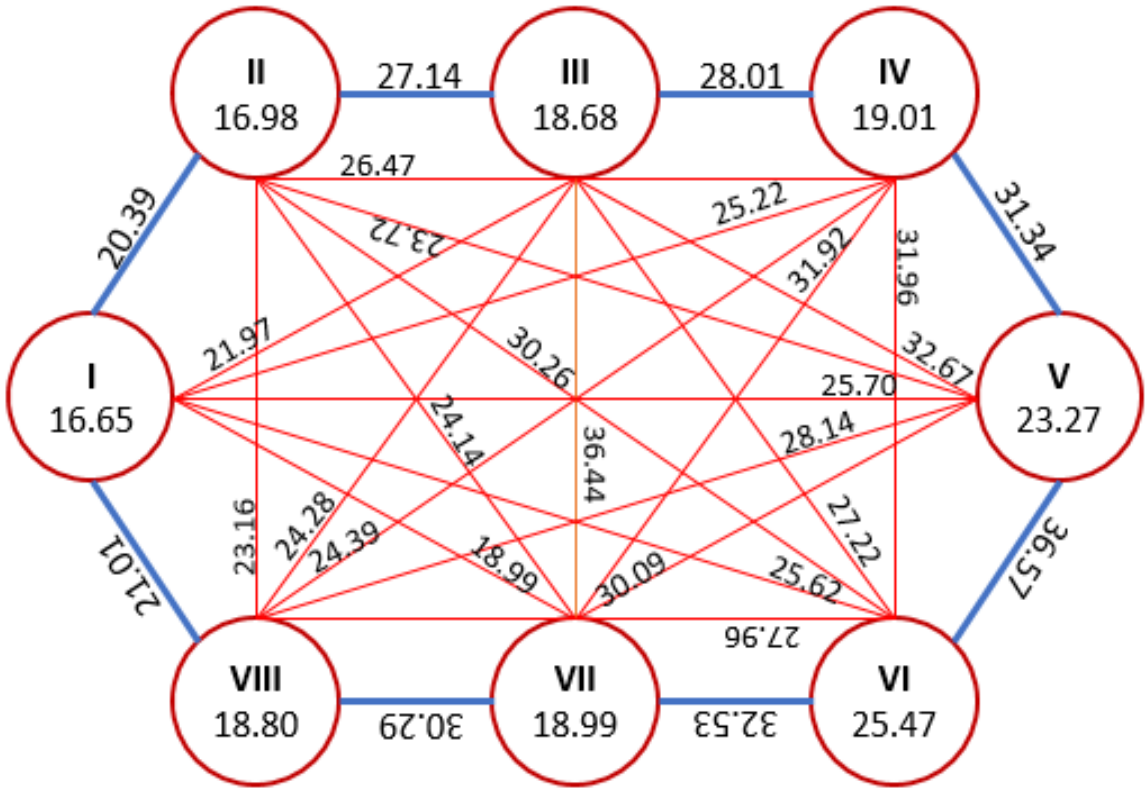


Fig.3. Cluster diagram for inter cluster and intra cluster D^2 values

VII and III (1328.15). The minimum inter cluster distance was found between I and II cluster (415.83) (Fig. 3.).

4.2.2. Cluster composition

Fifty three accessions of oriental pickling melon were grouped into eight clusters. The cluster wise distribution of 53 accessions is shown in Table.8.

Cluster I had the highest number of accessions (12) followed by cluster II (9) accessions. Cluster III (8) accessions, clusters VII (7) accessions, cluster VIII (6) accessions and clusters V and VI (4) accessions each and clusters IV had three accessions.

Cluster I comprised of 12 accessions namely CM007, CM008, CM014, CM015, CM017, CM023, CM025, CM035, CM039, CM048, CM050 and CM060. Cluster II comprised of 9 accessions namely CM019, CM040, CM042, CM055, CM056, CM058, CM059, CM061 and CM062.

Eight accessions *viz*; CM011, CM018, CM020, CM024, CM037, CM038, CM053 and CM057 were clubbed into cluster III. Seven accessions namely CM004, CM006, CM009, CM010, CM012, CM016 and CM028 were grouped into cluster VII. The accessions CM001, CM043, CM044, CM046, CM049 and CM052 were grouped into cluster VIII. Four accessions each were grouped into cluster V (CM022, CM045, CM047 and CM051) and VI (CM002, CM003, CM005 and CM036). The accessions CM032, CM033 and CM034 were clumped into cluster IV.

4.2.3. Cluster wise mean performance of characters

The cluster wise mean performance of 25 quantitative characters with respect to eight clusters are detailed in the Table.9.

4.2.3.1. Days to first female flower production

The lowest mean for days to first female flower production was observed in cluster II (27.98). The highest mean for days to first female flower production was observed in

Table.8. Cluster wise distribution of oriental pickling melon accessions

Cluster No.	Total number of accessions	Accessions included
I	12	CM007, CM008, CM014, CM015, CM017, CM023, CM025, CM035, CM039, CM048, CM050, CM060
II	9	CM019, CM040, CM042, CM055, CM056, CM058, CM059, CM061, CM062
III	8	CM011, CM018, CM020, CM024, CM037, CM038, CM053, CM057
IV	3	CM032, CM033, CM034
V	4	CM022, CM045, CM047, CM051
VI	4	CM002, CM003, CM005, CM036
VII	7	CM004, CM006, CM009, CM010, CM012, CM016, CM028
VIII	6	CM001, CM043, CM044, CM046, CM049, CM052

Table.9. Cluster wise mean performance of oriental pickling melon accessions

Sl. No.	Characters	I	II	III	IV	V	VI	VII	VIII
1	Days to first female flower production	30.05	27.98	29.71	29.56	29.60	31.40	30.40	30.26
2	Days to first male flower production	26.65	26.68	26.67	26.53	26.32	28.52	27.15	24.38
3	Node of first female flower	7.38	6.91	6.76	4.56	4.56	5.12	6.47	4.51
4	Node of first male flower	4.77	5.02	5.45	4.83	2.75	4.15	3.97	4.53
5	Vine length (cm)	249.22	255.83	298.23	128.66	265.47	286.35	266.35	302.93
6	Inter nodal length (cm)	9.15	8.61	9.87	6.73	8.69	8.33	8.99	7.98
7	Number of branches per plant	3.38	3.31	3.33	3.20	4.85	3.20	3.22	3.30
8	Fruit diameter (cm)	9.56	10.79	8.10	8.12	11.06	11.08	12.37	10.41
9	Fruit girth (cm)	28.19	30.36	20.62	25.99	34.18	23.61	39.80	27.08
10	Fruit length (cm)	21.42	22.74	15.95	14.60	29.05	15.15	21.02	26.57
11	Fruit weight (g)	803.75	1010.11	496.37	467.33	2647.50	656.25	1090.12	867.83
12	Fruit rind thickness (cm)	0.17	0.21	0.19	0.34	0.21	0.17	0.21	0.21
13	Flesh thickness (cm)	2.35	2.82	2.44	2.36	3.01	2.48	2.96	2.56
14	Seed cavity length (cm)	10.53	15.62	9.75	7.87	16.98	9.45	10.41	15.24
15	Seed cavity breadth (cm)	4.57	5.15	3.54	3.54	5.18	5.12	6.12	3.25

16	Seed length (cm)	0.66	0.71	0.72	0.63	0.75	0.70	0.71	0.67
17	Number of seeds per fruit	308.54	332.76	291.41	341.36	207.05	386.12	501.65	282.50
18	Number of fruits per plant	4.84	5.77	5.12	5.86	9.50	4.77	4.85	6.13
19	Days taken for fruit maturity	64.59	67.50	65.72	68.36	63.77	61.47	53.71	67.08
20	Days to first harvest	60.87	60.43	52.38	60.40	60.77	60.55	61.47	59.96
21	Days to last harvest	78.94	76.74	78.26	78.43	78.15	77.27	77.48	77.43
22	Marketable yield per plant (kg)	1.14	1.27	1.04	0.62	1.75	0.99	1.08	1.50
23	Days to fruit fly infestation after anthesis	8.04	9.19	8.23	10.63	9.42	6.92	7.91	8.28
24	Percentage of fruit fly infestation (per cent)	73.22	75.19	75.57	37.31	50.67	67.38	70.09	75.39
25	Yield per plant (kg)	2.99	3.80	2.32	2.20	8.17	2.26	3.37	3.04

cluster VI (31.40) followed by cluster VII (30.40).

4.2.3.2. Days to first male flower production

The lowest mean for days to first male flower production was observed in cluster VIII (24.38). The highest mean for days to first male flower production was observed in cluster VI (28.52) followed by cluster VII (27.15).

4.2.3.3. Node of first female flower

The lowest mean for node of first female flower production was observed in cluster VIII (4.51). The highest mean for node at first female flower production was observed in cluster I (7.38) followed by cluster II (6.91).

4.2.3.4. Node of first male flower

The lowest mean for node of first male flower production was observed in cluster V (2.75). The highest mean for node at first male flower production was observed in cluster III (5.45) followed by cluster II (5.02).

4.2.3.5. Vine length (cm)

The lowest mean vine length was observed in the cluster IV (128.66); the highest mean vine length was observed in cluster VIII (302.93) followed by the cluster III (298.23).

4.2.3.6. Inter nodal length (cm)

Cluster means for inter nodal length has the lowest mean in the cluster IV (6.73) and highest mean in cluster III (9.87) followed by cluster I (9.15).

4.2.3.7. Number of branches per plant

The lowest mean number of branches per plant was observed in the cluster IV and VI (3.20) and the highest mean number of branches per plant was in the cluster V (4.85) followed cluster I (3.38).

4.2.3.8. Fruit diameter (cm)

The lowest mean fruit diameter was observed in the cluster III (8.10) and highest mean fruit diameter was highest in the cluster VII (12.37) followed by cluster VI (11.08).

4.2.3.9. Fruit girth (cm)

The lowest mean fruit girth was observed in cluster III (20.62). Highest mean fruit girth was observed in the cluster VII (39.80) followed by cluster V (34.18).

4.2.3.10. Fruit length (cm)

The lowest mean was in the cluster IV (14.60). Fruit length has highest mean in cluster V (29.05) followed by cluster VIII (26.57).

4.2.3.11. Fruit weight (g)

The lowest mean fruit weight was observed in the cluster IV (467.33). Highest mean fruit weight was observed in the cluster V (2647.50) followed by cluster VII (1090.12).

4.2.3.12. Fruit rind thickness (cm)

The lowest mean fruit rind thickness was observed in the cluster I and VI (0.17). The highest mean fruit rind thickness was in the cluster IV (0.34).

4.2.3.13. Flesh thickness (cm)

Flesh thickness is one of the important characters regarding melons. The lowest mean flesh thickness was in the cluster I (2.35). The highest mean flesh thickness was observed in the cluster V (3.01) followed by cluster VII (2.96).

4.2.3.14. Seed cavity length (cm)

Consumer preferred melons should have low seed cavity length and breadth. The lowest mean seed cavity length was observed in the cluster IV (7.87). The highest mean seed cavity length was observed in the cluster V (16.98) followed by cluster II (15.62).

4.2.3.15. Seed cavity breadth (cm)

The lowest mean for seed cavity breadth was observed in the cluster VIII (3.25) and the highest mean seed cavity breadth was observed in the cluster VII (6.12) followed by cluster V (5.18).

4.2.3.16. Seed length (cm)

The lowest mean seed length was observed in the cluster V (0.63); the highest mean seed length was observed in the cluster V (0.75) followed by cluster III (0.72).

4.2.3.17. Number of seeds per fruit

The lowest mean number of seeds per fruit was observed in the cluster V (207.05). The highest mean number of seeds per fruit was in the cluster VII (501.65) followed by cluster VI (386.12).

4.2.3.18. Number of fruits per plant

The lowest mean number of fruits per plant was observed in the cluster VI (4.77). The highest mean number of fruits per plant was observed in the cluster V (9.50) followed by cluster VIII (6.13).

4.2.3.19. Days taken for fruit maturity

The lowest mean days taken for fruit maturity was observed in the cluster VII (53.71). The highest mean days taken for fruit maturity was in the cluster IV (68.36) followed by cluster II (67.50).

4.2.3.20. Days to first harvest

The lowest mean for days to first harvest was observed in the cluster III (52.38); the highest mean days to first harvest was in the cluster VII (61.47) followed by cluster I (60.87).

4.2.3.21. Days to last harvest

The lowest mean for days to last harvest was observed in the cluster II (76.74). The highest mean days to last harvest was in the cluster I (78.94) followed by cluster IV (78.43).

4.2.3.22. Marketable yield per plant (kg)

The lowest mean marketable yield per plant was recorded in the cluster IV (0.62). The highest mean marketable yield per plant was observed in the cluster V (1.75) followed by cluster VIII (1.50).

4.2.3.23. Days to fruit fly infestation after anthesis

The lowest mean number of days taken to infest fruits after anthesis was in the cluster VI (6.92). The highest mean number of days taken to infest the fruit after anthesis was in the cluster IV (10.63) followed by cluster V (9.42).

4.2.3.24. Percentage of fruit fly infestation

The lowest mean percentage of fruit fly infestation was recorded in the cluster IV (37.31). The highest mean fruit fly infestation was in the cluster III (75.57) followed by cluster VIII (75.39).

4.2.3.25. Yield per plant (kg)

Lowest mean yield per plant was recorded in the cluster IV (2.20). The highest mean yield per plant was in the cluster V (8.17) followed by cluster II (3.80).

4.3.0. Correlations and path analysis of yield and component caharacters

4.3.1. Genotypic correlations

Genotypic correlations for various yield attributing characters with yield were estimated and presented in the Table.10. Days to first female flower was significantly, positively correlated with days to first male flower production (rG =0.68), days to first female flower was significantly, negatively correlated with days taken for fruit maturity and days to fruit fly infestation after anthesis (rG = -0.42).

Table. 10. Genotypic correlation coefficient for different quantitative traits for oriental pickling melon accession

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
1	1																			
2	0.68**	1																		
3	-0.13	-0.09	1																	
4	-0.27	-0.03	0.56**	1																
5	0.16	0.06	-0.32*	0.21	1															
6	0.02	-0.08	0.47**	0.15	0.02	1														
7	-0.16	-0.09	-0.36	-0.32	-0.02	0.08	1													
8	0.04	0.01	-0.05	-0.32*	0.17	0.01	-0.05	1												
9	0.09	-0.07	-0.01	-0.27	0.08	0.05	0.19	0.73**	1											
10	-0.07	-0.04	-0.16	-0.07	0.08	-0.04	0.59**	0.37**	0.38**	1										
11	-0.01	-0.08	-0.16	-0.46**	0.05	0.03	0.84**	0.39**	0.48**	0.56**	1									
12	-0.23	-0.07	-0.05	0.21	-0.23	-0.08	-0.04	-0.02	0.15	-0.02	0.02	1								
13	0.03	0.13	0.23	0.22	0.19	0.19	-0.32	0.49**	0.37**	0.09	0.04	0.17	1							
14	-0.17	0.05	-0.11	-0.21	0.04	-0.12	0.57**	0.26	0.18	0.72**	0.56**	0.03	0.02	1						
15	-0.06	-0.10	0.12	-0.19	-0.03	0.03	0.11	0.53**	0.55**	0.09	0.33*	-0.03	-0.05	-0.04	1					
16	-0.25	-0.13	-0.29*	-0.17	0.13	-0.14	0.92**	0.11	0.14	0.44**	0.74**	0.33*	-0.03	0.49**	0.06	1				
17	-0.42**	-0.23	-0.25	0.21	0.18	-0.08	0.05	-0.06	-0.15	0.02	-0.04	0.36*	-0.03	-0.01	-0.08	0.38*	1			
18	-0.42**	-0.28*	-0.29*	-0.01	-0.07	-0.07	0.26	-0.06	0.08	0.17	0.23	0.68**	-0.01	0.13	0.07	0.49**	0.59**	1		
19	-0.05	0.08	0.21	0.21	0.18	0.11	-0.21	-0.03	-0.19	-0.01	-0.25	-0.74**	0.11	-0.09	0.03	-0.25	0.14	-0.50**	1	
20	-0.22	-0.09	-0.08	-0.32*	-0.07	-0.04	0.84**	0.28*	0.31*	0.57**	0.83**	0.04	-0.02	0.63**	0.33**	0.81**	0.07	0.23	-0.14	1

1. Days to first female flower production
2. Days to first male flower production
3. Node of first female flower
4. Node of first male flower
5. Vine length (cm)
6. Inter nodal length (cm)
7. Number of branches per plant
8. Fruit diameter (cm)
9. Fruit girth (cm)
10. Fruit length (cm)
11. Fruit weight (g)
12. Fruit rind thickness (cm)
13. Flesh thickness (cm)
14. Seed cavity length (cm)
15. Seed cavity breadth (cm)
16. Number of fruits per plant
17. Days taken for fruit maturity
18. Days to fruit fly infestation after anthesis
19. Percentage of fruit fly infestation
20. Yield per plant (kg)

Days to first male flower production had significant negative correlations with days to fruit fly infestation after anthesis (rG = - 0.28).

Node of first female flower was significantly, positively correlated with node of first male flower (rG =0.56) and inter nodal length (rG =0.47). Node of first female flower was significantly, negatively correlated with number of fruits per plant and days to fruit fly infestation after anthesis (rG = -0.29).

Node of first male flower had significant negative correlations with the fruit weight (rG = -0.46), fruit diameter and yield per plant (rG = -0.32).

Number of branches per plant was significantly, positively correlated with number of fruits per plant (rG =0.92), fruit weight and yield per plant (rG =0.84), fruit length (rG =0.59), and seed cavity length (rG =0.57).

Fruit diameter was had significant positive correlations with fruit girth (rG = 0.73), seed cavity breadth (rG =0.53), flesh thickness (rG = 0.49), fruit weight (rG = 0.39), fruit length (rG =0.37) and yield per plant (rG =0.28).

Fruit girth was significantly, positively correlated with seed cavity breadth (rG =0.55), fruit weight (rG= 0.48), fruit length (rG =0.38), flesh thickness (rG =0.37) and yield per plant (rG =0.31).

Fruit length had significant positive correlations with seed cavity length (rG =0.72), yield per plant (rG =0.57), fruit weight (rG =0.56) and number of fruits per plant (rG =0.44).

Fruit weight was significantly, positively correlated with yield per plant (rG =0.83), number of fruits per plant (rG =0.74), seed cavity length (rG =0.56) and seed cavity breadth (rG = 0.33).

Fruit rind thickness had significant positive correlations with days to fruit fly infestation after anthesis (rG =0.68), days taken for fruit maturity (rG =0.36) and number of fruits per plant (rG= 0.33). Fruit rind thickness was significantly, negatively correlated with percentage of fruit fly infestation (rG = -0.74).

Seed cavity length was significantly, positively correlated with yield per plant (rG = 0.63) and number of fruits per plant (rG =0.49). Seed cavity breadth was significantly, positively correlated with yield per plant (rG = 0.33).

Number of fruits per plant had significant positive correlations with yield per plant (rG = 0.81), days to fruit fly infestation after anthesis (rG=0.49) and days taken for fruit maturity (rG =0.38).

Days taken for fruit maturity was significantly, positively correlated days to fruit fly infestation after anthesis (rG=0.59).

Days to fruit fly infestation after anthesis had significant negative correlations with percentage of fruit fly infestation (rG=-0.50).

4.3.2. Phenotypic correlations

Phenotypic correlations of various yield attributing characters with yield were estimated and presented in the Table.11. Days to first female flower was significantly, positively correlated with days to first male flower production (rP=0.61).

Node of first female flower had significant positive correlations with node of first male flower (rP=0.42).

Number of branches per plant was significantly, positively correlated with with yield per plant (rP=0.54), fruit weight (rP=0.49) and number of fruits per plant (rP=0.45)

Fruit diameter showed significant positive correlations with fruit girth (rP=0.68), seed cavity breadth (rP=0.49) and flesh thickness (rP=0.44).

Fruit girth was significantly, positively correlated with seed cavity breadth (rP=0.53) and fruit weight (rP=0.48).

Fruit length had significant positive correlations with seed cavity length (rP=0.69), fruit weight (rP=0.54) and yield per plant (rP=0.51).

Fruit weight was significantly, positively correlated with yield per plant (rP=0.77), number of fruits per plant (rP=0.66) and seed cavity length (rP=0.55).

Fruit rind thickness had significant positive correlations with days to fruit fly infestation after anthesis (rP=0.53). Fruit rind thickness was significantly, negatively correlated with percentage of fruit fly infestation (rP= -0.58).

Seed cavity length was significantly positively correlated with yield per plant (rP=0.53) and number of fruits per plant (rP=0.42).

Table.11. Phenotypic correlation coefficient for different quantitative traits for oriental pickling melon genotypes

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
1	1*																			
2	0.61*	1*																		
3	-0.12	-0.09	1*																	
4	-0.19	-0.04	0.42*	1*																
5	0.08	0.02	-0.27	0.04	1*															
6	0.03	-0.09	0.36	0.12	-0.01	1*														
7	-0.12	-0.07	-0.19	-0.07	0.05	0.05	1*													
8	0.03	-0.05	-0.04	-0.21	0.15	0.01	0.03	1*												
9	0.12	-0.06	-0.03	-0.22	0.11	0.02	0.12	0.68*	1*											
10	-0.06	-0.04	-0.16	-0.08	0.11	-0.03	0.35	0.32	0.36	1*										
11	0.04	-0.07	-0.14	-0.36	0.09	0.03	0.49*	0.36	0.48*	0.54*	1*									
12	-0.19	-0.08	-0.01	0.19	-0.20	-0.04	-0.01	-0.01	0.14	-0.03	0.04	1*								
13	0.01	0.09	0.17	0.12	0.15	0.19	-0.26	0.44*	0.36	0.11	0.06	0.12	1*							
14	-0.12	0.07	-0.12	-0.17	0.08	-0.08	0.31	0.20	0.20	0.69*	0.55*	0.01	0.03	1*						
15	-0.06	-0.09	0.09	-0.15	-0.01	0.03	0.06	0.49*	0.53*	0.12	0.32	-0.03	-0.03	0.06	1*					
16	-0.17	-0.08	-0.22	-0.09	0.01	-0.13	0.45*	0.09	0.13	0.37	0.66*	0.26	-0.01	0.42*	0.07	1*				
17	-0.32	-0.22	-0.17	0.19	0.14	-0.06	0.12	-0.06	-0.09	0.04	0.01	0.24	0.04	0.04	-0.06	0.26	1*			
18	-0.32	-0.20	-0.28	-0.03	-0.01	-0.08	0.15	-0.05	0.08	0.17	0.23	0.53*	-0.01	0.14	0.08	0.39	0.43*	1*		
19	-0.05	0.13	0.16	0.12	0.12	0.10	-0.10	-0.05	-0.17	-0.09	-0.19	-0.58*	0.09	-0.06	0.01	-0.23	0.09	-0.42*	1*	
20	-0.16	-0.07	-0.04	-0.21	-0.07	-0.05	0.54*	0.28	0.29	.51*	0.77*	0.05	-0.03	0.53*	0.32	0.78*	0.06	0.18	-0.14	1*

1. Days to first female flower production
2. Days to first male flower production
3. Node of first female flower
4. Node of first male flower
5. Vine length (cm)
6. Inter nodal length (cm)
7. Number of branches per plant
8. Fruit diameter (cm)
9. Fruit girth (cm)
10. Fruit length (cm)
11. Fruit weight (g)
12. Fruit rind thickness (cm)
13. Flesh thickness (cm)
14. Seed cavity length (cm)
15. Seed cavity breadth (cm)
16. Number of fruits per plant
17. Days taken for fruit maturity
18. Days to fruit fly infestation after anthesis
19. Percentage of fruit fly infestation
20. Yield per plant (kg)

Number of fruits per plant had significant positive correlations with yield per plant (rP=0.78).

Days taken for fruit maturity was significantly, positively correlated with days to fruit fly infestation after anthesis (rP=0.43).

Days to fruit fly infestation after anthesis had significant negative correlations with percentage of fruit fly infestation (rP= -0.42).

4.3.3. Path coefficient analysis

The genotypic and phenotypic correlations between characters were subjected to path coefficient analysis for partitioning the direct and indirect effects of the traits on yield per plant, which was considered as dependent variable. The direct and indirect effects of various traits were given in Table.12.

4.3.3.1. Direct effects

In the table, diagonal values represented the direct effects and values on both sides of diagonal represented indirect effects. Number of branches per plant had highest direct positive effect on yield (0.634) followed by number of fruits per plant (0.455), seed cavity breadth (0.287), flesh thickness (0.232), seed cavity length (0.201), node at first female flower (0.166), fruit length (0.061) and fruit rind thickness (0.017).

Node of first male flower showed highest negative effect on yield (-0.281) followed by fruit girth (-0.155), vine length and days to fruit fly infestation after anthesis (-0.076), days to first female flower (-0.060), days taken for fruit maturity (-0.043), inter nodal length (-0.039), fruit diameter (-0.016), percentage of fruit fly infestation (-0.009), days to first female flower production (-0.007) and fruit weight (-0.001)

4.3.3.2. Indirect effects

Days to first female flower had direct negative effect on yield (-0.060) and indirect positive effects on yield through node at first male flower (0.055), days to fruit fly infestation after anthesis (0.024), days taken for fruit maturity (0.013), percentage of fruit fly infestation (0.004) and flesh thickness (0.003)

Table.12. Path coefficient showing direct and indirect effects

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19
1	**-0.060**	-0.004	-0.020	0.055	-0.006	-0.001	-0.075	-0.005	-0.019	-0.003	-0.000	-0.003	0.003	-0.023	-0.018	-0.076	0.013	0.024	0.004
2	-0.042	**-0.007**	-0.015	0.011	-0.001	0.003	-0.046	0.000	0.098	-0.002	0.001	-0.001	0.023	0.013	-0.026	-0.038	0.009	0.015	-0.001
3	0.008	0.006	**0.166**	-0.117	0.012	-0.014	-0.119	0.007	0.005	-0.009	0.002	-0.002	0.039	-0.027	0.027	-0.097	0.007	0.022	-0.001
4	0.013	0.002	0.069	**-0.281**	-0.003	-0.004	-0.047	0.003	0.034	-0.005	0.006	0.035	0.028	-0.034	-0.045	-0.043	-0.008	0.002	-0.001
5	-0.005	-0.001	-0.045	-0.012	**-0.076**	0.006	0.032	-0.002	-0.016	0.006	-0.001	-0.003	0.035	0.016	-0.001	0.008	-0.006	0.008	-0.001
6	-0.026	0.006	0.061	-0.032	0.001	**-0.039**	0.034	-0.002	-0.003	-0.001	-0.000	-0.007	0.046	-0.017	0.009	-0.057	0.002	0.006	-0.009
7	0.008	0.005	-0.031	0.021	-0.004	-0.021	**0.634**	-0.005	-0.018	0.021	-0.009	-0.003	-0.067	0.062	0.018	0.204	-0.057	-0.011	0.009
8	-0.002	0.000	-0.008	0.059	-0.011	-0.006	0.029	**-0.016**	-0.106	0.019	-0.006	-0.003	0.103	0.041	0.141	0.042	0.028	0.004	0.005
9	-0.008	0.004	-0.005	0.063	-0.008	-0.008	0.074	-0.011	**-0.155**	0.022	-0.009	0.002	0.084	0.041	0.153	0.057	0.004	-0.006	0.001
10	0.004	0.003	-0.026	0.023	-0.007	0.001	0.220	-0.005	-0.056	**0.061**	-0.001	-0.006	0.025	0.139	0.033	0.172	-0.023	-0.013	0.000
11	-0.003	0.005	-0.023	0.100	-0.007	-0.001	0.314	-0.005	-0.074	0.033	**-0.001**	0.007	0.014	0.110	0.091	0.299	-0.007	-0.017	0.001
12	0.013	0.006	-0.001	-0.056	0.015	0.001	-0.011	0.003	-0.022	-0.023	-0.000	**0.017**	0.028	0.002	-0.010	0.118	-0.010	-0.040	0.005
13	-0.001	-0.007	0.028	-0.034	-0.011	-0.078	-0.165	-0.007	-0.056	0.006	-0.001	0.002	**0.232**	0.007	-0.009	-0.008	-0.002	0.008	-0.008
14	0.008	-0.004	-0.019	0.047	-0.006	0.003	0.196	-0.003	-0.031	0.042	-0.001	0.000	0.008	**0.201**	0.001	0.191	-0.001	-0.011	0.006
15	0.004	0.006	0.015	0.043	0.004	-0.001	0.043	-0.007	-0.082	0.007	-0.006	-0.006	-0.007	0.001	**0.287**	0.033	0.002	-0.006	-0.001
16	0.011	0.000	-0.035	0.026	-0.001	0.004	0.285	-0.001	-0.019	0.023	-0.001	0.004	-0.004	0.084	0.021	**0.455**	-0.011	-0.034	0.002
17	0.022	0.001	-0.028	-0.054	-0.010	0.000	0.076	0.001	0.015	0.002	-0.000	0.004	0.011	0.008	-0.019	0.118	**-0.043**	-0.032	-0.000
18	0.022	0.001	-0.047	0.010	0.000	0.003	0.097	0.000	-0.013	0.011	-0.004	0.009	-0.002	0.028	0.023	0.181	-0.018	**-0.076**	0.009
19	0.003	-0.000	0.028	-0.035	-0.098	-0.003	-0.065	0.000	0.027	-0.000	0.003	-0.010	0.021	-0.014	0.005	-0.103	-0.004	0.032	**-0.009**

Residual effect=1.173

1. Days to first female flower production
2. Days to first male flower production
3. Node of first female flower
4. Node of first male flower
5. Vine length (cm)
6. Inter nodal length (cm)
7. Number of branches per plant
8. Fruit diameter (cm)
9. Fruit girth (cm)
10. Fruit length (cm)
11. Fruit weight (g)
12. Fruit rind thickness (cm)
13. Flesh thickness (cm)
14. Seed cavity length (cm)
15. Seed cavity breadth (cm)
16. Number of fruits per plant
17. Days taken for fruit maturity
18. Days to fruit fly infestation after anthesis
19. Percentage of fruit fly infestation

Days to first male flower showed direct negative effect on yield (-0.007) and it had indirect positive effects on yield through fruit girth (0.098), flesh thickness (0.023), days to fruit fly infestation after anthesis (0.015), seed cavity length (0.013), node of first male flower (0.011), days taken for fruit maturity (0.009), inter nodal length (0.003) and fruit weight (0.001).

Node of first female flower had direct positive effect on yield (0.166), indirect positive effects on yield through flesh thickness (0.039), seed cavity breadth (0.027), days to fruit fly infestation after anthesis (0.022), vine length (0.012), days to first female flower (0.008), fruit diameter, days taken to fruit maturity (0.007), days to first male flower (0.006), fruit girth (0.005) and fruit weight (0.002).

Node of first male flower had direct negative effect on yield (-0.281) and indirect positive effects on yield through node of first female flower (0.069), fruit rind thickness (0.035), fruit girth (0.034), flesh thickness (0.028), days to first female flower (0.013), fruit weight (0.006), fruit diameter (0.003), days to first male flower and days to fruit fly infestation after anthesis (0.002).

Vine length had direct negative effect on yield (-0.076) and indirect positive effect was noticed on yield through flesh thickness (0.035), number of branches per plant (0.032), seed cavity length (0.016), number of fruits per plant (0.008), inter nodal length and fruit length (0.006).

Inter nodal length had direct negative effect on yield (-0.039), indirect positive effects was noticed on yield through node of first female flower (0.061), flesh thickness (0.046), number of branches per plant (0.034), seed cavity length (0.009), days to fruit fly infestation after anthesis (0.006), days taken for fruit maturity (0.002) and vine length (0.001).

Number of branches per plant had direct positive effect on yield (0.634) and indirect positive effect was noticed on yield through number of fruits per plant (0.204), seed cavity length (0.062), node of first male flower and fruit length (0.021), seed cavity breadth

(0.018), percentage of fruit fly infestation (0.009), days to first female flower (0.008) and days to first male flower (0.005).

Fruit diameter had direct negative effect on yield (-0.016), indirect positive effects were noticed on yield through seed cavity breadth (0.141), flesh thickness (0.103), node of first male flower (0.059), number of fruits per plant (0.042), seed cavity length (0.041), number of branches per plant (0.029), days taken for fruit maturity (0.028), fruit length (0.019), percentage of fruit fly infestation (0.005) and days to fruit fly infestation after anthesis (0.004).

Fruit girth had direct negative effect on yield (-0.155) and indirect positive effects were noticed on yield through seed cavity breadth (0.153), flesh thickness (0.084), number of branches per plant (0.074), node of first male flower (0.063), number of fruits per plant (0.057), seed cavity length (0.041), fruit length (0.022), days to first male flower, days taken for fruit maturity (0.004) and percentage of fruit fly infestation (0.001).

Fruit length had direct positive effect on yield (0.061) and indirect positive effects were noticed on yield through number of branches per plant (0.220), number of fruits per plant (0.172), seed cavity length (0.139), seed cavity breadth (0.033), flesh thickness (0.025), node of first male flower (0.023), days to first female flower (0.004), days to first male flower (0.003) and inter nodal length (0.001).

Fruit weight had direct negative effect on yield (-0.001) and indirect positive effects were noticed on yield through number of branches per plant (0.314), number of fruits per plant (0.299), seed cavity length (0.110), node of first male flower (0.100), seed cavity breadth (0.91), fruit length (0.033), flesh thickness (0.014), fruit rind thickness (0.007), days to first male flower(0.005) and percentage of fruit fly infestation (0.001).

Fruit rind thickness had direct positive effect on yield (0.017) and indirect positive effects were noticed on yield through number of fruits per plant (0.118), flesh thickness (0.028), vine length (0.015), days to first female flower (0.013), days to first male flower

(0.006), percentage of fruit fly infestation (0.005), fruit diameter (0.003), seed cavity length (0.002) and inter nodal length (0.001).

Flesh thickness had direct positive effect on yield (0.232) and indirect positive effects were noticed on yield through node of first female flower (0.028), days to fruit fly infestation after anthesis (0.008), seed cavity length (0.007) and fruit length (0.006).

Seed cavity length had direct positive effect on yield (0.201) and indirect positive effects were noticed on yield through number of branches per plant (0.196), number of fruits per plant (0.191), node of first male flower (0.047), fruit length (0.042), days to first female flower, flesh thickness (0.008), percentage of fruit fly infestation (0.006) and inter nodal length (0.003).

Seed cavity breadth had direct positive effect on yield (0.287) and indirect positive effects were noticed on yield through node of first male flower and number of branches per plant (0.043), number of fruits per plant (0.033), node of first female flower (0.015), fruit length (0.007), days to first male flower (0.006), days to first female flower, vine length (0.004), days taken for fruit maturity (0.002) and seed cavity length (0.001).

Number of fruits per plant had direct positive effect on yield (0.455) and indirect positive effects were noticed on yield through number of branches per plant (0.285), seed cavity length (0.084), node of first male flower (0.026), fruit length (0.023), Seed cavity breadth (0.021), days to first female flower (0.011), inter nodal length, fruit rind thickness (0.004) and percentage of fruit fly infestation (0.002).

Days taken for fruit maturity had direct negative effect on yield (-0.043) and indirect positive effects were noticed on yield through number of fruits per plant (0.118), number of branches per plant (0.076), days to first female flower (0.022), fruit girth (0.015), flesh thickness (0.011), seed cavity length (0.008), days to first male flower and fruit diameter (0.001).

Days to fruit fly infestation after anthesis had direct negative effect on yield (-0.076) and indirect positive effects were noticed on yield through number of fruits per plant

(0.181), number of branches per plant (0.097), seed cavity length (0.028), seed cavity breadth (0.023), days to first female flower (0.022), fruit length (0.011), node of first male flower (0.010), fruit rind thickness, percentage of fruit fly infestation (0.009), inter nodal length (0.003) and days to first male flower (0.001).

Percentage of fruit fly infestation had direct negative effect on yield (-0.009) and indirect positive effects were noticed on yield through days to fruit fly infestation after anthesis (0.032), node of first female flower (0.028), fruit girth (0.027), flesh thickness (0.021), seed cavity breadth (0.005), days to first female flower and fruit weight (0.003).

4.4.0. Correlations and path analysis of fruit fly infestation and component characters

4.4.1. Genotypic correlations

Genotypic correlations of fruit characters of oriental pickling melon to fruit fly infestation were estimated and presented in the Table.13.

Fruit diameter was significantly, positively correlated with fruit rind thickness, flesh thickness (rG =1.03), days to fruit fly infestation after anthesis (rG =1.02), marketable yield per plant (rG = 0.98), fruit length (rG =0.96); negatively, significantly correlated with days taken for fruit maturity (rG = -1.05), percentage of fruit fly infestation (rG = -0.99).

Fruit girth had positive significant correlations with percentage of fruit fly infestation, fruit weight, days taken for fruit maturity (rG=0.85.0.84, 0.75) respectively; significantly, negative correlations with fruit rind thickness (rG = -0.82), flesh thickness (rG = -0.77), marketable fruit yield per plant (rG = -0.70), days to fruit fly infestation after anthesis (rG = -0.68) and fruit length (rG = -0.61).

Fruit length had significant positive correlations with days to fruit fly infestation after anthesis (rG =1.12), marketable yield per plant (rG =1.04), flesh thickness (rG =1.03) and fruit rind thickness (rG =0.95); negative significant correlations with days taken for fruit maturity (rG = -1.04), percentage of fruit fly infestation (rG = -1.04) and fruit weight (rG = -0.95).

Fruit weight was positively, significantly correlated with percentage of fruit fly infestation (rG=1.06) and days taken for fruit maturity (rG=0.97). Fruit weight had

Table.13. Genotypic correlations of traits to percentage of fruit fly infestation

	1	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**
1	1									
2	-0.98**	1								
3	0.96**	-0.61**	1							
4	-1.16**	0.84**	-0.95**	1						
5	1.03**	-0.82**	0.95**	-0.97**	1					
6	1.03**	-0.78**	1.03**	-0.96**	1.01**	1				
7	-1.05**	0.75**	-1.04**	0.97**	-1.01**	-0.99**	1			
8	0.98**	-0.70**	1.03**	-0.93**	0.96**	0.99**	-0.97**	1		
9	1.02**	-0.68**	1.12**	-0.96**	0.98**	0.97**	-0.97**	0.94**	1	
10	-0.99**	0.85**	-1.04**	1.06**	-0.98**	-0.98**	0.99**	-0.95**	-0.97**	1

1. Fruit diameter (cm)
2. Fruit girth (cm)
3. Fruit length (cm)
4. Fruit weight (g)
5. Fruit rind thickness (cm)
6. Flesh thickness (cm)
7. Days taken for fruit maturity
8. Marketable yield per plant (kg)
9. Days to fruit fly infestation after anthesis
10. Percentage of fruit fly infestation

significant negative correlations with fruit rind thickness (rG = -0.97), flesh thickness (rG= -0.96) and marketable yield per plant (rG= -0.93).

Fruit rind thickness was positively, significantly correlated with flesh thickness (rG=1.01), days to fruit fly infestation after anthesis (rG=0.98) and marketable yield per plant (rG=0.96). Fruit rind thickness had significant negative correlations with days taken for fruit maturity (rG= -0.93) and percentage of fruit fly infestation (rG= -0.98).

Flesh thickness was positively, significantly correlated with marketable yield per plant (rG= 0.99) and days to fruit fly infestation after anthesis (rG=0.97). Flesh thickness had significant negative correlations with days taken for fruit maturity (rG= -0.99) and percentage of fruit fly infestation (rG= - 0.98).

Days taken for fruit maturity was positively, significantly correlated with percentage of fruit fly infestation (rG=0.99). Days taken for fruit maturity had significant negative correlations with marketable yield per plant and days to fruit fly infestation after anthesis (rG= -0.97).

Marketable yield per plant was positively, significantly correlated with days to fruit fly infestation after anthesis (rG=0.94) and negative correlations with percentage of fruit fly infestation (rG= -0.95).

Days to fruit fly infestation after anthesis had significant negative correlations with percentage of fruit fly infestation (rG= -0.97).

4.4.2. Phenotypic correlations

Phenotypic correlations of fruit charactes with fruit fly infestation were estimated and presented in the Table.14. Fruit diameter had significant positive correlations with fruit rind thickness (rP=0.84), flesh thickness (rP=0.83), marketable yield per plant (rP=0.82), fruit length (rP=0.72) and days to fruit fly infestation after anthesis (rP=0.71). Fruit diameter was significantly, negatively correlated with days taken for fruit maturity (rP= - 0.84), percentage of fruit fly infestation (rP= - 0.78), fruit weight (rP= - 0.63) and fruit girth (rP= -0.29).

Fruit girth had significant positive correlations with fruit weight (rP=0.61), days taken for fruit maturity (rP=0.49) and percentage of fruit fly infestation (rP=0.46). Fruit

Table.14. Phenotypic correlations to percentage of fruit-fly infestation

	1	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**
1	1									
2	-0.29**	1								
3	0.72**	-0.09	1							
4	-0.63**	0.61**	-0.53**	1						
5	0.84**	-0.45**	0.62**	-0.73**	1					
6	0.83**	-0.49**	0.66**	-0.77**	0.93**	1				
7	-0.84**	0.49**	-0.66**	0.79**	-0.92**	-0.98**	1			
8	0.82**	-0.43**	0.69**	-0.72**	0.88**	0.95**	-0.94**	1		
9	0.71**	-0.46**	0.51**	-0.71**	0.84**	0.91**	-0.89**	0.79**	1	
10	-0.78**	0.46**	-0.62**	0.72**	-0.86**	-0.91**	0.92**	-0.86**	-0.84**	1

1. Fruit diameter (cm)
2. Fruit girth (cm)
3. Fruit length (cm)
4. Fruit weight (g)
5. Fruit rind thickness (cm)
6. Flesh thickness (cm)
7. Days taken for fruit maturity
8. Marketable yield per plant (kg)
9. Days to fruit fly infestation after anthesis
10. Percentage of fruit fly infestation

girth was significantly, negatively correlated with flesh thickness (rP= -0.49), days to fruit fly infestation after anthesis (rP= -0.46), fruit rind thickness (rP= -0.45) and marketable yield per plant (rP= -0.43).

Fruit length had significant positive correlations with marketable yield per plant (rP=0.69), flesh thickness (rP=0.66), fruit rind thickness (rP=0.62) and days to fruit fly infestation after anthesis (rP=0.51). Fruit length was significantly, negatively correlated with days taken for fruit maturity (rP= -0.66), percentage of fruit fly infestation (rP= - 0.62) and fruit weight (rP= -0.53).

Fruit weight had significant positive correlations with days taken for fruit maturity (rP=0.79) and percentage of fruit fly infestation (rP= 0.72). Fruit weight was significantly, negatively correlated with flesh thickness (rP= -0.77), fruit rind thickness (rP= -0.73), marketable yield per plant (rP= -0.72) and days to fruit fly infestation after anthesis (rP= -0.71).

Fruit rind thickness had significant positive correlations with flesh thickness (rP= 0.93), marketable yield per plant (rP= 0.88) and days to fruit fly infestation after anthesis (rP= 0.84). Fruit rind thickness was significantly, negatively correlated with flesh thickness (rP= -0.92) and percentage of fruit fly infestation (rP= - 0.86).

Flesh thickness had significant positive correlations with marketable yield per plant (rP= 0.95) and days to fruit fly infestation after anthesis (rP= 0.91). Flesh thickness was significantly, negatively correlated with days taken for fruit maturity (rP= -0.98) and percentage of fruit fly infestation (rP= - 0.91).

Days taken for fruit maturity had significant positive correlations with percentage of fruit fly infestation (rP= 0.92). Days taken for fruit maturity was significantly, negatively correlated with marketable yield per plant (rP= -0.94) and days to fruit fly infestation after anthesis (rP= -0.89).

Marketable yield per plant had significant positive correlations with days to fruit fly infestation after anthesis (rP= 0.79) and negatively correlated with percentage of fruit fly infestation (rP= -0.86).

Days to fruit fly infestation after anthesis had significant negative correlations with percentage of fruit fly infestation (rP= -0.84).

4.4.3. Path coefficient analysis

The genotypic and phenotypic correlations were subjected to path coefficient analysis for partitioning the direct and indirect effect of the traits on fruit fly infestation, which was considered as dependent variable. The direct and indirect effects of various traits were given in Table.15.

4.4.3.1. Direct effects

In the table, diagonal values represented the direct effects and values on both sides of diagonal represented indirect effects. Fruit rind thickness had highest positive direct effects on fruit fly infestation (1.004) followed by days taken for fruit maturity (0.747), fruit girth (0.285), and flesh thickness (0.215).

It had the highest negative effect on fruit diameter (-0.627) followed by days to fruit fly infestation after anthesis (-0.347), marketable yield per plant (-0.312), fruit weight (-0.202) and fruit length (-0.139).

4.4.3.2. Indirect effects

Fruit diameter had direct negative effect on fruit fly infestation (-0.627) and indirect positive effects were through fruit rind thickness (1.036), fruit weight (0.235) and flesh thickness (0.221).

Fruit girth had direct positive effect on fruit fly infestation (0.285) and indirect positive effects were through fruit diameter (0.613), days taken for fruit maturity (0.564), days to fruit fly infestation after anthesis (0.237), marketable yield per plant (0.219) and fruit length (0.085).

Fruit length had direct negative effect on fruit fly infestation (-0.139) and indirect positive effects were through fruit rind thickness (0.955), flesh thickness (0.222) and fruit weight (0.193).

Fruit weight had direct negative effect on fruit fly infestation (-0.202) and indirect positive effects were through fruit diameter (0.729), days taken for fruit maturity (0.727),

Table.15. Path coefficient showing direct and indirect effects to fruit-fly infestation

	1	2	3	4	5	6	7	8	9
1	**-0.627**	-0.278	-0.134	0.235	1.036	0.221	-0.785	-0.307	-0.355
2	0.613	**0.285**	0.085	-0.171	-0.818	-0.167	0.564	0.219	0.237
3	-0.604	-0.173	**-0.139**	0.193	0.955	0.222	-0.775	-0.323	-0.389
4	0.729	0.239	0.132	**-0.202**	-0.980	-0.206	0.727	0.289	0.331
5	-0.646	-0.232	-0.132	0.197	**1.004**	0.215	-0.749	-0.301	-0.342
6	-0.644	-0.222	-0.144	0.194	1.006	**0.215**	-0.741	-0.308	-0.337
7	0.658	0.215	0.144	-0.197	-1.007	-0.213	**0.747**	0.302	0.336
8	-0.616	-0.199	-0.144	0.187	0.967	0.213	-0.723	**-0.312**	-0.326
9	-0.641	-0.195	-0.156	0.193	0.989	0.209	-0.725	-0.294	**-0.347**

Residual effect=0.035

1. Fruit diameter (cm)
2. Fruit girth (cm)
3. Fruit length (cm)
4. Fruit weight (g)
5. Fruit rind thickness (cm)
6. Flesh thickness (cm)
7. Days taken for fruit maturity
8. Marketable yield per plant (kg)
9. Days to fruit fly infestation after anthesis

days to fruit fly infestation after anthesis (0.331), marketable yield per plant (0.289), fruit girth (0.239) and fruit length (0.132).

Fruit rind thickness had direct positive effect on fruit fly infestation (1.004) and indirect positive effects were through flesh thickness (0.215) and fruit weight (0.197).

Flesh thickness had direct positive effect on fruit fly infestation (0.215) and indirect positive effects through fruit rind thickness (1.006) and fruit weight (0.194).

Days taken for fruit maturity had direct positive effect on fruit fly infestation (0.747) and indirect positive effects through fruit diameter (0.658), days to fruit fly infestation after anthesis (0.336), marketable yield per plant (0.302), fruit girth (0.215) and fruit length (0.144).

Marketable yield per plant had direct negative effect on fruit fly infestation (-0.312) and indirect positive effects through fruit rind thickness (0.967), flesh thickness (0.213) and fruit weight (0.187).

Days to fruit fly infestation after anthesis had direct negative effect on fruit fly infestation (-0.347) and indirect positive effects through fruit rind thickness (0.989), flesh thickness (0.209) and fruit weight (0.193).

4.5.0. Identification of resistant source(s) to melon fruit fly (*Zeugodacus* spp.)

The mean fruit fly infestation data from three crop seasons *viz.*, March 2016 - May 2016, September 2016 - November 2016 and March 2017 - May of 2017 were for utilized pooled analysis for testing significance of means and the results are presented in the Table.16 (Fig.4.).

The rating scale suggested by Nath (1966) was followed to assess the reactions of accessions to melon fruit fly infestation. The fruit fly infestation was recorded from tender to mature stage of fruits based on 1-6 scale namely (i) immune (0.00 per cent), (ii) highly resistant (1-10 per cent), (iii) resistant (11-20 per cent),(iv) moderately resistant (21-50 per cent), (v) susceptible (51-75 per cent), (vi) highly susceptible (76-100 per cent). The accessions were grouped according to their relative resistance reactions as shown in the Table.17

Table.16. Percentage infestation of fruit fly over three seasons

Accessions	Species	S_1	S_2	S_3	Mean treatments
CM001	*Bactrocera cucurbitae*	52.72	62.73	57.73	57.73
CM002	- do -	43.63	47.22	45.42	45.42
CM003	- do -	73.08	77.98	75.53	75.53
CM004	- do -	73.30	80.00	76.65	76.65
CM005	- do -	74.35	81.30	77.82	77.84
CM006	- do -	81.60	72.25	76.93	76.93
CM007	- do -	68.50	65.83	67.16	67.16
CM008	- do -	57.50	51.15	54.33	54.33
CM009	- do -	81.65	80.00	80.83	80.83
CM010	- do -	80.45	65.55	72.99	72.99
CM011	- do -	79.90	64.52	72.21	72.21
CM012	- do -	19.50	15.50	17.50	17.50
CM014	*Bactrocera tau*	63.58	61.36	62.47	62.47
CM015	*Bactrocera cucurbitae*	61.55	57.19	59.37	59.37
CM016	- do -	72.85	66.64	69.74	69.74
CM017	- do -	76.35	67.31	71.83	71.83
CM018	- do -	77.85	68.00	72.93	72.92
CM019	- do -	89.80	62.57	76.18	76.18
CM020	- do -	71.13	58.33	64.72	64.72
CM022	- do -	49.90	55.31	52.60	52.61
CM023	- do -	75.00	64.63	69.81	69.81
CM024	- do -	66.58	69.09	67.83	67.83
CM025	- do -	76.60	59.26	67.93	67.93
CM028	- do -	81.30	61.19	71.23	71.25
CM032	- do -	73.30	78.48	75.89	75.89
CM033	- do -	18.99	17.71	18.35	18.35
CM034	- do -	19.65	17.52	18.58	18.58
CM035	- do -	73.47	70.96	72.21	72.21
CM036	- do -	78.49	67.79	73.14	73.14
CM037	- do -	83.17	62.69	72.93	72.93
CM038	- do -	79.53	76.84	78.18	78.18
CM039	- do -	82.74	63.15	72.94	72.94
CM040	- do -	75.10	64.36	69.73	69.73
CM042	- do -	77.53	68.85	73.18	73.18
CM043	- do -	80.00	77.94	78.96	78.96
CM044	- do -	87.90	79.75	83.82	83.82

CM045	- do -	43.89	39.06	41.47	41.47
CM046	- do -	76.78	67.24	72.01	72.01
CM047	- do -	54.15	54.50	54.32	54.33
CM048	- do -	84.20	73.87	79.04	79.04
CM049	- do -	75.70	75.96	75.83	75.83
CM050	- do -	77.94	71.82	74.87	74.87
CM051	- do -	54.75	62.50	58.62	58.62
CM052	- do -	79.25	79.49	79.37	79.37
CM053	- do -	69.70	65.59	67.64	67.64
CM055	- do -	86.50	75.29	80.89	80.89
CM056	- do -	28.02	20.60	24.31	24.31
CM057	- do -	76.75	63.55	70.15	70.15
CM058	- do -	77.28	78.56	77.92	77.92
CM059	- do -	80.00	79.66	79.83	79.83
CM060	- do -	81.30	71.43	76.36	76.36
CM061	- do -	88.70	63.72	76.20	76.21
CM062	- do -	73.85	75.75	74.80	74.80
	Mean	69.57	63.76	66.66	
	C.D (0.05) - Treatments	1.98			
	C.D (0.05) - Seasons	8.33			
	C.D (0.05) – Treatments x Seasons	NS			

S_1 – Season 1 S_2- Season 2 S_3- Season 3

NS- Non-Significant

Fig 4. Percentage of fruit fly infestation over three seasons

Table.17. Classification based on their relative degree of resistance to fruit fly

Scale	Rating	Fruit damage (per cent)	Accessions
1	Immune	0	Nil
2	Highly resistant	1-10	Nil
3	Resistant	11-20	CM012, CM033 and CM034
4	Moderately resistant	21-50	CM002, CM045 and CM056
5	Susceptible	51-75	CM008, CM010, CM011, CM014, CM015, CM016, CM017, CM018, CM020, CM022, CM023, CM024, CM025, CM028, CM035, CM036, CM037, CM047, CM050, CM051, CM053, CM057, CM061 and CM062
6	Highly susceptible	76-100	CM001, CM003, CM004, CM005, CM006, CM007, CM009, CM019, CM032, CM038, CM039, CM040, CM042, CM043, CM044, CM058, CM059, CM060, CM046, CM048, CM049, CM052 and CM055

Lowest mean infestation by melon fruit fly was recorded in CM012(17.50 per cent), followed by CM033(18.35 per cent), and CM034 (18.58 per cent) which were on par and these accessions were found resistant to fruit fly infestation from the present study (Plate10). Highest infestation by melon fruit fly was recorded in the accession CM044(83.82 per cent) followed by CM009 (80.83 per cent) andCM055 (80.89 per cent) which were found susceptible to fruit fly infestation from the present study.

4.5.1. Identification of species of *Zeugodacus*

Different species of melon fruit fly infesting oriental pickling accessions were identified with the help of Dr. David K.J, Scientist (Entomology), ICAR-National Bureau of Agricultural Insect Resources (NBAIR), Bengaluru, Karnataka. The specimens were identified as *Zeugodacus cucurbitae* in all the accessions except CM014, and *Zeugodacus tau* in the accession CM014. The genus *Bactrocera* is now renamed as the genus *Zeugodacus*. (Plate 11 and Plate 12).

4.5.2. Confirmation of resistance to melon fruit fly

4.5.2.1. Confirmation study in the field

Mean data on melon fruit fly infestation wa**s** recorded from three seasons *viz.*, March 2016 - May 2016, September 2016 - November 2016 and March 2017 - May of 2017 and the pooled mean data of three seasons were analyzed for significance of means and the results are presented in the Table.18

Highest number of days taken to fruit fly infestation after anthesis was recorded in the accession CM034 (11.73 days) followed by CM012 and CM033 (11.20 days) were on par and CM056 (10.93 days) was significantly different. It was clear that in these accessions, melon fruit fly infestation started approximately two weeks after anthesis hence, were succumbed to less infestation and were grouped as resistant accessions from the present study (Fig. 5).

Among the three seasons, lowest number of days taken to fruit fly infestation was in March 2017 - May of 2017, followed by September 2016- November 2016 and March 2016 - May 2016 in that order. There was no significant interactions for days to fruit fly infestation after anthesis over three seasons.

CM012 **CM033** **CM034**

Plate 10. Resistant accessions of oriental pickling melon

Male **Female**

Plate 11. Male and female fruit flies of *Zeugodacus cucurbitae*

Male **Female**

Plate 12. Male and female fruit flies of *Zeugodacus tau*

Table.18. Days to fruit fly infestation after anthesis over three seasons

Accessions	S_1	S_2	S_3	Mean treatments
CM001	6.10	6.00	5.90	6.00
CM002	6.60	7.00	6.60	6.73
CM003	6.80	6.60	7.00	6.80
CM004	6.60	6.70	6.50	6.60
CM005	6.50	6.10	6.60	6.40
CM006	5.90	5.80	5.90	5.86
CM007	7.50	7.50	7.20	7.40
CM008	8.00	7.50	7.70	7.73
CM009	7.90	8.30	8.20	8.13
CM010	7.90	7.90	8.00	7.93
CM011	8.30	8.10	8.60	8.33
CM012	11.60	11.00	11.00	11.20
CM014	7.10	7.10	7.80	7.33
CM015	6.70	6.00	6.70	6.46
CM016	6.30	6.00	6.50	6.26
CM017	5.20	5.30	5.70	5.40
CM018	6.80	7.10	6.90	6.93
CM019	8.20	8.10	8.10	8.13
CM020	9.80	9.60	9.60	9.66
CM022	9.30	9.10	9.00	9.13
CM023	8.50	7.90	7.80	8.06
CM024	8.30	8.80	7.70	8.26
CM025	9.00	8.40	8.00	8.46
CM028	9.20	9.20	8.60	9.00
CM032	8.80	8.70	8.50	8.66
CM033	11.30	11.20	11.10	11.20
CM034	11.80	11.70	11.70	11.73
CM035	8.00	7.90	7.90	7.93
CM036	7.80	8.00	7.80	7.86
CM037	7.20	7.10	7.30	7.20
CM038	8.30	8.30	7.40	8.00
CM039	9.00	8.60	8.80	8.80
CM040	9.20	9.50	8.70	9.13
CM042	11.00	10.20	10.20	10.46
CM043	7.60	7.70	8.10	7.80

CM044	8.70	8.90	8.60	8.73
CM045	10.40	9.40	9.00	9.60
CM046	9.10	8.80	8.70	8.86
CM047	8.80	8.50	8.70	8.66
CM048	9.70	9.30	9.20	9.40
CM049	9.60	9.50	9.30	9.46
CM050	9.30	9.30	9.40	9.33
CM051	9.20	9.50	9.10	9.26
CM052	8.60	9.00	8.80	8.80
CM053	8.10	8.40	8.10	8.20
CM055	8.90	8.80	8.90	8.86
CM056	11.50	10.20	11.10	10.93
CM057	9.00	8.70	9.30	9.00
CM058	8.50	8.60	8.90	8.66
CM059	8.90	9.00	9.10	9.00
CM060	8.50	8.70	8.80	8.66
CM061	8.20	8.50	8.30	8.33
CM062	8.40	8.20	8.40	8.33
	8.44	8.33	8.32	
			C.D (0.05) - Treatments	0.628
			C.D (0.05) - Seasons	NS
			C.D (0.05) – Treatments x Seasons	NS

S_1 – Season 1 S_2- Season 2 S_3- Season 3

NS-Non-Significant

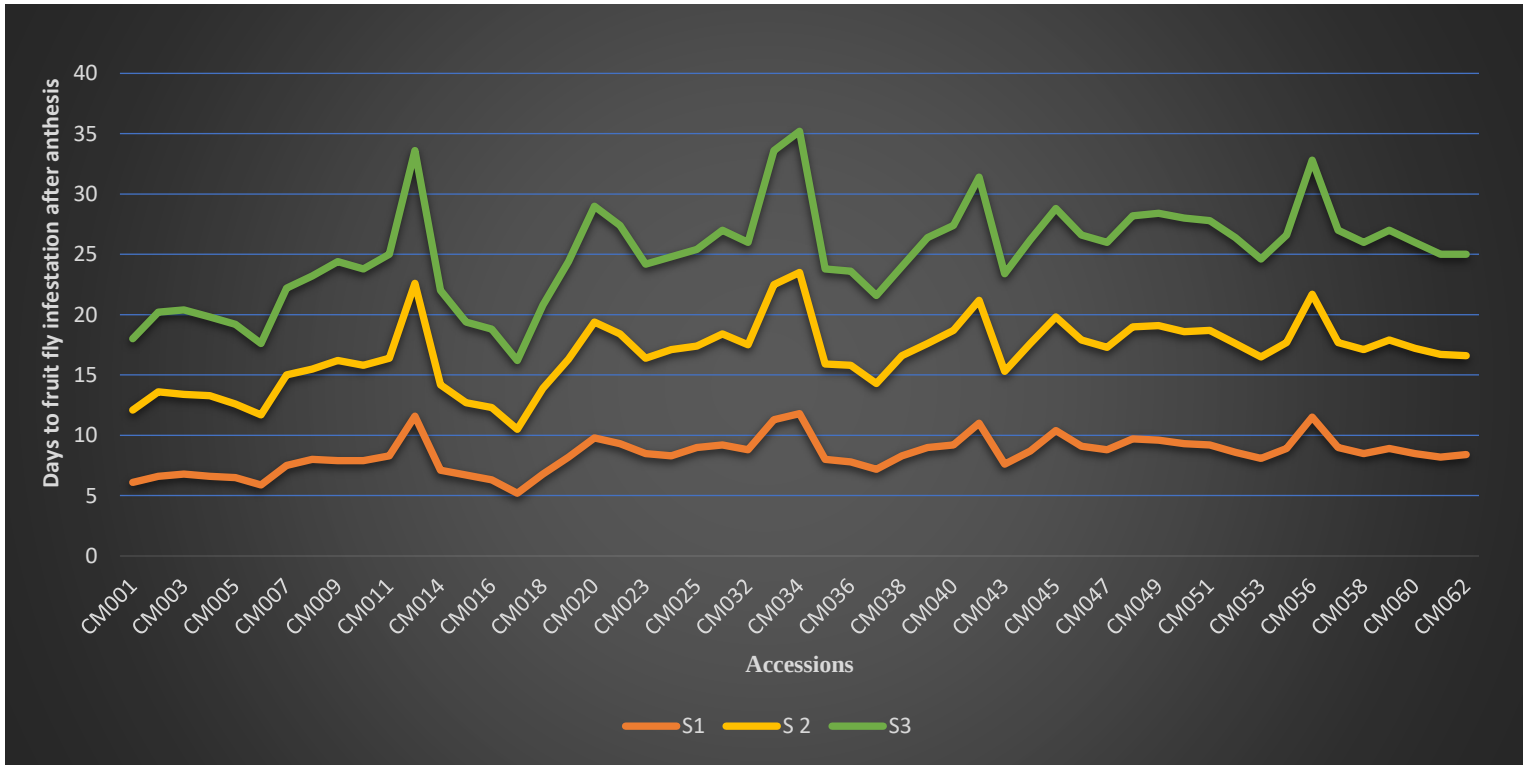


Fig 5. Days to fruit fly infestation after anthesis over three seasons

4.5.2.2. No choice assay

Fresh fruits of resistant accessions *viz*; CM012, CM033, CM034 and CM056 were kept under cage condition in the laboratory for one month to confirm resistance to melon fruit fly as per the methodology detailed under 3.3.2.3.

Freshly emerged fruit flies were used for the assay. From each infested fruit nearly 20-30 fruit flies were emerged after two weeks. Freshly emerged five male and female fruit flies were released in the cage, fed with sugar and jaggary solution, allowed random mating and allowed oviposition on the fruits kept inside the cage. After one month of study, there were no infestations by the fruit flies on the fruit kept under cage and the fruits were fresh outside as well as inside the cage (Plate13). Thus, it was confirmed that the accessions CM012, CM033, CM034 and CM056 exhibited resistance to fruit fly under cage condition also.

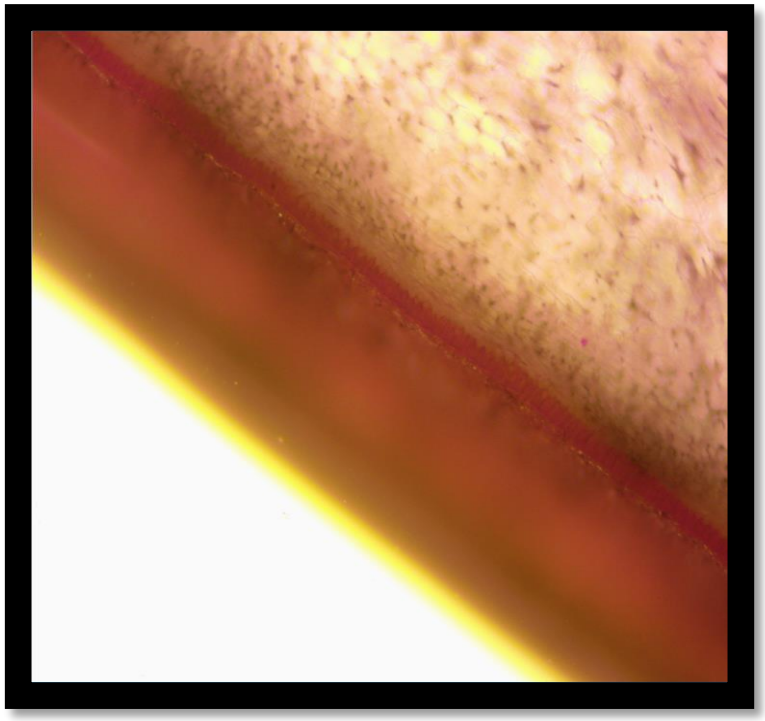
4.5.2.3. Anatomical studies

Anatomical studies were undertaken to record skin thickness in resistant and susceptible accessions. The accessions namely CM034 (resistant) and CM061 (susceptible) were selected. Transverse sections of skin were taken from fresh fruit piece and observed under Electron Microscope. Anatomical studies revealed that the resistant accession CM034 had a skin thickness of 348.55µm while susceptible accession CM061 had only a thickness of 65.65µm (Plate14). From the present study, it was revealed that more skin thickness favoured resistance to fruit fly infestation.

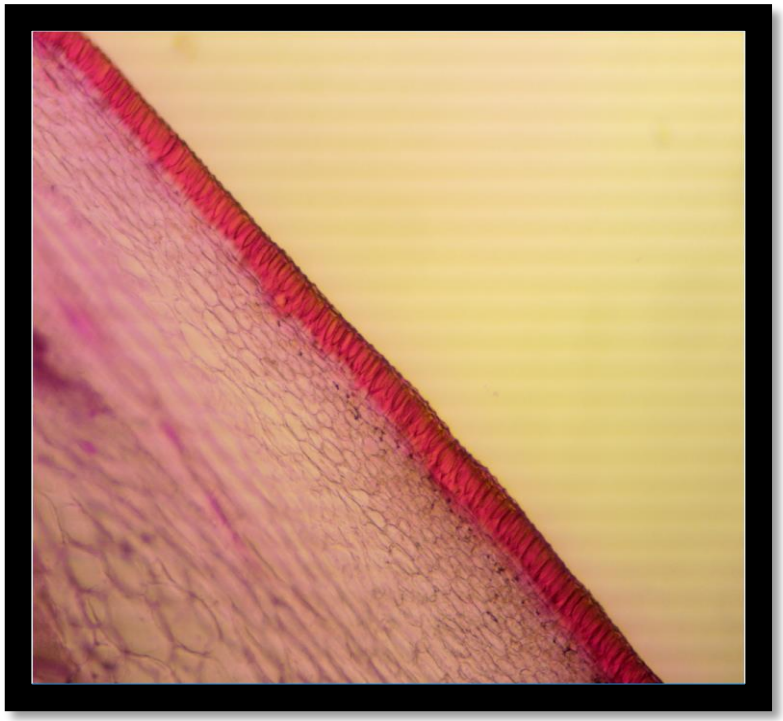
4.6.0. Incorporation of fruit fly resistance to high yielding accessions.

The accessions selected from the experiment I and wild species of *Cucumis melo* were used for the hybridization programme to transfer the resistant gene(s) from wild species to high yielding cultivated accessions. The accessions CM022, CM033, CM045, CM047, CM051, CM060, CM061 and CM062 were used as female parents and wild species *viz*., *Cucumis melo* var. *agrestis* (W-51), *Cucumis melo* var. *agrestis* (W-10) and *Cucumis melo* ssp. *callosus* were used as male parents. The accession CM033 was used as

Plate 13. Confirmation study and fruit showing no symptoms of fruit-fly attack



CM034



CM061

Plate 14. Anatomical studies

both male and female parent. The direct crosses were made to produce 31 F_1's as shown in Table 19. (Plate 15 and Plate 16).

Results of evaluation on qualitative characters such as flower colour, stem hairiness, fruit shape, and fruit colour at maturity, skin surface, skin hardness, and skin texture, taste of fruit, flesh colour, flesh texture, flesh flavour, fruit bitterness and seed colour of thirty one F_1's were presented in Appendix III, (Plate 17).

4.6.1 Mean performance of F_1s for quantitative characters

Quantitative data recorded from F_1s were analyzed for significance of means and the results are presented in Table.20.

4.6.1.1. Days to first female flower production

Among the F_1's, early female flower production was observed in CM061 X *Cucumis melo* var. *agrestis* (W-51) and CM062 X *Cucumis melo* ssp. *callosus* (31.86 days) produced female flower early. Female flower appeared late (38.80 days) in the F_1 s of CM022 X *Cucumis melo* var. *agrestis* (W-10).

4.6.1.2. Days to first male flower production

The lowest number of days taken to produce first male flower was observed in the F_1's of CM047X CM033, CM022 X CM033 (25.00 days) followed by CM022 X *Cucumis melo* var. *agrestis* (W-10) (25.20 days). Highest number of days taken to produce first male flower was noticed in F_1 of CM062 X CM033 (33.80 days), followed by CM051x *Cucumis melo* var. *agrestis* (W-10) (32.66 days).

4.6.1.3. Node at first female flower

Node at first female flower produced was lowest (2.26) in the F_1's of CM047 X *Cucumis melo* ssp. *callosus*. Female flower produced at the higher node (7.46) was in the F_1 s of CM051 X *Cucumis melo* ssp. *callosus*.

4.6.1.4. Node of first male flower

The node at first male flower produced in the lowest node (2.33) in the F_1's of CM047 X CM033 followed by CM047 X *Cucumis melo* ssp. *callosus*, CM045 X *Cucumis melo* var. *agrestis* (W-10) and CM051 X *Cucumis melo* var. *agrestis* (W-10) (2.40). The

Table. 19. Direct crosses of 31 F_1's

Sl. No.	**Crosses**
1	CM022 X *Cucumis melo* var. *agrestis* (W-10)
2	CM022 X *Cucumis melo* var. *agrestis* (W-51)
3	CM022 X *Cucumis melo* ssp. *Callosus*
4	CM022 X CM033
5	CM033 X *Cucumis melo* var. *agrestis* (W-10)
6	CM033 X *Cucumis melo* var. *agrestis* (W-51)
7	CM033X *Cucumis melo* ssp. C*allosus*
8	CM045X *Cucumis melo* var. *agrestis* (W-10)
9	CM045 X *Cucumis melo* var. *agrestis* (W-51)
10	CM045X *Cucumis melo* ssp. *Callosus*
11	CM045 X CM033
12	CM047X *Cucumis melo* var. *agrestis* (W-10)
13	CM047 X *Cucumis melo* var. *agrestis* (W-51)
14	CM047 X *Cucumis melo* ssp. *Callosus*
15	CM047 X CM033
16	CM051 X *Cucumis melo* var. *agrestis* (W-10)
17	CM051 X *Cucumis melo* var. *agrestis* (W-51)
18	CM051 X *Cucumis melo* ssp. *Callosus*
19	CM051 X CM033
20	CM060 X *Cucumis melo* var. *agrestis* (W-10)
21	CM060 X *Cucumis melo* var. *agrestis* (W-51)
22	CM060 X *Cucumis melo* ssp. *Callosus*
23	CM060X CM033
24	CM061 X *Cucumis melo* var. *agrestis* (W-10)
25	CM061 X *Cucumis melo* var. *agrestis* (W-51)
26	CM061 X *Cucumis melo* ssp. C*allosus*
27	CM061 X CM033
28	CM062 X *Cucumis melo* var. *agrestis* (W-10)
29	CM062 X *Cucumis melo* var. *agrestis* (W-51)
30	CM062 X *Cucumis melo* ssp. *Callosus*
31	CM062 X CM033

Cucumis melo var. *agrestis* (W-51, W-10) *Cucumis melo* ssp. *callosus* **CM033**

Plate 15. Male parents used in hybridization programme

CM022 **CM033** **CM045** **CM047**

CM051 **CM060** **CM061** **CM062**

Plate 16. Female Parents used in hybridization programme

Plate 17. Variability of fruit shape in F_1 generations

Table.20. Mean performance of F_1 of oriental pickling melon

Direct crosses of F_1's	1	2	3	4	5	6	7	8	9
CM022 X *Cucumis melo* var. *agrestis* (W-10)	38.80	25.20	6.06	2.73	222.53	9.46	4.13	8.46	27.36
CM022 X *Cucumis melo* var. *agrestis* (W-51)	35.20	26.46	5.60	2.73	159.86	9.11	3.60	9.13	28.78
CM022 X *Cucumis melo* ssp. *callosus*	35.53	27.46	4.06	3.93	219.33	5.20	2.93	7.60	24.24
CM022 X CM033	34.93	25.00	4.33	3.73	251.66	5.82	2.66	10.50	31.90
CM033 X *Cucumis melo* var. *agrestis* (W-10)	35.40	30.20	4.40	4.06	234.40	5.33	2.53	4.58	18.22
CM033 X *Cucumis melo* var. *agrestis* (W-51)	35.00	29.33	4.73	3.26	167.33	7.06	3.53	6.82	21.63
CM033X *Cucumis melo* ssp. *callosus*	35.66	29.53	3.46	3.60	105.40	6.96	3.26	6.15	23.22
CM045X *Cucumis melo* var. *agrestis* (W-10)	34.46	26.53	4.13	2.40	138.40	11.39	3.00	7.35	23.45
CM045 X *Cucumis melo* var. *agrestis* (W-51)	34.73	25.73	4.73	2.66	291.20	10.00	4.73	6.39	21.02
CM045X *Cucumis melo* ssp. *callosus*	35.20	26.73	4.20	2.80	217.93	9.33	3.46	6.74	22.91
CM045 X CM033	37.00	26.93	5.06	3.13	230.33	6.05	4.60	7.24	24.90
CM047X *Cucumis melo* var. *agrestis* (W-10)	35.86	25.53	4.33	2.86	223.53	5.74	3.26	6.67	23.80
CM047 X *Cucumis melo* var. *agrestis* (W-51)	35.20	26.00	4.40	4.06	133.00	8.91	3.40	6.74	19.51
CM047 X *Cucumis melo* ssp. *callosus*	35.06	27.80	2.26	2.40	194.20	9.94	3.60	7.06	22.43
CMO47 X CM033	36.60	25.00	5.60	2.33	181.06	5.48	3.80	7.50	23.26
CM051 X *Cucumis melo* var. *agrestis* (W-10)	37.93	32.66	3.93	2.40	108.13	12.09	4.13	6.65	23.19
CM051 X *Cucumis melo* var. *agrestis* (W-51)	35.40	28.46	5.40	3.26	233.06	10.47	3.93	7.60	23.36
CM051 X *Cucumis melo* ssp. *callosus*	36.13	28.33	7.46	2.86	263.80	7.17	2.86	8.71	32.71
CM051 X CM033	37.66	27.93	5.66	2.86	156.06	8.81	3.60	8.30	25.52

CM060 X *Cucumis melo* var. *agrestis* (W-10)	35.86	26.66	4.66	2.86	266.53	9.34	2.80	7.91	27.21
CM060 X *Cucumis melo* var. *agrestis* (W-51)	34.33	28.00	4.60	3.00	268.73	8.77	3.86	7.84	24.50
CM060 X *Cucumis melo* ssp. *callosus*	35.00	27.20	4.33	3.93	244.40	6.98	2.53	9.46	28.02
CM060X CM033	36.33	26.40	4.40	3.33	274.26	7.50	3.60	7.00	25.62
CM061 X *Cucumis melo* var. *agrestis* (W-10)	36.13	27.20	4.20	3.00	282.13	9.21	3.26	6.52	21.35
CM061 X *Cucumis melo* var. *agrestis* (W-51)	31.86	26.93	3.60	3.06	163.33	8.31	3.60	7.67	22.78
CM061 X *Cucumis melo* ssp. *callosus*	35.20	27.13	4.00	3.20	146.06	6.82	4.20	8.78	28.39
CM061 X CM033	35.46	26.13	4.73	3.13	241.53	8.13	4.13	9.04	29.79
CM062 X *Cucumis melo* var. *agrestis* (W-10)	34.86	26.20	5.06	2.93	254.93	8.66	3.86	8.01	23.19
CM062 X *Cucumis melo* var. *agrestis* (W-51)	35.60	25.26	4.66	2.86	226.06	8.00	3.60	5.92	19.44
CM062 X *Cucumis melo* ssp. *callosus*	31.86	25.93	4.80	3.86	210.40	6.40	4.13	5.65	19.44
CM062 X CM033	35.06	33.80	4.53	3.60	263.53	7.46	3.86	6.90	22.75
C.D. (0.05)	1.26	1.02	0.54	0.54	38.91	1.03	0.52	1.14	2.86

1. Days to first female flower production
2. Days to first male flower production
3. Node of first female flower
4. Node of first male flower
5. Vine length (cm)
6. Inter nodal length (cm)
7. Number of branches per plant
8. Fruit diameter (cm)
9. Fruit girth (cm)

Table 20. Contd….

Direct crosses of F_1's	10	11	12	13	14	15	16	17	18
CM022 X *Cucumis melo* var. *agrestis* (W-10)	22.51	696.66	0.18	2.28	15.09	4.39	0.69	657.60	4.53
CM022 X *Cucumis melo* var. *agrestis* (W-51)	28.78	1223.33	0.13	2.62	23.24	4.41	0.74	178.06	3.60
CM022 X *Cucumis melo* ssp. *callosus*	27.54	1260.00	0.16	2.44	18.50	3.55	0.68	218.33	3.86
CM022 X CM033	29.08	1990.00	0.21	3.12	23.20	5.30	1.06	257.26	3.33
CM033 X *Cucumis melo* var. *agrestis* (W-10)	9.18	298.00	0.16	0.72	6.37	3.02	0.52	265.53	4.13
CM033 X *Cucumis melo* var. *agrestis* (W-51)	13.56	336.66	0.16	1.44	7.02	3.80	0.55	141.66	4.33
CM033X *Cucumis melo* ssp. *callosus*	13.62	806.66	0.14	2.36	9.10	4.10	0.52	150.33	6.73
CM045X *Cucumis melo* var. *agrestis* (W-10)	15.96	645.00	0.16	2.16	9.47	3.64	0.67	218.80	5.33
CM045 X *Cucumis melo* var. *agrestis* (W-51)	12.71	533.66	0.19	1.33	6.80	3.66	0.68	623.60	4.93
CM045X *Cucumis melo* ssp. *callosus*	20.26	688.33	0.18	1.94	13.00	3.70	0.68	336.33	4.46
CM045 X CM033	20.08	800.00	0.16	1.58	9.61	4.69	0.66	286.60	5.66
CM047X *Cucumis melo* var. *agrestis* (W-10)	20.00	710.00	0.13	1.59	13.73	3.96	0.58	556.60	3.26
CM047 X *Cucumis melo* var. *agrestis* (W-51)	17.00	476.66	0.16	1.84	9.48	3.73	0.67	734.93	4.80
CM047 X *Cucumis melo* ssp. *callosus*	18.96	718.33	0.12	1.98	14.00	3.87	0.63	547.86	5.80
CM047 X CM033	21.14	763.33	0.13	1.98	11.47	3.95	0.67	543.00	5.60
CM051 X *Cucumis melo* var. *agrestis* (W-10)	13.66	626.66	0.19	1.46	5.89	3.69	0.62	397.13	6.93
CM051 X *Cucumis melo* var. *agrestis* (W-51)	24.22	866.66	0.17	2.12	15.83	3.72	0.68	302.80	4.33
CM051 X *Cucumis melo* ssp. *callosus*	30.12	2041.33	0.18	2.49	19.18	4.12	1.00	168.33	5.40
CM051 X CM033	28.47	1483.33	0.20	2.28	17.98	4.00	0.77	352.53	3.86

CM060 X *Cucumis melo* var. *agrestis* (W-10)	24.37	976.66	0.16	2.37	21.54	3.42	0.66	71.13	3.40
CM060 X *Cucumis melo* var. *agrestis* (W-51)	24.16	1050.00	0.14	2.01	15.84	3.86	0.83	152.46	3.33
CM060 X *Cucumis melo* ssp. *callosus*	29.99	1166.66	0.13	2.90	22.66	3.40	0.73	87.13	3.40
CM060X CM033	19.93	1416.66	0.16	1.86	6.80	3.78	0.68	588.33	5.33
CM061 X *Cucumis melo* var. *agrestis* (W-10)	13.46	676.66	0.07	1.69	6.88	3.35	0.70	524.73	3.93
CM061 X *Cucumis melo* var. *agrestis* (W-51)	15.31	913.33	0.16	1.36	10.07	3.87	0.72	634.33	8.06
CM061 X *Cucumis melo* ssp. *callosus*	29.30	1351.66	0.14	2.52	22.99	4.09	0.69	561.60	4.60
CM061 X CM033	26.96	1288.33	0.15	3.30	17.14	4.90	0.66	333.00	6.93
CM062 X *Cucumis melo* var. *agrestis* (W-10)	17.74	924.66	0.21	0.98	7.08	4.44	0.70	303.40	6.06
CM062 X *Cucumis melo* var. *agrestis* (W-51)	12.03	408.66	0.16	0.95	6.26	3.74	0.68	718.80	3.46
CM062 X *Cucumis melo* ssp. *callosus*	14.72	330.00	0.18	1.20	6.80	4.01	0.65	393.66	6.26
CM062 X CM033	17.52	771.73	0.13	1.58	9.81	3.23	0.62	206.93	5.33
C.D. (0.05)	3.69	482.83	0.03	0.42	2.16	0.46	0.10	192.26	1.52

10. Fruit length (cm)
11. Fruit weight (g)
12. Fruit rind thickness (cm)
13. Flesh thickness (cm)
14. Seed cavity length (cm)
15. Seed cavity breadth (cm)
16. Seed length (cm)
17. Number of seeds per fruit
18. Number of fruits per plant

Table 20. Contd….

Direct crosses of F_1's	19	20	21	22	23	24	25
CM022 X *Cucumis melo* var. *agrestis* (W-10)	49.40	55.33	83.20	1.17	0.52	7.86	53.93
CM022 X *Cucumis melo* var. *agrestis* (W-51)	49.26	52.66	91.33	1.61	0.99	8.46	49.05
CM022 X *Cucumis melo* ssp. *callosus*	49.00	54.00	91.73	1.66	1.06	7.60	56.73
CM022 X CM033	49.60	53.73	86.80	2.04	1.82	8.66	16.39
CM033 X *Cucumis melo* var. *agrestis* (W-10)	51.06	57.06	76.53	0.73	0.55	8.33	38.96
CM033 X *Cucumis melo* var. *agrestis* (W-51)	50.93	50.86	78.20	0.80	0.74	11.06	13.86
CM033X *Cucumis melo* ssp. *callosus*	50.46	50.60	74.86	1.69	1.54	10.40	17.16
CM045X *Cucumis melo* var. *agrestis* (W-10)	50.13	52.20	77.93	1.64	0.85	6.00	46.83
CM045 X *Cucumis melo* var. *agrestis* (W-51)	50.20	56.80	85.60	1.54	0.79	5.33	55.33
CM045X *Cucumis melo* ssp. *callosus*	48.46	52.00	84.26	1.52	0.98	10.80	49.48
CM045 X CM033	48.73	51.86	84.66	3.06	2.74	6.86	13.22
CM047X *Cucumis melo* var. *agrestis* (W-10)	50.93	51.73	74.80	1.16	0.66	6.06	40.01
CM047 X *Cucumis melo* var. *agrestis* (W-51)	50.73	51.93	85.80	1.16	0.43	6.46	70.56
CM047 X *Cucumis melo* ssp. *callosus*	51.26	54.06	77.86	2.11	0.83	5.80	42.22
CMO47 X CM033	49.93	55.60	79.60	1.84	1.41	7.86	26.88
CM051 X *Cucumis melo* var. *agrestis* (W-10)	50.00	53.26	87.66	1.34	0.82	7.00	34.35
CM051 X *Cucumis melo* var. *agrestis* (W-51)	50.60	57.73	86.00	1.52	0.86	6.06	52.91
CM051 X *Cucumis melo* ssp. *callosus*	49.60	56.40	83.60	2.34	1.91	6.46	24.12
CM051 X CM033	49.20	53.60	84.80	1.78	1.20	5.80	48.41
CM060 X *Cucumis melo* var. *agrestis* (W-10)	51.00	56.20	83.73	1.52	0.79	7.86	65.77

CM060 X *Cucumis melo* var. *agrestis* (W-51)	50.93	58.40	83.53	1.49	1.24	8.46	22.14
CM060 X *Cucumis melo* ssp. *callosus*	52.40	59.53	85.86	1.52	1.09	7.60	49.25
CM060X CM033	52.33	53.13	77.80	2.11	1.74	6.00	27.05
CM061 X *Cucumis melo* var. *agrestis* (W-10)	50.73	53.06	87.33	1.09	0.59	5.33	50.95
CM061 X *Cucumis melo* var. *agrestis* (W-51)	49.86	51.86	90.86	2.45	1.83	6.93	37.49
CM061 X *Cucumis melo* ssp. *callosus*	51.53	55.86	90.86	2.19	1.56	6.06	55.44
CM061 X CM033	51.20	55.06	83.73	3.26	2.23	6.46	49.59
CM062 X *Cucumis melo* var. *agrestis* (W-10)	49.46	55.80	83.60	2.14	1.48	5.80	49.76
CM062 X *Cucumis melo* var. *agrestis* (W-51)	49.46	53.06	88.02	0.84	0.50	6.00	50.41
CM062 X *Cucumis melo* ssp. *callosus*	49.66	54.13	87.00	1.56	1.03	5.33	46.02
CM062 X CM033	49.66	54.46	89.40	2.12	1.59	6.86	36.65
C.D. (0.05)	0.83	1.31	2.14	0.55	0.52	0.38	15.75

19. Days taken for fruit maturity
20. Days to first harvest
21. Days to last harvest
22. Yield per plant (kg)
23. Marketable yield per plant (kg)
24. Days to fruit fly infestation after anthesis
25. Percentage of fruit fly infestation

highest node (4.06) at which first male flower was appeared in the F_1's of CM033 X *Cucumis melo* var. *agrestis* (W-10) and CM047 X *Cucumis melo* var. *agrestis* (W-51) followed by CM022 X *Cucumis melo* ssp. *callosus*, CM060 X *Cucumis melo* ssp. *callosus* (3.93).

4.6.1.5. Vine length (cm)

The lowest vine length was recorded in the F_1's of CM033 X *Cucumis melo* ssp. *callosus* (105.40 cm) followed by CM051 X *Cucumis melo* var. *agrestis* (W-10) (108.13 cm) and CM047 X *Cucumis melo* var. *agrestis* (W-51) (133.00 cm). The highest vine length was in the F_1's of CM045 X *Cucumis melo* var. *agrestis* (W-51) (291.20 cm) followed by CM061 X *Cucumis melo* var. *agrestis* (W-10) (282.13 cm) and CM060 X CM033 (274.26 cm).

4.6.1.6. Inter nodal length (cm)

The lowest inter nodal length was in the F_1's of CM022 X *Cucumis melo* ssp. *callosus* (5.20 cm) followed by CM047 X CM033 (5.48 cm) and CM047 X *Cucumis melo* var. *agrestis* (W-10) (5.74 cm). The highest inter nodal length was obtained in the cross of CM051 X *Cucumis melo* var. *agrestis* (W-10) (12.09 cm) and CM045 X *Cucumis melo* var. *agrestis* (W-10) (11.39 cm).

4.6.1.7. Number of branches per plant

The lowest number of branches per plant was recorded in the F_1's of CM033 X *Cucumis melo* var. *agrestis* (W-10) and CM060 X *Cucumis melo* ssp. *callosus* (2.53) followed by CM022 X CM033 (2.66). The highest number of branches per vine was in the cross CM045 X *Cucumis melo* var. *agrestis* (W-51) (4.73) followed by CM045 X CM033 (4.60), CM061 X *Cucumis melo* ssp. *callosus* (4.20) and were on par.

4.6.1.8. Fruit diameter (cm)

The lowest fruit diameter was in the F_1's of CM033 X *Cucumis melo* var. *agrestis* (W-10) (4.58 cm), CM062 X *Cucumis melo* ssp. *callosus* (5.65 cm) and were on par. The highest fruit diameter was in CM022 X CM033 (10.50 cm) followed by CM060 X *Cucumis melo* ssp. *callosus* (9.46 cm) and were on par.

4.6.1.9. Fruit girth (cm)

The lowest fruit girth was recorded in the F_1's of CM033 X *Cucumis melo* var. *agrestis* (W-10) (18.22 cm), CM062 X *Cucumis melo* var. *agrestis* (W-51), and CM062 X *Cucumis melo* ssp. *callosus* (19.44 cm). Highest fruit girth was in the F_1's of CM051 X *Cucumis melo* ssp. *callosus* (32.71 cm) followed by CM022 X CM033 (31.90 cm) and were on par.

4.6.1.10. Fruit length (cm)

The lowest fruit length was obtained in F_1's of CM033 X *Cucumis melo* var. *agrestis* (W-10) (9.18 cm) followed by CM062 X *Cucumis melo* var. *agrestis* (W-51) (12.03 cm). The highest fruit length was in the F_1's of CM051 X *Cucumis melo* ssp. *callosus* (30.12 cm) followed by CM060 X *Cucumis melo* ssp. *callosus* (29.99 cm), CM061 X *Cucumis melo* ssp. *callosus* (29.30 cm) and were on par.

4.6.1.11. Fruit rind thickness (cm)

Lowest fruit rind thickness was recorded in the F_1's of CM061 X *Cucumis melo* var. *agrestis* (W-10) (0.07 cm). Fruit rind thickness was highest in the F_1's CM022 X CM033) and CM062 X *Cucumis melo* var. *agrestis* (W-10) (0.21 cm), followed by CM051 X CM033 (0.20 cm) and were on par.

4.6.1.12. Flesh thickness (cm)

Lowest flesh thickness was in the F_1's of CM033 X *Cucumis melo* var. *agrestis* (W-10) (0.72 cm). Highest flesh thickness was in the F_1's CM061 X CM033 (3.30 cm) followed by CM022 X CM033 (3.12 cm), CM060 X *Cucumis melo* ssp. *callosus* (2.90 cm) and were on par.

4.6.1.13. Seed cavity length (cm)

Seed cavity length was lowest in the F_1's of CM051 X *Cucumis melo* var. *agrestis* (W-10) (5.89 cm) followed by CM062 X *Cucumis melo* var. *agrestis* (W-51) (6.26 cm), CM033 X *Cucumis melo* var. *agrestis* (W-10) (6.37 cm) and were on par. Seed cavity length was highest in the F_1's of CM022 X *Cucumis melo* var. *agrestis* (W-51) (23.24 cm), CM022 X CM033 (23.20 cm), CM061 X *Cucumis melo* spp. *callosus* (22.99 cm) and were on par.

4.6.1.14. Seed cavity breadth (cm)

The lowest seed cavity breadth was obtained in the F_1's CM033 X *Cucumis melo* var. *agrestis* (W-10) (3.02 cm) followed by CM062 X CM033 (3.23 cm) and CM061 X *Cucumis melo* var. *agrestis* (W-10) (3.35 cm) were on par. Seed cavity breadth was highest in the F_1's of CM022 X CM033 (5.30 cm), CM061 X CM033 (4.90 cm) and were on par.

4.6.1.15. Seed length (cm)

The lowest seed length was recorded in two F_1's CM033 X *Cucumis melo* var. *agrestis* (W-10), CM033 X *Cucumis melo* ssp. *callosus* (0.52 cm), CM033 X *Cucumis melo* var. *agrestis* (W-51) (0.55 cm), CM047 X *Cucumis melo* var. *agrestis* (W-10) (0.58 cm) and were on par. Highest seed length was in the F_1's of CM022 X CM033 (1.06 cm) followed by CM051 X *Cucumis melo* ssp. *callosus* (1.00 cm) and were on par.

4.6.1.16. Number of seeds per fruit

The lowest number of seeds was observed in the F_1's CM060 X *Cucumis melo* var. *agrestis* (71.13), CM060 x *Cucumis melo* ssp. *Callosus* (87.13), CM033X *Cucumis melo* var. *agrestis* (W-51) (141.66) and were on par. Highest number of seeds per fruit was in the F_1's CM047 X *Cucumis melo* var. *agrestis* (W-51) (734.93) followed by CM062 X *Cucumis melo* var. *agrestis* (W-51) (718.80) and were on par.

4.6.1.17. Days taken for fruit maturity

Lowest days taken for fruit maturity was obtained in the F_1's CM045 X *Cucumis melo* ssp. *callosus* (48.46 days) followed by CM045 X CM033 (48.73 days), CM022 X *Cucumis melo* ssp. *callosus* (49.00 days) and were on par. Highest days taken to for fruit maturity was in the F_1's CM060 X *Cucumis melo* ssp. *callosus* (52.40 days) followed by CM060 X CM033 (52.33 days) and were on par.

4.6.1.18. Days to first harvest

Lowest number of days to first harvest was in the F_1's CM033 X *Cucumis melo* ssp. *callosus* (50.60 days) followed by CM033 X *Cucumis melo* var. *agrestis* (W-51) (50.86 days), CM047 X *Cucumis melo* var. *agrestis* (W-10) (51.73 days) and were on par. Highest

days to first harvest was in the F_1's CM060 X *Cucumis melo* ssp. *callosus* (59.53 days), CM060 X *Cucumis melo* var. *agrestis* (W-51) (58.40 days) and were on par.

4.6.1.19. Days to last harvest

Lowest number of days to last harvest was in the F_1's CM047 X *Cucumis melo* var. *agrestis* (W-10) (74.80 days), CM033 X *Cucumis melo* ssp. *callosus* (74.86 days), and were on par. Highest days taken for last harvest was noticed in the F_1's CM022 X *Cucumis melo* ssp. *callosus* (91.73 days) followed by CM022 X *Cucumis melo* var. *agrestis* (W-51) (91.33 days) and were on par.

4.6.1.20. Fruit weight (g)

The lowest fruit weight was obtained in the F_1's of CM033 X *Cucumis melo* var. *agrestis* (W-10) (298.00 g), CM062 X *Cucumis melo* ssp. *callosus* (330.00 g), CM033 X *Cucumis melo* var. *agrestis* (W-51) (336.66 g) and were on par. Highest fruit weight was in the F_1's of CM051 X *Cucumis melo* ssp. *callosus* (2041.33 g) followed by CM022 X CM033 (1990.00 g), CM051 X CM033 (1483.33 g), CM060 X CM033 (1416.66 g) and CM061 X *Cucumis melo* ssp. *callosus* (1351.66 g) and were on par

4.6.1.21. Number of fruits per plant

The lowest number of fruits per fruits was in the F_1's CM047 X *Cucumis* melo var. *agrestis* (W-10) (3.26), CM022 X CM033, CM060 X *Cucumis melo* var. *agrestis* (W-51) (3.33), CM060 x *Cucumis melo* ssp. *callosus* (3.40) and were on par. The highest number of fruits per plant was in the F_1's CM061 X *Cucumis melo* var. *agrestis* (W-51) (8.06), CM051 X *Cucumis melo* var. *agrestis* (W-10), CM061 X CM033 (6.93) and were on par.

4.6.1.22. Yield per plant (kg)

Lowest yield was observed in the F_1's CM033 X *Cucumis melo* var. *agrestis* (W-10) (0.73 kg), CM033 X *Cucumis melo* var. *agrestis* (W-51) (0.80 kg), and CM062 X *Cucumis melo* var. *agrestis* (W-51) (0.84 kg) and were on par. Highest yield per plant was in the F_1's CM061 X CM033 (3.26 kg) followed by CM045 X CM033 (3.04 kg) and were on par.

4.6.1.23. Marketable yield per plant (kg)

Lowest marketable yield per plant was in the F_1's CM047 X *Cucumis melo* var. *agrestis* (W-51) (0.43 kg), CM062 X *Cucumis melo* var. *agrestis* (W-51) (0.50 kg), CM022 X *Cucumis melo* var. *agrestis* (W-10) (0.52 kg), and were on par. Highest marketable fruit yield was in the F_1's CM045 X CM033 (2.74 kg) followed by CM061 X CM033 (2.23 kg) and were on par.

4.6.1.24. Days to fruit fly infestation after anthesis

The lowest number of days taken for fruit fly infestation after anthesis was in the F_1's, CM045 X *Cucumis melo* var. *agrestis* (W-51), CM061 X *Cucumis melo* var. *agrestis* (W-10) and CM062 X *Cucumis melo* ssp. *callosus* (5.33 days). Highest number of days taken for fruit fly infestation after anthesis was in CM033 X *Cucumis melo* var. *agrestis* (W-51) (11.06 days) followed by CM045 X *Cucumis melo* ssp. *callosus* (10.80 days) and were on par.

4.6.1.25. Percentage of fruit fly infestation

Percentage of fruit fly infestation was in the F_1's of CM045 X CM033 (13.22 per cent) followed by CM033 X *Cucumis melo* var. *agrestis* (W-51) (13.86 per cent), CM022 X CM033 (16.39 per cent), CM033 X *Cucumis melo* ssp. *callosus* (17.16 per cent) and were on par. Highest fruit fly infestation was noticed in the F_1's CM047 X *Cucumis melo* var. *agrestis* (W-51) (70.56 per cent), CM060 X *Cucumis melo* var. *agrestis* (W-10) (65.77 per cent), CM022 X *Cucumis melo* ssp. *callosus* (56.73 per cent) and were on par.

4.6.1.26. Incidence of different species of fruit fly

The species *Zeugodacus cucurbitae* was noticed during the cropping season. This species was the most common type infesting in all accessions.

4.6.1.27. Incidence of pests and diseases

Pests observed during the cropping season was pumpkin beetle (*Raphidopapa foveicollis*) and leaf eating caterpillar (*Diaphinia indica*). Plants were affected with mosaic disease.

4.7.0. Generation mean analysis

Considering the resistance to fruit fly, yield, yield attributes and absence of bitterness, the following cross combinations were chosen for generation mean analysis to elucidate inheritance.

1. Intra-specific cross of CM045 X CM033 (CrossI): F_1's exhibited more number of branches per plant. Days to attain horticultural maturity was less and inter nodal length was lowest in this cross. Yield per plant was highest, percentage of fruit fly infestation was low compared to other F_1's. It showed white flesh with sour taste (Plate 18).
2. Intra-specific cross of CM061 X CM033 (crossII): F_1's exhibited highest in fruit length, flesh thickness, number of fruits per plant and fruit yield per plant. Percentage of fruit fly infestation was moderate. The flesh colour was white with sour taste (Plate 19).
3. Inter-specific cross of CM051 X *Cucumis melo* ssp. c*allosus* (crossIII): F_1's exhibited highest fruit girth, fruit length and fruit weight. The days taken to attain horticultural maturity was low. Percentage of fruit fly infestation was moderate. This F_1 exhibits sour taste with white flesh (Plate 20).
4. Inter-specific cross of CM033 X *Cucumis melo* ssp. c*allosus* (crossIV): F_1's exhibited lowest vine length and maximum number of fruits per plant. The percentage of fruit fly infestation was very less so considered as resistant to fruit fly infestation. Fruits showed white flesh with sour taste (Plate 21).

The data was analyzed for significance of means and generation mean analysis to test the difference among six generations and to elucidate inheritance respectively.

4.7.1. Mean performance of six generations for quantitative characters.

Data on mean performances of P_1, P_2, F_1's, F_2's, B_1's and B_2's for all quantitative traits were analyzed and the results are presented in the Table.21, (Plate 22, Plate 23, Plate 24, Plate 25 and Plate 26).

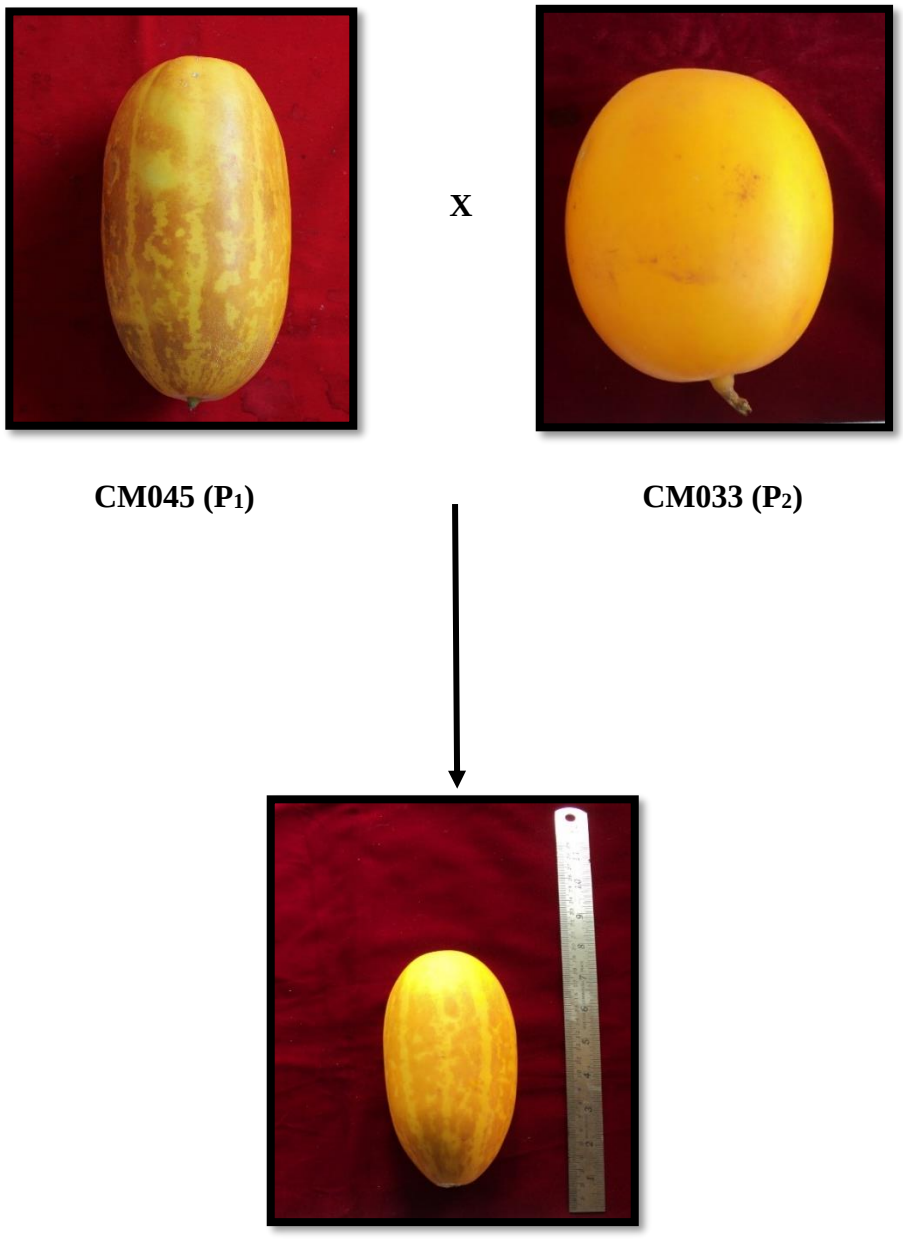


Plate 18. The Cross I (CM045 X CM033)

CM061 (P_1) **CM033 (P_2)**

CM061 X CM033 (F_1)

Plate 19. The Cross II (CM061 X CM033)

X

CM051 (P_1) ***Cucumis melo* ssp. *callosus* (P_2)**

CM051 x *Cucumis melo* ssp. *callosus* (F_1)

Plate 20. The Cross III (CM051 X *Cucumis melo* ssp. *callosus*)

CM033 (P_1) **X** ***Cucumis melo* ssp. *callosus* (P_2)**

CM033 x ***Cucumis melo* ssp. *callosus* (F_1)**

Plate 21. The Cross IV (CM033 X *Cucumis melo* ssp. *callosus*)

Table.21. Mean performance of six generations for quantitative characters

Pedigree	1	2	3	4	5	6	7	8	9
PARENTS									
CM033 (P_1 and P_2)	29.86	27.93	5.46	1.60	107.66	6.28	4.00	8.74	25.00
CM045 (P_1)	32.60	26.73	3.00	2.06	217.66	8.26	4.13	11.46	36.98
CM051 (P_1)	30.26	27.20	5.06	1.73	118.93	8.75	4.00	10.61	33.28
CM061 (P_1)	32.66	28.93	5.20	1.66	140.66	7.59	4.06	9.81	23.68
Cucumis melo ssp. *callosus* (P_2)	30.80	26.33	4.86	1.80	139.46	3.46	4.26	3.06	7.17
F_1 CROSSES									
CM045 X CM033	30.53	27.66	4.80	1.60	226.86	4.99	4.33	10.92	31.09
CM061 X CM033	31.40	26.66	4.33	1.66	219.6	7.90	4.06	7.90	22.67
CM051 X *Cucumis melo* ssp. *callosus*	31.73	27.33	5.20	1.60	223.93	7.79	3.46	9.33	31.52
CM033 X *Cucumis melo* ssp. *callosus*	33.66	27.13	4.86	1.80	92.46	6.69	4.00	9.70	26.51
F_2 CROSSES									
CM045 X CM033	31.80	27.93	4.86	1.53	239.20	4.68	4.60	10.88	31.30
CM061 X CM033	30.86	27.86	4.53	1.73	248.00	7.76	4.46	9.13	27.42
CM051 X *Cucumis melo* ssp. *callosus*	30.73	27.53	5.86	1.73	187.60	7.70	4.46	8.48	26.64
CM033 X *Cucumis melo* ssp. *callosus*	29.8	26.93	4.66	2.20	95.60	7.10	4.06	8.60	32.00
B_1 CROSSES									
(CM045 X CM033) X CM045	32.46	28.93	6.13	1.66	227.8	4.38	4.06	7.26	21.82

(CM061 X CM033) X CM061	30.66	27.77	4.46	2.06	249.46	7.53	3.80	10.23	31.59
(CM051 X *Cucumis melo* ssp. *callosus)* X CM051	31.13	26.4	5.46	1.80	218.4	7.23	3.86	8.18	26.04
(CM033 X *Cucumis melo* ssp. *callosus*) X CM033	30.33	26.8	5.00	1.73	118.6	7.26	3.93	7.96	25.77
B_2 CROSSES									
(CM045 X CM033) X CM033	31.86	27.33	5.60	1.86	270.73	4.90	4.00	7.50	21.89
(CM061 X CM033) X CM033	32.00	27.33	4.80	2.40	200.40	7.60	4.13	7.61	23.47
(CM051 X *Cucumis melo* ssp. *callosus*) X *Cucumis melo* ssp. *callosus*	31.93	27.13	5.46	2.00	196.06	7.70	4.26	8.98	30.01
(CM033 X *Cucumis melo* ssp. *callosus*) X *Cucumis melo* ssp. *callosus*	32.40	28.20	4.86	1.66	117.20	7.24	3.66	8.23	25.68
CD (0.05)	1.86	0.85	0.54	0.48	28.25	0.60	0.53	0.77	3.04

1. Days to first female flower production
2. Days to first male flower production
3. Node of first female flower
4. Node of first male flower
5. Vine length (cm)
6. Inter nodal length (cm)
7. Number of branches per plant
8. Fruit diameter (cm)
9. Fruit girth (cm)

Table 21. Contd…

Pedigree	10	11	12	13	14	15	16	17	18
PARENTS									
CM033 (P_1 and P_2)	12.62	612.00	0.40	2.22	6.01	4.26	0.48	307.26	8.20
CM045 (P_1)	30.56	995.33	0.23	2.32	16.29	4.02	0.70	118.00	7.93
CM051 (P_1)	23.85	1210.66	0.29	2.41	15.03	4.32	0.72	207.46	8.46
CM061 (P_1)	26.96	1230.00	0.14	2.20	15.16	3.67	0.62	289.06	9.33
Cucumis melo ssp. *callosus* (P_2)	6.10	19.53	0.37	0.80	1.75	0.60	0.26	281.46	18.73
F_1 CROSSES									
CM045 X CM033	18.20	610.00	0.27	2.46	8.57	4.43	0.68	286.60	8.53
CM061 X CM033	15.76	1020.00	0.18	1.72	13.67	3.98	0.68	333.00	7.33
CM051 X *Cucumis melo* ssp. *callosus*	25.86	1230.00	0.22	2.39	14.21	4.73	0.24	168.33	8.26
CM033 X *Cucumis melo* ssp. *callosus*	17.26	680.00	0.29	2.17	7.67	4.67	0.72	150.33	6.73
F_2 CROSSES									
CM045 X CM033	20.94	1093.33	0.19	2.85	13.67	4.46	0.77	308.86	13.26
CM061 X CM033	23.74	930.00	0.18	1.74	12.20	4.07	0.65	361.13	10.20
CM051 X *Cucumis melo* ssp. *callosus*	19.30	1260.00	0.20	1.93	11.94	4.70	0.60	180.86	9.20
CM033 X *Cucumis melo* ssp. *callosus*	17.22	440.00	0.20	1.97	7.24	4.80	0.69	158.26	10.93
B_1 CROSSES									

(CM045 X CM033) X CM045	16.85	350.66	0.15	2.24	12.68	4.00	0.58	294.46	10.06
(CM061 X CM033) X CM061	23.76	1050.00	0.19	2.13	7.46	3.85	0.66	284.66	6.53
(CM051 X *Cucumis melo* ssp. *callosus)* X CM051	25.96	1390.00	0.22	2.00	14.34	4.52	0.70	128.26	9.06
(CM033 X *Cucumis melo* ssp. *callosus*) X CM033	17.92	527.33	0.24	2.16	7.29	4.71	0.72	158.00	6.80
B_2 CROSSES									
(CM045 X CM033) X CM033	17.54	350.66	0.26	2.20	9.82	4.00	0.61	218.20	12.33
(CM061 X CM033) X CM033	13.60	393.33	0.20	1.88	6.72	3.91	0.66	257.66	8.46
(CM051 X *Cucumis melo* ssp. *callosus*) X *Cucumis melo* ssp. *callosus*	27.10	1296.66	0.23	1.98	11.94	4.73	0.66	119.20	7.26
(CM033 X *Cucumis melo* ssp. *callosus*) X *Cucumis melo* ssp. *callosus*	16.32	600.00	0.29	2.10	6.73	3.97	0.33	151.93	6.73
CD (5 per cent)	1.47	295.58	0.05	0.26	1.64	0.74	0.07	116.22	2.83

10. Fruit length (cm)
11. Fruit weight (g)
12. Fruit rind thickness (cm)
13. Flesh thickness (cm)
14. Seed cavity length (cm)
15. Seed cavity breadth (cm)
16. Seed length (cm)
17. Number of seeds per fruit
18. Number of fruits per plant

Table 21. Contd…

Pedigree	19	20	21	22	23	24	25
PARENTS							
CM033 (P_1 and P_2)	72.13	59.53	79.93	4.01	2.98	9.80	23.79
CM045 (P_1)	67.93	59.66	77.80	4.92	2.68	9.06	52.15
CM051 (P_1)	61.06	59.66	78.73	7.51	3.30	9.06	36.61
CM061 (P_1)	62.66	60.73	78.73	7.11	2.24	6.93	52.72
Cucumis melo ssp. *callosus* (P_2)	62.00	63.00	85.26	0.38	0.34	14.26	6.26
F_1 CROSSES							
CM045 X CM033	51.13	54.80	86.26	4.38	2.42	7.86	28.34
CM061 X CM033	59.66	56.06	80.46	5.34	1.92	6.73	35.35
CM051 X *Cucumis melo* ssp. *callosus*	59.93	60.46	83.53	8.06	6.40	7.60	14.55
CM033 X *Cucumis melo* ssp. *callosus*	59.60	59.66	73.20	3.77	3.13	10.13	18.41
F_2 CROSSES							
CM045 X CM033	61.93	61.20	84.20	9.06	4.57	8.60	25.12
CM061 X CM033	60.33	63.33	82.40	7.99	6.26	8.06	20.27
CM051 X *Cucumis melo* ssp. *callosus*	61.00	60.13	90.00	8.69	6.60	8.06	17.27
CM033 X *Cucumis melo* ssp. *callosus*	61.86	61.73	74.40	4.82	4.20	10.46	11.71
B_1 CROSSES							
(CM045 X CM033) X CM045	60.00	61.86	91.66	3.44	2.00	8.46	23.26

(CM061 X CM033) X CM061	55.20	68.33	91.60	5.95	3.21	8.20	21.27
(CM051 X *Cucumis melo* ssp. *callosus)* X CM051	60.66	64.40	88.20	10.18	7.26	8.40	18.07
(CM033 X *Cucumis melo* ssp. *callosus*) X CM033	62.53	62.73	81.73	4.02	3.20	12.46	13.80
B_2 CROSSES							
(CM045 X CM033) X CM033	61.06	64.40	93.26	3.94	2.52	8.00	27.12
(CM061 X CM033) X CM033	55.93	65.66	92.00	3.10	2.73	8.80	17.47
(CM051 X *Cucumis melo* ssp. *callosus*) X *Cucumis melo* ssp. *callosus*	61.53	63.33	90.93	8.07	4.18	8.40	27.59
(CM033 X *Cucumis melo* ssp. *callosus*) X *Cucumis melo* ssp. *callosus*	60.80	63.86	83.00	4.07	2.19	12.86	18.03
CD (0.05)	2.55	3.27	2.52	1.69	1.25	1.02	10.43

19. Days taken for fruit maturity
20. Days to first harvest
21. Days to last harvest
22. Yield per plant (kg)
23. Marketable yield per plant (kg)
24. Days to fruit fly infestation after anthesis
25. Percentage of fruit fly infestation

Plate 22. Variability of fruit shapes in six generations

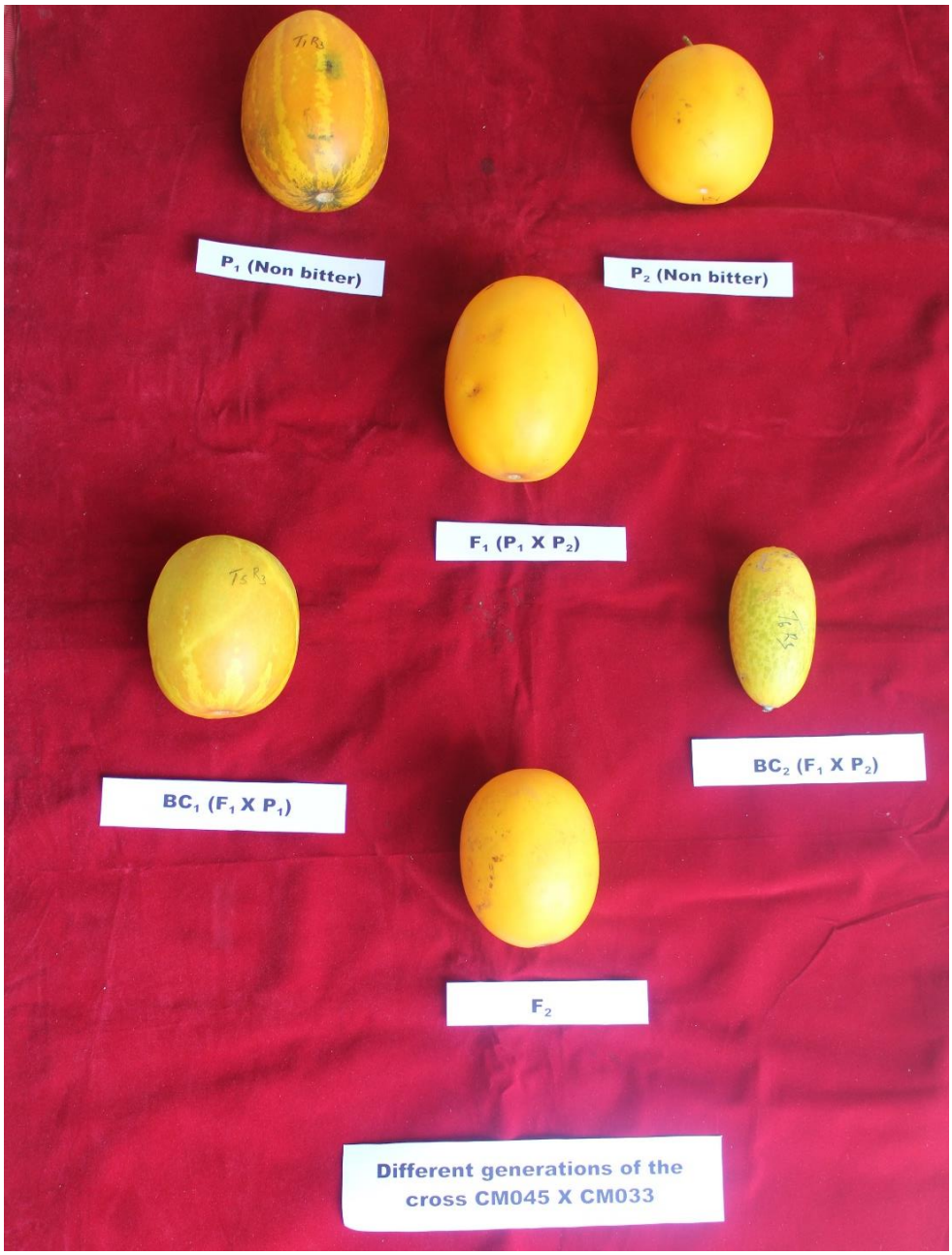


Plate 23. Six generations of Cross I (CM045 X CM033)

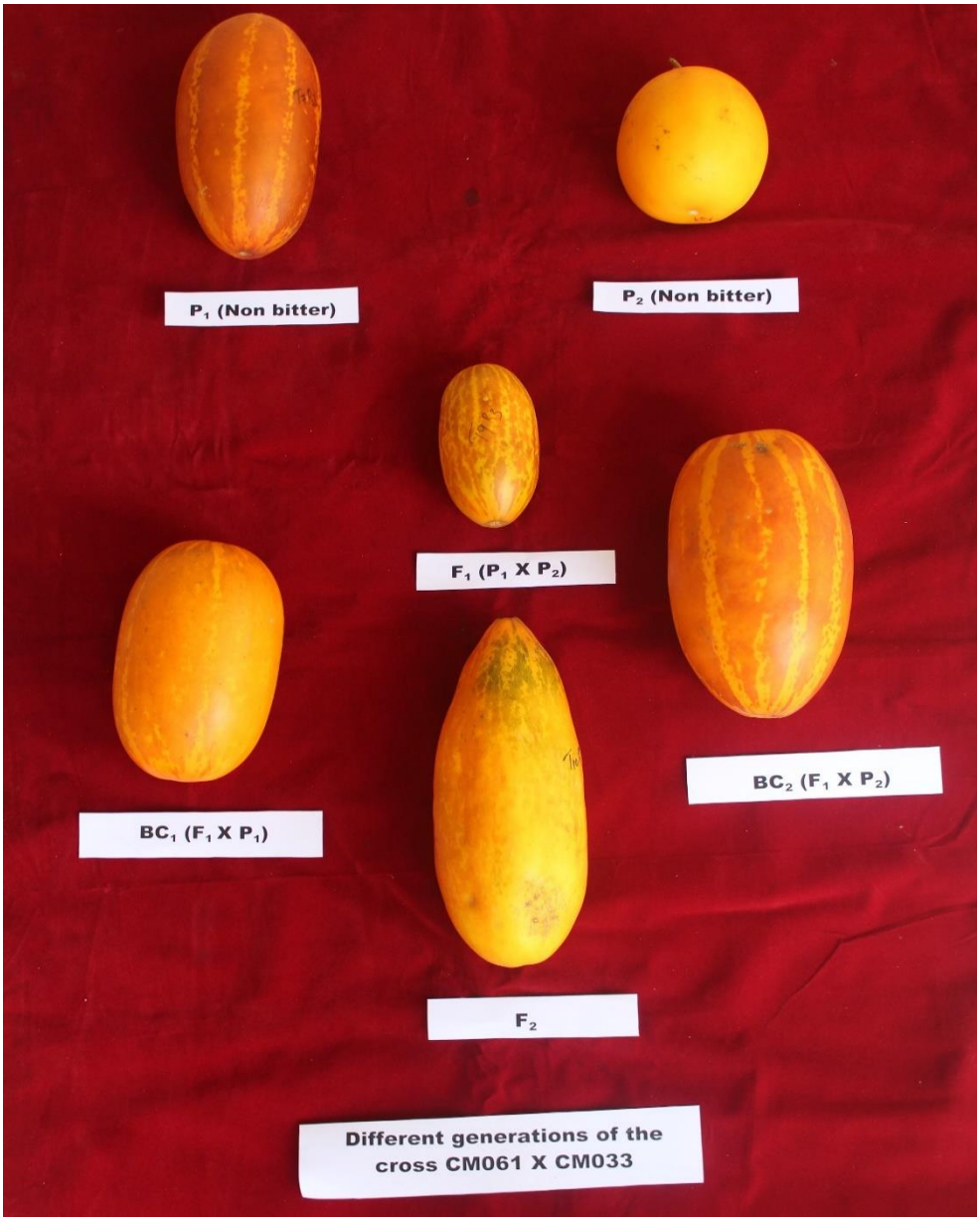


Plate 24. Six generations of Cross II (CM061 X CM033)

Plate 25. Six generations of Cross III (CM051 X *Cucumis melo* ssp. *callosus*)

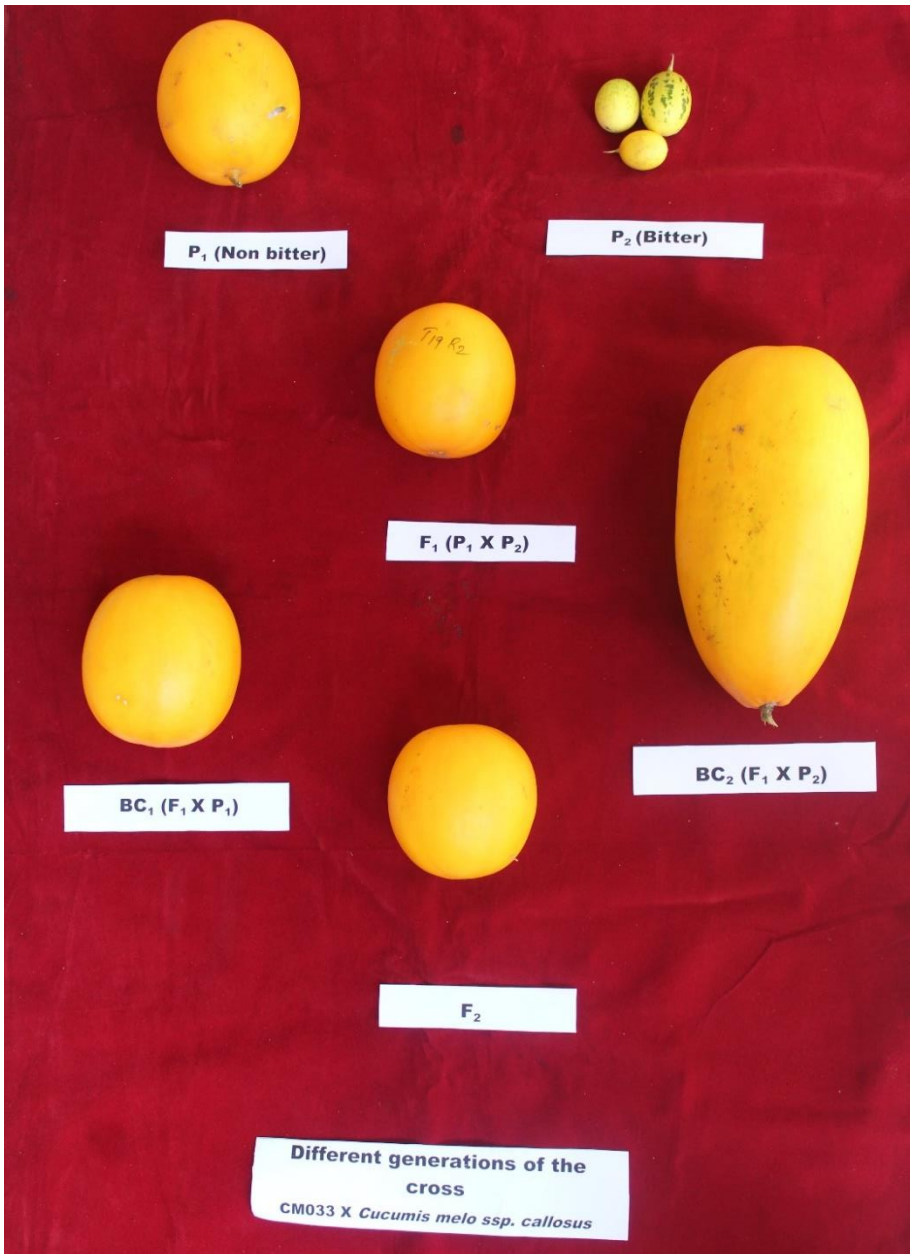


Plate 26. Six generations of Cross IV (CM033 X *Cucumis melo* ssp. *callosus*)

4.7.1.1. Days to first female flower production

Among the six generations, earliest female flower production was in the F_2 of cross IV (29.80 days), followed by P_1 (CM033) (29.86 days) and were on par. Highest number of days to female flower production was in the F_1 of Cross IV (CM033 X *Cucumis melo* subsp. *callosus*) as 33.66 days, followed by in the P_1 (CM033) as 32.60 days.

4.7.1.2. Days to first male flower production

First male flower production was earliest in P_1 (*Cucucmis melo* ssp. *callosus*) as 26.33 days, followed by B_1(CM051x *Cucumis melo* ssp. *callosus*) as 26.40 days. Highest number of days to first male flower production was in the P_1(CM061), B_1(CM045 x CM033) x CM045 as 28.93 days**.**

4.7.1.3. Node at first female flower

Lowest node (3.00) at which female flower produced was in the P_1(CM045), followed by in the F_1 of CM061 x CM033 as (4.33). Node number of first female flower was highest in the B_1(CM045xCM033) x CM045 as 6.13 followed by B_2(CM045xCM033) x CM033(5.60)**.**

4.7.1.4. Node at first male flower

Lowest node of first male flower (1.60) was in the P_1(CM033) followed by CM061 (1.66). Node of first female flower was highest in the B_2(CM061xCM033) x CM033(2.40) followed by in the F_2 (CM033x *Cucumis melo* ssp. *callosus*).

4.7.1.5. Vine length (cm)

Lowest vine length (92.46 cm) was in the F_1(CM033x *Cucumis melo* ssp. *callosus*), followed by the F_2 of the same cross (95.60 cm). Longest vine length was in the B_2 (CM045xCM033) x CM033 as 270.73 cm, followed by B_1(CM061xCM033) x CM061(249.46 cm).

4.7.1.6. Inter nodal length (cm)

Inter nodal length was lowest (3.46 cm) in the P_1(*Cucumis melo* ssp. *callosus*) followed by B_1(CM045xCM033) x CM045(4.38 cm). Highest inter nodal length (8.75 cm) was in the P_1 (CM051) followed by 7.79 cm in F_1(CM061xCM033).

4.7.1.7. Number of branches per plant

Lowest number of branches per plant (3.80) was in F_1(CM051x *Cucucmis melo* ssp. *callosus*), followed by B_1(CM061 x CM033) x CM061(3.80). Number of branches were highest (4.60) in F_2(CM045xCM033), followed by F_2(CM061xCM033) and CM061x CM033) as 4.46.

4.7.1.8. Fruit diameter (cm)

Fruit diameter was lowest (3.06 cm) in the P_1 (*Cucumis melo* ssp. *callosus*), followed by 7.26 cm in the B_1(CM061 x CM033) x CM061. Highest fruit diameter was in the P_1 CM045 (11.46 cm), followed by 10.92 cm in the F_1 (CM045x CM033).

4.7.1.9. Fruit girth (cm)

Fruit girth was lowest (7.17 cm) in the P_1 (*Cucumis melo* ssp. *callosus*). Highest fruit girth was in the P_1 CM045 (36.98 cm), followed by 33.28 cm in CM051.

4.7.1.10. Fruit length (cm)

Among six generations, lowest fruit length was in P_1(*Cucumis melo* ssp. *callosus*) (6.10 cm). Fruit length was highest in CM045 (30.56 cm) followed by CM061 (26.96 cm).

4.7.1.11. Fruit rind thickness (cm)

Lowest fruit rind thickness was in the P_1 (CM061) (0.14 cm) followed by 0.15 cm in B_1 (CM045 x CM033) x CM045. Fruit rind thickness was highest (0.40 cm) in the P_1(CM033) followed by 0.37 cm in P_1 (*Cucumis melo* ssp. *callosus*).

4.7.1.12. Flesh thickness (cm)

Among six generations, lowest flesh thickness (0.80 cm) was in P_1 (*Cucumis melo* ssp. *callosus*). Flesh thickness was highest (2.46 cm) in the F_1CM045 xCM033 followed by 2.41 cm in the P_1 (CM051).

4.7.1.13. Seed cavity length (cm)

Lowest seed cavity length (1.75 cm) was in the P_1 (*Cucumis melo* ssp. *callosus*). Seed cavity length was highest (16.29 cm) in P_1(CM045) followed by 15.16 cm in the P_1 (CM051).

4.7.1.14. Seed cavity breadth (cm)

Seed cavity breadth was lowest (0.06 cm) in the P_1 (*Cucumis melo* ssp. *callosus)*. Highest seed cavity breadth (4.73 cm) was in the F_1 (CM051 X *Cucumis melo* ssp. *callosus)* and B_2(CM051 x *Cucumis melo* ssp. *callosus*) x *Cucumis melo* ssp. *callosus* followed by 4.71 cm in B_1 (CM033 x *Cucumis melo* ssp. *callosus*) x CM033.

4.7.1.15. Seed length (cm)

Lowest seed length (0.26 cm) was in P_1 (*Cucumis melo* ssp. *callosus*). Seed length was highest 0.77 cm in F_2 (CM045 x CM033) followed by 0.72 cm in F_1 (CM033 x *Cucumis melo* ssp. *callosus*) and P_1 (CM051).

4.7.1.16. Number of seeds per fruit

Lowest number of seeds per fruit (118.00) was in P_1 (CM045) followed 119.20 in B_2 (CM051 x *Cucumis melo* ssp. *callosus*) x *Cucumis melo* ssp. *callosus*. Highest number of seeds (333.00) was in F_1 (CM061 x CM033).

4.7.1.17. Days taken for fruit maturity

Days taken for fruit maturity was lowest (51.13 days) in F_1(CM045 x CM033) followed by B_1(CM061 X CM033) X CM061 as 55.20 days. Highest number of days taken for fruit maturity (72.13 days) was in P_1 (CM033) followed by P_1 (CM045) (67.93 days).

4.7.1.18. Days to first harvest

Lowest days taken to first harvest was (54.80 days) in F_1 (CM045 X CM033) followed by F_1 (CM061 X CM033) (56.06 days). Highest number of days taken to first harvest (68.33 days) was in B_1 (CM061 X CM033) X CM061 followed by B_2 (CM061 X CM033) X CM033.

4.7.1.19. Days to last harvest

Days to last harvest was lowest (73.20 days) in F_1 (CM033 x *Cucumis melo* ssp. *callosus*) followed by F_2 (CM033 x *Cucumis melo* ssp. *callosus*) (74.40 days). Days to last harvest was highest in the B_2(CM045 x CM033) x CM033 as 93.26 days followed by B_2 (CM061 x CM033) x CM033 as 92.00 days.

4.7.1.20. Fruit weight (g)

Lowest fruit weight was in P_1 (*Cucumis melo* ssp. *callosus*) (19.53 g). Fruit weight was highest in the B_1 (CM051 x *Cucumis melo* ssp. *callosus)* x CM051 (1390.00 g) followed by B_2 (CM051 x *Cucumis melo* ssp. *callosus)* x *Cucumis melo* ssp. *callosus* (1296.00 g) and were significantly different.

4.7.1.21. Number of fruits per plant

Number of fruits per plant was lowest in F_1(CM033 x *Cucumis melo* ssp. *callosus*) and B_2(CM033x *Cucumis melo* ssp. *callosus*) x *Cucumis melo* ssp. C*allosus* (6.73). Highest number of fruits (18.73) was in P_1 (*Cucumis melo* ssp. *callosus*).

4.7.1.22. Yield per plant (kg)

The lowest fruit yield was in P_1 (*Cucumis melo* ssp. *callosus*) (0.38 kg). The highest fruit yield (10.18 kg) was in B_1 (CM051 x *Cucumis melo* ssp. *callosus*) x CM051 followed by F_2 (CM045 X CM033) (9.06 kg).

4.7.1.23. Marketable yield per plant (kg)

The lowest marketable yield per plant (0.34 kg) was in P_1 (*Cucumis melo* ssp. *callosus*). The highest marketable yield per plant (7.26 kg) was in the B_1 (CM051 x *Cucumis melo* ssp. *callosus*) x CM051 followed by F_2 CM051 x *Cucumis melo* ssp. *callosus* (6.60 kg).

4.7.1.24. Days to fruit fly infestation after anthesis

Lowest number of days taken for fruit fly infestatiton after anthesis was in F_1 (CM061 x CM033) (6.73 days) followed by P_1(CM061) (6.93 days). Highest number of days (14.26 days) taken to infest fruits after anthesis was in the P_1*Cucumis melo* ssp. *Callosus.*

4.7.1.25. Percentage of fruit fly infestation

Percentage of fruit fly infestation was lowest (6.26 per cent) in the P_1 (*Cucumis melo* ssp. *callosus*) and the highest fruit fly infestation (52.72 per cent) was observed in P_1 (CM061).

4.7.2. Mean performance of six generations for biochemical characters

Data on mean performances of P_1, P_2, F_1's, F_2's, B_1's and B_2's for eight biochemical traits were analyzed and the results are presented in the Table.22.

4.7.2.1. Total Soluble Solids (TSS) (^{o} Brix)

The lowest total soluble solids (2.00 ^{o} Brix) was in P_1 (*Cucumis melo* ssp. *callosus*) followed by F_1(CM045 x CM033) (3.00 ^{o} Brix). The highest TSS (5.33 ^{o} Brix) in P_1 (CM033).

4.7.2.2. Acidity (per cent)

Acidity was lowest (0.22 per cent) in B_1 (CM045 x CM033) x CM045 followed by B_1 of (CM051 x *Cucumis melo* ssp. *callosus)* (0.23 per cent). The highest acidity was

Table.22. Mean performance of six generations for biochemical characters

Pedigree	1	2	3	4	5	6	7	8
PARENTS								
CM033 (P_1 and P_2)	5.33	0.50	21.00	0.01	0.01	5.31	1.60	0.338
CM045 (P_1)	4.00	0.45	38.66	0.09	0.09	3.71	3.91	0.001
CM051 (P_1)	4.00	0.51	94.00	0.16	0.16	6.91	0.00	0.029
CM061 (P_1)	4.00	0.51	71.00	0.00	0.00	9.72	1.40	0.002
Cucumis melo ssp. *callosus* (P_2)	2.00	0.40	126.00	0.00	0.00	6.12	0.00	0.052
F_1 CROSSES								
CM045 X CM033	3.00	0.31	22.66	0.05	0.05	5.15	1.43	0.045
CM061 X CM033	4.00	0.84	25.00	0.00	0.00	5.30	1.66	0.005
CM051 X *Cucumis melo* ssp. *callosus*	4.00	0.39	74.00	0.01	0.01	7.04	0.00	0.327
CM033 X *Cucumis melo* ssp. *callosus*	4.33	0.24	104.66	0.17	0.17	3.07	0.00	0.022
F_2 CROSSES								
CM045 X CM033	3.66	0.50	40.33	0.08	0.08	9.15	0.90	0.000
CM061 X CM033	4.00	0.39	54.33	0.04	0.04	8.01	0.00	0.063
CM051 X *Cucumis melo* ssp. *callosus*	3.33	0.23	98.00	0.00	0.00	5.41	0.00	0.275
CM033 X *Cucumis melo* ssp. *callosus*	3.00	0.24	109.00	0.06	0.06	2.96	0.00	0.002
B_1 CROSSES								
(CM045 X CM033) X CM045	4.33	0.22	12.66	0.08	0.08	5.05	6.26	0.001

(CM061 X CM033) X CM061	4.00	0.38	83.33	0.03	0.03	5.71	1.80	0.035
(CM051 X *Cucumis melo* ssp. *callosus)* X CM051	4.00	0.23	69.33	0.10	0.10	4.31	0.46	0.031
(CM033 X *Cucumis melo* ssp. *callosus*) X CM033	4.00	0.39	38.33	0.06	0.06	3.64	0.00	0.005
B_2 CROSSES								
(CM045 X CM033) X CM033	3.66	0.22	46.00	0.01	0.01	8.05	1.46	0.003
(CM061 X CM033) X CM033	3.66	0.62	83.33	0.01	0.01	2.69	0.00	0.030
(CM051 X *Cucumis melo* ssp. *callosus*) X *Cucumis melo* ssp. *callosus*	3.00	0.23	79.00	0.02	0.02	1.76	0.00	0.013
(CM033 X *Cucumis melo* ssp. *callosus*) X *Cucumis melo* ssp. *callosus*	4.00	0.39	79.66	0.07	0.07	4.54	0.00	0.005
CD (0.05)	0.59	0.06	18.83	0.04	0.04	0.59	0.35	0.198

1. Total Soluble Solids (^{o} Brix) 2. Acidity (per cent) 3. Crude protein (mg/100g) 4. Total sugar (mg/100g)

5. Total soluble sugar (mg/100g) 6. Total phenol (mg/100g) 7. Silica (per cent) 8. Tannin (mg/100g)

observed (0.84 per cent) in F_1 (CM061 x CM033) followed by B_2 (CM061 x CM033) x CM033 (0.62 per cent).

4.7.2.3. Crude protein (mg/100g)

Crude protein content was lowest (12.66 mg) in B_1 (CM045 x CM033) x CM045 followed by P_1 (CM033) (21.00 mg). The highest crude protein content (126.00 mg) was in P_1 (*Cucumis melo* ssp. *callosus*) followed by F_2 (109.00 mg) in CM033 x *Cucumis melo* ssp. *callosus*.

4.7.2.4. Total sugars (mg/100g)

Total sugar was lowest (0.00 mg) in P_1 (CM061) followed by P_1 (*Cucumis melo* ssp. *callosus*), F_1 (CM061 x CM033) and F_2 (CM051 x *Cucumis melo* ssp. *callosus*). Total sugar content was highest (0.17 mg) in F_1 (CM033 x *Cucumis melo* ssp. *callosus*) followed by P_1 (CM051) (0.16 mg).

4.7.2.5. Total soluble sugars (mg/100g)

Total sugars was lowest (0.00 mg) in P_1 (CM061) followed by P_1 (*Cucumis melo* ssp. *callosus*), F_1 (CM061 x CM033) and F_2 (CM051 x *Cucumis melo* ssp. *callosus*). Total sugar content was highest (0.17 mg) in F_1 (CM033 x *Cucumis melo* ssp. *callosus*) followed by P_1 (CM051) (0.16 mg).

4.7.2.6. Total phenols (mg/100g)

Total phenol content was lowest (1.76 mg) in B_2 (CM051 x *Cucumis melo* ssp. *callosus*) x *Cucumis melo* ssp. *callosus* followed by B_2 (CM061 x CM033) x CM033 (2.69 mg). Highest total phenol content (9.72 mg) was noticed in P_1 (CM061) followed by F_2 (CM045 x CM033) (9.15 mg).

4.7.2.7. Silica (per cent)

Silica content was lowest (0.00 per cent) in P_1 (CM051) followed by P_1 (*Cucumis melo* ssp. *callosus*), F_1 (CM051 x *Cucumis melo* ssp. *callosus*), (CM033 x *Cucumis melo*

ssp. *callosus*); F_2 (CM061 x CM033), (CM051 x *Cucumis melo* ssp. *callosus*) and (CM033 x *Cucumis melo* ssp. *callosus*). Highest silica content (6.26 per cent) was observed in B_1 (CM045 x CM033) x CM045.

4.7.2.8. Tannins (mg/100)

Tannin content was lowest (0.000per cent) in F_2 (CM045 x CM033) followed by P_1 (CM045), B_1 (CM045 x CM033) x CM045 as 0.001per cent. Tannin content was highest (0.338 per cent) in P_1 (CM033).

4.7.3. Generation mean analysis

The character wise estimates of scaling tests, gene effects and chi-square values of four crosses of six generations are presented in Table 23 to Table 47.

4.7.3.1. Days to first female flower

The estimates of gene effects, simple scaling test and χ^2 values for the character concerned has been presented in the Table 23. χ^2 values and the estimates of gene effects were significant in CrossIV, indicating non- allelic interaction. The main effect (*m*) was not significant in all crosses indicating no variability among the hybrids.

Additive gene effects (*d*) were not significant in all four crosses. Significant dominant gene effects (*h*) was recorded in CrossIV (7.83).

Additive x additive (*i*) gene effects in positive direction was present only in CrossIV (*i*=6.27). Additive x dominance (*j*) gene effects and dominance x dominance (*l*) gene effects were non significant in all the crosses. Cross IV showed duplicate epistasis as it had opposite sign in *h* and *l.*

4.7.3.2. Days to first male flower

The estimates of gene effects, simple scaling test and χ^2 values for the character concerned has been presented in the Table.24. The estimates of gene effects and χ^2 values were significant in CrossI indicating non- allelic interactions. The main effect (m) was significant in all the crosses indicating absence of variability among the hybrids.

Additive gene effects (*d*) were significant in CrossI (*d*=1.60) and other three crosses were non-significant. Dominance gene effects (*h*) were non significant in all four crosses.

Table.23. Gene effects for days to first female flower production in oriental pickling melon

Cross	*m*	*d*	*h*	*i*	*j*	*l*	A	B	C	D	χ^2	Type of gene action
Cross I	31.80 34.89	0.60 0.44	0.73 0.16	1.47 0.32	-1.60 2.89	-6.53 -0.54	-1.73 -0.77	-3.33 -1.58	-3.60 -0.89	-0.73 -0.32	3.11	-
Cross II	30.87 52.09	-1.33 -1.65	1.20 0.40	1.87 0.65	-4.27 -2.06	-0.27 -0.06	2.93 1.79	-1.33 -0.84	3.47 1.15	-0.93 -0.65	5.46	-
Cross III	30.73 69.61	-0.80 -0.98	4.23 1.69	3.20 1.33	-1.40 -0.79	-4.47 -1.13	0.07 0.05	-1.33 -1.04	1.93 -0.86	-1.60 -1.33	2.73	-
Cross IV	29.80 113.8	-2.07 -2.45	7.83** 3.77	6.27** 3.19	-3.27 -1.77	-0.20 -0.05	4.67** 3.40	1.40 0.96	12.33** 7.21	-3.13** -3.19	56.71**	D

Cross I – CM045 X CM033

Cross II – CM061 X CM033

Cross III- CM051 X *Cucumis melo* ssp. *callosus*

Cross IV- CM033 X *Cucumis melo* ssp. *callosus*

D-Duplicate epistasis

Table.24. Gene effects for days to first male flower production in oriental pickling melon

Cross	*m*	*d*	*h*	*i*	*j*	*l*	A	B	C	D	χ^2	Type of gene action
Cross I	27.93** 112.56	1.60* 3.21	1.45 0.78	0.80 0.57	4.40** 4.07	-3.33 -1.43	-3.47** -3.57	0.93 1.53	-1.73 -1.44	-0.40 -0.57	17.98**	D
Cross II	27.87** 95.90	0.40 0.83	-2.47 -1.55	-1.33 -0.89	-1.47 -1.39	0.13 0.05	0.13 0.17	-1.33 -1.36	-2.53 -1.63	0.67 0.89	4.62	-
Cross III	27.53** 81.90	-0.73 -1.40	-2.50 -1.43	-3.07 -1.80	-2.33 -1.94	4.20 1.60	1.73 1.94	-0.60 -0.66	-1.93 -1.22	1.53 1.80	6.87	-
Cross IV	26.93** 64.22	-1.40 -2.00	1.20 0.54	2.27 1.04	-1.07 -0.72	-1.60 -0.48	0.86 0.84	-0.20 -0.17	2.93 1.58	-1.13 -1.04	3.01	-

Cross I – CM045 X CM033

Cross II – CM061 X CM033

Cross III- CM051 X *Cucumis melo* ssp. *callosus*

Cross IV- CM033 X *Cucumis melo* ssp. *callosus*

D- Duplicate epistasis

Additive x additive (*i*), dominance x dominance (*l*) gene effects were not significant in four crosses. Additive x dominance (*j*) gene effects (*j*=4.40) was significant in CrossI in positive direction; CrossI had opposite sign in *h* and *l* which indicated duplicate epistasis.

4.7.3.3. Node of first female flower

The estimates of gene effects, simple scaling test and χ^2 value for the character is presented in the Table 25. The estimates of scales (B and C) and χ^2 values were significant in two crosses, indicating the presence of non- allelic interactions. The main effect (m) was significant in all the crosses which showed presence of variability among the hybrids.

Additive gene effects (*d*) and dominant gene effects (*h*) were non significant in all four crosses.

Additive x additive (*i*) gene effects and dominance x dominance (*l*) gene effects were non significant in all crosses. Additive x dominance (*j*) gene effects was significant in CrossII (*j*= -1.40) in negative direction. Cross I and Cross II had opposite sign in *h* and *l* which indicated duplicate epistasis.

4.7.3.4. Node of first male flower

The estimates of gene effects, simple scaling test and χ^2 values for the character is presented in the Table.26. The estimates of scales (B and D) and χ^2 values were significant in one cross, which showed the presence of epistasis. The main effect (*m*) was significant in all the crosses which indicated variability among the hybrids.

Additive gene effects (*d*) was not significant in the four crosses. Dominant gene effects (*h*) was significant in CrossII (*h*=2.03) whereas, it was not significant in other three crosses.

Additive x additive (*i*) gene effects (*i*=2.00), dominant x dominant (*l*) gene effects significant in negative direction in CrossII (*l* = -4.33). Additive x dominance (*j*) gene effects was not significant in all the four crosses. All the interacting crosses had the opposite sign in *h* and *l* which indicated duplicate epistasis.

4.7.3.5. Vine length (cm)

The estimates of gene effects, simple scaling test and χ^2 values for the character is presented in the Table 27. The estimates of scales (A, B, C and D) and χ^2 values were

Table.25. Gene effects for node of first female flower in oriental pickling melon

Cross	*m*	*d*	*h*	*i*	*j*	*l*	A	B	C	D	χ^2	Type of gene action
Cross I	6.13** 19.06	0.40 1.37	-3.20 -2.24	-2.93 -2.08	0.13 0.20	1.33 0.74	-0.87 -1.78	-0.73 -1.48	-4.53** -3.33	1.47 2.07	13.64**	D
Cross II	4.47** 18.90	-0.27 -0.99	1.63 1.46	1.87 1.71	-1.40* -2.31	-3.00 -1.97	0.13 0.27	-1.27* -2.74	0.73 0.68	-0.93 -1.71	9.89*	D
Cross III	5.47** 25.39	0.27 0.96	0.30 0.28	-0.53 -0.52	0.87 1.43	1.00 0.64	-0.20 -0.35	0.67 1.32	-0.07 -0.06	0.27 0.52	2.81	-
Cross IV	5.00** 29.58	-0.07 -0.25	-0.73 -0.81	-0.40 -0.47	-0.40 -0.68	0.13 0.10	0.07 0.14	-0.33 -0.69	-0.67 -0.76	0.20 0.47	1.02	-

Cross I – CM045 X CM033

Cross II – CM061 X CM033

Cross III- CM051 X *Cucumis melo* ssp. *callosus*

Cross IV- CM033 X *Cucumis melo* ssp. *callosus*

D-Duplicate epistasis

Table.26. Gene effects for node of first male flower in oriental pickling melon

Cross	*m*	*d*	*h*	*i*	*j*	*l*	A	B	C	D	χ^2	Type of gene action
Cross I	1.53** 9.28	-0.20 -0.75	0.70 0.80	0.93 1.20	-0.87 -1.47	-1.13 -0.86	0.33 0.68	-0.53 -1.32	0.73 0.94	-0.47 -1.09	3.89	-
Cross II	1.73** 11.31	-0.33 -1.49	2.03* 2.55	2.00* 2.63	-0.73 -1.43	-4.33** -3.64	-0.80 -1.74	-1.53** -4.10	-0.33 -0.43	-1.00* -2.63	19.72**	D
Cross III	1.73** 8.40	-0.20 -0.76	0.50 0.50	0.67 0.68	-0.33 -0.57	-1.53 -1.09	-0.27 -0.56	-0.60 -1.45	-0.20 -0.22	-0.33 -0.68	2.26	-
Cross IV	2.00** 10.25	-0.27 -0.93	-0.30 -0.30	-0.27 -0.27	-0.33 -0.52	0.33 0.23	0.20 0.41	-0.13 -0.26	-0.20 -0.22	0.13 0.28	0.35	-

Cross I – CM045 X CM033

Cross II – CM061 X CM033

Cross III- CM051 X *Cucumis melo* ssp. *callosus*

Cross IV- CM033 X *Cucumis melo* ssp. *callosus* -

D - Duplicate epistasis

Table.27. Gene effects for vine length in oriental pickling melon

Cross	*m*	*d*	*h*	*i*	*j*	*l*	A	B	C	D	χ^2	Type of gene action
Cross I	239.20** 34.61	-42.93* -3.94	104.47* 2.84	40.27 1.14	-195.87** -8.56	-258.27** -4.62	-11.07 -0.64	-206.93** -9.99	-177.73** -5.06	-20.13 -1.14	115.69**	D
Cross II	248.00** 45.44	49.07** 4.32	6.47 0.19	-92.27* -2.93	58.53* 2.46	-126.53* -2.32	-138.67** -8.73	-80.13** -3.57	-311.07** -10.33	46.13* 2.93	124.99**	D
Cross III	187.60** 25.82	22.33 1.94	173.27** 4.58	78.53 2.12	65.20* 2.71	-201.20** -3.57	-93.93** -5.33	-28.73 -1.53	-44.13 -1.36	-39.27 -2.12	29.19**	D
Cross IV	95.60** 33.86	1.40 0.29	61.37** 4.00	89.20** 5.99	24.87 2.06	-135.27** -5.73	-35.47** -4.17	-10.60 -1.13	43.13** 3.19	-44.60** -5.99	39.99**	D

Cross I – CM045 X CM033

Cross II – CM061 X CM033

Cross III- CM051 X *Cucumis melo* ssp. *callosus*

Cross IV- CM033 X *Cucumis melo* ssp. *callosus*

D-Duplicate epistasis

significant in all the crosses, which showed the presence of epistasis. The main effect (*m*) was significant in all the crosses, indicated variability among the hybrids.

Additive gene effects (*d*) was significant in the CrossI(*d*=-42.93) and CrossII (*d*= 49.07). Dominant gene effects (*h*) was significant in CrossI(*h*=104.47) CrossIII(*h*=173.27), and CrossIV (*h*=61.37).

Additive x additive (*i*) gene effects was significant in CrossII (*i*= -92.27) in negative direction, CrossIV (*i*=89.20) in positive direction.

Significant additive x dominant (*j*) gene effects recorded in CrossI (*j*=-195.87) in negative direction; CrossII (*j*=58.53) and CrossIII (*j* = 65.20) had significant positive *j* effects. Dominant x dominant (*l*) gene effects were significant in negative direction in all the four crosses. All crosses showed opposite sign in *h* and *l* which indicated duplicate epistasis.

4.7.3.6. Inter nodal length (cm)

The estimates of gene effects, simple scaling test and χ^2 values for the character is presented in the Table.28. The estimates of scales (A, B, C and D), χ^2 were significant in CrossI, CrossII and CrossIV which indicated the presence of epistasis. The main effects (*m*) were significant in all the four crosses, indicated significant variability among the hybrids.

Additive gene effect (*d*) was not significant in all the crosses. Significant dominant gene effects (*h*) were recorded in CrossI (*h*=-2.41) which was in desirable direction.

Additive x dominant (*j*) gene effect were significant with negative estimates in crosses CrossI (*j*=-3.01), CrossIII (*j*=-6.23) and CrossIV (*j*=2.79) which were in desirable direction.

Significant dominant x dominant (*l*) gene effects were observed in CrossI (6.08) and CrossIV (-6.49) which was in desirable direction. Three crosses showed opposite sign in *h* and *l* which indicated duplicate epistasis.

4.7.3.7. Number of branches per plant

Results of simple scaling test, gene effects and χ^2 values for the character is presented in the Table.29. The estimates of scales and χ^2 were significant in one cross. The main effect (*m*) was significant in all the four crosses, indicated significant variability among the hybrids.

Table.28. Gene effects for inter nodal length in oriental pickling melon

Cross	*m*	*d*	*h*	*i*	*j*	*l*	A	B	C	D	χ^2	Type of gene action
Cross I	4.68** 39.13	-0.52 -2.71	-2.41** -3.81	-0.13 -0.22	-3.01** -6.55	6.08** 6.33	4.48** 15.67	1.47** 3.78	5.81** 10.05	0.07 0.22	264.98**	D
Cross II	7.76** 28.94	-0.07 -0.17	0.20 0.14	-0.76 -0.55	-1.45 -1.60	0.16 0.08	0.43 0.67	-1.03 -1.56	-1.36 -1.22	0.38 0.55	4.34	-
Cross III	7.71** 54.83	-0.47 -1.31	0.73 0.78	-0.96 -1.06	-6.23** -8.36	-1.11 -0.69	2.08** 3.45	-4.15** -8.00	-3.03** -4.19	0.48 1.06	92.85**	D
Cross IV	7.11** 64.25	0.02 0.07	2.42** 3.23	0.60 0.82	-2.79** -4.49	-6.49** -5.05	-1.55** -3.91	-4.34** -8.53	-5.29** -9.54	-0.30 -0.82	137.33**	D

Cross I – CM045 X CM033

Cross II – CM061 X CM033

Cross III- CM051 X *Cucumis melo* ssp. *callosus*

Cross IV- CM033 X *Cucumis melo* ssp. *callosus*

D-Duplicate epistasis

Table.29. Gene effects for number of branches per plant in oriental pickling melon

Cross	*m*	*d*	*h*	*i*	*j*	*l*	A	B	C	D	χ^2	Type of gene action
Cross I	4.60** 24.18	0.07 0.24	-2.00 -2.04	-2.27* -2.39	0.00 0.00	2.93 2.02	0.33 0.63	0.33 0.77	-1.60 -1.78	1.13* 2.39	5.88	-
Cross II	4.47** 27.03	-0.33 -1.39	-1.97* -2.31	-2.00* -2.45	-0.73 -1.35	2.33 1.85	0.53 1.20	-0.20 -0.47	-1.67 -2.04	1.00* 2.45	8.04*	D
Cross III	4.47** 17.47	-0.40 -1.78	-2.27 -1.99	-1.60 -1.43	-0.53 -1.00	0.53 0.37	-0.27 -0.66	-0.80 -1.92	-2.67* -2.40	0.80 1.43	7.73	-
Cross IV	4.07** 22.38	0.27 1.34	-0.83 -0.97	-1.07 -1.29	1.00 2.17	1.40 1.19	-0.33 -0.96	0.67 1.63	-0.73 -0.85	0.53 1.29	5.78	-

Cross I – CM045 X CM033

Cross II – CM061 X CM033

Cross III- CM051 X *Cucumis melo* ssp. *callosus*

Cross IV- CM033 X *Cucumis melo* ssp. *callosus*

D-Duplicate epistasis

Additive gene effects (*d*) were not significant in all the crosses. Significant dominant gene effects (*h*) was recorded in CrossII (*h*= -1.97), additive x additive (*i*) gene effects (*i*= -2.00) with significant negative estimate which was not in a desirable direction. None of the crosses showed significant estimates for additive x dominant (*j*) and dominant x dominant (*l*) gene effects. In CrossII, which showed opposite sign in *h* and *l* indicated duplicate epistasis. In all other three crosses additive x dominant model is sufficient to explain the gene effects.

4.7.3.8. Fruit diameter (cm)

The estimates for either of A, B, C and D gene effects and χ^2 values were significant in all crosses which indicated that additive dominance model was inadequate to explain gene effects, Table.30. The main effect (*m*) was significant in all the four crosses which indicated significant variability among the hybrids.

Additive gene effects (*d*) were significant in CrossII (*d*=2.62) and was positive, which was in the desirable direction and in CrossIII (*d* = -0.80) in negative direction. Dominant gene effects (*h*) were significant in CrossI, CrossII and CrossIII. Highest magnitude (*h* = 2.70) of positive effects were found in the CrossIII which was in the desirable direction.

Additive x additive (*i*) gene effects showed significant negative estimate in CrossI (*i* = -13.99). Significant *j* effects (*j* =4.61) with positive estimate was shown in CrossII which was in desirable direction whereas, CrossI, CrossIII and CrossIV showed significant *j* effects with negative estimates. Dominant x dominant (*l*) gene effects were significant only in CrossI with positive estimate (*l*=26.51).

Duplicate epistasis was observed in CrossI and CrossIII due to the presence opposite signs of *h* and *l*. Complementary epistasis was noted Cross II and CrossIV due to the presence of same sign in *h* and *l*.

4.7.3.9. Fruit girth (cm)

The estimates of either of the simple scales (A, B, C and D), gene effects and χ^2 values were significant for this trait (Table.31). All the crosses were interacting (χ^2 significant) which suggested that additive - dominance model was inadequate to explain

Table.30. Gene effects for fruit diameter in oriental pickling melon

Cross	*m*	*d*	*h*	*i*	*j*	*l*	A	B	C	D	χ^2	Type of gene action
Cross I	10.88** 83.52	-0.23 -1.02	-13.16** -18.44	-13.99** -20.15	-3.19** -6.15	26.51** 23.98	7.86** 17.47	4.67** 15.32	-1.46* -2.36	6.99** 20.15	595.88**	D
Cross II	9.13** 60.58	2.62** 9.78	-2.44* -2.78	-0.84 -1.04	4.61** 5.38	-0.05 -0.04	-2.75** -3.53	1.86** 4.89	-1.73 -1.89	0.42 1.04	37.68**	C
Cross III	8.48** 42.39	-0.80* -2.80	2.70* 2.50	0.40 0.41	-9.15** -14.85	-2.77 -1.66	3.39** 5.20	-5.76** -9.87	-1.97 -1.92	-0.20 -0.41	237.67**	D
Cross IV	8.61** 38.18	-0.27 -0.91	1.25 1.11	-2.04 -1.88	-7.25** -11.20	1.88 1.15	3.55** 6.96	-3.70** -6.26	-2.19 -1.96	1.02 1.88	141.29**	C

Cross I – CM045 X CM033

Cross II – CM061 X CM033

Cross III- CM051 X *Cucumis melo* ssp. *callosus*

Cross IV- CM033 X *Cucumis melo* ssp. *callosus*

D-Duplicate epistasis

C-Complementary epistasis

Table.31. Gene effects for fruit girth in oriental pickling melon

Cross	*m*	*d*	*h*	*i*	*j*	*l*	A	B	C	D	χ^2	Type of gene action
Cross I	20.94** 51.44	-0.69 -1.74	-18.37** -9.94	-14.97** -8.28	-19.31** -22.94	25.77** 10.80	15.05** 20.90	-4.25** -6.55	-4.17* -2.33	7.49** 8.27	602.37**	D
Cross II	23.74** 57.15	10.16** 16.72	-23.91** -11.14	-20.21** -9.82	5.31** 4.13	15.92** 4.90	-4.80** -3.66	0.51 0.67	-24.51** -11.90	10.11** 9.82	191.29**	D
Cross III	19.30** 48.04	-1.13 -0.82	39.81** 12.31	28.93** 9.02	-20.01** -7.09	-53.39** -9.14	-2.22 -0.81	-22.23** -29.21	4.48* 2.47	-14.47** -9.02	916.64**	D
Cross IV	17.23** 67.67	1.60 2.64	8.66** 5.39	-0.43 -0.27	-0.94 -0.76	-17.17** -6.39	-8.33** -13.58	-9.27** -8.19	-18.02** -15.61	0.21 0.27	388.00**	D

Cross I – CM045 X CM033

Cross II – CM061 X CM033

Cross III- CM051 X *Cucumis melo* ssp. *callosus*

Cross IV- CM033 X *Cucumis melo* ssp. *callosus*

D-Duplicate epistasis

the gene action. The main effect (*m*) was significant in all the four crosses, indicated significant variability among the hybrids.

Additive gene effect (*d*) was significant in CrossII (*d*= 10.16) with positive estimate which was in the desirable direction.

Dominant gene effects (*h*) were significant in all four crosses of which two had significant positive estimate CrossIII and CrossIV (*h*=39.81) and (*h*=8.66) respectively and were in desirable direction.

Among the epistatic effects, additive x additive (*i*) gene effects were significant in three crosses with highest positive estimate (*i*=28.93) in CrossIII, which was in desirable direction.

Additive x dominant (*j*) gene effects were significant in three crosses. The highest magnitude (*j*=5.33) of significantly positive effect was found in CrossII whereas, in other two crosses *j* had significantly negative estimates.

Significant dominant x dominant (*l*) gene effects were observed in four crosses with high positive estimates in CrossI (*l*=25.77) and CrossII (*l*=15.92) whereas, in two cross *l* effects were negatively significant. Duplicate epistasis was found in all the crosses due to the presence of opposite sign in *h* and *l*.

4.7.3.10. Fruit length (cm)

The estimates for either of the simple scales (A, B, C and D), gene effects and χ^2 values were significant for this trait (Table.32). The main effect (*m*) was significant in all the four crosses indicating significant variability among the hybrids.

Significant additive gene effects (*d*= 8.12) in Cross II with positive estimate; Cross III (*d* = -3.97) with negative estimates were observed. Dominance gene effects (*h*) were significant in three crosses in which Cross III (*h*=16.83) had positive estimate which was in desirable direction.

Among the epistatic effects, additive x additive (*i*) gene effects were significant in three crosses with highest positive estimate (*i*=5.33) in Cross III which was in desirable direction.

Table.32. Gene effects for fruit length in oriental pickling melon

Cross	*m*	*d*	*h*	*i*	*j*	*l*	A	B	C	D	χ^2	Type of gene action
Cross I	31.31** 74.63	-0.07 -0.13	-37.70** -17.75	-37.80** -18.69	-12.13** -8.09	74.55** 24.07	24.44** 20.37	12.31** 11.39	-1.05 -0.49	18.90** 18.69	635.09**	D
Cross II	27.42** 56.97	8.12** 10.77	-0.43 -0.17	0.45 0.18	15.99** 9.50	-18.13** -4.89	-16.83** -16.31	-0.85 -0.61	-17.23** -7.98	-0.23 -0.18	284.39**	C
Cross III	26.65** 93.72	-3.97** -5.56	16.83** 7.26	5.53* 3.03	-34.04** -10.94	-14.15** -3.37	12.71** 11.27	-21.33** -7.24	-3.08 -1.00	-2.77* -3.03	229.23**	D
Cross IV	32.00** 65.32	0.09 0.13	-12.11** -4.75	-25.08** -10.52	-17.97** -12.49	2.28 0.60	-2.41 -1.92	-20.39** -14.41	-47.88** -18.01	12.54** 10.52	507.17**	D

Cross I – CM045 X CM033

Cross II – CM061 X CM033

Cross III- CM051 X *Cucumis melo* ssp. *callosus*

Cross IV- CM033 X *Cucumis melo* ssp. *callosus*

D-Duplicate epistasis

C- Complementary epistasis

Additive x dominant (*j*) gene effects were significant in four crosses. The highest magnitude of significantly positive effect (*j*=15.99) was found in Cross II whereas, in other three crosses *j* had significantly negative estimates.

Significant dominant x dominant (*l*) gene effects were observed in three crosses with highest positive estimate (*l*=74.55) in Cross I. In two crosses, *l* effects had significantly negative estimate whereas, in one cross *l* effects was not significant. Duplicate epistasis was found in Cross I, Cross III and Cross IV due to the presence of opposite sign in *h* and *l*. Complementary epistasis is observed in Cross II due to presence of same sign in *h* and *l*.

4.7.3.11. Fruit weight (g)

The estimates of gene effects, simple scaling test and χ^2 values for the character is presented in the Table.33. The estimates of scales (A, B, C and D) were significant and also χ^2 values in four crosses indicating the presence of epistasis. The main effect (*m*) was significant in all the four crosses indicating significant variability among the hybrids.

Additive gene effects (*d*) was significant in CrossII with high positive estimates (*d*= 656.67), which was in the desirable direction.

Significant dominant gene effects (*h*) were recorded in three crosses, in which CrossIV had significant positive estimate (*h*=722.53) which was in desirable direction.

Additive x additive (*i*) gene effects were significant in three crosses, in which CrossIV showed significantly high positive estimate (*i*=494.67).

Additive x dominant (*j*) gene effect were significantly positive (*j*=593.33) estimates in CrossII which was in desirable direction and other three crosses showed negative *j* estimates for this trait.

Significant dominant x dominant (*l*) gene effects were observed in three crosses out of which, CrossI and CrossII had significant positive estimates (*l*= 4395.33 and 1726.67) respectively. Four crosses showed opposite sign in *h* and *l* which indicated duplicate epistasis.

4.7.3.12. Fruit rind thickness (cm)

The estimates of simple scaling test, gene effects and χ^2 values is presented in Table.34. The estimates of either of the simple scales (A, B, C and D) were significant in

Table.33. Gene effects for fruit weight in oriental pickling melon

Cross	*m*	*d*	*h*	*i*	*j*	*l*	A	B	C	D	χ^2	Type of gene action
Cross I	1093.33** 15.58	0.00 0.00	-3164.33** -10.33	-2970.67** -10.10	-383.33* -2.38	4395.33** 11.78	904.00** 6.24	520.67** 5.02	-1546.00** -4.69	1485.33** 10.10	139.44**	D
Cross II	930.00** 17.56	656.67** 6.59	-683.33* -2.17	-833.33* -2.86	593.33* 2.72	1726.67** 3.38	150.00 0.64	743.33** 5.60	60.00 0.19	416.67* 2.86	51.08**	D
Cross III	1260.00** 11.62	93.33 0.57	948.23 1.69	333.33 0.61	-1004.47* -2.80	-2016.47* -2.42	-339.33 -1.26	-1343.8** -4.64	-1349.8* -2.62	-166.67 -0.61	24.72**	D
Cross IV	440.00** 11.34	-72.67 -1.35	722.53** 3.25	494.67* 2.62	-1001.07** -6.92	-485.07 -1.37	505.33** 3.08	-495.73** -3.78	504.27 1.79	-247.33* -2.62	56.65**	D

Cross I – CM045 X CM033

Cross II – CM061 X CM033

Cross III- CM051 X *Cucumis melo* ssp. *callosus*

Cross IV- CM033 X *Cucumis melo* ssp. *callosus*

D- Duplicate epistasis

three crosses indicating inadequacy of additive –dominance model for explaining the gene action. In one cross, χ^2 value was not significant and indicated that additive – dominance model was adequate to explain the gene action.

Significant additive gene effects (*d*) were observed in CrossI with negative estimates (-0.11), dominant gene effects (*h*) were non significant for all the crosses.

Among the interaction effects, additive x additive (*i*) gene effects were significant in Cross IV (*i*= 0.27). Additive x dominant gene effects (*j*) were not significant in all crosses. Dominant x dominant gene effects (*l*) were significant with positive estimates in Cross I(*l*=0.30).

CrossI had complementary epistasis due to the presence of the same sign in *h* and *l* estimates. Duplicate epistasis was observed in two crosses, due to presence of opposite sign in *h* and *l*.

4.7.3.13. Flesh thickness (cm)

The estimates for either of the simple scales (A, B, C and D) were significant, gene effects and χ^2 values were also significant for this trait (Table.35). All the crosses were interacting (χ^2 significant), thereby suggested that additive- dominance model was inadequate to explain the gene action.

The main effect (*m*) was significant in all the four crosses indicating significant variability among the hybrids.

Additive gene action (*d*) was non significant in four crosses. Dominance gene effects (*h*) were significant in three crosses with the highest magnitude (*h*=1.41) was found in CrossIV. In general, magnitude of dominant (*h*) effect were higher than the additive (*d*) gene effects.

Among the epistatic effects, additive x additive (*i*) gene effects were significant in two crosses with the highest magnitude (*i* =1.05) positive estimate in CrossII.

Additive x dominant gene effects (*j*) showed significantly negative estimates in two crosses, with highest magnitude (*j*= -1.57) of *j* effects in CrossIII.

Significant dominant x dominant (*l*) gene effects were observed in two crosses with the highest magnitude (*l*=3.11) of positive estimate in CrossI.

Table.34. Gene effects for fruit rind thickness in oriental pickling melon

Cross	*m*	*d*	*h*	*i*	*j*	*l*	A	B	C	D	χ^2	Type of gene action
Cross I	0.19** 12.61	-0.11** -5.71	0.01 0.13	0.05 0.74	-0.05 -1.03	0.30* 2.78	0.20** 5.36	0.15** 3.97	0.41** 5.21	-0.03 -0.74	42.58**	C
Cross II	0.19** 11.30	-0.01 -0.32	0.02 0.21	0.04 0.51	0.11 2.46	-0.03 -0.30	-0.05 -1.76	0.06 1.52	0.05 0.63	-0.02 -0.51	6.97	-
Cross III	0.21** 31.00	-0.01 -0.62	-0.03 -0.62	0.08 1.58	0.05 1.06	0.12 1.22	0.07 1.75	0.13** 3.70	0.28** 5.96	-0.04 -1.58	36.84**	D
Cross IV	0.20** 10.25	-0.05 -1.56	0.21 2.00	0.27* 2.57	-0.05 -0.68	-0.05 -0.32	0.13* 2.22	0.08 1.45	0.48** 5.20	-0.13* -2.57	27.93**	D

Cross I – CM045 X CM033

Cross II – CM061 X CM033

Cross III- CM051 X *Cucumis melo* ssp. *callosus*

Cross IV- CM033 X *Cucumis melo* ssp. *callosus*

D-Duplicate epistasis

C-Complementary epistasis

Table.35. Gene effects for flesh thickness in oriental pickling melon

Cross	*m*	*d*	*h*	*i*	*j*	*l*	A	B	C	D	χ^2	Type of gene action
Cross I	2.85** 35.76	0.05 0.55	-2.33** -6.09	-2.52** -6.98	-0.01 -0.07	3.11** 5.91	0.30 1.51	0.29 1.85	-1.93** -4.79	1.26** 6.98	50.98**	D
Cross II	1.75** 20.15	0.25 2.17	0.57 1.34	1.05* 2.54	0.50 2.11	-1.25 -2.08	-0.35 -2.05	0.15 0.75	0.86* 2.19	-0.53* -2.54	12.57**	D
Cross III	1.93** 31.07	0.02 0.17	1.04** 2.93	0.25 0.74	-1.57** -6.19	-0.24 -0.43	0.79** 4.59	-0.78** -3.55	0.27 0.85	-0.13 -0.74	40.79**	D
Cross IV	1.97** 26.00	0.05 0.54	1.41** 3.79	0.64 1.76	-1.11** -5.24	-2.01** -3.85	-0.13 -0.83	-1.24** -7.44	-0.73** -2.17	-0.32 -1.76	55.99**	D

Cross I – CM045 X CM033

Cross II – CM061 X CM033

Cross III- CM051 X *Cucumis melo* ssp. *callosus*

Cross IV- CM033 X *Cucumis melo* ssp. *callosus*

D-Duplicate epistasis

Duplicate epistasis was observed in four crosses due to the presence of opposite sign in *h, l*.

4.7.3.14. Seed cavity length (cm)

The estimates of simple scaling tests, gene effects and χ^2 values has been presented in Table.36. Significance of either of the scales (A, B, C and D) indicated the presence of epistasis. This was further confirmed by the significant $\chi 2$ values. The main effect (*m*) was significant in all the four crosses indicating significant variability among the hybrids

Among the interacting crosses, additive (*d*) gene effects were significant in three crosses with positive estimates in CrossI and CrossII (*d*=2.87) and (*d*= 0.74) respectively. Dominance (*h*) gene effects were significant in four crosses with positive estimates in CrossIII and CrossIV (*h*=20.45) and (*h*=3.30) respectively.

Additive x additive (*i*) effects were significant in three crosses with positive estimates in CrossIII (*i*=14.63). Highly significant additive x dominant (*j*) gene effects were recorded in four crosses with highest magnitude of negative estimates in CrossIII (*j*= -18.33) which was in desirable direction.

Three crosses showed significant dominant x dominant gene effects (*l*). The highest magnitude (*l* = -31.83) of significantly negative estimate was observed in CrossIII which was in desirable direction. Opposite sign in *h* and *l* were exhibited in four crosses, indicating duplicate epistasis.

4.7.3.15. Seed cavity breadth (cm)

Results of simple scaling tests and gene effects is presented in the Table.37. Estimates of simple scales and χ^2 values were significant in three crosses. The main effect (*m*) was significant in all the crosses indicating significant variability among the hybrids. Additive dominance model was adequate in one cross as this cross was considered as non -interacting.

Among the interacting crosses, additive gene effects (*d*) were significant, negative (*d* = -0.65) in CrossIII which was in desirable direction. Dominant gene effects (*h*) were

Table.36. Gene effects for seed cavity length in oriental pickling melon

Cross	*m*	*d*	*h*	*i*	*j*	*l*	A	B	C	D	χ^2	Type of gene action
Cross I	13.67** 44.54	2.87** 3.86	-12.26** -6.27	-9.68** -5.03	-4.55* -2.88	4.12 1.26	-0.51 -0.47	-5.05** -4.29	-15.24** -10.94	4.84** 5.03	138.13**	D
Cross II	12.21** 31.97	0.74* 2.92	-16.90** -9.95	-20.44** -12.70	-8.57** -8.98	39.67** 18.61	13.90** 15.78	5.33** 8.45	-1.21 -0.65	10.22** 12.70	405.46**	D
Cross III	11.95** 40.08	-2.53** -3.76	20.45** 11.03	14.63** 8.14	-18.33** -12.60	-31.83** -10.34	0.57 0.44	-17.77** -21.40	-2.57 -1.72	-7.31** -8.14	471.22**	D
Cross IV	7.25** 27.32	0.56 1.50	3.30* 2.48	-0.93 -0.72	-2.25* -2.94	-4.89* -2.54	-1.79* -2.56	-4.04** -8.05	-6.76** -5.60	0.47 0.72	77.94**	D

Cross I – CM045 X CM033

Cross II – CM061 X CM033

Cross III- CM051 X *Cucumis melo* ssp. *callosus*

Cross IV- CM033 X *Cucumis melo* ssp. *callosus*

D-Duplicate epistasis

Table.37. Gene effects for seed cavity breadth in oriental pickling melon

Cross	*m*	*d*	*h*	*i*	*j*	*l*	A	B	C	D	χ^2	Type of gene action
Cross I	4.59** 44.24	-0.08 -0.60	-2.93** -5.76	-2.85** -5.79	-0.46 -1.40	4.77** 6.62	1.19** 4.37	0.73** 3.31	-0.94 -1.93	1.43** 5.80	44.10**	D
Cross II	4.01** 30.84	-0.03 -0.26	-0.25 -0.43	-0.49 -0.85	-0.00 -0.00	0.40 0.53	-0.05 -0.22	-0.05 -0.23	-0.59 -1.06	0.25 0.85	1.14	-
Cross III	4.70** 53.84	-0.65** -4.21	2.18** 4.27	-0.40 -0.86	-5.07** -13.54	-2.90** -3.52	0.89** 2.73	-4.19** -13.31	-3.70** -6.84	0.20 0.86	282.23**	D
Cross IV	4.81** 31.37	0.36 1.33	-0.43 -0.51	-2.88** -3.53	-2.61** -4.72	0.51 0.39	0.12 0.28	-2.49** -6.04	-5.25** -7.54	1.44** 3.53	86.35**	D

Cross I – CM045 X CM033

Cross II – CM061 X CM033

Cross III- CM051 X *Cucumis melo* ssp. *callosus*

Cross IV- CM033 X *Cucumis melo* ssp. *callosus*

D-Duplicate epistasis

significant in CrossI and CrosIII. The highest magnitude of negative estimates (*h* = -2.93) of was recorded in CrossI, which was in desirable direction.

Additive x additive (*i*) gene effects were significant in CrossI (*i*=-2.85) and CrossIV (*i*=-2.88), which were in desirable direction.

Additive x dominant (*j*) gene effects were significant in CrossIII (*j*= -5.07) and CrossIV (*j*= -2.61) negative estimates.

Dominant x dominant (*l*) gene effects were significant in CrossI (*l*= 4.77) and CrossIII (*l*= -2.90). Three crosses showed opposite sign in *h* and *l* which indicated duplicate epistasis.

4.7.3.16. Seed length (cm)

The estimates of gene effects, simple scaling tests and χ^2 values for the character is presented in the Table.38. The estimates of scales (A, B, C and D) were significant and also χ^2 values in three crosses indicating the presence of epistasis. The main effect (*m*) was significant in all the four crosses indicating significant variability among the hybrids.

Additive gene effects (*d*) were significant in CrossIV (*d*=0.39). Significant dominant gene effects (*h*) were recorded in two crosses namely CrossI (*h*= -0.61) and CrossIV (*h*= -0.33) had significant negative estimate which was in desirable direction.

Additive x additive (*i*) gene effects were significant in Cross I (*i*= -0.69) and CrossIV (*i*= -0.65) with negative estimates. Additive x dominant (*j*) gene effects were significant, with positive estimates in CrossIV (*j* =0.49) and negative estimates in CrossI (*j*=-0.27) and CrossIII (*j*= -0.39) which were in desirable directions.

Significant dominant x dominant (*l*) gene effects were observed in three crosses out of which CrossIII (*l*= -1.56) has significant negative estimates. Three crosses showed opposite sign in *h* and *l* which indicated duplicate epistasis.

4.7.3.17. Number of seeds per fruit

The estimates of gene effects, simple scaling tests and χ^2 values for the character is presented in the Table 39. The estimates of scales (A, B, C and D) and χ^2 values were significant in all the crosses, indicating the presence of epistasis. The main effect (*m*) was significant in all the crosses indicating variability among the hybrids.

Table.38. Gene effects for seed length in oriental pickling melon

Cross	*m*	*d*	*h*	*i*	*j*	*l*	A	B	C	D	χ^2	Type of gene action
Cross I	0.77** 27.23	-0.03 -0.88	-0.61** -4.60	-0.69** -5.38	-0.27** -4.03	0.85** 4.78	0.21** 4.12	-0.06 -1.05	-0.54** -4.20	0.35** 5.38	49.47**	D
Cross II	0.65** 20.31	0.00 0.00	0.09 0.58	0.05 0.37	0.05 0.69	-0.04 -0.19	-0.02 -0.31	0.03 0.53	0.07 0.45	-0.03 -0.37	0.66	-
Cross III	0.60** 19.44	0.04 1.14	0.07 0.51	0.32* 2.26	-0.39** -4.89	-1.56** -7.93	-0.43** -6.64	-0.81** -13.92	-0.92** -6.64	-0.16* -2.26	219.36**	D
Cross IV	0.69** 33.62	0.39** 12.66	-0.33** -3.10	-0.65** -6.33	0.49** 6.74	0.80** 4.98	-0.17** -3.08	0.32** 5.63	-0.51** -4.97	0.33** 6.33	81.72**	D

Cross I – CM045 X CM033

Cross II – CM061 X CM033

Cross III- CM051 X *Cucumis melo* ssp. *callosus*

Cross IV- CM033 X *Cucumis melo* ssp. *callosus*

D-Duplicate epistasis

Table.39. Gene effects for number of seeds per fruit in oriental pickling melon

Cross	*m*	*d*	*h*	*i*	*j*	*l*	A	B	C	D	χ^2	Type of gene action
Cross I	308.87** 27.23	76.278 2.50	-136.17 -1.53	-210.13* -2.77	341.80** 3.62	183.27 1.15	-184.33* -2.73	157.47 2.02	-237.00* -2.29	105.07* 2.77	54.84**	D
Cross II	361.13** 11.90	27.00 1.09	-333.47* -2.35	-359.87* -2.75	89.07 1.00	554.40** 2.91	52.73 0.95	141.80 1.59	-165.33 -1.01	179.93* 2.75	9.08*	D
Cross III	180.87** 8.69	9.07 1.11	-304.67** -3.37	-228.53* -2.69	92.13* -2.69	559.20** 5.14	119.27** 3.42	211.40** 5.97	102.13 0.98	114.27* 2.69	42.85**	D
Cross IV	158.27** 12.86	6.07 0.44	-166.90* -2.49	-13.20 -0.23	-33.00 -0.44	302.07** 2.94	160.93* 2.25	127.93** 4.94	275.67** 3.19	6.60 0.23	30.35**	D

Cross I – CM045 X CM033

Cross II – CM061 X CM033

Cross III- CM051 X *Cucumis melo* ssp. *callosus*

Cross IV- CM033 X *Cucumis melo* ssp. *callosus*

D-Duplicate epistasis

Additive gene effects (*d*) was not significant in all the four crosses. Dominant gene effects (*h*) was significant in cross in CrossII (*h*= -333.47), CrossIII (*h*= -304.67) and CrossIV (*h*= -166.90) and were in desirable direction.

Additive x additive (*i*) gene effects were significant in cross CrossI *(i* = -210.13), CrossII (*i*= -359.87), CrossIII (*i*= -228.53) and were in desirable direction.

Additive x dominance (*j*) gene effects were significant in CrossI and CrossIII in positive direction. Dominant x dominant (*l*) gene effects were significant in CrossII (*l*=554.40), CrossIII (*l*=559.20) and CrossIV (*l*=302.07). All the four crosses had the opposite sign in *h* and *l* which indicated duplicate epistasis.

4.7.3.18. Number of fruits per plant

Results of simple scaling tests and gene effects is presented in Table 40. The estimates of scales and χ^2 were significant in all the crosses. The main effect (*m)* was significant in all the four crosses indicating significant variability among the hybrids.

Additive gene effects (*d*) were not significant in all the crosses. Dominant gene effects (*h*) were significant, negative in CrossII, CrossIII and CrossIV.

Among the interaction effects, additive x additive (*i*) gene effects were significant in CrossII and CrossIV with negative estimates. Highly significant additive x dominant (*j*) gene effects were in CrossII (*j*= -5.53) and CrossIII (*j*=13.87) which were in desirable direction.

Significantly positive dominance x dominance gene effects (*l*) were found in CrossII (l=12.47), CrossIII (l=15.20) and CrossIV (l=20.20) and were desirable direction.

CrossI had complementary epistasis due to the presence of the same sign in *h* and *l* estimates. Duplicate epistasis was noted in CrossII, CrossIII and CrossIV which had *h* and *l* with opposite signs.

4.7.3.19. Days taken for fruit maturity

The estimates of gene effects, simple scales (A, B, C and D) and χ^2 values were significant for this trait (Table 41). Only CrossII were found interacting and other three

Table.40. Gene effects for number of fruits per plant in oriental pickling melon

Cross	*m*	*d*	*h*	*i*	*j*	*l*	A	B	C	D	χ^2	Type of gene action
Cross I	13.27** 8.29	-2.27 -1.49	-7.80 -1.09	-8.27 -1.17	-4.27 -1.32	-3.33 -0.37	-3.67 -1.73	-7.93** -3.14	-19.87** -3.03	4.13 1.17	19.89**	C
Cross II	10.20** 12.48	-1.93 -1.84	-11.97** -3.04	-10.80* -2.78	-5.53* -2.49	12.47* 2.28	3.60* 2.85	-1.93 -0.98	-9.13* -2.60	5.40* 2.78	18.75**	D
Cross III	9.20** 11.41	1.80 2.24	-9.47* -2.52	-4.13 -1.15	13.87** 6.24	15.20** 3.02	-1.40 -0.93	12.47** 6.39	6.93 1.74	2.07 1.15	45.92**	D
Cross IV	10.93** 12.12	0.07 0.09	-18.50** -4.69	-16.67** -4.29	2.07 1.18	20.20** 4.20	0.73 0.54	2.80* 2.21	-13.13** -3.42	8.33** 4.29	21.67**	D

Cross I – CM045 X CM033

Cross II – CM061 X CM033

Cross III- CM051 X *Cucumis melo* ssp. *callosus*

Cross IV- CM033 X *Cucumis melo* ssp. *callosus*

D-Duplicate epistasis

C-Complementary epistasis

Table. 41. Gene effects for days taken for fruit maturity in oriental pickling melon

Cross	*m*	*d*	*h*	*i*	*j*	*l*	A	B	C	D	χ^2	Type of gene action
Cross I	61.93** 105.09	-1.07 -1.52	-24.50** -8.75	-5.60 -2.04	2.07 1.27	5.80 1.51	-0.93 -0.65	1.13 1.21	-5.40 -2.06	2.80 2.04	7.09	-
Cross II	60.33** 151.43	-0.73 -0.71	-24.67** -8.26	-19.07** -7.27	3.73 1.51	46.67** 8.81	11.93** 5.65	15.67** 7.09	8.53** 2.60	9.53** 7.27	80.99**	D
Cross III	61.00** 125.01	-0.87 -1.13	-1.20 -0.43	0.40 0.16	-0.80 -0.46	-1.87 -0.43	-0.33 -0.20	-1.13 -0.67	-1.07 -0.34	-0.20 -0.16	0.47	-
Cross IV	61.87** 142.23	1.73 1.80	-5.53 -1.93	-0.80 -0.31	-2.80 -1.11	2.00 0.41	2.00 0.85	-0.80 -0.50	0.40 0.13	0.40 0.31	1.27	-

Cross I – CM045 X CM033

Cross II – CM061 X CM033

Cross III- CM051 X *Cucumis melo* ssp. *callosus*

Cross IV- CM033 X *Cucumis melo* ssp. *callosus*

D-Duplicate epistasis

crosses χ^2 values was not significant. Hence, the additive dominance model was adequate to explain the gene action. The main effect (*m*) was significant in all the crosses indicating variability among the hybrids.

Additive (*d*) gene effects were non significant for all of the crosses. Significant dominance (*h*) gene effects were found in CrossI (*h*= -24.50) and CrossII (*h*=-24.67) and were in desirable direction.

Among the epistatic effects, additive x additive (*i*) gene effects were significant in CrossII (*i*= -19.07) were in desirable direction. Additive x dominant (*j*) gene effects were not significant in all the crosses. Significant dominance x dominance (*l*) gene effects were observed in CrossII (*l*=46.67). Duplicate epistasis was observed in CrossII due to the presence of opposite sign *h* and *l.*

4.7.3.20. Days to first harvest

Results of simple scaling tested and gene effects is presented in Table 42. The estimates of scales, gene effects and χ^2 were significant in all the crosses. The main effect (*m*) was significant in all the four crosses indicating significant variability among the hybrids

Additive gene effects (*d*) were significant in CrossI (*d*= -2.53) in desirable direction. Dominant gene effect (*h*) were significant in CrossII (*h*=9.67) and CrossIII (*h*= 14.07).

Among the interaction effects, additive x additive (*i*) gene effects were significant in CrossI (*i*=7.73), CrossII (*i*=14.67) and CrossIII (*i*=14.93). Significant additive x dominant (*j*) gene effects were found in CrossI (*j*= -5.20) which were in desirable direction; CrossII (*j*=6.00) and CrossIII (*j*=5.47) were significantly positive.

Four crosses showed significant, negative estimates for dominance x dominance (*l*) gene effects and was in desirable direction. Duplicate epistasis was noted in all the crosses, which had *h* and *l* with opposite signs.

Table.42. Gene effects for days to first harvest in oriental pickling melon

Cross	*m*	*d*	*h*	*i*	*j*	*l*	A	B	C	D	χ^2	Type of gene action
Cross I	61.20** 112.27	-2.53* -2.54	2.93 0.96	7.73* 2.62	-5.20* -2.34	-31.47** -6.53	-9.27** -5.41	-14.47** -8.67	-16.00** -5.93	-3.87* -2.62	100.89**	D
Cross II	63.33** 65.33	2.67* 2.37	9.67* 2.12	14.67* 3.27	6.00* 2.53	-48.40** -7.85	-19.87** -11.33	-13.87** -7.25	-19.07** -4.52	-7.33** -3.27	161.35**	D
Cross III	60.13** 63.94	1.07 1.15	14.07** 3.25	14.93** 3.56	5.47* 2.64	-26.80** -4.71	-8.67** -4.49	-3.20 -2.06	3.07 0.71	-7.47** -3.56	26.24**	D
Cross IV	61.73** 55.59	-1.13 -0.94	5.20 0.99	6.27 1.24	-5.47 -2.10	-18.67* -2.60	-3.47 -1.73	-8.93** -3.50	-6.13 -1.16	-3.13 -1.24	12.51**	D

Cross I – CM045 X CM033

Cross II – CM061 X CM033

Cross III- CM051 X *Cucumis melo* ssp. *callosus*

Cross IV- CM033 X *Cucumis melo* ssp. *callosus*

D-Duplicate epistasis

4.7.3.21. Days to last harvest

Results of simple scaling test and gene effects is presented in the Table 43. Estimates of scales, χ^2 values were significant in all four crosses. Hence, additive - dominance model was inadequate to explain the gene action.

The main effect (*m*) was significant in all the crosses indicating significant variability among the hybrids.

Among the interacting crosses, additive gene effects (*d*) were significant in CrossIII (*d*= -2.73). Dominance gene effects (*h*) were significant, positive in CrossI (*h*=40.47), CrossII (*h*=36.90) and CrossIV (*h*=22.13) and were in desirable direction.

Additive x additive (*i*) gene effects were significant, positive in CrossI (*i*=33.07), CrossII (*i*=37.60) and CrossIV (*i*=34.93) and were in desirable direction. Additive x dominance (*j*) gene effects were non – significant.

Dominance x dominance (*l*) gene effects were significant in all the four crosses with negative estimates. Three crosses showed opposite sign in *h* and *l* which indicated duplicate epistasis and CrossIII showed complementary epistasis.

4.7.3.22. Yield per plant (kg)

The estimates of simple scaling tests, gene effects, and χ^2 values is presented in Table 44. Significance of either of the scales (A, B, C and D) indicated the presence of epistasis. This was further confirmed by significant χ^2 values. Hence, additive – dominance model was inadequate to explain the gene action. The main effect (*m*) was significant in all the crosses indicating significant variability among the hybrids

Additive (*d*) gene effects were higher in magnitude than dominance (*h*) effects. Among the interacting crosses, additive (*d*) gene effects were significant in CrossII (*d*=2.86) with positive estimates. Dominance (*h*) gene effects were significant in CrossI (*h*= -21.55) and Cross II (*h*=-13.85) in negative direction.

Among the interaction effects, additive x additive (*i*) effects were significant in CrossI (*i*= -21.46) and CrossII (*i*= -13.85) with negative estimates. Highly significant additive x dominance (*j*) gene effects with negative estimates were found in only CrossIV (*j*= -5.72).

Table.43. Gene effects for days to last harvest in oriental pickling melon

Cross	*m*	*d*	*h*	*i*	*j*	*l*	A	B	C	D	χ^2	Type of gene action
Cross I	84.20** 116.13	-1.60 -1.42	40.47** 10.79	33.07** 9.01	-1.07 -0.43	-72.67** -13.06	-19.27** -10.33	-20.33** -11.25	-6.53 -1.99	-16.53** -9.01	217.76**	D
Cross II	82.40** 104.89	-0.40 -0.29	36.90** 8.79	37.60** 9.05	4.07 1.41	-81.53** -12.74	-24.00** -12.24	-19.93** -9.11	-6.33 -1.87	-18.80** -9.05	225.92**	D
Cross III	90.00** 174.28	-2.73* -3.16	-0.20 -0.07	-1.73 -0.64	1.07 0.48	-25.47** -5.65	-14.13** -7.78	-13.07** -7.89	-28.93** -10.04	0.87 0.64	135.11**	C
Cross IV	73.93** 116.25	-1.60 -1.35	22.13** 6.22	34.93** 10.06	-3.60 -1.43	-45.33** -8.10	-3.40 -1.62	-7.00** -4.16	24.53** 8.19	-17.47** -10.06	115.42**	D

Cross I – CM045 X CM033

Cross II – CM061 X CM033

Cross III- CM051 X *Cucumis melo* ssp. *callosus*

Cross IV- CM033 X *Cucumis melo* ssp. *callosus*

D-Duplicate epistasis

C-Complementary epistasis

Table.44. Gene effects for yield per plant in oriental pickling melon

Cross	*m*	*d*	*h*	*i*	*j*	*l*	A	B	C	D	χ^2	Type of gene action
Cross I	9.06** 10.95	-0.49 -1.19	-21.55** -6.26	-21.46** -6.29	-1.91 -1.81	24.37** 6.38	2.41* 2.69	0.49 0.69	-18.56** -5.40	10.73** 6.29	43.86**	D
Cross II	7.99** 12.18	2.86** 4.47	-13.99** -4.66	-13.85** -4.74	2.46 1.60	17.40** 4.42	0.55 0.39	3.01* 2.92	-10.29** -3.44	6.92** 4.74	28.86**	D
Cross III	8.69** 13.02	2.11 2.21	5.83 1.74	1.72 0.52	-2.90 -1.40	-14.21** -2.94	-4.79* -2.94	-7.69** -5.27	-10.77** -3.64	-0.86 -0.52	40.29**	D
Cross IV	4.82** 8.95	-0.05 -0.09	-2.35 -0.95	-3.09 -1.28	-5.72** -4.74	0.49 0.15	1.56 1.51	-4.16** -4.76	-5.69* -2.39	1.55 1.28	34.07**	D

Cross I – CM045 X CM033

Cross II – CM061 X CM033

Cross III- CM051 X *Cucumis melo* ssp. *callosus*

Cross IV- CM033 X *Cucumis melo* ssp. *callosus*

D-Duplicate epistasis

Significant, positive dominance x dominance (*l*) gene effects were in CrossI (*l*=24.37), CrossII (*l*=17.40) and were in desirable direction; CrossIII (*l*= -14.21). Opposite signs of *h* and *l* were exhibited in all the crosses, indicating duplicate epistasis.

4.7.3.23. Marketable yield per plant (kg)

The estimates of simple scaling tests, gene effects, and $\chi 2$ values is presented in Table 45. Significance of either of the scales (A, B, C and D) indicated the presence of epistasis. The main effect (*m)* was significant in all the crosses indicating significant variability among the hybrids.

Additive (*d*) gene effect were significant in CrossIII (*d*= 3.09) and CrossIV (*d*=1.01) with positive estimates and were in desirable direction. Dominance (*h*) gene effects were significant in Cross I (*h*=-1.62) and CrossII (*h*=-13.39) with negative estimates.

Among the interaction effects, additive x additive (*i*) effects was significant in Cross I (*i*=-9.22), CrossII (*i*=-13.16) and CrossIV (*i*= -6.01) with negative estimates. Highly significant additive x dominance (*j*) gene effects with positive estimates were found in CrossIII (*j*= 3.22) and were in desirable direction.

Significant, positive dominance x dominance (*l*) gene effects were found in CrossI (*l*=10.68) and CrossII (*l*=9.45) in desirable direction. Opposite signs of *h* and *l* were exhibited in all the crosses, indicating duplicate epistasis.

4.7.3.24. Days to fruit fly infestation after anthesis

Results of simple scaling tests and gene effects is presented in the Table 46. Significance of either of the simple scales (A, B, C and D) indicated the presence of epistasis. Hence, additive- dominance model was inadequate to explain the gene action. The main effect (*m*) was significant in all the crosses indicating significant variability among the hybrids.

Among the interacting crosses, additive gene effects (*d*) were significant in CrossII (*d*=-0.60). Dominance gene effects (*h*) were significant with negative estimates in CrossI (*h*=-3.03), CrossIII (*h*=-2.73) and CrossIV (*h*=6.73) which were in desirable direction.

Table.45. Gene effects for marketable yield per plant in oriental pickling melon

Cross	*m*	*d*	*h*	*i*	*j*	*l*	A	B	C	D	χ^2	Type of gene action
Cross I	4.57** 10.72	-0.52 -1.83	-9.62** -5.30	-9.22** -5.13	-0.74 -1.11	10.68** 5.05	1.09* 2.39	0.36 0.65	-7.76** -4.35	4.61** 5.13	30.93**	D
Cross II	6.26** 11.23	0.48 0.88	-13.39** -5.39	-13.16** -5.30	0.79 0.71	9.45** 3.01	-2.25* -2.64	-1.46 -1.98	-16.87** -7.49	6.58** 5.30	64.88**	D
Cross III	6.60** 11.81	3.09** 5.69	1.07 0.42	-3.51 -1.41	3.22* 2.75	-2.94 -0.90	-4.83** -4.75	-1.61 -1.94	-9.95** -4.09	1.75 1.41	32.59**	D
Cross IV	4.20** 8.41	1.01* 2.82	-3.92 -1.81	-6.01* -2.83	0.27 0.37	3.58 1.38	-1.35 -1.72	1.08* -2.21	-8.45** -3.92	3.01* 2.83	16.85**	D

Cross I – CM045 X CM033

Cross II – CM061 X CM033

Cross III- CM051 X *Cucumis melo* ssp. *callosus*

Cross IV- CM033 X *Cucumis melo* ssp. *callosus*

D-Duplicate epistasis

Table.46. Gene effects for days to fruit fly infestation after anthesis in oriental pickling melon

Cross	*m*	*d*	*h*	*i*	*j*	*l*	A	B	C	D	χ^2	Type of gene action
Cross I	8.60** 45.21	0.47 1.20	-3.03* -2.73	-1.47 -1.35	1.67 1.98	3.13 1.75	0.00 0.00	1.67 2.97*	0.20 0.23	0.73 1.35	9.06*	D
Cross II	8.07** 39.11	-0.60* -2.65	0.13 0.14	1.73 1.84	1.60* 2.79	-5.60** -4.18	-2.73** -6.01	-1.13* -2.49	-2.13* -2.16	-0.87 -1.84	37.75**	D
Cross III	8.07** 52.63	0.00 0.00	-2.73** -3.02	1.33 1.55	5.20** 6.69	3.60* 2.46	-0.13 -0.22	5.07** 9.56	6.27** 7.59	-0.67 -1.55	102.09**	D
Cross IV	10.47** 31.13	-0.40 -0.65	6.73** 3.57	8.80** 4.83	2.27 1.59	-14.80** -4.99	-4.13** -4.08	-1.87 -1.71	2.80* 1.70	-4.40** -4.83	29.01**	D

Cross I – CM045 X CM033

Cross II – CM061 X CM033

Cross III- CM051 X *Cucumis melo* ssp. *callosus*

Cross IV- CM033 X *Cucumis melo* ssp. *callosus*

D-Duplicate epistasis

Additive x additive (*i*) gene effects were significant in CrossIV (*i*=8.80) which were in desirable direction. Additive x dominance (*j*) gene effects were significant in CrossII (*j*=1.60) and CrossIII (*j*=5.20) with positive estimates and were in desirable direction.

Dominance x dominance (*l*) gene effects were significant in CrossIII (*l*=3.60) with positive estimates and were in desirable directions; CrossII (*l*= -5.60) and CrossIV (*l*= -14.80) with negative estimates. Four crosses showed opposite sign in *h* and *l* which indicated duplicate epistasis.

4.7.3.25. Percentage of fruit fly infestation.

The estimates of gene effects, simple scaling tests and χ^2 values for the character is presented in the Table 47. The estimates of simple scales (A, B, C and D) and χ^2 values were significant in all the crosses, indicating the presence of epistasis. The main effect (*m*) was significant in all the crosses indicating variability among the hybrids.

Additive gene effects (*d*), dominance gene effects (*h*), additive x additive (*i*) gene effects were non-significant in all the crosses.

Significant, negative additive x dominance (*j*) gene effects in CrossI (*j*=-36.09), CrossIII (*j*=-49.40) and CrossIV (*j*= -32.82) were found in desirable direction. Dominance x dominance (*l*) gene effects were significant, positive in CrossII (*l*=82.06). All the crosses showed opposite sign in *h* and *l* which indicated duplicate epistasis.

4.7.4. Correlation of biochemical traits of six generations to fruit fly infestation

Correlation of biochemical traits with percentage of fruit fly infestation was worked out and presented in Table 48.

Total Soluble Solids (TSS) was significantly, positively correlated with percentage of fruit fly infestation (r =0.36), silica (r =0.35) and acidity (r =0.25); negatively correlated with crude protein content (r = -0.50).

Acidity was significantly, positively correlated with percentage of fruit fly infestation (r =0.33) and total phenols (r =0.23). Significantly, negatively correlated with crude protein (-0.29), total sugars and total soluble sugars (r = -0.25).

Table.47. Gene effects for percentage of fruit fly infestation in oriental pickling melon

Cross	*m*	*d*	*h*	*i*	*j*	*l*	A	B	C	D	χ^2	Type of gene action
Cross I	25.12** 6.48	-3.87 -0.59	-9.34 -0.44	0.28 0.01	-36.09* -2.59	31.58 0.95	33.98** 3.41	-2.12 -0.16	32.14 1.58	-0.14 -0.01	13.26**	D
Cross II	20.27** 136.65	3.79 0.74	-10.86 -1.02	-3.60 -0.35	-12.62 -1.11	82.06** 3.84	45.54** 5.28	32.92** 4.23	74.86** 12.73	1.80 0.35	185.30**	D
Cross III	17.28** 4.69	-9.53 -1.35	15.34 0.72	22.23 1.09	-49.40* -2.82	-41.57 -1.23	15.03 1.20	-34.37* -2.68	2.89 0.15	-11.11 -1.09	9.13*	D
Cross IV	11.71** 7.37	-4.23 -1.48	13.65 1.38	16.83 1.97	-32.82** -4.04	-0.51 -0.03	24.57** 3.32	-8.25 -1.26	33.14* 2.83	-8.41 -1.97	19.19**	D

Cross I – CM045 X CM033

Cross II – CM061 X CM033

Cross III- CM051 X *Cucumis melo* ssp. *callosus*

Cross IV- CM033 X *Cucumis melo* ssp. *callosus*

D-Duplicate epistasis

Table.48. Correlations of biochemical traits to percentage of fruit fly infestation in six generations

	1	2	3	4	5	6	7	8	9
1	1								
2	0.25*	1							
3	0.11	-0.25*	1						
4	-0.50**	-0.29*	0.11	1					
5	0.04	0.23*	-0.23*	-0.11	1				
6	0.11	-0.25*	1.00**	0.10	-0.23*	1			
7	0.35**	0.05	0.02	-0.61**	0.04	0.02	1		
8	0.16	0.01	-0.20	0.04	0.09	-0.23*	-0.16	1	
9	0.36**	0.33**	0.01	-0.43**	-0.23*	0.01	-0.41**	-0.13	1

1. Total Soluble Solids (^{o} Brix)
2. Acidity (per cent)
3. Crude protein (mg/100g)
4. Total sugar (mg/100g)
5. Total soluble sugar (mg/100g)
6. Total phenol (mg/100g)
7. Silica (per cent)
8. Tannin (mg/100g)
9. Percentage of fruit fly infestation

Total soluble sugars was significantly, positively correlated with total sugars (r =1.00) and negatively correlated with total phenols (r = -0.23).

Crude protein was significantly, negatively correlated with silica content (r= -0.61) and percentage of fruit fly infestation (r= -0.43).

Total phenols was significantly, negatively correlated with percentage of fruit fly infestation and total sugars (r = -0.23). Total phenols was negatively, significantly correlated with percentage of fruit fly infestation and total sugars (r = -0.23). Total sugars was significantly, negatively correlated with tannins (r = -0.23).

Silica content was significantly, negatively correlated with percentage of fruit fly infestation (r= -0.41). Tannin was negatively correlated with percentage of fruit fly infestation (r = -0.13).

4.7.5. No choice assay in six generations.

No choice assay was done to confirm the resistance to fruit fly under the cage conditions as detailed in section 3.3.2.3. The results revealed that even after one month of assay none of the fruits of the six generations were infested by the fruit flies. Thus, it was confirmed that these generations possessed resistance to fruit fly (Plate 27).

4.8.0. Sensory Evaluations

Sensory qualities of fresh as well as cooked fruit flesh *viz*., colour, flavour, texture, taste and after taste were assessed in all the genotypes of six generations of four crosses and the results obtained are presented in Table 49 and Table 50, (Plate 28 and Plate 29).

4.8.1. Sensory Evaluations of fresh fruits

4.8.1.1 Flesh colour

The P_1 (Cross II) was more appealing in the flesh colour with the score, rank of (8.00), (16.60) followed by B_1 (Cross IV) and B_2 (Cross IV) (7.70), (15.75). The lowest score obtained for flesh colour was in the B_2 (Cross II) and B_2 (Cross III) (5.60), (9.35).

Plate 27. No choice assay in six generations

Table.49. Sensory evaluation of fruit fresh (Raw)

Treatments	Parameters						Total Score
	Colour	Flavor	Texture	Taste	After Taste	Overall Acceptability	
CM045 (P_1)	7.30 (13.25)	6.40 (10.10)	7.30 (16.05)	7.50 (16.70)	7.50 (16.00)	7.50 (15.20)	43.50
CM033 (P_2)	6.40 (9.70)	6.60 (11.25)	6.90 (13.50)	6.50 (11.95)	6.50 (10.25)	6.50 (10.35)	39.40
CM045 x CM033 (F_1)	7.40 (14.50)	6.10 (11.95)	7.50 (16.85)	5.80 (10.20)	5.80 (13.00)	5.80 (13.75)	38.40
CM045 x CM033 (F_2)	6.10 (7.90)	5.90 (8.70)	6.20 (8.85)	5.40 (7.10)	5.40 (8.10)	5.40 (9.80)	34.40
(CM045 x CM033) x CM045 (B_1)	7.50 (14.35)	6.40 (10.75)	6.40 (10.50)	7.00 (14.75)	7.00 (12.35)	7.00 (12.15)	41.30
(CM045 x CM033) x CM033 (B_2)	6.10 (8.75)	5.50 (6.90)	5.90 (6.95)	5.50 (8.50)	5.50 (6.75)	5.50 (7.90)	34.00
CM061 (P_1)	8.00 (16.60)	7.00 (13.35)	7.20 (15.00)	7.50 (16.25)	7.50 (12.80)	7.50 (14.50)	44.70
CM033 (P_2)	6.30 (8.40)	7.00 (14.85)	7.20 (14.65)	6.50 (11.95)	6.50 (11.85)	6.50 (13.05)	40.00
CM061 x CM033 (F_1)	7.20 (13.85)	5.90 (10.60)	6.50 (12.55)	5.80 (9.45)	5.80 (11.55)	5.80 (10.90)	37.00
CM061 x CM033 (F_2)	6.40 (9.90)	6.40 (10.90)	6.80 (12.35)	6.30 (10.40)	6.30 (11.25)	6.30 (9.55)	38.50
(CM061 x CM033) x CM061 (B_1)	7.10 (12.20)	7.50 (16.60)	5.90 (9.50)	6.80 (13.15)	6.80 (12.20)	6.80 (12.25)	40.90
(CM061 x CM033) x CM033 (B_2)	5.60 (7.25)	1.10 (1.35)	2.30 (2.70)	1.40 (1.25)	1.40 (1.15)	1.40 (1.30)	13.20
CM051 (P_1)	6.90	6.70	6.80	6.10	6.10	6.10	38.70

	(12.50)	(13.15)	(12.20)	(10.10)	(13.10)	(12.15)	
CM051 x *Cucumis melo* ssp. *callosus* (F_1)	5.70 (8.15)	7.10 (14.65)	7.40 (15.25)	7.20 (15.25)	7.20 (13.10)	7.20 (14.80)	41.80
CM051 x *Cucumis melo* ssp. *callosus* (F_2)	6.70 (10.45)	7.00 (13.15)	7.40 (15.60)	7.40 (15.80)	7.40 (15.40)	7.40 (14.55)	43.30
(CM051 x *Cucumis melo* ssp. *callosus*) x CM051 (B_1)	5.80 (7.60)	5.90 (8.45)	5.60 (10.15)	6.30 (10.10)	6.30 (11.10)	6.30 (9.30)	36.20
(CM051 x *Cucumis melo* ssp. *callosus*) x *Cucumis melo* ssp. *callosus* (B_2)	5.60 (9.35)	2.70 (5.05)	3.20 (4.05)	4.00 (6.60)	4.00 (5.85)	4.00 (5.10)	23.50
CM033 (P_1)	6.60 (10.00)	6.30 (9.90)	6.10 (8.15)	6.40 (10.45)	6.40 (12.60)	6.40 (10.50)	38.20
CM033 x *Cucumis melo* ssp. *callosus* (F_1)	6.90 (11.65)	6.50 (12.85)	6.60 (11.10)	6.20 (11.40)	6.20 (12.50)	6.20 (12.40)	38.60
CM033 x *Cucumis melo* ssp. *callosus* (F_2)	7.60 (15.15)	7.20 (15.70)	6.80 (12.15)	7.10 (15.20)	7.10 (15.55)	7.10 (15.15)	42.90
(CM033 x *Cucumis melo* ssp. *callosus*) x CM033 (B_1)	7.70 (15.75)	7.20 (16.45)	7.00 (14.40)	7.10 (15.60)	7.10 (12.60)	7.10 (14.50)	43.20
(CM033 x *Cucumis melo* ssp. *callosus*) x *Cucumis melo* ssp. *callosus* (B_2)	7.70 (15.75)	7.30 (16.35)	6.10 (10.50)	6.40 (11.05)	6.40 (13.95)	6.40 (13.85)	40.30
Kendall' s W value	0.239	0.388	0.371	0.360	0.305	0.319	

Cross I – CM045 X CM033 **Cross II – CM061 X CM033**
Cross III- CM051 X *Cucumis melo* ssp. *callosus* **Cross IV- CM033 X *Cucumis melo* ssp. *callosus***

Plate 28. Sensory evaluations of fresh fruits in six generations

4.8.1.2. Flesh flavour

Flavour was maximum in B_2 (Cross IV) (7.30), (16.35) followed by F_2 (Cross IV) and B_1 (Cross IV) (7.20), (15.70). The flavour was minimum in B_2 (Cross II)

4.8.1.3. Texture

The score, rank for texture was maximum in F_1 (Cross I) (7.50), (16.85) followed by F_2 (Cross II) (7.40), (15.60). B_2 (Cross II) (2.30), (2.70) recorded minimum for texture.

4.8.1.4. Taste

Taste was maximum in P_1 (Cross I) and P_1 (Cross II) (7.50), (16.70) followed by F_2 (Cross III) (7.40), (15.80). Less preferred taste was obtained in B_2 (Cross II) (1.40), (1.25).

4.8.1.5. After Taste

The score, rank for after taste was highest in P_1 (Cross I) (7.50), (16.00) followed by F_2 (Cross III) (7.40), (15.40). Lowest taste was obtained in B_2 (Cross II) (1.40), (1.15).

4.8.1.6. Overall acceptability

Highest score, rank of 7.50(15.20) was obtained by P_1 (Cross I) and P_1 (Cross II) and lowest for B_2 (Cross II) (1.40), (1.30).

4.8.1.7. Total score

A careful study of total scores of different genotypes showed that P_1 (Cross II) with total score of 44.70 was most preferred followed by P_1 (Cross I) (43.50). Least preferred genotypes was B_2 (Cross II) (13.20) due to bitterness present in the fruit flesh.

4.8.2. Sensory Evaluations of cooked fruits

4.8.2.1. Colour

The P_1 (Cross II) was obtained attractive flesh colour of score, rank (8.10), (18.20) followed by F_2 (Cross IV) (7.50), (14.55). The lowest score was recorded in B_2 (Cross II) (4.80), (5.80).

4.8.2.2. Flavour

Flavour was maximum in P_1 (Cross I) and the score, rank was (7.30), (18.55) followed by P_1 (Cross II) (7.20), (17.80). The least value recorded for flavour is in B_2 (Cross II) (4.80), (2.50).

Table.50. Sensory evaluation of fruit flesh (Cooked)

Treatments	Parameters						Total Score
	Colour	Flavor	Texture	Taste	After Taste	Overall Acceptability	
CM045 (P_1)	7.40 (13.65)	7.30 (18.55)	7.70 (18.70)	7.30 (17.95)	7.30 (18.45)	7.40 (18.60)	44.40
CM033 (P_2)	6.30 (7.40)	6.50 (13.90)	6.80 (14.30)	6.40 (13.40)	6.20 (11.65)	6.20 (12.00)	38.40
CM045 x CM033 (F_1)	7.40 (13.55)	6.60 (15.40)	6.40 (11.65)	6.40 (13.80)	6.30 (13.10)	6.90 (15.85)	40.00
CM045 x CM033 (F_2)	7.40 (13.70)	6.70 (15.80)	7.10 (16.80)	6.70 (14.80)	6.90 (16.35)	6.90 (15.75)	41.70
(CM045 x CM033) x CM045 (B_1)	7.20 (12.70)	5.90 (10.65)	6.50 (12.65)	6.80 (15.45)	6.70 (14.75)	6.80 (15.00)	39.90
(CM045 x CM033) x CM033 (B_2)	7.20 (12.15)	6.10 (12.25)	6.50 (12.60)	5.80 (11.15)	6.10 (12.80)	6.20 (12.10)	37.90
CM061 (P_1)	8.10 (18.20)	7.20 (17.80)	7.40 (18.10)	7.00 (17.10)	6.50 (14.60)	7.30 (17.45)	43.50
CM033 (P_2)	7.10 (11.60)	7.10 (9.00)	6.30 (11.20)	5.50 (10.25)	5.00 (6.95)	5.70 (9.55)	36.70
CM061 x CM033 (F_1)	7.00 (11.15)	7.00 (9.80)	6.10 (9.95)	5.90 (12.20)	5.80 (11.15)	6.00 (11.40)	37.80
CM061 x CM033 (F_2)	7.10 (12.25)	7.10 (7.85)	6.70 (13.80)	6.10 (12.50)	6.40 (13.75)	6.40 (13.20)	39.80
(CM061 x CM033) x CM061 (B_1)	5.80 (9.55)	5.80 (8.30)	5.50 (6.85)	5.00 (8.45)	4.80 (8.15)	4.90 (8.85)	31.80
(CM061 x CM033) x CM033 (B_2)	4.80	4.80	3.00	1.40	1.30	1.30	16.60

	(5.80)	(2.50)	(1.30)	(1.15)	(1.10)	(1.20)	
CM051 (P_1)	6.90 (10.30)	6.90 (9.05)	5.70 (6.70)	5.60 (10.45)	5.70 (11.00)	3.30 (5.50)	34.10
CM051 x *Cucumis melo* ssp. *callosus* (F_1)	6.30 (7.45)	6.30 (4.80)	5.60 (6.15)	4.20 (5.10)	4.50 (6.15)	4.20 (5.35)	31.10
CM051 x *Cucumis melo* ssp. *callosus* (F_2)	6.70 (9.65)	6.70 (10.65)	6.70 (14.35)	6.00 (11.90)	6.10 (12.10)	6.00 (11.35)	38.20
(CM051 x *Cucumis melo* ssp. *callosus*) x CM051 (B_1)	7.00 (13.00)	5.50 (8.85)	6.00 (8.45)	4.90 (8.10)	5.20 (8.45)	5.60 (9.95)	34.20
(CM051 x *Cucumis melo* ssp. *callosus*) x *Cucumis melo* ssp. *callosus* (B_2)	7.20 (12.50)	6.30 (13.90)	6.00 (10.20)	3.80 (5.35)	3.50 (5.85)	3.40 (5.45)	30.20
CM033 (P_1)	7.30 (12.95)	6.10 (12.85)	6.10 (10.80)	5.60 (11.30)	5.40 (10.30)	6.00 (11.75)	36.50
CM033 x *Cucumis melo* ssp. *callosus* (F_1)	6.60 (12.30)	6.00 (11.45)	5.90 (7.90)	5.90 (12.85)	6.30 (15.45)	6.10 (13.60)	36.80
CM033 x *Cucumis melo* ssp. *callosus* (F_2)	7.50 (14.55)	6.60 (15.65)	6.90 (15.55)	6.80 (16.65)	6.90 (17.35)	6.80 (16.40)	41.50
(CM033 x *Cucumis melo* ssp. *callosus*) x CM033 (B_1)	7.00 (11.05)	6.10 (12.50)	6.50 (12.45)	6.20 (13.90)	6.00 (13.05)	6.20 (12.80)	38.00
(CM033 x *Cucumis melo* ssp. *callosus*) x Cucumis *melo* ssp. *callosus* (B_2)	6.40 (8.25)	6.00 (11.50)	6.50 (12.55)	5.40 (9.20)	5.60 (10.50)	5.60 (9.90)	35.50
Kendall's W value	0.237	0.404	0.478	0.438	0.453	0.487	

Cross I – CM045 X CM033
Cross II – CM061 X CM033
Cross III- CM051 X *Cucumis melo* ssp. *callosus*
Cross IV- CM033 X *Cucumis melo* ssp. *callosus*

Plate 29. Sensory evaluation of cooked fruits in six generations

4.8.2.3. Texture

For texture, the score, rank recorded maximum was in the P_1 (Cross I) (7.70), (18.70) followed by P_1 (Cross II) (7.40), (18.10). Lowest value recorded in the B_2 (Cross II) (3.00), (1.30).

4.8.2.4. Taste

Most preferred taste was obtained in P_1 (Cross II) (7.30), (17.95) followed by P_1 (Cross I) (7.00), (17.10). Lowest preferred taste was in B_2 (Cross II) (1.40) (1.15).

4.8.2.5. After taste

After taste, the highest score was obtained in P_1 (Cross II) (7.30), (18.45) followed by F_2 (Cross I) and F_2 (Cross IV) (6.90), (1635). The lowest score was recorded in B_2 (Cross II) (1.30), (1.10).

4.8.2.6. Overall acceptability

Overall acceptability was maximum in P_1 (Cross I) (7.40), (18.60) followed by P_1 (Cross II) (7.30), (17.45). Least acceptability was found in B_2 (Cross II) (1.30), (1.20).

4.8.2.7. Total score

By analyzing total scores of different genotypes, it was found that total score was maximum P_1 (Cross I) (44.40) followed by P_1 (Cross II) (43.50). Lowest total score was in the genotype B_2 (Cross II)(16.60) both in fresh as well cooked fruits due to the presence of bitterness.

Discussion

5. DISCUSSION

Cucumis melo is an important cucurbitaceous crop across wide areas of the world. Great morphological variation exists in fruit characteristics such as size, shape, colour, texture, and composition. *Cucucmis melo* is therefore, considered as the most diverse species of the genus *Cucumis* (Whitaker and Davis 1962, Kirkbride 1993). The species comprises feral, wild and cultivated varieties, the latter including sweet "dessert" melons, as well as non-sweet forms that are consumed raw, pickled or cooked. *Cucumis melo* (melon) genotypes widely differ in morphological and biochemical traits.

Oriental pickling melon *(Cucumis melo* var. *conomon* L.) is an important summer vegetable crop especially in rice fallows of Kerala. Melons of Kerala, exhibits tremendous variability in fruit shape, size, skin characters, flesh colour, cavity space, keeping quality and reaction towards pests and diseases (Rahki and Rajamony, 2005). Fruit fly (*Zeugodacus cucurbitae*) is one of the most important pests of cucurbits, which damages the crop to large extend. Nearly 50 per cent of cucurbits are reported partially or completely damaged by the pest every year. The attack is severe especially after rains when humidity is high. Systematic study to characterize variability in morphological, biochemical and reaction to pests and diseases of melons of Kerala is scarce. Information on genetics of inheritance of traits being basic to any crop improvement program, the present study was undertaken in fifty three accessions of oriental pickling melon to estimate genetic variability, heritability, genetic advance with respect to morphological, biochemical and reaction to melon fruit fly and to elucidate the nature of inheritance.

5.1. Genetic variability

Genetic variability is the basic need for a plant breeder to initiate any breeding programme. The estimates of phenotypic, genotypic coefficient of variability give a clear picture of amount of variations present in the germplasm. Although, from the present study, estimates of PCV were higher than GCV, a close association between them for earliness and yielding contributing traits *viz.*, days to first female flower production, days to first

male flower production, node of first female flower, node of first male flower, days to fruit maturity, days to first harvest, days to last harvest, vine length, inter nodal length, fruit diameter, fruit girth, number of fruits per plant, marketable yield per plant, and yield per plant indicated that genotypic variations contributed more to the expression of these traits than environmental factors and hence, selection based on phenotypic values is feasible for improvement of these traits. Similar results in oriental pickling melon were reported by Rastogi and Deep (1990); Rakhi and Rajamony (2005). Similar trend was observed in the estimates of PCV and GCV for traits contributing to fruit fly resistance *viz.*, fruit rind thickness, flesh thickness and days to fruit fly infestation after anthesis. None concerned has reported similar findings so far.

Comparatively wide differences between PCV and GCV estimates for fruit length, seed cavity length, seed length and number of seeds per fruit indicated a greater degree of environmental influences on expression of these traits and selection based on phenotypic values in these traits would not be rewarding. Similar results were reported by Lakshmi *et al*. (2017) for fruit length in oriental pickling melon.

High heritability was observed for traits like days to first male flower production (98.83), days to first harvest (95.69), number of fruits per plant (95.15), inter nodal length (92.36), yield per plant(91.87) vine length (91.14), marketable yield per plant (90.41), fruit rind thickness (87.75), seed cavity breadth (84.12), percentage fruit fly infestation (88.35) and days to fruit fly infestation after anthesis (82.28) signifying that these traits are genetically controlled and there could be greater correspondence between phenotypes and breeding values while selecting individuals. Similar results were earlier reported by Rakhi and Rajamony (2005).

High heritability coupled with high genetic advance was observed for vine length, days to first harvest, marketable yield per plant, and days to fruit fly infestation after anthesis, percentage fruit fly infestation and yield per plant. It showed that variation in these traits is due to high additive gene effects consequently, scope for improving these traits through selection is more. These results are in agreement with those of Mariappan and

Pappiah (1990) in cucumber, Krishnaprasad *et al*. (2004), Pandey *et al*. (2005), Singh and Lal (2005), Torkadi *et al.* (2007) in muskmelon; Rakhi and Rajamony (2005), Lakshmi *et al*. (2017) in culinary melon.

Although, high heritability was observed for days to first female flower production ,days to first male flower production, inter nodal length, number of branches per plant, fruit diameter, seed cavity breadth, number of fruits per plant and days to fruit maturity, genetic advance was indicating the role of non-additive gene action, which resulted in no scope for selection. Similar results were reported by Joshi *et al*., (1981) in cucumber, Rakhi and Rajamony (2005) for fruit length, fruit girth and yield per plant in culinary melon; Kumar *et al.* (2008), Yogesh *et al*. (2009) in cucumber.

Present investigations revealed that overall selection for high yielding culinary melon types should focus on node of first female flower, vine length, number of seeds per fruit, and number of fruits per plant, days to last harvest and percentage of fruit fly infestation.

5.2. Genetic divergence

Mahalanobis D^2 analysis is one of the potent tools used for measuring genetic divergence. In breeding programmes, it helps to estimate the differentiation force at inter and intra cluster level with which breeders could choose genetically divergent parents for developing hybrids with more heterosis. If the distance between the clusters is larger, the divergence between the accessions is more and vice versa.

From the present study, after computing D^2 values for all the possible pairs, 53 accessions were grouped into 8 clusters, which indicated a large genetic diversity in the accessions. Maximum number of accessions were accommodated in cluster I (12), followed by Cluster II (9), Cluster III (8), Cluster VII (7), Cluster VIII (6), Cluster V and VI (4each) and Cluster IV (3). The clustering indicated a wide range of variations in the cluster means for most of the characters. Accessions from different geographical regions were grouped into the same clusters indicating no relationship between geographic distribution and

genetic divergence, while accessions collected from same locations were grouped into different clusters, showing great genetic diversity. Similar results were reported by Kabir *et al*. (2009), Kumar *et al*. (2013 a) and Kahn *et al*. (2016).

The magnitude of intra- cluster distance was not always proportional to the number of accessions in the cluster as was the case of Cluster VII, which contained seven accessions; its intra-cluster distance (360.97) was lesser than Cluster VI (649.02), which had only four accessions. The intra- cluster distances in all the clusters were less than the inter cluster distance which indicated that the accessions within the same cluster were closely related. The maximum inter cluster D^2 value (1337.80) was observed between Cluster VI and Cluster V; the minimum was between Cluster II and Cluster I (415.83). The lower intra-cluster (I), higher inter cluster values (VI, V) also suggested that the accessions were homogeneous within, heterogenous between clusters. Therefore, the accessions grouped in clusters VI and V are expected to provide high heterosis in hybridization, wide variability in genetic architecture. These results are in agreement with Khatun *et al*. (2010); Rabbani *et al*. (2012) and Kahn *et al*. (2016).

Cluster V consisting of four accessions *viz.*, CM022, CM045, CM047 and CM051 performed better for number of branches per plant, fruit length, fruit weight, flesh thickness and seed cavity length, seed length, number of fruits per plant, marketable yield per plant and yield per plant. Cluster IV consisting of three accessions namely, CM032, CM033 and CM034 performed better for fruit rind thickness, days taken for fruit maturity, days to fruit fly infestation after anthesis, and percentage of fruit fly infestation. Cluster IV recorded lowest mean values for most the traits *viz.*, vine length, inter nodal length, number of branches per plant, fruit length, fruit weight, seed cavity length, seed length, marketable yield per plant and yield per plant. Thus, results of divergence analysis revealed that the accessions CM022, CM045, CM047 and CM051 of Cluster V could be selected for better yield, used in hybridization program. Similar findings were reported by Kumar *et al*. (2013a) and Lakshmi *et al.* (2017).

From the present study, four accessions *viz.*, CM012 (17.50 per cent), CM033 (18.35 per cent), CM034 (18.58 per cent) and CM056 (24.31 per cent) recorded resistance to melon fruit fly infestation. The accession CM012 was grouped in Cluster VII. Accessions CM033 and CM034 were grouped into Cluster IV and the accession CM056 was clubbed into the cluster II. None concerned has reported similar results so far.

Results of divergence analysis from the present study revealed that the hybridization program for incorporation of melon fruit fly resistance into high yielding genotypes, may be focused on a breeding strategy in which the accessions namely, CM012, CM033 and CM034 of Cluster IV could be selected for resistance to fruit fly; the accessions *viz.*, CM022, CM045, CM047 and CM051 of Cluster V for better yield. None concerned has reported similar findings so far.

5.3. Correlation and Path analysis

The knowledge on degree of associations of yield with yield contributing, horticultural traits is of great importance because yield is not an independent character; it is the result of interactions of number of component traits among themselves as well as environmental interactions. The phenotypic expression of each trait is due to the genotype, the environment and interaction of the both. Therefore, correlation analysis of yield with various characters has been executed to find out the yield contributing factors. Genotypic correlations reveal existence of real association while, phenotypic correlations may occur by chance. Knowledge on the associations of component traits with yield per plant may greatly help in making selection more precise and accurate.

Although correlation coefficients are helpful in determining the components of complex trait like yield, they do not provide an exact picture of the relative degree of direct and indirect influences. The ultimate yield depends upon a large number of factors influencing the final expression of this trait. Path analysis will give a clear picture to the association of characters towards yield through direct or indirect effects. Wherever there is direct effects, such traits can be improved through selection; trait showing indirect effects through hybridization. The residual effects were low (1.17) which suggested that the most

of the characters under study were explained and the variability was present in the accessions.

5.2.1. Correlations of quantitative traits to yield

From the present study, yield had direct significant positive correlations with number of branches per plant, fruit length, seed cavity length, seed cavity breadth and number of fruits per plant. Genotypic correlation coefficients were higher than the phenotypic correlation coefficients for all these characters, which indicated less influence of environmental factors on these traits. Heritability estimates for these traits were also high. Therefore, direct simultaneous selection for higher mean values of these traits would improve yield. This was in confirmation with the results of Chaudhary *et al*. (2004), Kahn *et al*. (2016) and Sharma *et al*. (2018).

Days to first female flower production and node of first female flower had negative correlation and direct positive effect on yield. It meant that, selection based on lower mean value of these traits would improve yield Kahn *et al*. (2016)

Fruit girth, fruit diameter, fruit weight and days taken for fruit maturity had positive correlations with direct negative effects on yield. Hence, selection for yield should not focus on these traits. Similar findings were reported by Hossain *et al*. (2010) in cucumber.

Days to first male flower production, node of first male flower, vine length, inter nodal length, days to fruit fly infestation after anthesis and percentage of fruit fly infestation had negative correlations with direct negative effects on yield. Hence, while attempting selection for improving yield these traits should not be focused on. These results are in accordance with Babu *et al*. (2013) in oriental pickling melon; Singh and Singh (2015) and Kumari *et al*. (2018) in bitter gourd.

5.3.2. Correlations and path analysis to fruit fly infestation

Path analysis provides a clear picture to the associations of traits towards fruit fly infestation through direct, indirect effects. Wherever there is direct effects, such traits can be improved through selection and indirect effects are there such traits through breeding

methods. The residual effect was very low (0.035), suggested that the most of the traits in the present study was explained, variability was present in the accessions.

Correlation analysis of percentage of fruit fly infestation to quantitative traits revealed that it was directly, positively correlated with fruit girth, fruit weight and days taken for fruit maturity. GCV were higher than the PCV for all these traits, which indicated less influence of environmental factors on these traits. Heritability estimates for these traits were moderate to high indicated high scope for improving these traits through selection.

The present study revealed that fruit rind thickness and flesh thickness showed significant negative correlations with direct positive effects on percentage of fruit fly infestation. These traits recorded close association between PCV and GCV (63.48, 70.21; 58.36, 69.27), high heritability (81.75, 70.98), GA (2.09, 9.39) and GAM (118.24, 101.30) respectively. Hence, direct selections can be made based on higher mean values of these traits for lower percentage of fruit fly infestation. Similar results were observed by Haldhar *et al*. (2015a) in watermelon and Haldhar *et al*. (2015b) in ridge gourd, Haldhar *et al*. (2018) in snap melon.

5.5. Generation mean analysis

Generation mean analysis is a first-degree statistic and a simple, useful technique for characterizing gene effects for a polygenic character (Hayman, 1958). It determines the presence and absence of non-allelic interactions. The significance of the parameters was tested by means of the corresponding standard errors which were calculated using either the variance of the population means in a six parameter model or from error variance in a three parameter model. The crosses in which chi-square (χ^2) was significant were considered as interacting (non-allelic or epistasis) otherwise non- interacting (allelic).

The interacting crosses were further classified into two groups namely, complementary and duplicate epistasis. The epistasis was complementary when *h* and *l* had same signs (either + or -) while *h* and *l* had opposite signs represented duplicate epistasis.

The data were subjected to A, B, C and D scaling test of Mather (1949) for testing the adequacy of additive and dominance model. The gene effects (additive and dominance)

and interactions (additive x additive, additive x dominance and dominance x dominance) for each character were estimated according to Hayman (1958) and Jinks and Jones (1958).

The A and B scaling tests provide evidence for the presence of all three types of interactions viz., additive x additive (*i)*, additive x dominance (*j)* and dominance x dominance (*l*) gene effects. The C scale test provides information about the presence of dominance x dominance type of interaction effects while D scaling test is evident about the presence of additive x additive type of gene interactions.

Generation mean analysis comprising of six generations is P_1, P_2, F_1, F_2, B_1 and B_2 generations offer great scope of obtaining information on genetics of inheritance of various qualitative, quantitative traits. For systematic improvement of yield along with quantitative traits requires a precise knowledge on nature of gene action (mono factorial or epistasis) and association of traits with yield and among themselves.

The analysis of variance for six generations revealed significant differences among the generation means for all the traits for all the crosses except for days to first female flower in CrossI,II and III; for days to first male flower in Cross II,III and IV; for node at first female flower in CrossIII and IV; for node at first male flower in CrossI,III and IV; for number of branches per plant in cross I,III and IV ; for inter nodal length in CrossII; for fruit rind thickness in Cross II; for seed cavity breadth in CrossII; for seed length in cross II and for days taken for fruit maturity in CrossI,III and IV.

The individual scaling test of Mather (1949) and joint scaling test of Cavalli (1952) revealed the presence of non-allelic interactions in majority of the crosses for all the traits.

A careful assessment of the results revealed that characters related to earliness *viz*., days to first female flower, days to first male flower, node number of first female flower, node number of first male flower, days taken for fruit maturity, days to first harvest and days to last harvest were in general, largely determined by dominance (*h*) and dominance x dominance (*l*) components and was in favourable direction. Duplicate epistasis was observed in most of the crosses for all these traits. Thus, it could be inferred that there is predominance of dominance, dominance x dominance components in the inheritance of

earliness traits. Therefore, improvement in earliness in flowering, fruiting and harvesting may be achieved by heterosis breeding. Reports of Srivastava and Premnath (1976) and Celine and Sirohi (1998) in bitter gourd supported the results in the present study. Further, reports by Janakiram and Sirohi (1990), and Pichaimuthu (1991) in bottle gourd are also in agreement with the present findings. Sanandia *et al.* (2008) also reported predominance of dominance, dominance x dominance components in the inheritance of earliness characters in sponge gourd.

Estimates for components of generation means for vine length, inter nodal length and number of branches per vine revealed that largely dominance (*h*) and dominance x dominance (*l*) effects showed higher influence in the desired direction than additive (*d*) effects for these traits in all the interacting crosses which indicated that hybrid production would be helpful to exploit these traits in desired direction. Duplicate epistasis was observed for all traits in all the interacting crosses. Similar results in bitter gourd were reported by reported by Sirohi and Chuadhary, (1979) and Sirohi *et al.* (1986).

In general, both additive (*d*) and dominance (*h*) effects were highly significant in desired direction for fruit weight, fruit length, fruit girth, and fruit diameter in four crosses of oriental pickling melon. Any one or all of the interaction effects *viz*., additive x additive (*i*), additive x dominance (*j*) and dominance x dominance (*l*) were largely significant coupled with duplicate epistasis. Predominant role of dominance gene effects, additive x additive (*i*), and dominance x dominance (*l*) effects suggested that hybridization followed by selection could be adopted for improvement of these traits. Findings of Patil *et al*. (2014); Javanmard *et al*. (2018); Singh *et al.* (2018) were in agreement with the present results.

Flesh thickness and fruit rind thickness are largely governed in desirable direction by dominance gene effects, additive x additive (*i*), dominance x dominance (*l*) effects coupled with duplicate epistasis. Thus, it was inferred that hybridization followed by selection would be helpful in improving these traits. Similar results in muskmelon was reported by Javanmard *et al*. (2018); Singh *et al.* (2018).

In general, dominance (*h*) gene effects in desired direction, significant additive x additive(*i*), additive x dominance(*j*) and dominance x dominance (*l*) effects combined with duplicate epistasis were observed for seed cavity length, seed cavity breadth, seed length and number of seeds per fruit. This meant that hybridization followed by judicious selection would be appropriate to improve these traits. Similar results were reported by Javanmard *et al*. (2018) in muskmelon.

Number of fruits per plant, yield per plant and marketable yield per plant were largely governed by additive gene effects *(d)* additive x dominance (*j*), dominance x dominance (*l*) effects in the desired direction coupled with duplicate epistasis. Thus, it was inferred that progeny selection by following proper selection methods as well as hybridization would be appropriate breeding methodologies for improvement of these traits. The presence of duplicate epistasis would be detrimental for making rapid progress, making it difficult to fix genotypes with increased level of character manifestation because positive effect of one parameter will be cancelled out by the negative effect of another. Hence, early generation inter mating besides accumulating the favourable genes and maintaining heterozygosity are likely to give better results. These findings are in agreement with the reports of Celine and Sirohi (1998).

From the present study, additive x dominant (*j*), dominance x dominance (*l*) effects were predominant combined with duplicate epistasis was important in percentage fruit fly infestation in oriental pickling melon. This meant that hybridization and selection could improve this trait. None, concerned has reported similar findings so far. However, days to fruit fly infestation after anthesis was governed by additive (*d*), dominance (*h*) and dominance x dominance (*l*) effects desirable direction combined with duplicate epistasis. Thus, it was inferred that simple selection or hybridization and selection could be adopted to improve this trait. None concerned has reported similar results so far.

5.6. Correlation of biochemical traits of six generations to fruit fly infestation

Total Soluble Solids were significantly, positively correlated with percentage of fruit fly infestation, silica and acidity. Therefore, it can be inferred that Total Soluble Solids

will be low in fruit fly resistant accession and more in susceptible accessions. These results were in agreement with Haldhar *et al*. (2018).

Acidity was significantly, positively correlated with fruit fly infestation and total phenols which indicated that acidity will be more in susceptible accessions than resistant ones. Similar findings was noticed by Haldhar *et al*. (2013)

Total soluble sugars and total sugars were positively correlated with percentage fruit fly infestation and tannin. Total sugars were found to be lowest in resistant in accessions and highest in susceptible accessions. These results are in line with findings of Nath *et al*. (2017).

Crude protein, total phenols, silica and tannin contents were negatively, significantly correlated with percentage of fruit fly infestation. Therefore, it can be inferred that crude protein, total phenols, silica and tannin will be high in fruit fly, resistant accessions and low in susceptible accessions. Similar findings were reported by Gogi *et al*. (2010) in bitter gourd, Haldhar *et al*. (2015a) in watermelon, Haldhar *et al*. (2015b) in ridge gourd and Haldhar *et al*. (2017a).

From the present study, results of correlation studies of biochemical traits revealed that lower contents of Total Soluble Solids, Total soluble sugars and total sugars; higher contents of crude protein, total phenols, silica and tannins favoured resistance to fruit fly.

5.7. Sensory evaluations

Evaluation of sensory qualities of fresh, cooked fruits of six generations in four crosses revealed that highest overall acceptability for fresh, cooked fruits was in CM045 (P_1) Cross I and CM061 (P_1) CrossII. Two high yielding accessions used as parents were more acceptable than other generations. None concerned has reported similar findings.

Summary

6. SUMMARY

The present investigations were carried out at Department of Vegetable Science, College of Horticulture, Vellanikkara, with the objective(s) to identify the superior genotypes with resistance to melon fruit fly in oriental pickling melon and to incorporate the resistance to melon fruit fly in high yielding genotypes through hybridization and to elucidate the genetics of inheritance . Fifty three oriental pickling melon accessions were collected, evaluated for yield, quality, resistance to fruit fly and genetic diversity. Based on results of divergence analysis, eight high yielding accessions, four accessions with resistance to melon fruit fly were selected Hybridization was attempted to incorporate melon fruit fly resistance to high yielding accessions. Best performing four F_1 were advanced to F_2, B_1 and B_2 generations. Generation mean analysis was done to elucidate the genetics of inheritance. The salient findings of the present investigations are here under.

1. In the present study, fifty three oriental pickling melon accessions were catalogued as per Minimal Descriptor of Vegetable Crops- *Cucumis melo* (L.)- NBPGR (2000). High variability was observed for all the morphological traits except flower colour. Majority of the accessions were having oblate, elongate and globular fruit shapes. Flesh colour was white, creamy white and white with orange shade. Most of the accessions were having stem hairiness and none of the accessions were having fruit bitterness.
2. A close associations were observed between GCV and PCV estimates for earliness and yielding contributing traits *viz*, days to first female flower production, days to first male flower production, node of first female flower, node of first male flower, days to fruit maturity, days to first harvest, days to last harvest, vine length, inter nodal length, fruit diameter, fruit girth, number of fruits per plant, marketable yield per plant and yield per plant.
3. The estimates genotypic coefficient of variations were close for the traits contributing to fruit fly resistance *viz*, fruit rind thickness, flesh thickness and days to fruit fly infestation after anthesis.

4. Wide differences were noticed between PCV and GCV estimates for fruit length, fruit weight, seed cavity length, seed length and number of seeds per fruit indicated a greater degree of environmental influence on expression of these traits and selection based on these traits would not be rewarding for improvement of oriental pickling melon.
5. High heritability was observed for 11 traits *viz*., days to first male flower production, days to first harvest, number of fruits per plant, inter nodal length, yield per plant, vine length, marketable yield per plant, fruit rind thickness, seed cavity breadth, percentage fruit fly infestation and days to fruit fly infestation after anthesis, signifying that these traits are genetically controlled and there could be greater correspondence between phenotypes and breeding values while selecting individuals.
6. High heritability coupled with high genetic advance was observed for vine length, days to first harvest, marketable yield per plant, and days to fruit fly infestation after anthesis, percentage fruit fly infestation and yield per plant indicating the presence of additive gene and consequently a distinct possibility of improving these traits by simple selection.
7. High heritability coupled with low to moderate genetic advance was observed for days to first female flower production, days to first male flower production, inter nodal length, number of branches per plant, fruit diameter, seed cavity breadth, number of fruits per plant and days to fruit maturity, indicating the role of non-additive gene action hence, hybridization would be rewarding to improve these traits.
8. Genetic diversity analysis revealed that eight clusters were formed from 53 accessions. Wide range of genetic divergence was observed among the accessions in oriental pickling melon and this may be taken into account for selecting the parents for hybridization, future improvement of this crop.
9. Among the eight clusters, the accessions grouped in cluster VI and V showed maximum inter cluster distance which is useful for exploiting heterosis. Cluster

means for yield, yield contributing traits were high in cluster V (CM022, CM045, CM047 and CM051).

10. Cluster IV consisting of three accessions namely, CM032, CM033 and CM034 performed better for fruit rind thickness, days taken for fruit maturity, days to fruit fly infestation after anthesis, and percentage of fruit fly infestation.

11. The lowest inter cluster distance was observed between the cluster I and II which suggested that accessions in these clusters are closely related.

12. The genotypic correlation coefficients were mostly higher than the phenotypic correlation coefficients, thus indicating the preponderance of genetic control in the expression of most of characters. The genotypic correlation coefficient for number of branches per plant, fruit diameter, fruit girth, fruit length, fruit weight, seed cavity length, seed cavity breadth and number of fruits per plant showed significant positive correlations with yield per plant and also inter correlated among themselves indicating that these traits can be relied upon selection programme for enhancement in yield.

13. The genotypic correlation coefficients for fruit girth, fruit weight and days taken for fruit maturity showed significant positive correlations with respect to fruit fly infestation. Fruit diameter, fruit length, fruit rind thickness, flesh thickness, marketable yield per plant and days to fruit fly infestation after anthesis showed significant negative correlations to fruit fly infestation. Hence, that these traits lead to less fruit fly infestation and favoured resistance to fruit fly.

14. The path analysis revealed that number of branches per plant, number of fruits per plant, seed cavity breadth, flesh thickness, seed cavity length, node of first female flower, fruit length and fruit rind thickness had high positive effects on yield per plant. Therefore, these characters can be relied upon for improving yield per plant.

15. The path analysis in respect of percentage of fruit fly infestation and correlated traits showed that fruit rind thickness, flesh thickness, days taken for fruit maturity and fruit girth had direct negative effects on fruit fly infestation.

16. Based on the yield and genetic divergence, the accessions namely CM022, CM045, CM047 and CM051 were selected as promising accessions for yield and yield contributing traits which may be utilized in hybridization programme

17. The fruit fly resistant accessions were CM012, CM033, CM034 and CM056. Two different species of fruit fly were identified. *Zeugodacus cucurbitae* infesting most of the accessions and *Zeugodacus tau* infesting the accession CM014 only.

18. Anatomical studies revealed that resistant accession CM034 had more skin thickness(348.55µm) which favoured resistance to fruit fly infestation than the susceptible accession CM061 with a skin thickness of 65.65µm

19. Hybridization was undertaken to incorporate fruit fly resistance into high yielding accessions. Eight high yielding accessions *viz*., CM022, CM033, CM045, CM047, CM051, CM060, CM061 and CM062 was selected as female parents; fruit fly resistant genotypes (*Cucumis melo* var. *agrestis* (W-10), *Cucumis melo* var. *agrestis* (W-51), *Cucumis melo* ssp. *callosus* and CM033) were selected as male parents to generate 31 F_1 hybrids(CM033 was used both as male and female parent).

20. Thirty one F_1's were evaluated for morphological characters and resistance to fruit fly. High variability was observed for all the qualitative and quantitative traits.

21. Based on yield, qualitative traits, absence of bitterness and resistance to fruit fly, four F_1's (CM045 x CM033 (Cross I), CM061 x CM033 (Cross II), CM051 x *Cucumis melo* ssp. *callosus* (Cross III), CM033 x *Cucumis melo* ssp. *callosus* (Cross IV) were advanced to F_2, B_1, and B_2 generations for generation mean analysis.

22. Generation mean analysis revealed that related to earliness *viz*., days to first female flower, days to first male flower, node number of first female flower, node number of first male flower, days taken for fruit maturity, days to first harvest and days to last harvest were in general, largely determined by dominance (*h*) and

dominance x dominance (*l*) components and was in favourable direction. Therefore, improvement in earliness in flowering, fruiting and harvesting may be achieved by heterosis breeding.

23. Number of fruits per plant, fruit rind thickness (Cross I), fruit girth (Cross II), fruit diameter (Cross II & III), day to last harvest (Cross III) exhibited complementary epistasis with significant additive (*d*), additive x dominance (*j*) and dominance x dominance (*l*) gene effects revealed that selection from segregating population could improve these traits.

24. Yield contributing traits, fruit fly resistance traits were governed by additive x additive (*i*), additive x dominance *(j*) and dominance x dominance (*l*) coupled with duplicate epitasis indicated that hybridization followed by selection is appropriate.

25. Correlations of biochemical traits of six generations with fruit fly infestation revealed that lower content of total soluble solids, total soluble sugars, total sugars; higher content of crude protein, total phenol, silica and tannins favored resistance to fruit fly infestation.

26. Sensory qualities of fresh, cooked fruits of six generations in four crosses revealed that highest overall acceptability for fresh, cooked fruits was in CM045 (P_1) CrossI and CM061 (P_1) of Cross II.

References

REFERENCES

Akashi, Y., Fukuda, N., Wako, T., Masuda, M. and Kato, K. 2002. Genetic variation and phylogenetic relationship in East and South Asian melons *Cucumis melo* L. based on the analysis of five isozymes. *Euphytica*. 125: 385-396.

Am, M., Sridharam, S., Mohan, C. and Awasthi, N. S. 2017. Varying infestation of fruit fly *Bactrocera cucurbitae* (Coquillett) in different cucurbit crops. *J. Entomol. Zool. Stud*. 5(3): 1419-1421.

Amerine, M. A., Pangborn, R. N., and Roessler, E. B. 1965. *Principles of Sensory Evaluation of Food.* Academic press, London, 350p.

Babu, R. R., Rao, N. H. and Reddy, R. V. S. K. 2013. Correlation and path analysis in oriental pickling melon (*Cucumis melo* L. var. *conomon*) genotypes. *J. Res.* 42(3):62-66.

Burton, G. W. 1952. Quantitative inheritance in grasses. *Proc. 6th. Int. Grassld. Cong*. 1: 277-283.

Cavalli, L. L. 1952. An analysis of linkage in quantitative inheritance. Quantitative Inheritance H.M.S.O. London. pp 135-144.

Celine, V. A. and Sirohi, P. S. 1998. Generation mean analysis for earliness and yield in bitter gourd (*Momordica charantia* L.). *Veg. Sci*. 25: 50-53.

Chaudhary, B. R., Fageria, M. S. and Dhaka, R. S. 2004. Correlation and path coefficient analysis in muskmelon (*Cucumis melo* L.) *Indian J. Hort*. 61 (2):162-258.

Christenson, L. D. and Foote, R. H. 1960. Biology of fruit flies. *Annu. Rev. Entomol*. 32: 381-383.

Dewey and Lu. 1959. *Path analysis – A primer*. Box wood press, Pacific Grove, CA.

Dhillon, M. K., Naresh, J. S., Singh, R. and Sharma, N. K. 2005a. Evaluation of bitter gourd (*Momordica charantia* L.) genotypes to melon fruit fly *Bactrocera cucurbitae* (Coquillett). *Indian J. Plant Prot.* 33: 55-59.

Dhillon, M. K., Singh, R., Naresh, J. S. and Sharma, H. C. 2005b. The melon fruit fly, *Bactrocera cucurbitae*: A review of its biology and management, *J. Insect Sci*., 5: 1-16.

Doharey, K. L.1983. Bionomics of fruit flies (*Dacus* spp.) on some fruits. *Indian J. Entomol*. 45: 406-413.

Falconer, D. S. 1967. *Introduction to Quantitative Genetics* (3rd Ed.). Oliver and Boyd. Edinburgh. pp**:** 312-318.

Gogi, M. D., Ashfaq, M., Arif, M. J. and Khan, M. A. 2009. Screening of bitter gourd (*Momordica charantia*) germplasm for sources of resistance against melon fruit fly (*Bactrocera cucurbitae*) in Pakistan. *Int. J. Agric. Biol*. 11: 746-750.

Gogi, M. D., Ashfaq, M., Arif, M. J., Sarfraz, R. M. and Nawab, N. N. 2010. Investigating phenotypic structures and allelochemical compounds of the fruits of *Momordica charantia* L. genotypes as source of resistance against *Bactrocera cucurbitae* (Coquillett) (Diptera, Tephritidae). *Crop Prot*. 29: 884-890.

Gondi, S. P., Ganiger, V. M., Bhuvaneshwari, G., Madalageri, M. B., Kotikal, Y. K. and Manjunatha, G. 2016. Evaluation of oriental picking melon (*Cucumis melo* L. var. *conomon*) genotypes for pest and disease reaction under Northern Dry Zone of Karnataka. *J. Environ. Ecol.* 7(1):29-36.

Haldhar, S. M., Bhargava, R., Choudhary, B. R., Pal, G. and Kumar, S. 2013. Allelochemical resistance traits of muskmelon (*Cucumis melo*) against the fruit fly (*Bactrocera cucurbitae*) in a hot arid regions of India. *Phytoparasitica.* 41: 473-481.

Haldhar, S. M., Choudhary, B. R., Bhargava, R. and Meena, S. R. 2015 a. Antixenotic and allelochemical resistance traits of watermelon against *Bactrocera cucurbitae* in a hot arid regions of India. *Fla. Entomol*. 98 (3): 827-834.

Haldhar, S. M., Choudhary, B. R., Bhargava, R. and Gurjar, K. 2015 b. Host plant resistance (HPR) traits of ridge gourd (*Luffa acutangala* (Roxb) L.) against melon fruit fly (*Bactrocera cucurbitae* (Coquillett)) in hot arid regions of India. *Scientia Horticulturae* 194: 168-174.

Haldhar, S. M., Samadia, D. K., Bhargava, R. and Choudhary, B. R. 2018. Hosts plant accessions determine bottom up effect of snap melon (*Cucumis melo* var. *momordica*) against melon fly (*Bactrocera cucurbitae* (Coquillett)). *Breed. Sci*. 68: 499-507.

Haldhar, S. M., Samadia, D. K., Bhargava, R. and Singh, D. 2017. Host plant genotype determine bottom up effect of *Cucumis melo* var. *callosus* against melon fruit fly. *Crop Prot*. 98: 157-165.

Hayman, B. I. 1958. The separation of epistatic from additive and dominance variation in generation means. *Heredity* 12: 371-390.

Hayman, B. I. and Mather, K. 1955. The description of genetic interaction in continuous variation. *Biometrics* 16: 369-381.

Hollingsworth, R., Vagalo, M. and Tsatsia, F. 1997. Biology of melon fly, with special reference to the Solomon Island, In: Allwood, A.J. and Drew, R.A.I. editors. Management of fruit flies in the Pacific. *Proc. Aust. Country Ind. Agric. Res*. 76:140-144.

Hossain, M. F., Rabbani, M. G., Hakim, M. A., Amanullah, A. S. M., Ahsanullah, A. S. M. 2010. Studies on variability, character association and yield performance of cucumber (*Cucumis sativus* L.). *Bangladesh Res. Publications J.* 4(3): 297-311.

Huang, H. Y. and Hseieh, C. H. 2017. Genetic research on fruit colour traits of the bitter gourd (*Momordica charantia* L.). *Hortic. J*. 86(2): 238-243.

Ingoley, P., Mehta, P. K., Chauhan, Y. S., Singh, N. and Awasthi, C. P. 2005. Evaluation of cucumber genotypes for resistance to fruit fly, *Bactrocera cucurbitae* Coq. under mid hill conditions of Himachal Pradesh. *J. Ent. Res*. 29(1): 57-60.

Janakiram, T. and Sirohi, P. S. 1990. Genetics of fruit maturity in bottle gourd. *South Indian Hort.* 38:3

Javanmard, T., Abadi, F. S. S. and Bihamta, M. R. 2018. Estimation of some genetic parameters through generation mean analysis in melon. *Indian J. Agric. Res*.52: 619-624.

Jinks, J. L. and Jones, R. M. 1958. Estimation of the components of heterosis. *Genetics*, 43: 223-234.

John, K. J., Scariah, S., Nissar, V. A. M., Latha, M., Gopalakrishnan., S., Yadav, S. R. and Bhat, K.V. 2013. On the occurrence, distribution, taxonomy and genepool relationship of *Cucumis callosus* (Rottler) Cogn. the wild progenitor of *Cucumis melo* L. from India. *Genet. Resour. Crop Evol.* 60: 1037-1046.

Johnson, H. W., Robinson, H. F. and Comstock, R. E. 1955a. Estimation of genetic and environmental variability in soyabeans, *Agron. J*.47: 314-318

Johnson, H. W., Robinson, H. F. and Comstock, R. E. 1955b. Estimates of phenotypic and genotypic correlation in soybean and their implications in selection. *Agron. J.* 47**:** 477- 482.

Joshi, S., Joshi, M.C. and Vishnoi, A.K. 1981. Genotypic and phenotypic variability in cucumber. Veg. Sci. 8(2):114-119.

Kabir, M.Y., Khan, A.S.M.M.R. and Hassain, M.S. 2009.Genetic divergence in pointed gourd. *J. Agric. Rural Dev.* 7(1&2):87-92.

Kapoor, V.C. 1993. *Indian Fruit Flies*. Oxford and IBH Publishing Co., New Delhi, India. 228p.

KAU (Kerala Agricultural University) 2016. *Package of Practises Recommendations: Crops* (15 th Ed.). Kerala Agricultural University, Thrissur, 393 p.

Khan, A.S.M.M.R., Eyasmin, R., Rashid, M.H., Ishtiaque, S. and Chaki, A.K. 2016. Variability, heritability, character association, path analysis and morphological diversity in snake gourd. *Agric. Natural Resource*. 50:483-489.

Khandelwal, R.C. and Nath, P. 2011. Inheritance of resistance to fruit fly in watermelon. *Genome*. 20 (1): 31-34.

Khatun, M., Rabbani, M. G. and Rahaman, E. H. S. 2010. Estimate of genetic diversity in snake gourd (*Trichosanthes cucumerina*). *Bangladesh J. Agric. Res*. 35: 95-100.

Kirkbride, J. H. 1993. Biosystematic monograph of the genus *Cucumis* (Cucurbitaceae). *Parkway Publishers*, Bonne, North Carolina, USA, 159p.

Krishnaprasad, V. S. R., Rai, M., Pan, R. S. and Singh, A. K. 2004 a. Combining ability and standardization potence in crosses between *Cucumis sativus* L. x *Cucumis hardwickii*. *Indian J. Hort.* 61(2): 128-131.

Kumar, A., Kumar, S. and Pal, A. K. 2008. Genetic variability and character association for fruit yield and yield traits in cucumber. *Indian J. Hort*. 65(4): 423-428.

Kumar, R. and Wehner, T.C. 2013. Quantitative analysis of generation for inheritance of fruit yield in watermelon. *Hort. Sci*. 48(7): 844-847.

Kumar, R., Ameta, K.D., Dubey, R.B. and Pareek, S. 2013 a. Genetic variability, correlation and path analysis in sponge gourd (*Luffa cylindrica* Roem.). *Afr. J. Biotechnol*. 12: 539-543.

Kumar, R., Kumar, S., Kumar, D. and Kansal, S. 2018. Heterosis and combining ability and gene action studies for insect pest and disease resistance in cucumber. *Electr. J. Plant Breed*. 9 (3): 815-828.

Kumari, A., Singh, A. S., Moharana, D. P., Kumar, A. and Kumar, N. 2018. Character relationship and path coefficient analysis for yield and yield components in diverse genotypes of cucumber (*Cucumis sativus* L.). *The Pharma. Inno. J*. 7(5): 33-38.

Lakshmi, L. M., Lingaiah, H. B., Rao, A. M., Raju, T. B. P., Pitchaimuthu, M. and Gowda, D.M. 2017. Variability and genetic divergence studies for economic traits in indigenous oriental pickling melon (*Cucumis melo var. conomon*) genotypes. *Electr. J. Plant Breed*. 8(1): 365-370.

Lenka, D. and Misra, H. 1973. Path coefficient analysis of yield in rice varieties. *Indian J. Agric. Sci***.** 46: 376-379.

Lush, J. L. 1940. Intra-sire correlation and regression of offspring on dams as a method of estimating heritability of characters. *Amer. Soc. Anim. Prod*.33: 293- 301.

Mahajan, V., Mukherjee, S. C. and Shaw, S. S.1997. Use resistant vegetable varieties: a best alternative to tackle diseases and insect pest. *Farmer and Parliament*. 33: 29-30.

Mahalanobis, P. C. 1936. On the generalized distances in statistics. *Proc. Nat. Acad. Sci. India*. 2: 49-55

Mariappan, S. and Pappiah, C. M. 1990. Genetic studies in cucumber (*C. sativus* L.). *South Indian Hort.* 38:70-74.

Mather, K. 1949. Biometrical genetics. The study of variation. Methuen and Co. Ltd. London. pp.162.

Mather, K. and Jinks. 1971. Introduction to Biometrical Genetics (3rd ed.). Champman and Hali Ltd. London. pp.189.

Ma, J. F., Tamai, M., Ichii, M., and Wu, K. 2002. A rice mutant defective in active silicon uptake. *J. Plant Physiol*. 130: 2111-2117.

Miyatake, T., Irabu, T., Higa, R., 1993. Oviposition punctures in cucurbit fruits and their economic damage caused by the sterile female melon fly, *Bactrocera cucurbitae* (Coquillett). *Proc. Plant Prot. Kyushu*. 39: 102-105.

Munshi, A. D. and Alvarez, J. M. 2005. Hybrid melon development. *J. New Seeds*, 6(4): 321-360

Nagappan, K., Kamalnathan, S., Santharaman,T. and Ayyasamy, M.K.1971. Insecticidal trial for the control of the melon fruit fly, *Dacus cucurbitae* Coq. infesting snake gourd, *Trichosanthes anguina. Madras Agric. J.* 58: 688-690.

Nath, P. 1966. Varietal resistance of gourds to the fruit fly. *Indian J. Hortic*. 23: 69-79.

Nath, P., Pandey, A. K.,Kumar, A., Rai, A. B. and Palanivel, H. 2017. Biochemical resistance traits of bitter gourd against fruit fly (*Bactrocera cucurbitae* (Coquillett)) infestation. *J. Agric. Sci*. 9(2): 217-225.

NBPGR [National Bureau of Plant Genetic Resources].2000. Indian Horticulture Database, National Bureau of Plant Genetic Resources, New Delhi. Pp136-145.

NHB [National Horticulture Board].2018. NHB home page [online]. Available: http://www.nhb.gov.in [03. Mar. 2018].

Nuez, F., Pico, B., Iglesias, A., Esteva, J. and Juarez, M. 1999. Genetics of Melon yellow virus resistance derived from *Cucumis melo* ssp. *agrestis*. *Eur. J. Plant Pathol*. 105: 454-464.

Pal, A. B., Srinivasan, K. and Doijode, S. D. 1984. Source of resistance to melon fruit fly in bitter gourd and possible mechanism of resistance. *SABRAO J*. 16: 57-69.

Pandey, S., Rai, M. and Singh, B. 2005. Genetic variability and character association in muskmelon (*Cucumis melo* L.). *Indian J. Plant Genet. Resour*. 18(2): 212-216.

Parathasarathy, V. A. and Sambandam, C. N. 1989. Taxonomy of *Cucumis callosus* (Rottl.) Cogn. the wild melon of India. *Cucurbit Genet. Coop. Rep*. 3: 66-67.

Patil, D. S., Musmade, A. M. and Jagtap, V. S. 2014. Generation mean analysis of yield and its component in muskmelon (*Cucumis melo* L.). *Asian J. Hortic*. 9: 81-88.

Pitchaimuthu, M. 1991. Heterosis in bottle gourd (*Lagenaria siceraria* (Mol) Standl). Ph.D Thesis, IARI, New Delhi, 189p.

Pitrat, M. 2013a. Phenotypic diversity in melon and cultivated melons (*Cucumis melo* L.). *Plant Biotech.* 30(3): 273-278.

Rabbani, M. G., Naher, M. J. and Hoque, S. 2012. Variability, character association and diversity analysis of ridge gourd (*Luffa acutangula* Roxb.) genotypes of Bangladesh. *SAARC. J. Agric*. 10:1-10.

Rabindranath, K. and Pillai, K. S. 1986. Control of fruit fly of bitter gourd using synthetic pyrethroids. *Entomol*. 11: 262-272.

Rakhi, R. and Rajamony, L. 2005. Variability, heritability and genetic advances in land races of culinary melon (*Cucumis melo* L.). *J. Tropic. Agric*. 43(1-2):79-82.

Ram, H. H. 2014. *Vegetable Breeding Principles and Practices*. Kalyani Publishers, Ludhiana, 591p.

Rani, K. R., Reddy, K. R. and Raju, C. S. 2013. Study of gene effects for yield and its component traits in bitter gourd (*Momordica charantia* L.) by generation mean analysis. *Electr. J. Plant Breed.* 4(3):1237-1241.

Rao, C. R. 1952. *Advance Statistics Method in Biometrical Research*. John Wiley and Sons, New York, 390pp.

Rastogi, K. B. and Deep, A. 1990. Variability studies in cucumber (*Cucumis sativus* L.). *Veg. Sci*. 17: 224-226.

Robinson, H. F., Comstock, R. S. and Harvey, P. H 1949. Estimates of heritability and the degree of dominance in corn. *Agron. J*. 41: 353-359.

Roy, A., Bal, S. S., Fergany, M., Kaur, S., Singh, H., Malik, A. A., Singh, J., Monforte, A. J. and Dhillon, N. P. S. 2012. Wild melon diversity in India (Punjab State). *Genet. Resour. Crop Evol*. 59: 755-767.

Sadasivam, S. and Manickam, A. 2008. *Biochemical Methods* (3rd Ed.). New Age International Publishers, New Delhi,168p.

Sakulphrom, S., Chankaew, S. and Sauitchon, J. 2018. Genetic analysis and heritability of fruit character in muskmelon (*Cucumis melo* L.) using extreme parental difference. *J. Agric. Sci*. 40(1): 1-7.

Samadia, D. K. and Pareek, O. P. 2000. Two *Cucumis* (Kachri) varieties of arid regions. *ICAR News.* 6(2): 15-16.

Sanandia, S. T., Mehta, D. R. and Tarpara, V. D. 2008. Generation mean analysis for earliness in sponge gourd (*Luffa Cylindrica* (L.) Roem.). *Natnl. J. Pl. Improv*. 10(2): 126-128.

Sharma, M., Singh, V., Singh, S. K. and Dhangrah, V. K. 2016. Exploitation of gynoecious lines in cucumber (*Cucumis sativus* L.) for heterosis breeding. *Int. J. Bio. Resour. Stress Manag*. 7(2):184-190.

Sharma, S., Kumar, R., Chatterjee, S. and Sharma, H. R. 2018. Correlation and path analysis studies for yield and its attributes in cucumber (*Cucumis staivus* L.). *Int. J. Chem. Stud*. 6(2): 2045-2048.

Shashikumar, K. T., Pitchaimuthu, M. and Rawal, R. D. 2010. Generation mean analysis of resistance to downy mildew in adult muskmelon plants**.** *Euphytica*. 173:121-127.

Sivasubramanian, S. and Menon, M.P. 1973. Genotypic and phenotypic variability in rice. *Madras Agric. J.* 60.

Shivaji, J. S. 2014. Evaluation of F_1 hybrids of cucumber and their nutrition management under Konkan agro climatic conditions. PhD. (Hort.) Thesis, Dr. Balasaheb Sawant Konkan Krishi Vidhyapeeth, Dapoli, 67p.

Singh, G. and Lal, T. 2005. Genetic variability, heritability and genetic advance for yield and its contributing traits in muskmelon. *J. Res. Punjab Agric. Univ*. 42(2): 168-174.

Singh, H. K. and Singh, D. R. 2015. Association and path co-efficient analysis among yield and its components in bitter gourd (*Momordica charantia* L.). *Asian J. Hort*. 10(2): 212-215.

Singh, M. 1997. Variability studies in some lines of cucumber (*Cucumis sativus* L.). M.Sc. (Hort.) Thesis, Dr. Y.S. Parmar University of Horticulture and Forestry, Nauni, Solan, H.P,175p

Singh, S., Pandey, S., Raghuwanshi, R. and Singh, B. 2018. Generation mean analysis for fruit traits in infra-specific population of melon. *Green Farming* 9(6): 954-958.

Singh, S. V., Mishra, A., Bisan, R. S., Malik, Y. P. and Mishra, A. 2000. Host preference of red pumpkin beetle, *Aulacophora foveicollis* and melon fruit fly, *Dacus cucurbitae*. *Indian J. Entomol*. 10: 249-266

Sirohi, P. S and Choudhary, B. 1979. Gene effects in bitter gourd (*Momordica charantia* (L.)). *Veg. Sci.* 6: 106-112.

Sirohi, P. S., Sivakami, N. and Choudhary, B.1986. Genetic analysis in long fruited bottle gourd. *Indian J. Agric. Sci.* 56(9): 623-625.

Sivaprasad, M. K. 2013. Studies on performance of muskmelon (*Cucumis melo* L.) hybrids under Northern Dry Zone of Karnataka, MSc. (Hort.) Thesis, UHS, Bagalkot. 72p.

Snedecor, G. W. 1961. *Statistical Methods*.Iowa state university press America**.** Iowa, U.S.A.313p.

Srivastavu, V. K. and Premnath. 1976. Diallel analysis in *Momordica charantia* L. *Proc. Third Int. Symp. Sub-Trop. Hort*., Banglore. 1. *Improve. Hort. Plant Med. Plants* 157p.

Taha, M., Eljack, A. E. and Omara, S. 2007. Estimation of genetic variability and broad sense heritability of some traits in melon (*Cucumis melo* L.). *Sudan J. Agric. Res*. 8: 51-57.

Thakur, M., Kumar, R. and Kansal, S. 2019. Heterosis, combining ability and gene action studies in cucumber for different biotic stresses to develop resistant hybrids. *Genetika* 51(1): 199-212.

Thyagaraj, G. N., Puttaraju, T. B. and Santhosh, N. 2013. Evaluation of F_1 hybrids in oriental pickling melon (*Cucumis melo* var. *conomon*) for important pest and diseases. *Green Farming*. 4(3): 291-293.

Torkadi, S. S., Musmade, A. M. and Mangave, K. K. 2007. Genetic variability studies in musk melon. *J. Soils and Crops*. 17(2): 308-311.

Whitaker, T.W. and Davis, G.N. 1962. Cucurbits. *Interscience*, New York, pp250.

Yogesh, C., Yadav, S. K., Brijpal, B. and Dixit, S.K. 2009. Genetic variability, heritability and genetic advance for some traits in cucumber. *Indian J. Hort*. 66(4): 488-491.

Zalapa, J. E., Staub, J. E. and Creight, M. J. D. 2006. Generation mean analysis of plant architectural traits and fruit yield in melon. *Plant Breed*. 125: 482-487.

Abstract

BREEDING FOR RESISTANCE TO FRUIT FLY (*Zeugodacus* spp.) IN ORIENTAL PICKLING MELON (*Cucumis melo* (L.) var. *conomon* Mak.)

by

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ABSTRACT

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"Breeding for resistance to fruit fly (*Zeugodacus* spp.) in oriental pickling melon (*Cucumis melo* (L.) var. *conomon* Mak.)

ABSTRACT

Melon fruit fly (*Zeugodacus* spp.) is one of the major pests in cucurbits and it causes a loss of 32-100 per cent depending upon seasons and prevailing climatic conditions. The developing resistant varieties either by selection from germplasm lines or through backcross breeding is an economical way to reduce fruit loss in oriental pickling melon. Keeping this in view, the present investigations entitled "Breeding for resistance to fruit fly (*Zeugodacus* spp.) in oriental pickling melon (*Cucumis melo* (L.) var. *conomon*. Mak.)" was undertaken to identify sources of resistance to fruit fly infestation form germplasm; to incorporate fruit fly resistance into high yielding genotypes and to study the genetics of inheritance. Two separate experiments were designed for the study.

Fifty three oriental pickling melon accessions were catalogued as per Minimal Descriptor of Vegetable Crops- *Cucumis melo* (L.)- NBPGR (2000). High variability was observed for all the morphological traits except flower colour. Oblate followed by globular and elongate were the predominant fruit shapes. White, creamy white, white with orange shade were observed for flesh colour. Fruit taste was sour, sweet; none of the accessions had bitterness. The traits *viz.,* node of first female flower, vine length, number of seeds per fruit, number of fruits per plant, days to last harvest and percentage of fruit fly infestation exhibited high GCV, PCV, heritability and GA which indicated that these traits were highly heritable and could be improved through selection.

Yield per plant was positively, significantly correlated with number of branches per plant, fruit diameter, fruit girth, fruit length, fruit weight, seed cavity length, seed cavity breadth and number of fruits per plant. High heritability was exhibited by all these traits. Therefore, simultaneous selection for these traits would improve yield. Significant negative correlations to fruit fly infestation were observed for traits *viz*., fruit diameter, fruit rind thickness, flesh thickness, marketable yield per plant, days to fruit fly infestation after

anthesis. These traits exhibited high heritability hence, direct selection of higher mean values would improve yield and fruit fly resistance.

Mahalanobis D^2 analysis grouped the 53 accessions into 8 clusters. Cluster I had maximum number of accessions (12) followed by cluster II (9). The maximum inter cluster D^2 value was between cluster VI and cluster V. Cluster mean for yield contributing traits were high in cluster V which consisted the promising accessions *viz.,* CM022, CM045, CM047 and CM051. Cluster mean for fruit fly resistance contributing traits were high in cluster IV and cluster VI, where the promising accessions with respect to fruit fly resistance *viz.,* CM012, CM033, CM034 and CM056were distributed. Two species of fruit fly were identified *viz., Zeugodacus cucurbitae* and *Zeugodacus tau* during the crop seasons.

Hybridization was undertaken to incorporate fruit fly resistance into high yielding accessions from wild as well as resistant genotypes. Accessions *viz.,* CM022, CM033, CM045, CM047, CM051, CM060, CM061 and CM062 selected as female parents; fruit fly resistant genotypes (*Cucumis melo* var. *agrestis* (W-10), *Cucumis melo* var. *agrestis* (W-51), *Cucumis melo* ssp. *callosus* and CM033) were selected as male parents. Thirty one F_1's were evaluated for morphological characters and resistance to fruit fly. High variability was observed for all the morphological traits except flower colour. Oblate followed by elliptical and elongate were the predominant fruit shapes. White, creamy white, white with orange shade were observed for flesh colour. Fruit taste was sour, sweet and bitter. Based on yield, quality, absence of bitterness and resistance to fruit fly, four F_1's were selected *viz.,* CM045 x CM033(3.04kg) (Cross I), CM061 x CM033 (3.26kg) (Cross II), CM051 x *Cucumis melo* ssp. *callosus* (2.34kg) (Cross III), CM033 x *Cucumis melo* ssp. *callosus* (1.96kg)(Cross IV) for generation mean analysis.

Generation mean analysis revealed that earliness traits were predominantly determined by dominance *(h)* gene effects coupled with duplicate epistasis. Hence improvement of earliness in flowering, fruiting and harvesting may be achieved by heterosis breeding. Yield contributing traits were governed by additive x additive *(i),* additive x dominance *(j)* and dominance x dominance *(l)* coupled with duplicate epistasis

which indicated that hybridization followed by selection is appropriate. Fruit fly resistance traits were largely determined by additive x additive (*i*), additive x dominance (*j*) and dominance x dominance (*l*) effects coupled with duplicate epistasis. Selection and or hybridization followed by selection can be used. Number of fruits per plant, fruit rind thickness (Cross I), fruit girth (Cross II), fruit diameter (Cross II & III), day to last harvest (Cross III) exhibited complementary epistasis with significant additive (*d*), additive x dominance (*j*) and dominance x dominance (*l*) gene effects revealed that selection from segregating population could improve these traits.

Correlations of biochemical traits of six generations to fruit fly infestation revealed that lower content of total soluble solids, total soluble sugars, total sugars; higher content of crude protein, total phenols, silica and tannins favoured resistance to fruit fly infestation.

Evaluation of sensory qualities of fresh, cooked fruits of six generations in four crosses revealed that highest overall acceptability for fresh, cooked fruits was in CM045 (P_1) Cross I and CM061 (P_1) CrossII.

The present investigations revealed that high variability was observed for all the morphological traits and resistance to fruit fly in oriental pickling melon accessions. Two species of fruit fly *viz., Zeugodacus cucurbitae* and *Zeugodacus tau* were identified during the crop seasons which infested different accessions. High heritability was observed for yield and fruit fly resistance. Fruit diameter, fruit rind thickness and flesh thickness exhibited high heritability, significant positive correlations with yield and significant negative correlations with fruit fly infestation. Simultaneous selection based on these traits would improve yield as well as fruit fly resistance. High magnitude of fruit rind thickness, flesh thickness and days to fruit fly infestation after anthesis along with hairiness on stem and fruit contributed to fruit fly resistance. High crude protein, total phenols, tannins and silica content of fruits contributed resistance to fruit fly whereas, high sugars, total sugars, total soluble solids favored fruit fly infestation. Generation mean analysis revealed that selection from segregating generations, heterosis breeding would be appropriate to improve yield along with fruit fly resistance.

Appendices

Appendix I. Score card for the sensory evaluation of flesh in oriental pickling melon fruit (Fresh and Cooked)

Parameters	T_1	T_2	T_3	T_4	T_5	T_6	T_7	T_8	T_9	T_{10}	T_{11}	T_{12}	T_{13}	T_{14}	T_{15}	T_{16}	T_{17}	T_{18}	T_{19}	T_{20}	T_{21}	T_{22}	T_{23}	T_{24}
Colour																								
Flavour																								
Texture																								
Taste																								
After taste																								
Overall acceptability																								
Total																								

Name:

Date:

Signature:

Nine point hedonic scale

Like extremely	9	Neither like or dislike	5
Like very much	8	Dislike slightly	4
Like moderately	7	Dislike moderately	3
Like slightly	6	Dislike very much	2
		Dislike extremely	1

Appendix II. Qualitative traits in oriental pickling melon accessions

Variety	Flower colour	Stem hairiness	Fruit shape	Fruit colour at maturity	Skin surface	Skin hardness	Skin texture
CM001	Yellow	Present	Pyriform	Yellowish with orange and green shades	Smooth	Hard	Plain
CM002	Yellow	Present	Oblate	Yellowish with green and orange stripes	Cracked	Intermediate	Stripped
CM003	Yellow	Absent	Globular	Yellow	Smooth	Hard	Plain
CM004	Yellow	Present	Oblate	Yellowish with orange shade	Smooth	Hard	Plain
CM005	Yellow	Absent	Globular	Orange with yellowish colour	Smooth	Hard	Plain
CM006	Yellow	Absent	Globular	Yellowish with light orange shade	Smooth	Hard	Plain
CM007	Yellow	Absent	Globular	Yellow colour	Smooth	Hard	Plain
CM008	Yellow	Absent	Globular	Yellow colour	Smooth	Intermediate	Plain
CM009	Yellow	Present	Globular	Yellowish with orange shade	Smooth	Hard	Plain
CM010	Yellow	Present	Oblate	Yellow colour	Smooth	Hard	Plain
CM011	Yellow	Absent	Elongate	Light yellow with green stripes	Smooth	Hard	Striped
CM012	Yellow	Present	Ovate	Orange with light yellow shade	Smooth	Hard	Plain
CM014	Yellow	Present	Ovate	Yellowish with orange shade	Smooth	Hard	Plain
CM015	Yellow	Absent	Oblate	Yellow	Smooth	Hard	Plain
CM016	Yellow	Present	Globular	Orange with yellow colour	Smooth	Intermediate	Plain
CM017	Yellow	Absent	Oblate	Orange colour with yellow stripes on the top of fruit	Smooth	Hard	Plain
CM018	Yellow	Absent	Globular	Yellow with green stripes	Smooth	Hard	Striped

CM019	Yellow	Absent	Elongate	Orange with yellow stripes	Smooth	Intermediate	Striped
CM020	Yellow	Absent	Elliptical	Orange with green stripes	Smooth	Hard	Striped
CM022	Yellow	Present	Oblate	Orange with green colour stripes	Smooth	Hard	Striped
CM023	Yellow	Present	Elliptical	Light yellow with green stripes	Smooth	Intermediate	Striped
CM024	Yellow	Absent	Elongate	Orange with green stripes	Smooth	Hard	Striped
CM025	Yellow	Absent	Oblate	Yellowish with green stripes	Smooth	Hard	Striped
CM028	Yellow	Absent	Oblate	Yellowish with orange tinch	Smooth	Hard	Plain
CM032	Yellow	Present	Globular	Plain yellow	Smooth	Hard	Plain
CM033	Yellow	Present	Globular	Plain yellow	Smooth	Hard	Plain
CM034	Yellow	Present	Oblate	Yellow with orange stripes	Smooth	Hard	Striped
CM035	Yellow	Present	Globular	Plain yellow with greenish stripes	Smooth	Hard	Striped
CM036	Yellow	Absent	Ovate	Yellowish with green stripes	Smooth	Hard	Striped
CM037	Yellow	Present	Pyriform	Light orange with orange and green stripes	Cracked	Hard	Striped
CM038	Yellow	Absent	Elliptical	Yellow with green and orange stripes	Cracked	Hard	Striped
CM039	Yellow	Absent	Globular	Yellow	Smooth	Hard	Plain
CM040	Yellow	Absent	Ovate	Orange with green stripes	Smooth	Hard	Striped
CM042	Yellow	Absent	Oblate	Green with orange and yellow stripes	Cracked	Intermediate	Striped
CM043	Yellow	Present	Elongate	Yellow with orange stripes	Smooth	Hard	Striped
CM044	Yellow	Present	Elongate	Yellowish with orange shade	Smooth	Hard	Plain
CM045	Yellow	Present	Elongate	Yellowish with orange stripes	Cracked	Intermediate	Striped

CM046	Yellow	Absent	Oblate	Yellow with dark orange stripes	Cracked	Intermediate	Striped
CM047	Yellow	Present	Elongate	Yellowish with orange stripes	Cracked	Hard	Striped
CM048	Yellow	Absent	Elongate	Yellow with orange stripes	Cracked	Hard	Striped
CM049	Yellow	Absent	Elongate	Orange with yellow stripes	Smooth	Intermediate	Striped
CM050	Yellow	Absent	Elongate	Yellow with green stripes	Smooth	Intermediate	Striped
CM051	Yellow	Present	Ovate	Orange with green and yellow stripes	Smooth	Intermediate	Striped
CM052	Yellow	Present	Oblate	Yellow with dark orange stripes	Smooth	Hard	Striped
CM053	Yellow	Present	Elliptical	Yellow with orange stripes	Cracked	Hard	Striped
CM055	Yellow	Present	Oblate	Orange with green stripes	Cracked	Intermediate	Striped
CM056	Yellow	Present	Elliptical	Orange with yellow stripes	Smooth	Hard	Striped
CM057	Yellow	Present	Oblate	Light yellow with dark green stripes	Smooth	Hard	Striped
CM058	Yellow	Present	Elongate	Yellow with green stripes	Cracked	Intermediate	Striped
CM059	Yellow	Present	Oblate	Yellow with orange stripes	Cracked	Hard	Striped
CM060	Yellow	Present	Elongate	Orange with dark green stripes	Cracked	Hard	Striped
CM061	Yellow	Present	Elongate	Yellowish with green and orange stripes	Cracked	Intermediate	Striped
CM062	Yellow	Present	Elongate	Yellow with orange stripes	Cracked	Hard	Striped

Appendix II. Contd…

Variety	Taste of Fruit	Flesh Colour	Flesh Texture	Flesh Flavour	Fruit Bitterness	Seed Colour
CM001	Sweet	White	Crispy	Moderate	Absent	Cream
CM002	Sour	White	Soft	Moderate	Absent	Cream
CM003	Sweet	White	Soft	Moderate	Absent	Cream
CM004	Sweet	Creamy white	Intermediate	Strong	Absent	Creamy white
CM005	Sour	White	Crispy	Mild	Absent	Cream
CM006	Sweet	White	Crispy	Mild	Absent	Cream
CM007	Sweet	Creamy white	Crispy	Mild	Absent	Light ream
CM008	Sweet	White	Intermediate	Moderate	Absent	Cream
CM009	Sweet	White	Intermediate	Moderate	Absent	Creamy white
CM010	Sour	White	Crispy	Strong	Absent	Creamy white
CM011	Sweet	White	Intermediate	Mild	Absent	Cream
CM012	Sour	White with orange shade	Soft	Mild	Absent	Cream
CM014	Sour	White	Crispy	Mild	Absent	Cream
CM015	Sweet	White	Crispy	Moderate	Absent	Cream
CM016	Sour	White	Intermediate	Mild	Absent	Cream

CM017	Sour	White	Intermediate	Strong	Absent	Cream
CM018	Sour	White	Intermediate	Strong	Absent	Cream
CM019	Sour	White	Intermediate	Strong	Absent	Cream
CM020	Sour	White	Soft	Strong	Absent	Cream
CM022	Sour	White with orange shade	Crispy	Strong	Absent	Light cream
CM023	Sour	White	Soft	Moderate	Absent	Cream
CM024	Sweet	White	Intermediate	Mild	Absent	Ream
CM025	Sour	White	Soft	Moderate	Absent	Cream
CM028	Sour	White	Intermediate	Strong	Absent	Cream
CM032	Sweet	Creamy white	Intermediate	Strong	Absent	Cream
CM033	Sweet	White with orange shade	Intermediate	Strong	Absent	Light cream
CM034	Sour	Creamy white	Crispy	Strong	Absent	Cream
CM035	Sour	White	Crispy	Strong	Absent	Cream
CM036	Sour	White with orange shade	Crispy	Strong	Absent	Cream
CM037	Sour	White	Intermediate	Strong	Absent	Light cream
CM038	Sour	Creamy white	Intermediate	Strong	Absent	Cream
CM039	Sour	White	Intermediate	Strong	Absent	Cream
CM040	Sour	White	Soft	Strong	Absent	Cream
CM042	Sour	White	Crispy	Moderate	Absent	Cream
CM043	Sour	White	Crispy	Mild	Absent	Cream

CM044	Sour	White	Crispy	Moderate	Absent	Cream
CM045	Sour	White	Intermediate	Strong	Absent	Cream
CM046	Sour	White	Intermediate	Moderate	Absent	Cream
CM047	Sour	White	Intermediate	Mild	Absent	Cream
CM048	Sour	White	Crispy	Mild	Absent	Cream
CM049	Sour	White	Intermediate	Strong	Absent	Cream
CM050	Sour	White	Crispy	Strong	Absent	Cream
CM051	Sour	White with orange shade	Intermediate	Strong	Absent	Creamy white
CM052	Sour	Creamy white	Crispy	Strong	Absent	Cream
CM053	Sour	White	Intermediate	Mild	Absent	Cream
CM055	Sour	White	Intermediate	Mild	Absent	Light cream
CM056	Sour	White	Soft	Strong	Absent	Cream
CM057	Sour	White	Soft	Strong	Absent	Cream
CM058	Sour	White	Soft	Strong	Absent	Cream
CM059	Sour	White	Crispy	Strong	Absent	Cream
CM060	Sour	White	Soft	Strong	Absent	Cream
CM061	Sour	White	Soft	Strong	Absent	Cream
CM062	Sour	White	Soft	Strong	Absent	Cream

Appendix III. Qualitative traits of F_1 in oriental pickling melon

Cross	Flower colour	Stem hairiness	Fruit shape	Fruit colour at maturity	Skin surface	Skin hardness
CM047X *Cucumis melo* var. *agrestis* (W-10)	Yellow	Present	Pyriform	Yellow with green stripes	Cracked	Hard
CM047 X *Cucumis melo* var. *agrestis* (W-51)	Yellow	Present	Elliptical	Yellow with dark orange stripes	Smooth	Hard
CM047 X *Cucumis melo* ssp. *callosus*	Yellow	Present	Elliptical	Light yellow with green stripes	Smooth	Hard
CMO47 X CM033	Yellow	Present	Elliptical	Yellow with orange stripes	Smooth	Hard
CM045X *Cucumis melo* var. *agrestis* (W-10)	Yellow	Absent	Oblate	Light yellow with orange stripes	Cracked	Intermediate
CM045 X *Cucumis melo* var. *agrestis* (W-51)	Yellow	Present	Elongate	Yellow with green stripes	Cracked	Hard
CM045X *Cucumis melo* ssp. *callosus*	Yellow	Present	Elliptical	Yellow with orange stripes	Cracked	Soft
CM045 X CM033	Yellow	Present	Elliptical	Yellow with orange stripes	Smooth	Hard
CM051 X *Cucumis melo* var. *agrestis* (W-10)	Yellow	Present	Globular	Yellow	Smooth	Hard
CM051 X *Cucumis melo* var. *agrestis* (W-51)	Yellow	Present	Elongate	Yellow with orange stripes	Smooth	Hard

CM051 X *Cucumis melo* ssp. *callosus*	Yellow	Present	Elongate	Dark yellow with orange stripes	Smooth	Hard
CM051 X CM033	Yellow	Present	Elongate	Yellow with orange stripes	Smooth	Hard
CM022 X *Cucumis melo* var. *agrestis* (W-10)	Yellow	Present	Elliptical	Yellow with orange stripes	Cracked	Hard
CM022 X *Cucumis melo* var. *agrestis* (W-51)	Yellow	Present	Elongate	Yellow with orange and green stripes	Cracked	Hard
CM022 X *Cucumis melo* ssp. *callosus*	Yellow	Absent	Pyriform	Yellow with orange stripes	Cracked	Hard
CM022 X CM033	Yellow	Present	Oblate	Yellow	Smooth	Hard
CM060 X *Cucumis melo* var. *agrestis* (W-10)	Yellow	Present	Elliptical	Yellow with orange stripes	Cracked	Hard
CM060 X *Cucumis melo* var. *agrestis* (W-51)	Yellow	Present	Oblate	Yellow with green stripes	Smooth	Hard
CM060 X *Cucumis melo* ssp. *callosus*	Yellow	Present	Elongate	Yellow with orange stripes	Smooth	Hard
CM060X CM033	Yellow	Present	Elongate	Yellow with orange stripes	Smooth	Hard
CM061 X *Cucumis melo* var. *agrestis* (W-10)	Yellow	Present	Oblate	Light yellow with green stripes	Smooth	Hard
CM061 X *Cucumis melo* var. *agrestis* (W-51)	Yellow	Present	Oblate	Yellow with orange and green stripes	Smooth	Hard

CM061 X *Cucumis melo* ssp. *callosus*	Yellow	Present	Pyriform	Yellow with green stripes	Smooth	Hard
CM061 X CM033	Yellow	Absent	Oblate	Dark yellow with orange colour scattered	Smooth	Hard
CM062 X *Cucumis melo* var. *agrestis* (W-10)	Yellow	Present	Oblate	Yellow with orange stripes	Smooth	Hard
CM062 X *Cucumis melo* var. *agrestis* (W-51)	Yellow	Present	Oblate	Yellow with orange and green stripes	Smooth	Intermediate
CM062 X *Cucumis melo* ssp. *callosus*	Yellow	Present	Elliptical	Yellow with green stripes	Smooth	Intermediate
CM062 X CM033	Yellow	Present	Oblate	Yellow with green stripes	Cracked	Hard
CM033 X *Cucumis melo* var. *agrestis* (W-10)	Yellow	Present	Oblate	Yellow with green stripes	Smooth	Soft
CM033 X *Cucumis melo* var. *agrestis* (W-51)	Yellow	Present	Ovate	Light yellow with yellow stripes	Smooth	Hard
CM033X *Cucumis melo* ssp. *callosus*	Yellow	Present	Ovate	Yellow	Smooth	Hard

Appendix III. Contd…

Variety	**Skin Texture**	**Taste of Fruit**	**Flesh Colour**	**Flesh Texture**	**Flesh Flavour**	**Fruit Bitterness**	**Seed Colour**
CM047X *Cucumis melo* var. *agrestis* (W-10)	Striped	Little bitter	White	Intermediate	Strong	Present	Light cream
CM047 X *Cucumis melo* var. *agrestis* (W-51)	Striped	Bitter	White	Intermediate	Strong	Present	Cream
CM047 X *Cucumis melo* ssp. *callosus*	Striped	Little bitter	White	Soft	Strong	Present	Light brown
CMO47 X CM033	Striped	Sour	White	Crispy	Strong	Absent	Ream
CM045X *Cucumis melo* var. *agrestis* (W-10)	Striped	Bitter	White	Soft	Moderate	Present	Cream
CM045 X *Cucumis melo* var. *agrestis* (W-51)	Striped	Bitter	White	Intermediate	Strong	Present	Light cream
CM045X *Cucumis melo* ssp. *callosus*	Striped	Bitter	White	Soft	Strong	Present	Cream
CM045 X CM033	Striped	Sour	White	Soft	Strong	Absent	Cream
CM051 X *Cucumis melo* var. *agrestis* (W-10)	Plain	Bitter	White	Crispy	Strong	Present	Cream
CM051 X *Cucumis melo* var. *agrestis* (W-51)	Striped	Bitter	White	Crispy	Strong	Present	Cream

CM051 X *Cucumis melo* ssp. *callosus*	Striped	Sour	Creamy white	Intermediate	Strong	Absent	Cream
CM051 X CM033	Striped	Sour	Creamy white	Soft	Strong	Absent	Cream
CM022 X *Cucumis melo* var. *agrestis* (W-10)	Striped	Bitter	Creamy white	Soft	Strong	Present	Cream
CM022 X *Cucumis melo* var. *agrestis* (W-51)	Striped	Bitter	White	Soft	Strong	Present	Creamy white
CM022 X *Cucumis melo* ssp. *callosus*	Striped	Sour	Light yellow tinch	Soft	Strong	Absent	Cream
CM022 X CM033	Plain	Sweet sour	White	Intermediate	Strong	Absent	Cream
CM060 X *Cucumis melo* var. *agrestis* (W-10)	Striped	Bitter	Creamy white	Soft	Strong	Present	Cream
CM060 X *Cucumis melo* var. *agrestis* (W-51)	Striped	Bitter	White	Soft	Strong	Present	Cream
CM060 X *Cucumis melo* ssp. *callosus*	Striped	Sour	White	Soft	Moderate	Absent	Cream
CM060X CM033	Striped	Sweet sour	Creamy white	Soft	Moderate	Absent	Cream
CM061 X *Cucumis melo* var. *agrestis* (W-10)	Striped	Bitter	Creamy white	Crispy	Strong	Present	Cream

CM061 X *Cucumis melo* var. *agrestis* (W-51)	Striped	Sour	White	Soft	Strong	Absent	Cream
CM061 X *Cucumis melo* ssp. *callosus*	Striped	Sweet sour	White	Soft	Strong	Absent	Cream
CM061 X CM033	Scattered	Sour	White	Soft	Moderate	Absent	Cream
CM062 X *Cucumis melo* var. *agrestis* (W-10)	Striped	Bitter	Creamy white	Soft	Strong	Present	Cream
CM062 X *Cucumis melo* var. *agrestis* (W-51)	Striped	Sour and bitter	White	Intermediate	Strong	Present	Cream
CM062 X *Cucumis melo* ssp. *callosus*	Striped	Bitter	White	Intermediate	Mild	Present	Cream
CM062 X CM033	Striped	Sour	White	Crispy	Strong	Absent	Cream
CM033 X *Cucumis melo* var. *agrestis* (W-10)	Striped	Sour	White	Crispy	Strong	Absent	Cream
CM033 X *Cucumis melo* var. *agrestis* (W-51)	Striped	Sour	White	Soft	Mild	Absent	Cream
CM033X *Cucumis melo* ssp. *callosus*	Smooth	Sweet sour	White	Intermediate	Strong	Absent	Cream