ANALYSIS OF GENETIC DIVERSITY OF INDIAN MELON (*Cucumis melo* L.) LAND RACES AND ITS COMPARISON WITH GLOBAL REFERENCE MELON POPULATIONS

Dissertation

Submitted to the Punjab Agricultural University
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in
Vegetable Crops
(Minor Subject: Plant Breeding and Genetics)

By

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(L-2008-A-13-D)

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CERTIFICATE I

This is to certify that the dissertation entitled, **"Analysis of genetic diversity of Indian melon (*Cucumis melo* L.) land races and its comparison with global reference melon populations"** submitted for the degree of **Ph.D.** in the subject of **Vegetable Crops** (Minor subject: Plant Breeding and Genetics) of the Punjab Agricultural University, Ludhiana is a bonafide research work carried out by **Mr Ajaz Ahmed Malik** (Admn. No. L-2008-A-13-D) under my supervision and that no part of this dissertation has been submitted for any other degree.

The assistance and help received during the course of investigation have been fully acknowledged.

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CERTIFICATE II

This is to certify that the dissertation entitled, **"Analysis of genetic diversity of Indian melon (*Cucumis melo* L.) land races and its comparison with global reference melon populations"** submitted by **Mr Ajaz Ahmed Malik** (Admn. No. L-2008-A-13-D) to the Punjab Agricultural University, Ludhiana, in partial fulfillment of the requirements for the degree of **Ph.D.** in the subject of **Vegetable Crops** (Minor subject: Plant Breeding and Genetics) has been approved by the Student's Advisory Committee after an oral examination on the same.

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ABSTRACT

The present investigation entitled, "Analysis of genetic diversity of Indian melon (*Cucumis melo* L.) land races and its comparison with global reference melon populations" was conducted at Department of Vegetable Science and School of Agricultural Biotechnology, Punjab Agricultural University Ludhiana, during the years 2009 and 2010. Eighty-eight melon accessions collected from Uttrakhand and Uttar Pradesh states of India representing four agro-ecological regions (six sub-regions) and eight reference accessions from USA were characterized and evaluated for nineteen morphological traits of plant and fruit, biochemical traits such as T S S, ascorbic acid content, titrable acidity and dry matter content, SSR genotyping and reaction to diseases. Significant differences were noted among all the accessions for all the characters observed. Phenotypic and genotypic coefficients of variation were found to be high for fruit weight and node at which first hermaphrodite flower appears. High heritability alongwith high genetic advance was recorded for fruit weight, node at which first hermaphrodite flower appears, fruit length, seed cavity length, number of primary branches per vine and total soluble solids content. D^2 analysis grouped the accessions into ten clusters. The reference accessions obtained from USA and land races collected from different agro-ecological zones of India were found to be scattered in different clusters. No parallelism was found between genetic and geographic diversity. DNA polymorphism was utilized to cluster the genotypes into different clusters based on similarity as well as dissimilarity coefficients. On basis of SSR analysis, dendrogram clustered 96 accessions into three major groups. There was a significant correlation between botanical groups and the clustering pattern. Accessions belonging to *cantalupensis* cluster together in cluster I, accessions of *reticulatus* group cluster together in cluster II and *momordica* group cluster together in cluster III. However, some accessions of *cantalupensis* and *reticulatus* were intermixed in cluster I and II. Reference accessions cluster together forming a genetically unique assemblage in sub-group IIA and shared similarity coefficient of 0.65 with sub-group IIB. This suggested that reference accessions shared genetic affinities with Indian melon accessions that could not have been predicted based on their geographic origin. Four accessions were free from CMV and two accessions exhibited immune reaction to downy mildew. The results inferred that these melon accessions could be used to broaden the genetic base of melon.

Keywords: CMV, downy mildew, genetic advance, heritability, melon, SSR

Signature of Major Advisor

Signature of the Student

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ਪ੍ਰਮੁੱਖ ਸਲਾਹਕਾਰ ਦੇ ਹਸਤਾਖ਼ਰ

ਵਿਦਿਆਰਥੀ ਦੇ ਹਸਤਾਖ਼ਰ

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CHAPTER – I

INTRODUCTION

Muskmelon (*Cucumis melo* L. 2*n* = 2*x* = 24) belongs to family Cucurbitaceae, subfamily *Cucurbitoideae* tribe *Melothrieae* and subtribe *Cucumerinae.* The center of origin of muskmelon is not known with certainty but as the wild species of *Cucumis* occur in Africa, it is likely that it originated in that continent. However, a recent study shows that melon is of Asian origin (Sebastian *et al,* 2010). Melons exhibit a wide range of morphological, physiological and biochemical diversity (Eduardo, 2007). The species *Cucumis melo* is a polymorphic taxon encompassing a large number of botanical and horticultural varieties or groups. Although the species is generally known as melon, it is also called sweet melon, muskmelon casab and cantaloupe (Nayar and Singh, 1998).

Melon (*Cucumis melo* L.) is an important horticultural crop grown in temperate, subtropical and tropical regions of world. Production of muskmelon in the world is about 61.13 million tonnes. China is major producer of muskmelon with a production of 322.4 million tonnes followed by Turkey (37.0 million tonnes), Iran (27.1 million tonnes), U.S (23.6 million tonnes) and Spain (22.2 million tonnes) (Anon, 2011a). In India, it is cultivated on an area of 31.5 thousand ha with a total production of 0.64 million tonnes and productivity of 20 tonnes per ha (Anon, 2011b). In India, it is extensively cultivated in hot and dry areas of Uttar Pradesh, Punjab, Rajasthan, Madhya Pradesh, Bihar and Karnataka. In Punjab, it is cultivated on an area of 3,007 ha, with a total production of 0.58 million tonnes and productivity of 19 tonnes per ha (Anon, 2011c).

Melon (*Cucumis melo* L.) is relished as dessert fruit and fetches premium price in the market compared to other vegetables. It is a popular vegetable grown under both rainfed and irrigated conditions. Muskmelon fruits are also canned or used for syrup or jam preparation. Melon seeds are eaten slightly roasted or edible oil can be extracted from them. Its seed oil is useful in relieving painful discharge and suppression of urine. Muskmelon has gained commercial importance due to its short duration and high production potential as well as its high nutritive value. The positive nutritional characteristics of muskmelon and their potential as a source of anti-oxidants, make muskmelon ideal candidate for crop improvement. Muskmelon fruit is a rich source of Vitamin C (6mg - 60mg/100g fw), Vitamin A (500 IU - 4200 IU/100g fw) and also minerals like Potassium (130 mg - 330mg/100g fw), Calcium (5mg - 18mg/100g fw), Iron (0.2mg - 5mg/100g fw), Magnesium (8mg - 17mg/100g fw), Phosphorous (7mg - 57mg/100g fw) (Salunkhe and Kadam, 1998).

Cucumis melo is one of the most diverse and highly polymorphic species in *Cucurbitaceae* (Danin-Poleg *et al,* 2001 and Decker-Walters *et al,* 2002). Intraspecific classification of such variability has been quite challenging and confusing. There have been

several attempts to taxonomically subdivide melons into sub-species, botanical varieties or groups. The species of *C. melo* L. was first described by Linne in 1753 (Stepansky *et al,* 1999a). In one popular classification, the original melon groupings of Naudin (1859) were subdivided by Munger and Robinson into seven horticultural groups viz., (i) *C. melo var. agrestis* Naud. (wild melon) (ii) *C. melo var. flexuosus* Naud. (snakemelon) (iii*) C. melo var. conomon* Mak (pickling melon, Chinese white cucumber) (iv) *C. melo var. cantalupensis* Naud. (cantaloupe or muskmelon) (v*) C. melo var. inodorus* Naud. (winter melons, honeydew, Casaba) (vi*) C. melo var. chito* (mango melon) and var. *dudaim* Naud (Queen's pocket melon) and (vii) *C. melo var. momordica* (Phoot or snap melon). Pitrat *et al* (2000) proposed the most recent classification of the species *C. melo* L. following the basic taxonomic rank of the International Code of Botanical Nomenclature (Greuter *et al,* 2002). Accordingly, the species *C. melo* L. was sub-divided into two sub-species: *agrestis* and *melo*. These subspecies were defined based on the hairiness of the ovary. Although, subspecies *melo* has spreading hairs, subspecies *agrestis* has appressed hairs (Kirkbride, 1993). The groups: *conomon*, *makuwa*, *chinensis*, *acidulus* and *momordica* are within subsp. *agrestis*; *cantalupensis*, *reticulatus*, *adana*, *chandalak*, *ameri*, *inodorus*, *flexuosus*, *chate*, *tibish*, *dudaim* and *chito* are within subsp. *melo*. More recently Burger *et al* (2010) indicated the myriad of horticultural types recognized by Kirkbride (1993) and Pitrat *et al* (2000).

Crop improvement depends largely on availability of genetic variability in germplasm, their effective evaluation and utilization. This genetic variability is responsible for the different traits in species and has enabled crop species to adapt to the variety of environments that exist in the world. It also provides the raw materials by which new species arise through evolution. Before aiming at an improvement in melon for yield, quality and disease resistance, it is necessary to have a thorough knowledge of genetic variability present in the crop. Adequate genetic variability ensures better chances of producing new forms (Aremu, 2011). During the domestication process, although plants retained several horticultural important traits like big fruit, desirable flavour and high yield but they lost other undesirable traits which confer disease resistance and high secondary metabolites. Thus, plants lost some of the alleles related to horticulturally undesirable or nonselected traits. Selection of these traits decreased the genetic base of following population (Zamir, 2001). However, modern breeding methodologies of today produce high-yielding crops which are important for the agriculturist and the genetic variation of crop plants becomes narrower because new varieties are developed from crosses between genetically related species (Tanksley and McCouch, 1997). Unfortunately, crop species have been driven into a genetic bottleneck. The allelic variation of genes in a population starts to decrease and it brings a dramatic loss of heterogeneity. The narrow genetic base of some plant species poses serious threat to these species. Crop species with narrow genetic variation are more susceptible to

diseases, insect-pests and environmental changes (Zitter *et al,* 1996). Pests and diseases cause great losses to melon crops around the world. Their distribution and impact on melon plants varies around the world (Tahir and Yousif, 2009). Melon and its related species and genera co-exist in India and have rich genetic resources, which are characterized by a considerable amount of variability for horticultural traits and insect-pests and disease resistance (Roy *et al,* 2011). Therefore, efforts should be made to collect and conserve the genetic resources of melon in India. To enhance the utilization of such genetic resources they should also be evaluated for different characters including disease and insect-pests resistance.

Genetic diversity in plants, has traditionally been established using morphological and biochemical markers. Many studies aimed at assessing the genetic diversity in germplasm collections using biochemical /allozyme markers have been carried out but their use in the recent years has declined due to their limited number. Conventionally, varietal identification and genetic diversity in plants is based on phenotypic evaluation of morphological characteristics that demands collection of extensive data at different locations, however, many traits having polygenic control are influenced by environment. Also, the level of polymorphism for morphological characteristic in elite germplasm is sometimes too limited and inadequate to allow for varietal discrimination. The cultivar evaluation and estimation of genetic diversity using phenotypic markers only have several limitations. Morphological markers are a few in numbers, depend on developmental stage of plant and are influenced by environmental variation (Wang *et al,* 2008).

Contrarily, the molecular markers/ DNA based markers overcome all the limitations encountered in the use of the biochemical and morphological markers. They are more authentic and provide an accurate and powerful tool for analyzing the relationship among accessions based on estimation of genetic similarity. There are mainly two types of molecular markers - hybridization based molecular markers (RFLPs) and PCR based molecular markers (RAPDs, AFLPs and SSRs). The RFLPs, RAPDs, AFLPs and SSRs markers are used for estimating the genetic diversity and can detect variation both in coding and non-coding regions of DNA. In the recent past, RFLPs were used for the varietal identification, fingerprinting, classification and estimation of genetic variability in the germplasm but these have now been replaced lately by PCR based markers.

Genetic markers like random amplified polymorphic DNA (RAPD) and Simple Sequence Repeat (SSR) markers have been used intensively to characterize melon germplasm to define different classes and relationships (Garcia *et al* 1998, Katzir *et al* 1996, Lopez-Sese *et al* 2002, Mliki *et al* 2001, Monforte *et al* 2003, Staub *et al* 1997, Stepansky *et al* 1999a).The Simple Sequence Repeat (SSR) markers are widely preferred for genotype characterization, genome analysis and gene mapping in various crop species (Fang *et al,* 2000), as these are PCR based, co-dominant, robust, reliable, reproducible, hypervariable,

informative and easy to use (Zhao *et al,* 1992).They can also provide greater power of discrimination than RFLP or RAPD markers (Akagi *et al*, 1996). Moreover, SSR genotypic data, from a number of loci have potential to provide unique allelic profiles or DNA fingerprints for establishing the precise genotypic identity (Yun-Xin *et al,* 2005). But the relative genetic distances among different muskmelon accessions endemic to India and global melon populations have still not been defined. Therefore, present study is aimed at determining whether diversity in botanical and horticultural traits displayed by these muskmelon accessions is reflected at DNA level. Also, less information is available on genetic diversity of melon with respect to available germplasm. Therefore, characterization and evaluation of the germplasm at genotypic level, supplemented by phenotypic help to know the horticultural worth of the germplasm and the genetic relationship among various muskmelon accessions would prove useful in genetic improvement of muskmelon. This would also help in the augmentation of core collections, their utilization and conservation. The, present study was undertaken with the following objectives:

i) Characterization and evaluation of muskmelon germplasm collected from different agro-ecological regions of Uttar Pradesh and Uttarakhand.

ii) Analysis of DNA variation (SSR) in the muskmelon accessions and their relatedness.

iii) Comparison of Indian melon (*Cucumis melo* L.,) land races with global reference populations using SSR markers.

CHAPTER – II

REVIEW OF LITERATURE

The literature relevant to the present investigation has been reviewed under the following heads:

2.1Characterization on the basis of morphological characters

2.2 Characterization on the basis of biochemical characters

2.3 Characterization on the basis of SSR markers

2.4 Characterization on the basis of reaction to diseases

2.1 Characterization on the basis of morphological characters

Genetic variability is defined as the extent to which heritable material differs within a group of plants. Genetic variability is most valuable and essential basic raw materials to meet the current and future needs of crop improvement programmes (Van-Hintum, 1995). A wider genetic base, thus, assumes priority in plant breeding research aimed at developing new varieties for increased crop production. The diversity comprises native landraces, local selections, elite cultivars and wild relatives of crop plants. For plant breeders, in their endeavour directed towards increased agricultural production, there is a pressing need for more genetic diversity to work upon and solve to varied kinds of problems and needs. The wider the range of choice a breeder will have in selecting the appropriate kind of diversity, the better will be the chances for his success for any particular goal. Selection is impossible without diversity and new varieties cannot be developed without it. This makes access to this variation essential for breeders. Thus knowledge, access and use of the available diversity in domesticated and "wild" accessions are essential for broadening the genetic base of modern melon cultivars and for sustainable genetic improvement (Dhillon *et al,* 2012). Species with greater genetic diversity are more likely to evolve in response to a changing environment than those with low diversity while population that lacks genetic diversity may experience low fertility, high mortality among offsprings, even in the environments that are not changing (Bekele, 1983). Demissie and Bjornstrand (1996) reported that devising appropriate sampling procedures for germplasm collection and conservation, obtaining core collections for efficient germplasm management are essential for effective utilization of germplasm in plant breeding programmes. Hence, knowledge of genetic diversity and relatedness in germplam is needed for the crop improvement programmes, management and evaluation (Staub *et al,* 1997). Melon landraces are cultivated throughout India, but earlier collection efforts have focused mainly on the regions in northern India. India is divided into 21 agroecological regions comprising 131 agroecological subregions (Sehgal *et al,* 1992). This regional and sub-regional approach should be adopted for future melon explorations in India in order to retain and conserve existing genetic variability in melon (Dhillon *et al,* 2012).

Among different parts of a melon plant, fruit has the highest diversity in shape (round, flattened or elongated), flesh colour (orange, orange light or pink, green, white or even mixture of these colours), rind colour (green, yellow, white, orange, red, gray or blend of these colours), rind texture (smooth, warty, striped, netted, rough or combination of these textures) (Kirkbride, 1993). Staub *et al* (2004) assessed genetic diversity among seventeen melon land races and inbred lines of group *cantalupensis*, *inodorus* and *flexuosus* in which average fruit weight ranged from 176 to 439 g, number of fruits per vine from 0.8 to 4.3. Fruits of group *flexuosus* were mostly elongated in shape, while mostly ovoid in groups *inodorus* and *cantalupensis.*

In an investigation of twenty seven melon accessions, Dhillon *et al* (2007) reported number of fruits per plant from 1 to 3.5 and average fruit weight from 0.23 to 1.4 kg along with greater variability in fruit shape viz., round, acron, oblate, ovate, elongated, elliptical, pyriforms and fruit colour viz., light yellow, white and yellow. Lotti *et al* (2008) assessed one hundred and fifty-three genotypes of melon belonging to *inodorus* and *cantalupensis* and found wide range of variability among the accessions in fruit weight (0.6 to 4.1kg), fruit length (12.2 to 35.6cm), fruit width (10.7 to 20.2cm), days to harvesting (92.3 to 127.0) and fruit skin primary colour (white, white-green, yellow-green, green, green-white, green-yellow, green-orange, yellow-green, yellow-orange, yellow, orange-green, orange). Similarly, in an another study on genetic diversity among forty-two melon accessions Dhillon *et al* (2009) reported that number of fruits per vine ranged from 1 to 2.1 and average fruit weight from 0.21 to 3.27 kg and majority of the accessions (51%) had light yellow fruit colour and prolate type fruit shape. Also greater variability in fruit weight (0.4-1.6 kg), fruit length (8.6-15.2cm) and fruit width (9.0-13.8cm) was observed by Ohashi *et al* (2009). Yi-San *et al* (2009) studied genetic diversity in forty-one melon accessions belonging to groups *cantalupensis, conomon, agrestis and momordica* and observed significant variation in fruit weight (10.00-400.00 g) among melon accessions. While studying genetic diversity in melon Dwivedi *et al* (2010) reported great variability in fruit length (2.0-11.2cm), fruit width (2.0-6.9 cm) and fruit weight (110.7-1980.0g).

Szamosi *et al* (2010) studied morphological evaluation and comparison of fifty-eight Hungarian and Turkish melon genotypes and reported wide range of diversity among melon genotypes belonging to these regions. Among Hungarian melon, the average fruit weight ranged from 734.0 to 1333.7, fruit diameter from 8.5 to 24.5, fruit length from 7.9 to 29.8, diameter of seed cavity from 3.3 to 10.9 and seed cavity length from 4.7 to 18.7, however, among Turkish melon the average fruit weight ranged from 653.50 to 1017.70, fruit diameter from 4.2 to 16.7, fruit length from 5.5 to 26.7, diameter of seed cavity from 2.7 to 14.2 and seed cavity length from 4.0 to 12.17. Fergany *et al* (2011) documented no of fruits per vine from 2.5 to 9.0, fruit weight from 0.17 to 1.73kg and four types of fruit shape (elongated,

oblate, elliptical and pyriform). They also observed large variability in primary skin colour (yellow, orange, light green and green), secondary skin colour (green, dark green and orange) and days to marketable maturity of fruit from 50.1 to 77.2.

Dhillon *et al* (2007) evaluated twenty seven melon accessions and observed that 44% accessions had long vine (>250 cm), 37% had medium vine (150-250cm) and 19% had short vine (< 150cm) and number of primary branches per vine ranged from 2.9 to 11.8. Similarly in an another study on genetic diversity among forty-two melon accessions Dhillon *et al* (2009) revealed that majority of the accessions (81.5%) had shallow leaf lobbing and number of primary branches per vine ranged from 2.4 to 10.2. Also Fergany *et al* (2011) estimated genetic diversity among fifty melon land races and reported that number of primary branches per vine ranged from 2.0 to 7.5. They also reported large variability in leaf size (large, medium, and small) and stem shape (round and angular).

Liu *et al* (2004) assessed seventy-two accessions of *Cucumis melo* L. for 35 morphological characters with emphasis on shelf-life and the relationship between shelf-life and related characters. Principle component analysis (PCA) revealed that *Cucumis melo* var. *acidulus* and *Cucumis melo* var. *makuwa,* both of which belong to the oriental melon were closely related, while American cantaloupe var. *reticulatus* and European cantaloupe var. *cantalupensis* were rather closely related. Scattered diagram also indicated that *Cucumis melo* var. *saccharinus* was closer to *Cucumis melo* var. *inodorus* than other varieties*.* Accessions with good shelf life were mostly found in var. *saccharinus* and *inodorus.* Neitzke *et al* (2009) studied 26 morphological characters and genetic dissimilarity of fourteen melon landraces cultivated in South Brazil. Great genetic variability was revealed for fruit traits in the melon landraces from South Brazil, with potential use in plant breeding, with an emphasis on the accession C71 due to its sweet taste and orange pulp and the C72 due to its high values for fruit weight and flesh thickness. Solmaz *et al* (2010) subjected Principle Component Analysis (PCA) on seventy-eight melon accessions collected from Eastern and Central Anatolia region of Turkey reported that the Turkish melon accessions have large diversity for all the traits examined except green colour of cotyledon and colour of petals.

Kalloo *et al* (1982) performed multivariate analysis of genetic divergence in forty-five muskmelon genotypes and obtained 14 clusters where maximum genetic distance was observed between cluster XI and XII concluding that the clustering pattern of the strains usually did not follow the geographical distribution pattern. Mathew *et al* (1986) reported that genetic distance, measured by using Mahalanobis D^2 statistic was greatest between muskmelon (var. *inodorus*) and snake melon (var. *flexuosus*) and the least between long melon (var.*utilissimus*) and snapmelon. Fruit number per plant contributed 80 percent to the total divergence and was recommended for explotation of diversity in breeding programmes. However, in an another study on genetic diversity of thirty-two muskmelon genotypes

collected from diverse regions, Hosoki *et al* (1990) identified two main groups in dendrogram prepared by cluster analysis and within each cluster many genotypes tended to group on the basis of their geographical origin. However, cluster analysis of morphological and biochemical traits indicated largest divergence between *indorus* cultivars as one group and more exotic varieties *conomon, chito, dudain, agrestis* and *momordica* as a second group (Stepansky *et al*, 1999a). Singh and Lal (2000) studied multivariate analysis in fifty-one accessions of muskmelon and grouped them into thirteen clusters. The maximum inter-cluster distance was between cluster VII and XII and minimum between cluster I and II. Maximum divergence was provided by node at which first female flower opens (11.0%), fruit weight (10.1%) and TSS content (9.3%) emphasizing the importance of these characters in breeding programme.

McCreight *et al* (2004) analyzed genetic variation of three hundred and seventy-eight melons accessions collected from India and twenty six accessions from China with ninteen isozyme loci. 'Top Mark' and 'Green Flesh Honeydew' which represented two distinct *Cucumis melo* ssp *melo* groups: *cantalupensis* and *inodorus*, respectively, were used as reference cultivars. They calculated genetic distance and initial cluster analysis among accessions. Group 1 was unique and consisted of only two *Cucumis melo* ssp *agrestis* accessions. Two large branches were detected at cluster node 2. One branch comprised three groups of 3, 12 and 34 accessions, while other branch contained seven groups of 2, 3, 14, 16 and 47 accessions and reference accessions. Of the one hundred and forty-eight accessions, one hundred and thirty-two were distributed unequally across the 11 groups. The fourteen Chinese accessions originating from seven provinces were also dispersed unequally in the four major cluster groups. 'Top Mark' and 'Green Flesh Honeydew' were genetically distinct and uniquely clustered in the same group. Singh and Dhillon (2006) assessed genetic divergence for 14 characters and grouped them into 11 clusters based on D^2 values. The clustering pattern of the genotypes did not follow the geographical distribution pattern. The intracluster distance was maximum in cluster VIII and minimum in clusters VIII, IX, X and XI. Maximum intercluster distance was calculated between X and VII clusters and minimum between V and III, which hinted there use in muskmelon breeding programme. Tomar *et al* (2008) calculated genetic distance and initial cluster analysis among fifty diverse melon accessions on the basis of relative magnitude of D^2 values. The maximum genetic distance was observed between clusters II and V followed by cluster IV and V, cluster V and VI and cluster I and II. However, cluster III and VII displayed lowest degree of divergence. The mean value of most characters was highest in cluster III, while cluster II and VI showed highest values for two characters. Cluster II showed lowest mean values for maximum characters. Total soluble sugars followed by total soluble solids and fruit yield per plant contributed maximum towards divergence.

Deol *et al* (1974) found that the highest phenotypic co-efficient of variation for sex ratio (46.41%), the lowest for the number of days taken to first picking (8.40%). The highest genotypic co-efficient of variation for the sex ratio (40.49%) and the lowest for number of days to first picking (5.49%). In an another study, Nandpuri *et al* (1975) observed the highest genotypic coefficient of variability (GCV) for yield per plant (52.10%) followed by number of fruits per plant (43.60%) and highest phenotypic coefficient of variation (PCV) for fruit weight (57.68%) and lowest for days taken from transplanting to maturity of the first fruit (8.66%). Similarly, highest GCV and PCV for total yield per plant followed by marketable yield per plant, fruit weight, main stem length and internodal length whereas the lowest value for titrable acidity were recorded (Swamy *et al,* 1985). Lal and Singh (1997) estimated high phenotypic as well as genotypic coefficient of variation in fifty-one genotypes of muskmelon for node at which first hermaphrodite flower opened, marketable fruit yield per vine, total fruit yield per vine and fruit weight, indicating greater amount of variability among genotypes. Boujghagh *et al* (1997) observed wide range of phenotypic and genotypic variability among fifty-five accessions of muskmelon assembled from diverse geographical origin, for all the characters under both green house and field conditions revealing that plant vigour, disease resistance, fruit weight, soluble solids content had high estimates of genotypic coefficient of variation. In an another study, highest PCV and GCV were observed by Kumar *et al* (2004) for fruit yield per plant followed by fruit weight and number of branches per vine for eighteen traits in thirty-three genotypes of muskmelon.

Heritability estimates (broad sense) were high for number of fruits per plant, yield per plant, total soluble solids, vine length and days taken from transplanting to maturity (Nandpuri *et al*, 1975). Swamy *et al* (1985) observed that the highest genetic advance for fruit yield per plant closely followed by number of fruits per plant, while the heritability values were moderate to high for most of the characters studied. They also noted high heritability along with high genetic advance for sutures, netting, shape index, flesh thickness, average fruit weight, total yield per plant and titratable acidity, predicting their improvement through selection. Kalloo *et al* (1983) reported high heritability estimates along with high genetic advance for yield per plant (31.44), number of fruits (20.73) and fruit weight (19.53) hinting at their exploitation through mass selection. Similarly, the high heritability and high genetic advance were noticed for number of fruits per vine, TSS, flesh thickness and yield per vine (Vijay, 1987). Lal and Singh (1997) found broad sense heritability of 74.0 per cent for number of fruits per vine and 98.00 per cent for nodes at which first female flower appeared. They also observed highest heritability as well as highest genetic advance for node at which first hermaphrodite flower appeared suggesting that these characters can be considered for genetic improvement. Rakhi and Rajamony (2005) observed high heritability coupled with high genetic advance for fruit length, average fruit weight and keeping quality of fruit

indicating improvement of these traits through selection. Pandey *et al* (2005) observed high heritability along with high genetic advance for number of days to 50% female flower anthesis, TSS content and number of days to first male flower anthesis. Torkadi *et al.* (2007) estimated high heritability coupled with high genetic advance for average fruit weight and fruit cavity, thus, suggesting the presence of additive gene action and improvement of these traits through direct selection. Choudhary *et al* (2011) reported high heritability and genetic advance for fruit yield per plant, flesh weight per fruit and average fruit weight in seventy genotypes of muskmelon which indicated existence of considerable amount of genetic variability.

Khanna (1969) observed positive correlation between total soluble solids content and ascorbic acid content in nine varieties of muskmelon. Chhonkar *et al* (1979) reported that fruit yield in melon had strong and positive genotypic and phenotypic correlation with the fruit weight and vine length. The number of sub-branches, number of nodes and number of leaves on the main branch showed negative association with yield. The genotypic correlation coefficient indicated that fruit weight was the most important character for improvement of fruit yield. Singh and Nandpuri (1978) found positive and significant correlation of yield with number of fruits per plant, weight of fruit, length of vine and days to first hermaphrodite flower opening in muskmelon. Salk (1982) suggested that total yield per vine in melon was positively correlated with number of fruits per vine. Positive correlation was found between flesh thickness, fruit weight and fruit diameter but selection for the last two characters did not result greater flesh thickness in a fruit of given diameter. Swamy (1986) reported that yield per vine was positively correlated with number of fruits, fruit weight, number of nodes on main stem, stem length, internode length, number of primary branches and fruit index which were negatively correlated with TSS content, ascorbic acid and dry matter content.

More *et al* (1987) recorded maximum flesh area (57.40%) in round fruits showing that variation in fruit shape influenced the flesh area percentage and flesh: cavity (F: C) ratio. Shape index had negative association with F: C ratio in oblong fruits, whereas such significant association was not established in flat and round fruits. Dhaliwal *et al* (1996) observed that association of yield per plant was positively correlated with fruit weight, fruit number per vine and flesh thickness indicating that fruit weight and fruit number per vine were negatively correlated with each other. Kaur *et al* (1997) reported that Vitamin C was positively correlated with total sugars but negatively related with free reducing sugars, fruit weight and flesh thickness, while fruit weight was positively associated with flesh thickness. In quality evaluation of melon cultivars, Pardo *et al* (2000) observed that flavour was positively correlated with pH and soluble solids content which confirmed consumer's preference for fruit with high sugar content. Taha *et al* (2003) found positive and significant association between the number of fruits/vine with the number of primary branches, netting

development with number of primary branches, netting development with total soluble solids, number of primary branches with number of secondary branches, fruit weight with plant length, earliness with flavour and netting development with flesh thickness. Also earliness with netting development, total soluble solids with earliness and the number of primary branches with stem length were found to be negatively associated. Choudhary *et al* (2004) observed that the yield per plant had significant positive correlation with fruit weight, fruits per plant, number of fruit per vine, harvest duration, rind thickness, shelf life and vine length. Pandey *et al* (2005) recorded positive and significant correlation with fruit weight, fruit diameter, fruit length, flesh thickness and rind thickness at both phenotypic and genotypic level. The fruit weight, fruit diameter, fruit length, flesh thickness and rind thickness had positive correlation coefficient among themselves. Singh and Lal (2005) found that fruit weight, flesh thickness and vine length had a significant positive correlation with marketable yield. Chamnan and Kasem (2006) reported that fruit width displayed negative correlation with fruit length and fruit shape. Fruit shape and fruit size were not related to fruit number per plant and yield while fruit number per vine had highly positive correlation with yield per plant. Choudhary *et al* (2011) suggested that fruit yield per vine showed a significant positive correlation with equatorial diameter of fruit, seed cavity diameter, average fruit weight and fruit flesh weight per fruit.

2.2 Characterization on the basis of biochemical characters

Major biochemical changes take place in melon fruit during maturation and ripening (Pech *et al,* 2002). The melon fruit ripening process requires a high metabolic activity, i.e. synthesis and/or degradation of structural, soluble and enzymatic proteins, novel mRNAs, changes in plant hormones levels and DNA transcription, as well as accumulation of original pigments, organic acids and sugars, and the release of volatile compounds (Villanueva *et al,* 2004). All these anabolic and catabolic events need both energy and a carbon nitrogen framework as building blocks, which are supplied *via* respiration. The two most important respiratory substrates found in melon fruit are sugars and organic acids (Seymour and McGlasson, 1993). Sucrose, glucose and fructose are the major sugars found in the mesocarp of ripe melon fruits. High levels of sucrose cause fruit sweetness in melon (Hubbard *et al,* 1990). Sweetness is the most important edible quality attribute of ripe melon fruits (Artes *et al,* 1993). The total soluble solids (TSS) content is a reliable indicator of quality. The large genetic variability observed in melon germplasm for TSS and sugar concentration is accounted for mainly by differences in the levels of sucrose (Hubbard *et al*, 1989). Large variability for TSS often occurs among fruits of the same cultivar. This variability is also attributed to differences in sucrose rather than hexose levels (Burger *et al*, 2000). Increase in sugar levels during fruit ripening is a result of sucrose accumulation, glucose and fructose levels which vary minimally (Hughes and Yamaguchi, 1983). In an extensive study,

Stepansky *et al* (1999b) found considerable variation in sugar content and composition in mature flesh of fifty-six melon genotypes belonging to *cantaloupensis, inodorus, conomon, chito, dudaim, momordica, flexuosus, agrestis,* and some non-defined varieties. Among the fourteen genotypes classified as *cantaloupensis,* total sugars ranged between 40-100 mg/g fw and sucrose was 50-70% of the total sugar, although a few accessions had lower levels. Within the *inodorus* group, both low and high sucrose-accumulating genotypes were observed. Some genotypes attained only 30mg/g fw total sugar, mostly glucose and fructose, whereas others had a high sucrose accumulation (50 mg/gfw). Among the six *conomon* genotypes analyzed, there were fruits with almost no sucrose (line 85-893) accumulation as well as genotypes with intermediate and high sucrose levels. In the *chito* and *dudaim* varieties, five genotypes were evaluated, four out of which accumulated less than 10 mg/g fw sucrose, but interestingly, the last one (PI 164320) had an unusual sugar pattern profile as it accumulated high levels of total sugar, mostly due to elevated glucose and fructose levels. Most members of the *agrestis* group accumulated extremely low levels of sugars, however, two accessions (PI 164493 and PI 436532) had high total sugars (41 and 58 mg/gfw, respectively). The *momordica* and *flexuosus* genotypes did not accumulate significant amounts of sucrose or hexose. They concluded that in the sweeter melon varieties, sucrose was generally the most significant component that contributed to variation in total sugars.

Reddy *et al* (1990) reported that medium total soluble solids (TSS) varieties had very high variation for TSS content. Ram *et al* (2002) suggested exclusive improvement of TSS without any adverse effect on other traits as TSS did not show any significant correlation with any other plant or fruit characters in muskmelon. Bianco and Pace (2006) studied twenty-one melon accessions belonging to the *cantalupensis* and *inodorus* groups. Soluble solids ranged from 3.9% (Melone 12 K) to 15.2% (Melone d'inverno giallo). Dhillon *et al* (2007) reported that total soluble solid ranged from 2.0 to 5.30^0B among twenty-seven snapmelon accessions. Similarly, Lotti *et al* (2008) observed total soluble solids content between 4.8 and 14.8^0B, while studying one hundred and fifty-three melon accessions belonging to *inodorus* and *cantalupensis* group. Oumouloud *et al* (2008) evaluated forty-six melon accessions belonging to *inodorus, cantalupensis, makuwa* and *conomon* groups and reported TSS varied from 8.9-13.4% and melon belonging to *inodorus* and *cantalupensis* showed higher value for this trait. Similarly, Yi-San *et al* (2009) assessed genetic diversity of forty-one melon accessions belonging to group *cantalupensis, agrestis, momordica* and *conomon* and found wide variability in TSS value (2.8-11 ^{0}B). Among *agrestis* accessions it ranged from 4.2 to 7 ^{0}B, in *momordica* accessions it ranged from 2.8 to 6.5 ^{0}B, in *cantalupensis* it ranged from 3.8 to 10.2 ^{0}B and in *conomon* it ranged from 4.0 to 11.0 ^{0}B. In an another study on genetic diversity among forty-two melon landraces Dhillon *et al* (2009) found that great variability was observed for total soluble solids content ranging from 3 to 7.8 ^{0}B. Wide range in TSS content

(6-15%) of musk melon was reported by Ohashi *et al* (2009), while Fergany *et al* (2011) documented total soluble solids between 2.1 and 6.4 °B.

Fruit acidity is attributed to the accumulation of organic acids in the vacuole of the mesocarp cells. This accumulation is complex and poorly understood metabolic process which comprises components of organic acid metabolism together with H^+ transport physiology into the fruit vacuole. Often, the organic acids and their relative amount that are accumulated is peculiar, that is, specific to a given genus or species. In *Cucumis*, citrate is reported as major acid. Citric and malic acids are the most important organic acids found in the flesh of different melon varieties (Burger *et al,* 2003). Similarly, Amor *et al* (1998) reported that the major organic acids found in wild-type and transgenic *cantaloupe* melon fruit were citric and malic acids. Artes *et al* (1993) described that titratable acidity in four melon varieties ranged from 0.14% to 0.50%. However, there was a genetic variability for the organic acid accumulation in *Cucumis melo*, some of the sour accessions, such as 'Faqqous' accumulate primarily malic acid while some others accumulate high levels of citrate. Titratable acidity in the range of (0.08-0.61%) was reported by Dhillon *et al (*2007) while investigating genetic diversity among twenty-seven melon accessions. In an another study Dhillon *et al* (2009) reported wide variability in titratable acidy (0.03-0.65%) among forty-two melon accessions belonging to different agro-ecological zones of India. Similarly, Fergany *et al* (2011) evaluated fifty melon land races and observed titratable acidity in the range of 0.12 to 0.57.

Developmental studies show that the accumulation of acid and sucrose are temporally separated. The sweet melons of Group *reticulatus, cantalupensis* and *inodorous* are unique among sweet dessert fruits where organic acids play little role in determining their quality. (Yamaguchi *et al,* 1977). Leach *et al* (1989) assessed the carbohydrate, organic acid composition and aroma profiles of mature samples of thirty cultivars of *Cucumis melo* and found wide range of variation in sugar acid ratios and significant variations in aroma profiles. Although sweet melon cultivars have low acid levels, other *C. melo* groups have fruits with relatively high acidity at maturity (Pitrat *et al,* 2000). These fruits are consumed when young, similar to a cucumber, before developmental accumulation of acidity. These high-acid groups do not accumulate the high level of sugars characteristic of sweet melon group, though the genetic combination of high sugar and high acid level can be obtained (Burger *et al*, 2006) and present a novel melon flavour which could be exploited to develop new and exotic market types of melons. Albuquerque *et al* (2006) studied the effects of sugar, citric, malic, succinic and ascorbic acid level on melon flavour perception and reported consumers preferences based on instrumentally measured characteristics concluding that flavour was the most important parameter for the consumer decision correlating flavour with sweetness (with the sucrose content) and sourness. Burger *et al* (2003) reported that the high organic acid fruit

content characteristic conferred by a single dominant gene, called *So,*which is found only in melon varieties that do not accumulate high levels of sugars and which are used for non-dessert purposes. In the recessive condition (*so*), melon fruits have a low-organic acid attribute. Furthermore, these authors stated that the evolution of horticultural sweet melon varieties required the sequential selection of three recessive mutations, first a recessive mutation that allowed for non-bitter fruit (*bif*), second a recessive mutation for low-acid fruit (*so*) and third a recessive mutation for high sucrose fruit (*suc*). Though low organic acid level is a genetically regulated feature, several environmental factors, such as salinity can affect quantitatively, the organic acid level in melon fruit (Amor *et al*, 1999).

Obando *et al* (2009) estimated the soluble sugar content and organic acid composition of melon fruit flesh using near-isogenic lines (NILs) derived from the Spanish cultivar Piel de Sapo (PS) and the exotic Korean accession Shongwan Charmi (PI 161375). These data were used to map 60 quantitative trait loci (QTLs) which include 18 for individual sugars, eight for sucrose equivalents, five for the glucose-to-fructose ratio, seven for the total sugar content and 21 for organic acids. Within the QTLs that were associated with the sugar profile, 27 defined the sugar content: eight for fructose, six for glucose, four for sucrose and nine for sucrose equivalents. Within the 32 QTLs mapped for sensory traits, 27 were associated with lower scores in taste (nine QTLs), sweetness (eight QTLs) or global quality appreciation (nine QTLs), two with increased fruit sourness or sweetness and three with increased fruit bitterness. The QTLs defined herein may assist breeders to understand the overall organoleptic balance (sweetness and sourness) in melon fruit, particularly those located within linkage groups III, V, VI, and VIII to XI.

Zhang *et al* (2009) studied the inheritance of melon sugar content, sour content and sugar acid ratio traits in mutant inbred line (76-2) with sour taste and 'Huangpicui' by joint analysis method of multiple generations, which showed that the sugar content was controlled by two pairs of equal additive major genes plus additive-dominant polygene (E-4 model). The heritability of major gene was 88.8%, while heritability the polygenes was 6.94%. However the inheritance of sour content fitted one pair of additive dominance major gene plus additive dominance-epitasis polygene (D-0 model). The heritability for major gene was 26.68% and the heritability for polygenes was 72.77%. Sugar acid ratio trait fitted two pairs of additive-dominance-epitasis major genes plus additive-dominant polygene (E-1 model). The heritability for major gene was 82.86%, while the heritability for polygenes was 16.02%.

Vitamin C (ascorbic acid) contained in melon is an important nutrient for human health (Lester and Crosby, 2002). Burger *et al* (2004) reported from three hundred and fifty melon accessions a few accessions having consistently high soluble solids and sucrose content and high ascorbic acid content. Sharma and Lal (2004) found that the average dry matter content ranged from 6.63 to 11.17% and vitamin C content ranged from 8.35 to

23.12mg/100g of fruit. Bianco and Pace (2006) documented from twenty-one melon accessions belonging to the *cantalupensis* and *inodorus* group that ascorbic acid ranged from 9 to 31 mg/100 g fw. Moon *et al* (2006) found that DVRM-1 and Hara Madhu had the highest values for carotenoid and ascorbic acid contents. Dhillon *et al* (2007) reported wide variability in ascorbic acid from 1.6 to 34.1 mg/ 100g of fresh fruit weight among forty-two melon accessions belonging to different agro-ecological zones of India. However, ascorbic acid ranged from 0.5 to 12.9 mg/ 100g of fresh fruit weight, while studying genetic diversity among twenty-seven melon accessions (Dhillon *et al,* 2009). Also Fergany *et al* (2011) observed ascorbic acid in the range of (1.4 to 9 mg/ 100g of fresh fruit weight). A genetic linkage map in melon was constructed by Park *et al* (2009) using an F_2 population derived from the melon (*Cucumis melo*) cross of 'Deltex' x TGR 1551 to map quantitative trait loci (QTL) for sucrose, total soluble solids (TSS), ratio of sucrose to total sugars (RSTS) and ascorbic acid. A single QTL for ascorbic acid was placed on LG 5. This map could be of great utility in identifying QTLs for fruit sweetness, quality, size, and shape traits as well as disease resistance.

2.3 Characterization on the basis of SSR markers

In melon, all the marker types like AFLPs, RAPDs, RFLPs and SSRs have been used for germplasm characterization (Staub *et al,* 2000), specifying male sterility gene (Park *et al,* 2009), gene mapping (Danin-Poleg *et al,* 2000) and estimation of genetic diversity (Staub *et al,* 2004). In recent years, in addition to morphological characterization based on morphology, cross compatibility or physiology, molecular markers have been used for studying genetic diversity and phylogenetic relationships in melon (Tanaka *et al,* 2007). In 1985, isozyme analysis was performed by Perl-Treves and associates who used 29 nuclear-coded enzymes in twenty-one *Cucumis* species. Similarly, Akashi *et al* (2002) used five isozymes on one hundred and fourteen melon accessions. Neuhausen *et al* (1992) worked on melon genetic diversity by using restriction fragment length polymorphism (RFLP) analysis and found that amount of genetic variability detected by RAPDs among the lines analyzed was higher than detected by RFLPs. Garcia *et al* (1998) successfully used random polymorphic DNA (RAPD) anaysis in melon. They determined the genetic relationships among thirty-two breeding lines of melon belonging to seven varietal types and most of the breeding lines were Galia and Piel de Sapo genotypes. Stepansky *et al* (1999a) used inter-SSR-PCR and RAPD techniques to detect differences between North American and European *cantalupensis* and *inodorus* varieties and exotic melon subspecies *agrestis* genotypes (e.g. *conomon, dudaim* and *momordica*). Cluster analysis indicated that the largest divergence was between North American and European *cantalupensis* and *inodorus* cultivars as one group and more exotic varieties *conomon*, *chito, dudaim, agrestis* and *momordica* as second group.

Mo-Suk *et al* (1999) employed eight polymorphic RAPD primers to differentiate

fifty-two Korean land races and lines into two distinct groups, grouping melon lines into sub-groups (netted and non-netted fruit types). Silberstein *et al* (1999) studied diverse melon types using cluster analysis based on 18 RAPD primers data and found that the North American and European muskmelon cultivars deviated largely from *Cucumis melo* var. *momordica* from India, var. *conomon, chito* and *dudaim* from Far East and var. *agrestis* from Africa. Dessert melon var. *inodorus* and var. *cantalupensis* were not differentiated indicating abundant genetic variation in land races and wild accessions in melon germplasm. Further assaying with RFLP probes disclosed numerous *Pst-l* digested repetitive sequences in melon genome and *EcoRI* as the most productive restriction enzyme in detecting polymorphism. Mliki *et al* (2001) assessed genetic diversity among exotic and reference array (RA) melon (*Cucumis melo* L.) accessions at 49 RAPD putative loci using 29 decamer primers. Using multidimensional scaling and cluster analysis, they revealed that the genetic differences inherited between the African gene pools were associated with the geographical proximity of African countries in the germplasm array examined. The data also indicated that the genetic diversity of US and European commercial germplasm (*cantalupensis* and *inodorus*) could be enhanced by the introduction of genetic variation from African accessions. Lopez-Sese *et al* (2003) studied genetic relationships among one hundred and twenty-five Spanish melon (*Cucumis melo* L.) accessions using a standard molecular marker array consisting of 34 random amplified polymorphic DNA (RAPD) marker bands (19 primers) and seventy-two reference accessions (RA) drawn from previous studies. The RA array consisted of a broad range of horticultural groups and of melon market classes. Genetic diversity was highest in accessions of African origin and lowest in accessions of Spanish origin. Additional RAPD markers (49 primers, 141 bands) and 22 selected agronomic traits (quantitative and qualitative) were used to assess the genetic diversity among Spanish accessions. Cluster analysis using fruit characteristics grouped accessions into cultivars, RAPD based genetic-distance estimate did not provide consistent accession grouping either by cultivar or geographic origin. The highest level of polymorphism was detected among melons originating from the central region of Spain.

Using molecular random polymorphic DNA (RAPD), morphological and pathological characters, Staub *et al* (2004) detected greatest variation in group *flexuosus* among all other groups, *cantalupensis, inodorus* and *flexuosus* germplasm. Based on comparative analysis of this Greek germplasm and an array of previously characterized reference accessions, genetic affinity and distinctness of Greek accessions from various melons of diverse origin revealed potential usefulness of these Greek melon land races for enhancement of market classes. Diversity among thirty-six snapmelon landraces, collected from 2 agro-ecological regions of India (9 agro-climatic sub-regions) was assayed by Dhillon *et al* (2007) using RAPD primers. RAPD based grouping analysis inferred that Indian

snapmelon was rich in genetic variation where regional and sub-regional approach should be followed across India for acquisition of additional melon land races. Accessions of var. *agrestis* and *momordica* clustered together and accessions of var. *reticulatus* had separate cluster. Tanaka *et al* (2007) classified genetic diversity of sixty-nine accessions from India, Myanmar, Korea and Japan which were grouped into three major clusters and sub clusters. Cluster I and II comprised group *conomon* var. *makuwa* and var. *conomon* from East India, which indicated that genetic variation decreased from India towards East. Yi-San *et al* (2009) studied genetic diversity in forty-one accessions of melon, of which thirty-six accessions were of small-seed type. The gene diversity was 0.239, higher than that for group *conomon* from East Asia and equivalent to Indian melon populations. Melon accessions were classified into six major clusters, however, the largest cluster IV mainly comprised group *conomon* which was closely related to cluster V consisting of mainly group *agrestis*. The accessions of group *cantalupensis* were grouped into clusters II or VII which were distantly related to groups *conomon* and *agrestis*.

Phan *et al* (2010) studied genetic diversity among fifty-nine melon land races from Vietnam and reported that morphological characters of the melon land race fruits were highly diversified. Among the five types of cultivated melon, "Dua le" and "Dua vang" were classified as *conomon* var. makuwa, whereas "Dua gang" as *conomon* var. conomon, and "Dua bo" as *momordica*, however, "Dua thom" could not be classified into a proper group or variety. The gene diversity based on random amplified polymorphic DNA (RAPD) and simple sequence repeat analysis was small and equivalent to that of Chinese *conomon*. A cluster analysis revealed that "Dua bo", "Dua le", "Dua vang" and "Dua gang" were grouped in cluster II. Clusters III and IV consisted mainly of *conomon* accessions from China and Japan. "Dua thom" was classified into cluster V with landraces from Yunnan Province, China. The comparison of two hundred and ninety-one melon accessions from Africa and Asia using RAPD profile clearly showed that "Dua thom" and Yunnanese land races were closely related with the small-seed type melons from Myanmar, Bangladesh, and northeastern India. The other four types were related closely with *conomon* and *agrestis* accessions from China, Korea, and Japan, indicating their involvement in the differentiation and establishment of the *conomon* group in East Asia. Soltani *et al* (2010) assessed diversity among Iranian melon land races of groups *flexuosus* and *dudaim* for morphological and physiological traits alongwith random amplified polymorphic DNA (RAPD) and reported that thirty-one morphological and physiological traits had significant variation among accessions. The *flexuosus* accessions had typical morphological characters like elongated fruit shape, light skin colour, ribs on fruit skin and non-sweet flesh. Characters distinct from typical accessions, such as short fruits, dark green skin colour, five carpels, sweet flesh, were especially in ribless accessions. Cluster analysis of morphological and physiological characters divided Iranian melon into seven

groups. *Dudaim* (cluster VII) was clearly separated from *flexuosus* in which typical (cluster I) accessions and atypical accessions (clusters III-VI) were grouped separately. The diversity index shown by RAPD was 0.201 in twenty five *flexuosus* accessions and was rich in genetic diversity. Cluster analysis using RAPD divided *flexuosus* accessions into eight subclusters and clarified genetic similarity between Iranian melon accessions and reference accessions of large-seed type (groups *inodorus* and *cantalupensis*) suggesting that large-seed *flexuosus, inodorus* and *cantalupensis* were not differentiated genetically, probably due to spontaneous inter-group hybridization.

Simple sequence repeats (SSRs) known as microsatellites are small, tandemly repeated segments of DNA (Chiba *et al,* 2003). SSRs, in general, have a high level of transferability to related species and for this reason, these markers are significantly valuable (Varshney *et al,* 2005). Usually microsatellites are 2 to 5 bp in length and are repeated a number of times (Danin-Poleg *et al,* 2001) with the most useful SSRs having the core motif repeated from 9 to 45 times. Some of the major core motifs that are used in the development of SSR markers for melon includes TGA, GAT, CTT, GGA, AT and CT. This method has many advantages for genetic fingerprinting as they are rapid, reliable (Diwan and Cregan 1997), abundant (Lagercrantz *et al,* 1993), co-dominant, highly heterozygous (Powell *et al* 1996) and highly polymorphic (Akkaya *et al,* 1995). The discriminatory power of PCR based Randomly Amplified Polymorphic DNA (Williams *et al,* 1990) and Simple Sequence Repeats in the analysis of melon germplasm, their technical simplicity and low cost suggested their immense potential for germplasm assessment and management (Katzir *et al,* 1996). Danin-Poleg *et al* (2001) evaluated 40 SSR markers (30 melon and 10 cucumber) to detect polymorphism in melon and cucumber genotypes. Phylogenetic analysis among the cucumber and melon accessions based on SSR data clearly demonstrated the distinction between the 'exotic' groups and the sweet cultivated groups of melon.

Based on microsatellite variation in melons, Monforte *et al* (2003) described two distinct groups of melons, first including accessions from Mediterranean and other from China, Japan, Korea and India. Cluster analysis suggested the division of these accessions into two major groups, largely corresponding to the division of *C. melo* in the two subspecies *agrestis* and *melo.* Szabo *et al* (2005) analyzed the microsatellite profile of fourty-seven melon cultivars and landraces from 15th century. Dendogram produced by SPSS11 based on presence versus absence of SSR alleles revealed that medieval melon had the closest genetic similarity to a registered melon cultivar 'Hogoloyo' selected from an old Hungarian melon land race, which indicated that cloned DNA sequences recovered from the DNA of medieval melon can be used for molecular breeding of modern cultivar *via* gene transfer. Nakata *et al* (2005) studied genetic diversity among sixty seven Japanies melon accessions belonging to group *cantaluoensis, inodorus and conomon* by 25 RAPD and 9 SSR markers. Genetic

variation among these accessions was compared to variation in thirty-four reference array (RA). Cluster analysis resulted in 11 of 15 *conomon* accessions forming a group with South African RA accessions and suggests an Asiatic origin for South African melon accessions or an independent domestication involving similar ancestors. Also genetic difference existed between subspecies *agrestis* and *melo.* Sheng *et al* (2007) measured genetic diversity among forty-six Chinese melon accessions of diverse origin using 50 SSR markers. Cluster analysis grouped genotypes into nine clusters, the results indicated that genetic diversity of the Chinese melons could be enhanced by introduction of genetic variation from Chinese accessions of different origins. Further, it would be advantageous to acquire more accessions from geographically varied regions to ensure the retention of existing genetic diversity in China. Kohpayegani and Behbahani (2008) evaluated thirty-five accessions from Iran using fifteen SSR markers. The number of alleles detected by SSR ranged from 1 to 8 with an average of 2.80. Cluster analysis grouped genotypes into five clusters inferring significant differences between the Iranian genotypes.

Dhillon *et al* (2009) studied the genetic diversity among forty-two snapmelon land races collected from four agro-ecological regions of eastern India (eight agro-ecological subregions) by measuring variation at 16 simple sequence repeat (SSR) marker loci, and various traits including plant habit and fruit type, yield (two associated traits), disease resistance and biochemical composition (total soluble solids, ascorbic acid, carotenoids and titrable acidity), their study revealed that there was a high level of genetic variability within snapmelon germplasm. Comparison of the genetic variability between snapmelons of eastern India and melons from north, south and central regions of India and reference accessions of melon from Spain, France, Japan, Korea, Maldives, Iraq, Zambia, Israel using SSRs showed that Indian snapmelon germplasm was not closely related to melon accessions from other parts of the world and found regional differences between Indian melon accessions, indicating that east Indian snapmelon has unique traits. Tzitzikas *et al* (2009) assessed genetic diversity and population structure of traditional Greek and Cypriot melon cultigens (*Cucumis melo* L.) based on 17 SSR markers. All SSR markers were polymorphic with a total number of 81 alleles, whereas all cultigens could be distinguished with at least one SSR, except cultigens 43 and 41. Reference accessions also showed larger genetic variability with an average of four alleles per locus and 0.65 gene of diversity compared with an average of 2.47 alleles per locus and 0.30 of gene diversity for the Greek/Cypriot cultigens which revealed that Cypriot cultigens were more closely related to the *inodorus* 'Piel de Sapo', whereas the Greek cultigens were located in an intermediate position between the *inodorus* 'Piel de Sapo' and the *cantalupensis* 'Vedrantais'. The cultigen 'Kokkini' was the most divergent among the Greek and Cypriot cultigens. This association between geographic origin and genetic similarity among Greek and Cypriot cultigens indicated geographic isolation. Most of the cultivars from

the same cultivar group (i.e. *inodorus*, *cantalupensis*) clustered together, but some exceptions were found, suggesting that former *inodorus* landraces would have been transformed to *cantalupensis* as a result of intercrossing and further selection by farmers.

Chen *et al* (2010) studied genetic diversity among sixty-one melon accessions using sequence-related amplified polymorphism technique. Sixteen primer combinations with clear band pattern and polymorphism were selected. The polymorphic rate was 58.63% and 28.56 loci and 16.56 polymorphic loci were amplified by each pair of primers on an average. The genetic similarity coefficient of the 61 accessions ranged from 0.48 to 0.93, with an average of 0.73 which suggested that there was rich genetic diversity among the melon accessions and grouped them into two groups, which were thick-skinned melon and thin-skinned melon. Fergany *et al* (2011) assessed the genetic diversity among fifty melon landraces collected from three agro-ecological regions of South India (six agro-ecological sub-regions) by measuring variation at 17 SSR loci, morphological traits of plant habit and fruit, two yield-associated traits, pest and disease resistance, biochemical composition (ascorbic acid, carotenoids and titrable acidity) and mineral content (P, K, Fe, Zn). Which revealed that the genetic variability between Indian melons from north, south and east regions and reference accessions of melon from Spain, France, Japan, Korea, Iraq, Zambia showed regional differentiation between Indian melon accessions and that Indian germplasm was weakly related to melon accessions from other parts of the world. Kong *et al* (2011) assessed twenty-seven melon accessions, including twenty-one thin-skinnned melon landraces with SSR markers. The number of alleles detected by SSR ranged from 2 to 5 with an average of 3. The PIC value for each locus varied from 0.21 to 0.68 with the mean of 0.46. Cluster analysis by UPGMA partitioned the accessions into groups of thin-skinned melon and thick-skinned melon. However, SSR markers failed to discriminate the thin-skinned melon from other thin-skinned melon accessions. Escribano *et al* (2012) studied genetic relationships between Spanish melon accessions and reference accessions (RA) using 52 SSR markers based on genetic distance. Spanish genotypes differed substantially from (RA) accessions, thus defining their genetic uniqueness.

Garcia-Mas *et al* (2000) measured genetic diversity among six genotypes by using three different types of molecular markers viz., RAPD, AFLP and RFLP. Cluster analysis performed with the three types of markers separated the genotypes into two main groups one having the sweet type, cultivated melons and other having exotic type, non-cultivated melons. Staub *et al* (2000) successfully used RAPD and SSR markers loci to characterize genetic relationships in four *Cucumis melo* subsp. *melo* groups (*cantalupensis, inodorus, conomon and flexuosus*). Decker-Walters *et al* (2002) classified the origin of New World melon, North American *chito* and *dudaim* accessions using RAPD and SSR data for forty-two North American populations, ten accessions of var. *chito* and *dudaim*, ten other world accessions

and four other varieties of *Cucumis melo* var. *conomon, flexuosus, inodorus* and *cantaloupensis* which inferred that New World populations were distinct and should be classified as ssp. *agrestis* var. *taxamus* and showed the greatest genetic affinities to var. *chito* and to cultivars from Eastern Asia, including var. *conomon*. The population structure of fifteen Spanish melon (*Cucumis melo* L) accessions, mostly of Group *inodorus*, was assessed by Lopez-Sese *et al* (2002) using 100 random amplified polymorphic DNA (RAPD) bands produced by 36 primers and allelic variation at 12 microsatellite (SSR) loci. Cluster analysis using RAPD and SSR based genetic distance estimates resulted in similar and consistent groupings of most of the accessions and high level of heterogeneity observed indicated that the Spanish accessions possessed a relatively broad genetic background. On the basis of SSR and RAPD analysis of twenty-two accessions, a 190 point genetic map was constructed by Zalapa *et al* (2007) using 114 RAPD, 43 SSR, 32 AFLP markers and one phenotypic trait to detect quantative trait loci (QTL)for yield related traits using recombinant inbred lines derived from exotic and elite US western shipping melon germplasm which indicated that genes present in highly branched melon types have potential for increasing yield in US western shipping type germplasm *via* marker assisted selection. Nimmakayala *et al* (2009) studied molecular diversity among thirty-eight melon accessions by using two different types of molecular markers viz., AFLPs and SSR. Molecular diversity was estimated based on a robust set of 465 polymorphisms gathered by AFLPs and SSR polymorphisms, ranged from 0.70 to 1.00 among various accessions. Clustering analysis performed with the two types of markers separated the genotypes into three classical morphotypes, namely, *aestivalis, europeus* and *hiemalis,* under the convar *Europeus*, which is also known as *adana*. The polymorphisms generated were specific to the grouping of fruit types and days to maturity being useful for future breeding programme

2.4 Characterization on the basis of reaction to diseases

Downy mildew disease in melon, caused by *Pseudoperonospora cubensis* (Berk and Curt) Rostow, is worldwide in occurrence. It is widespread in tropical, semi-arid and temperate regions of the world (Kucharek, 2000). Downy mildew was observed to cause disease on melons as early as the 19th century (Colucci *et al,* 2006). Nowadays, downy mildew epidemics threaten muskmelon production in over 50 countries, causing significant economic losses (Lebeda and Urban, 2004). The first resistance breeding research was carried out in the 1940s in the USA, where four cultivars (Cuban Castilian, Green Fleshed Rocky Dew, Orange Fleshed Rocky Dew and Smith´s Perfect) with high levels of resistance against *P. cubensis* were described (Ivanoff, 1944).

Amin *et al* (1982) screened fifty genotypes of melon against downy mildew and found no resistance. Similarly, Thomas and Canigila (1997) assessed seventeen USA Honey dew melon (*Cucumis melo*) through artificial inoculations under controlled conditions for

resistance to *Pseudoperonospora cubensis* and reported that all cultivars tested were susceptible to downy mildew. Thomas and Jourdain (1992) reported that based on disease index (DI), PI 124112 was highly resistant (DI = 3.7) and PI 124111, PI 122847, PI 124210, PI 145594, and PI 165525 were resistant (DI = 3.0, 2.8, 2.6, 2.7, and 2.5, respectively) and forty-nine accessions were identified as moderately resistant. Kalloo *et al* (1993) reported that Hara Madhu was highly susceptible to *Pseudoperonospora cubensis* with an average of 52.4% incidence, while Hissar Madhur showed lower incidence (34.2%), being an early variety. Six snapmelon genotypes evaluated against downy mildew using disease parameters such as leaf death score (LDS), mean disease score, number of lesions per unit area and area disease progress curve (ADPC), which showed that genotypes SP-3 and KP-7 had less disease score than other genotypes (Lal *et al*, 1994) . Singh *et al* (1996) reported genotypes SP-2, SP-3, KP-2, KP-7, KP-9 and EC163888 to be resistant against *P.cubensis*. Pan and More (1996) screened 72 melon genotypes for cucumber green mottle mosaic virus (CGMMV), powdery mildew (*Sphaerotheca fuliginea*) and Fusarium wilt (*Fusarium oxysporium f.sp.melonis*) resistance under artificial conditions and for downy mildew (*Pseudoperonospora cubensis*) resistance under natural epiphytotic conditions. They found that wild *Cucumis* species *Cucumis figari* exhibited absolute resistance to CGMMV, Fusarium wilt and high level of resistance to downy mildew; phoot or snapmelon (*Cucumis melo* var. *momordica*), a non-desert form of Indian origin, was highly resistant to CGMMV and moderately resistant to Fusarium wilt and Iroquois was resistant to powdery mildew and moderately resistant to downy mildew and CGMMV.

Dhiman *et al* (1997) evaluated snapmelon (*Cucumis melo* var. *momordica*), wild melon, their F_1 hybrids and commercial melon cultivars, Hara Madhu, Punjab Sunehri, MM-28 and Pusa Madhuras for resistance to downy mildew (*Pseudoperonospora cubensis*). Low disease incidence was recorded for genotype KP 7, KP 3, SP 3, KP 4, 89-2 and SP 4. TP 5 had the highest disease incidence (20.8%). Thomas (1999) assessed one hundred and eighty melon accessions under field conditions for resistance against downy mildew. Based on disease index **(**DI), PI 271329 and PI 401644 were identified as most resistant with overall DI 2.6 and 2.8, whereas respectively, sixty eight accessions were identified as resistant and one hundred and ten accessions as moderately resistant. More *et al* (2002) screened three hundred and sixty-eight genotypes of muskmelon including dessert and non dessert forms of Indian origin for downy mildew resistance. The lowest disease intensity of downy mildew was recorded in genotypes 55-2 (14.15%), 55-1 (15.67%), 113 (17.65%), 144 (18.38%) and 531 (19.09). Disease index in genotype 78-1 and 78-3 ranged from 20.60 to 25.24 % while PI 124111F and PI 124112 obtained from Israel exhibited 47.24 % and 46.34 % downy mildew incidences, respectively and these were categorized as moderately resistant to downy mildew. Choudhary *et al* (2004) studied the reaction of *Pseudoperonospora cubensis* on foliage of

thirty-six genotypes (8 parents and 28 F_1 hybrids) of muskmelon under field conditions. The per cent disease intensity (PDI) for downy mildew ranged from 8.67 to 52.27% in parents (lowest in MHY-3 and highest in Hara Madhu) and among F_1 hybrids, the lowest PDI was recorded in RM-43 x MHY-3 (12.73%) followed by MHY-3 x Hara Madhu (14.20%) and MS-1 x MHY-3 (14.93%). Among all genotypes, cultivar RM-43 and MHY-3 and hybrid RM-43 x MHY-3 were resistant. Dhillon *et al* (2007) evaluated twenty seven melon accessions for resistance to downy mildew under field conditions and on the basis of per cent disease index (PDI), three accessions (IC 267353, IC 274029 and KP 7) were identified as resistant, eleven as susceptible and thirteen as moderately susceptible.

Within the genus *Cucumis*, *C. melo* is the only species with relatively well-investigated race specificity and available effective sources of resistance against *Pseudoperonospora cubensis* (Thomas, 1986). Muskmelon (*Cucumis melo*) is a very variable species from morphological, genetic and molecular aspects. Despite of this fact, all of its forms are easily crossable. Its intraspecific taxonomic units and genotypes display the basic differences in resistance/susceptibility to *P. cubensis* and are therefore used for differentiation of pathotypes and races (Lebeda *et al*, 2008). Initial studies on variability among isolates of *P. cubensis* were performed by Thomas *et al* (1987), who reported the existence of five pathotypes among isolates collected from Israel, Japan, and USA. These studies were based on compatible reactions with species of *Cucumis*, *Citrullus* and *Cucurbita*. Cohen *et al* (2003) reported a sixth pathotype, isolated from Israel. Shetty *et al* (2002) found that European and North American pathotypes were more closely related and Asian pathotypes were more distinct.

Development of cultivars with inherent resistance to downy mildew is one of the most effective and economical means of controlling the disease (Epinat and Pitrat, 1994). Cohen *et al* (1985) observed that in a cross between *Cucumis melo* line PI -124111F (resistant) and *Cucumis melo* var. *reticulatus* cv. Ananas Yokneam (susceptible). F_1 plants were intermediate in resistance to downy mildew and F_2 and backcross segregation data revealed that resistance was governed by two partially dominant genes. Thomas *et al* (1988) while studying reaction to the parental lines and progenies to sporangial inoculation with *Pseudoperonospora cubensis* reported that the resistance in line MR-1 was conferred by two incompletely dominant genes designated as PC-1 and PC-2. Kenigbuch and Cohen (1989) while studying a cross between *Cucumis melo,* downy mildew susceptible variety WI-998 and resistant genotype PI -124111F, observed that F_1 plants were moderately resistant to pathotype type 3 of *Pseudoperonospora cubensis*. The backcross progeny of F_1 to susceptible parent (WI-998) segregated into 3 susceptible: 1 moderately resistant while progeny from backcross to resistant parent (PI -124111F) segregated into 3 moderately resistant: 1 resistant, inferring a partially dominant digenic inheritance of resistance against pathotype 3 of

Pseudoperonospora cubensis. Somkuwar and More (1996) reported from crosses, Phoot (R) x Pusa Madhuras (S), Phoot (R) x Monoecious-3 (S) and Phoot (R) x Lucknow Safed (S) that all the three crosses showed duplicate type of gene action for downy mildew resistance. Two dominant genes were involved for resistance in Phoot x Monoecious-3 and Phoot x Pusa Madhuras crosses, where two recessive genes governed the downy mildew resistance in Phoot x Lucknow Safeda. Perchepied *et al* (2005) reported genetic analysis of partial resistance to downy mildew using a recombinant inbred line (RIL) population derived from 'PI 124112' and using quantitative evaluation. In most cases, monogenic or digenic resistance to downy mildew has been reported.

Other important disease of muskmelon is cucumber mosaic virus (CMV) (Karchi *et al,* 1975). CMV is the type member of the *Cucumovirus* genus in the family *Bromoviridae* and has the largest host range of any virus throughout the temperate regions of the world.It is spread naturally by more than 60 aphid species in a non-persistent manner (Palukaitis *et al*, 1992). Cucumber mosaic, first described in 1916 (Doolittle, 1916), was one of the earliest melon diseases attributed to a virus (Jagger, 1916). Reports of the disease soon came from elsewhere in the USA and later from Europe and Africa (Price, 1934) and other parts of the world. In the early days, tools for determining the presence of specific viruses were limited and as many as 40 different plant diseases were later shown to be caused by CMV (Kaper and Waterworth, 1981). Daryono *et al* (2003) screened forty melon cultivars collected from 17 Asian countries for resistance to an Indonesian isolate of cucumber mosaic virus (CMV-B2) by manual inoculation and examined by enzyme-linked immunosorbent assay (ELISA) and found resistance in Yamatouri, Miyamauri, Mawatauri, Sanuki-shirouri and Shinjong. In another study, Diaz *et al* (2003) evaluated two hundred and sixty-eight *Cucumis melo* accessions for resistance to cucumber mosaic virus (CMV), papaya ring spot virus (PRSV-W), watermelon mosaic virus (WMV) and zucchini yellow mosaic virus (ZYMV), on the basis of symptoms development and systematic infection based on double antibody sandwich enzyme linked immuno sorbent assay found that accessions C-189, PI 161375 had resistance to CMV and accessions C-768 and C-425 exhibited very mild symptoms of WMV, while accessions C-885 and C-769 exhibited resistance to PRSV-W, WMV and ZYMV.

Dhillon *et al* (2007) investigated resistance to cucumber mosaic virus (CMV) in twenty- seven melon accessions and on the basis of per cent disease incidence and per cent disease severity reported one resistant namely, IC 274014, ten highly susceptible, eleven susceptible and five moderately susceptible accessions against CMV. In another study Dhillon *et al* (2009) studied forty-two melon landraces collected from four agro-ecological regions of east India and on the basis of per cent disease incidence and per cent disease severity revealed that three accessions from Assam viz., SM72, SM73, and SM82 and one accession from West Bengal (SM-67) as resistant against CMV. Similarly, Fergany *et al*

(2011) screened fifty melon accessions for resistance to CMV and on the basis of per cent disease incidence and per cent disease severity, two accessions AM-25 and AM-82 were categorized as resistant, thirteen accessions as highly susceptible, fourteen accessions as susceptible, eight as moderately susceptible and thirteen as moderately resistant. Ekbc *et al* (2010) screened sixty Turkish melon accessions for resistance to ZYMV, WMV and CMV and reported resistance in four accessions ('CU 100', 'CU 287', 'CU 305' and 'CU 328') to ZYMV and three accessions ('CU 305', 'C 264', and 'C 276') to WMV, however, none of the genotype had resistant to CMV.

Resistance to CMV was first reported in three varieties of oriental melons (*C. melo* var. *conomon*) accessions (Freeman Cucumber, White Melon and Ginmakuwa) from east Asia and appeared to be dominant (Enzie, 1943). In an another study involving the cultivar Freeman's Cucumber, resistance was conditioned by three recessive genes (Karchi *et al*, 1975). The same genes were identified in the Korean accession, PI 161375 (Risser *et al*, 1977). Gimenez *et al* (2003) reported a resistance mechanism aganist melon necrotic spot virus controlled by a single recessive gene in melon. Soria *et al* (2003) found that melon accession TGR-1551 showed a clear and total resistance to CMV. The genetic analysis of the progenies obtained from crossing this accession with susceptible Spanish cultivar 'Bola de Oro' showed that resistance to mosaic virus transmission was conferred by a single dominant gene. Daryono *et al* (2003) studied the inheritance of resistance to CMV-B2 in melon cultivars controlled by a single dominant gene. Essafi *et al* (2008) reported that resistance to cucumber mosaic virus (CMV) in melon is oligogenic in nature, when accessions PI 161375 and cv, "Sonwang Charmi" (SC) were used.

CHAPTER – III

MATERIALS AND METHODS

The present investigation was carried out at Department of Vegetable Science and School of Agricultural Biotechnology, Punjab Agricultural University Ludhiana, during the years 2009 and 2010. The melon diversity was characterized for morphological characters, biochemical traits, at molecular level using SSR markers and for reaction to diseases. Details of each method are presented below:

3.1 Experiment I: Genetic diversity for different morphological traits

3.1.1 Experiment material

The experimental material comprised eighty-eight melon open pollinated accessions collected from Uttrakhand and Uttar Pradesh states of India representing four agro-ecological regions and six sub-regions within these states and eight reference accessions from USA. Details of accessions and their distribution as per agro-ecological zones and sub-zones are presented in Table 3.1 and Fig. 1.

3.1.2 Experimental procedure

The accessions were planted in a Randomized Block Design (RBD) with three replications in spring-summer season for two consecutive years, 2009 and 2010. The soil type of the experimental field was sandy loam in nature. The mean annual rainfall was 704.5 mm per year and the annual mean maximum and minimum temperatures were 21.2–41.2 and 5.8–27.1 ^{0}C respectively. Nursery was sown on 22th February in 2009 and on 18th February in 2010 in polythene bags of 15 cm x 10 cm size and 100- gauge thickness punched at the base and filled with a mixture of soil, well-rotten farm yard manure and silt in equal proportions. Seedlings were transplanted in the field at two true leaf stage on 19th of March in 2009 and on 21th March in 2010 at a spacing of 3.0 m x 0.45 m. Ten plants of each accession were transplanted in a randomized complete block design. Five randomly chosen plants from each accession of each replication were used for recording data and the mean data of five plants was used for statistical analysis. The observations on various qualitative and quantitative characters were recorded.

Table 3.1: Sources of melon accessions.

Sr. No.	Accession	Zone	Sub zone	District	State
1	MM-3833 *C. melo* var. *cantalupensis*	13	13.1	Gorakhpur	Uttar Pradesh
2	MM-3837 *C. melo* var. *cantalupensis*	13	13.1	Gorakhpur	Uttar Pradesh
3	MM-3839 *C. melo* var. *cantalupensis*	13	13.1	Gorakhpur	Uttar Pradesh
4	MM-3843 *C. melo* var. *cantalupensis*	13	13.1	Gorakhpur	Uttar Pradesh

Sr. No.	Accession	Zone	Sub zone	District	State
5	MM-3849 *C. melo* var. *cantalupensis*	13	13.1	Gorakhpur	Uttar Pradesh
6	MM-3850 *C. melo* var. *cantalupensis*	13	13.1	Gorakhpur	Uttar Pradesh
7	MM-3851 *C. melo* var. *cantalupensis*	13	13.1	Gorakhpur	Uttar Pradesh
8	MM-3855 *C. melo* var. *cantalupensis*	13	13.1	Gorakhpur	Uttar Pradesh
9	MM-3856 *C. melo* var. *cantalupensis*	13	13.1	Gorakhpur	Uttar Pradesh
10	MM-3857 *C. melo* var. *cantalupensis*	9	9.2	Pratapgarh	Uttar Pradesh
11	MM-3858 *C. melo* var. *cantalupensis*	13	13.1	Gorakhpur	Uttar Pradesh
12	MM-3859 *C. melo* var. *cantalupensis*	13	13.1	Gorakhpur	Uttar Pradesh
13	MM-3860 *C. melo* var. *reticulatus*	13	13.1	Gorakhpur	Uttar Pradesh
14	MM-3864 *C. melo* var. *cantalupensis*	13	13.1	Gorakhpur	Uttar Pradesh
15	MM- 3866 *C. melo* var. *cantalupensis*	13	13.1	Gorakhpur	Uttar Pradesh
16	MM- 3868 *C. melo* var. *cantalupensis*	13	13.1	Gorakhpur	Uttar Pradesh
17	MM-3874 *C. melo* var. *cantalupensis*	13	13.1	Gorakhpur	Uttar Pradesh
18	MM-3881 *C. melo* var. *cantalupensis*	13	13.1	Gorakhpur	Uttar Pradesh
19	MM-3884 *C. melo* var. *cantalupensis*	13	13.1	Gorakhpur	Uttar Pradesh
20	MM-3885 *C. melo* var. *reticulatus*	13	13.1	Gorakhpur	Uttar Pradesh
21	MM-3887 *C. melo* var. *momordica*	13	13.1	Gorakhpur	Uttar Pradesh
22	MM- 3889 *C. melo* var. *cantalupensis*	13	13.1	Gorakhpur	Uttar Pradesh
23	MM- 3901 *C. melo* var. *reticulatus*	9	9.2	Mau	Uttar Pradesh
24	MM-3903 *C. melo* var. *cantalupensis*	9	9.2	Mau	Uttar Pradesh
25	MM- 3909 *C. melo* var. *cantalupensis*	9	9.2	Azamgarh	Uttar Pradesh

Sr. No.	Accession	Zone	Sub zone	District	State
26	MM-3917 *C. melo* var. *cantalupensis*	9	9.2	Mau	Uttar Pradesh
27	MM-3947 *C. melo* var. *cantalupensis*	9	9.2	Mau	Uttar Pradesh
28	MM-3955 *C. melo* var. *cantalupensis*	14	14.5	U.S. Nagar	Uttarakhand
29	MM-3956 *C. melo* var. *cantalupensis*	14	14.5	U.S. Nagar	Uttarakhand
30	MM-3961 *C. melo* var. *cantalupensis*	14	14.5	U.S. Nagar	Uttarakhand
31	MM-3962 *C. melo* var. *momordica*	13	13.1	Gorakhpur	Uttar Pradesh
32	MM-3963 *C. melo* var. *cantalupensis*	14	14.5	U.S. Nagar	Uttarakhand
33	MM-3965 *C. melo* var. *cantalupensis*	14	14.5	U.S. Nagar	Uttarakhand
34	MM-3966 *C. melo* var. *reticulatus*	13	13.1	Gorakhpur	Uttar Pradesh
35	MM-3968 *C. melo* var. *reticulatus*	14	14.5	U.S. Nagar	Uttarakhand
36	MM-3973 *C. melo* var. *cantalupensis*	9	9.1	Bijnour	Uttar Pradesh
37	MM-3974 *C. melo* var. *momordica*	13	13.1	Gorakhpur	Uttar Pradesh
38	MM-3976 *C. melo* var. *reticulatus*	9	9.1	Bijnour	Uttar Pradesh
39	MM-3977 *C. melo* var. *reticulatus*	9	9.1	Bijnour	Uttar Pradesh
40	MM-3979 *C. melo* var. *cantalupensis*	9	9.1	Bijnour	Uttar Pradesh
41	MM-3980 *C. melo* var. *cantalupensis*	9	9.1	Bijnour	Uttar Pradesh
42	MM-3981 *C. melo* var. *cantalupensis*	9	9.1	Bijnour	Uttar Pradesh
43	MM-3982 *C. melo* var. *momordica*	13	13.1	Gorakhpur	Uttar Pradesh
44	MM-3983 *C. melo* var. *cantalupensis*	9	9.1	Bijnour	Uttar Pradesh
45	MM-3985 *C. melo* var. *cantalupensis*	9	9.1	Bijnour	Uttar Pradesh
46	MM-3986 *C. melo* var. *cantalupensis*	9	9.1	Bijnour	Uttar Pradesh
47	MM-3994 *C. melo* var. *momordica*	14	14.5	U.S. Nagar	Uttarakhand
48	MM-3998 *C. melo* var. *momordica*	13	13.1	Gorakhpur	Uttar Pradesh

Sr. No.	Accession	Zone	Sub zone	District	State
49	MM-4002 *C. melo* var. *cantalupensis*	9	9.1	Bijnour	Uttar Pradesh
50	MM-4003 *C. melo* var. *cantalupensis*	9	9.1	Bijnour	Uttar Pradesh
51	MM-4004 *C. melo* var. *momordica*	13	13.1	Gorakhpur	Uttar Pradesh
52	MM-4005 *C. melo* var. *momordica*	13	13.1	Gorakhpur	Uttar Pradesh
53	MM-4013 *C. melo* var. *cantalupensis*	9	9.1	Bijnour	Uttar Pradesh
54	MM-4018 *C. melo* var. *cantalupensis*	9	9.1	Bijnour	Uttar Pradesh
55	MM-4021 *C. melo* var. *cantalupensis*	9	9.1	Bijnour	Uttar Pradesh
56	MM- 4026 *C. melo* var. *cantalupensis*	9	9.1	Bijnour	Uttar Pradesh
57	MM-4030 *C. melo* var. *cantalupensis*	9	9.1	Bijnour	Uttar Pradesh
58	MM-4057 *C. melo* var. *cantalupensis*	9	9.1	Bijnour	Uttar Pradesh
59	MM-4059 *C. melo* var. *reticulatus*	9	9.1	Bijnour	Uttar Pradesh
60	MM-4063 *C. melo* var. *cantalupensis*	9	9.2	Varanasi	Uttar Pradesh
61	MM-4065 *C. melo* var. *reticulatus*	9	9.2	Varanasi	Uttar Pradesh
62	MM-4066 *C. melo* var. *reticulatus*	9	9.2	Lucknow	Uttar Pradesh
63	MM-4067 *C. melo* var. *cantalupensis*	9	9.2	Lucknow	Uttar Pradesh
64	MM-4068 *C. melo* var. *cantalupensis*	9	9.2	Raibareli	Uttar Pradesh
65	MM- 4091 *C. melo* var. *momordica*	13	13.1	Gorakhpur	Uttar Pradesh
66	MM-4098 *C. melo* var. *cantalupensis*	13	13.1	Gorakhpur	Uttar Pradesh
67	MM-4243 *C. melo* var. *cantalupensis*	4	4.3	Allahabad	Uttar Pradesh
68	MM-4247 *C. melo* var. *momordica*	13	13.1	Gorakhpur	Uttar Pradesh
69	MM-4248 *C. melo* var. *cantalupensis*	9	9.2	Lucknow	Uttar Pradesh
70	MM-4250 *C. melo* var. *cantalupensis*	9	9.2	Varanasi	Uttar Pradesh
71	MM-4251 *C. melo* var. *cantalupensis*	9	9.2	Varanasi	Uttar Pradesh

Sr. No.	Accession	Zone	Sub zone	District	State
72	MM-4252 *C. melo* var. *reticulatus*	4	4.3	Allahabad	Uttar Pradesh
73	MM-4253 *C. melo* var. *cantalupensis*	9	9.2	Jaunpur	Uttar Pradesh
74	MM-4256 *C. melo* var. *cantalupensis*	4	4.3	Allahabad	Uttar Pradesh
75	MM-4267 *C. melo* var. *momordica*	13	13.1	Gorakhpur	Uttar Pradesh
76	MM- 4268 *C. melo* var. *reticulatus*	9	9.2	Lucknow	Uttar Pradesh
77	MM-4270 *C. melo* var. *cantalupensis*	9	9.2	Jaunpur	Uttar Pradesh
78	MM-4271 *C. melo* var. *reticulatus*	9	9.2	Jaunpur	Uttar Pradesh
79	MM-4276 *C. melo* var. *cantalupensis*	9	9.2	Lucknow	Uttar Pradesh
80	MM-4277 *C. melo* var. *reticulatus*	9	9.2	Lucknow	Uttar Pradesh
81	MM-4278 *C. melo* var. *cantalupensis*	9	9.2	Lucknow	Uttar Pradesh
82	MM-4279 *C. melo* var. *reticulatus*	9	9.2	Lucknow	Uttar Pradesh
83	MM- 4282 *C. melo* var. *cantalupensis*	9	9.2	Lucknow	Uttar Pradesh
84	MM-4283 *C. melo* var. *cantalupensis*	9	9.2	Lucknow	Uttar Pradesh
85	MM-4305 *C. melo* var. *cantalupensis*	9	9.2	Lucknow	Uttar Pradesh
86	MM-4342 *C. melo* var. *cantalupensis*	9	9.2	Lucknow	Uttar Pradesh
87	MM-4409 *C. melo* var. *cantalupensis*	9	9.1	Bijnour	Uttar Pradesh
88	MM-5736 *C. melo* var. *momordica*	13	13.1	Gorakhpur	Uttar Pradesh
89	AR Hale's *C. melo* var. *reticulatus*			U.S.A	
90	Dulce-B.B *C. melo* var. *reticulatus*				
91	Gulf Coast *C. melo* var. *reticulatus*				
92	Gulf Stream *C. melo* var. *reticulatus*				
93	Jucumba *C. melo* var. *reticulatus*				
94	Rocky Ford *C. melo* var. *reticulatus*				
95	Hannah's Choice *C. melo* var. *reticulatus*				
96	Chujuc *C. melo* var. *reticulatus*				

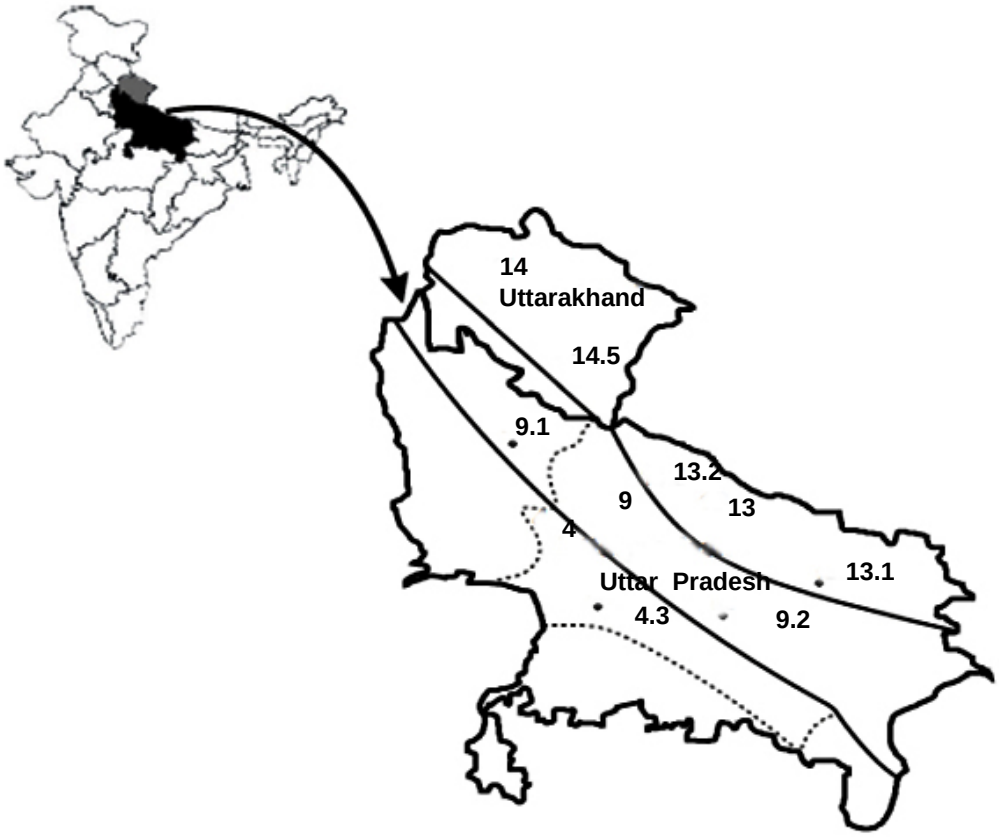


Fig. 1: Distribution of melon accessions as per agro-ecological zones and sub-zones

3.1.3 Morphological characters

3.1.3.1 Node at which first hermaphrodite flower appears

Number of nodes from the base of the vine was counted and average for each of the five random plants were taken.

3.1.3.2 Number of primary branches per plant

Number of primary branches was counted and the mean value for each of the five random plants were computed for each replication.

3.1.3.3 Days from sowing to marketable maturity.

The number of days taken from sowing to first fruit harvest was computed from five plants in each replication and mean value was taken.

3.1.3.4 Days from sowing to last fruit harvest

The number of days taken from sowing to last fruit harvest was computed from five plants in each replication and mean value was taken.

3.1.3.5 Stem pubescence

Stem pubescence was recorded at peak fruiting stage as absent or present.

3.1.3.6 Stem shape

Stem shape (round or angular) was recorded at peak fruiting stage.

3.1.3.7 Leaf margin

Recorded at complete foliage stage as unifid, bifid and multifid lobed from the five randomly selected plants for each replication.

3.1.3.8 Fruit weight (g)

Fruit harvested in each picking from five representative vines in each replication of each accession were summed up and fruit weight in grams was determined.

3.1.3.9 Fruit shape

Fruit shape was observed at fully ripe fruit stage from randomly selected fruits for each replication as globular (round), flattened and elliptical.

3.1.3.10 Fruit skin primary colour

Primary skin colour of fruit was observed visually as white, cream, light yellow, yellow, light orange, orange, brown and green

3.1.3.11 Fruit skin secondary colour

Secondary skin colour of fruit was observed visually as white, cream, light yellow, orange, brown and green

3.1.3.12 Fruit length (cm)

Length of fruit was measured as the distance from blossom end to stem end. Five fruits from each replication of every accession were measured for their length.

3.1.3.13 Fruit breadth (cm)

The fruits taken for measuring length were also used for measuring breadth in centimeters. Five fruits from each replication of each accession were measured for their breadth.

3.1.3.14 Seed cavity length (cm)

Five fruits from each replication of each genotype were measured for their seed cavity length from longitudinal section.

3.1.3.15 Seed cavity breadth (cm)

Five fruits from each replication of each genotype were measured for their seed cavity breadth from horizontal section.

3.1.3.16 Rind thickness (mm)

The rind thickness of five fruits from each replication for every accession was measured with the help of Vernier Calipers and the mean value in mm was calculated.

3.1.3.17 Netting

The presence or absence of netting was noted on the fruits from each replication.

3.1.3.18 Number of fruits per plant

Five vines were randomly selected per plot and the number of fruits at marketable maturity was counted and average was done per vine basis.

3.1.3.19 Shelf life

A sample of three fruits per accession was harvested at maturity and placed on shelves in a ventilated room to determine shelf life at room temperature which ranged from 34-38 ^{0}C. Fruits were discarded at 24 hr interval at first visual signs of deterioration which was a slight wrinkling and softening of the fruit due to desiccation. The process of discarding continued till the last fruit became unmarketable.

3.2 Biochemical traits

All above studied accessions were used for biochemical study. The mature ripe fruits, which were used for morphological study, were used for analysis of various biochemical characters in this experiment.

3.2.1 Total soluble solids content (%)

A hand refractometer was used for direct determination of T.S.S. (^{0}B) from fresh juice extracted from fully ripened fruits.

3.2.2 Ascorbic acid content (mg/100 g of fresh fruit flesh)

Two ml of juice was added to an equal volume of metaphosphoric acid + acetic acid solution in a conical flask and titrated with standardized dye solution (dichlorophenol indophenol dye).

Ascorbic acid content was determined using the method given by Heinze *et al* (1944). Ascorbic acid was calculated as under:

(Y/X) x (100/Z) mg Ascorbic acid/100 ml fruit juice.

Where, Y = Volume of dye used in titrating 'Z' volume of juice.

X = Volume of dye used in titrating 1 mg of vitamin C.

Z = Volume of fruit juice taken for titration.

3.2.3 Titrable acidity (%)

Two ml of fruit juice was neutralized with N/10 NaOH. Phenolphthalein was used as indicator of end point of titration.

Acidity was calculated as: 0.0064(g anhydrous citric acid/100ml juice).

3.2.4 Dry matter content (%)

100 grams of fresh fruit was kept at 65^0 C in pre-weighed pertri dish in oven for 48 hours (until dry weight became constant). Then petri dish was re-weighed and dry matter content (%) was calculated as:

$$\text{Dry matter content (\%)} = \frac{\text{Dry weight x 100}}{\text{Fresh weight}}$$

3.3 Statistical analysis

3.3.1 Analysis of variance

The mean value of five plants for each replication of ninety-six accessions was used for analysis of variance. The analysis of variance for randomized block design was based on the following model:

$$Y_{ij} = \mu + g_i + b_j + e_{ij}$$

(i= 1, 2 ----------g)

(ij= 1, 2 ----------b)

Where,

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

μ = Population mean

g_i = Effect of i^{th} genotype

b_j = Effect of j^{th} replication

e_{ij} = Experimental error associated with the i^{th} genotype grown in j^{th} replication.

The following procedure was adopted for the estimation of different statistical parameters.

Analysis of variance

Source of variation	Degree of freedom	Mean squares	Expected mean squares
Replication (r)	(r-1)	Mr	$\sigma^2 + g\,\sigma^2 r$
Genotype (g)	(g-1)	Mg	$\sigma^2 e + r\,\sigma^2 g$
Error	(r-1) (g-1)	Me	$\sigma^2 e$
Total	rg-1		

The mean squares due to replication and genotypes were tested against error variance by 'F' test at (r-1), (r-1) (g-1) and (g-1), (r-1) (g-1) degree of freedom, respectively at 5 and 1 per cent levels of significance.

3.3.2 Coefficient of variability

These were calculated at phenotypic and genotypic levels by the formula suggested by Burton and De-Vane (1953).

Phenotypic coefficient of variability (PCV)

$$PCV = \sqrt{\frac{\text{Phenotypic variance } (\sigma^2 p)}{\text{General Mean of population } (\bar{X})}} \times 100$$

Genotypic coefficient of variability (GCV)

$$GCV = \sqrt{\frac{\text{Genotypic variance } (\sigma^2 g)}{\text{General Mean of population } (\bar{X})}} \times 100$$

Heritability (%)

Heritability (broad sense) was calculated as per formula given by Burton and De Vane (1953) and Johnson *et al* (1955).

$$Hbs = \frac{\sigma^2 g}{\sigma^2 p} \times 100$$

Where, Hbs = Heritability (broad sense)

$\sigma^2 g$ = Genotypic variance

$\sigma^2 p$ = Phenotypic variance

Genetic advance

The expected genetic advance resulting from selection of five per cent superior individuals was calculated by the formula suggested by Burton and De Vane (1953) and Johnson *et al* (1955).

$$GA = k.\ \sigma p.Hbs$$

Where,

GA = Genetic advance

k = 2.06 (selection differential at 5 per cent selection index)

σ.p. = Phenotypic standard deviation

Hbs = Heritability (broad sense)

Genetic gain

Genetic advance expressed as per cent of population mean was calculated by the method given by Johnson *et al* (1955) as follows:

$$\text{Genetic gain (\%)} = \frac{\text{Genetic advance (GA)}}{\text{Population mean } (\bar{X})} \times 100$$

Correlation coefficient

The correlation coefficients at phenotypic and genotypic level were estimated from variances and covariances of all characters as suggested by Al-Jibouri *et al* (1958).

Phenotypic correlation coefficient (r_p)

$$r_p = \frac{\sigma_{pxy}}{\sqrt{\sigma^2_{px} \times \sigma^2_{py}}}$$

Where,

σ_{pxy} = Phenotypic covariance between two characters x and y

σ^2_{px} = Phenotypic variance of the x character

σ^2_{py} = Phenotypic variance of the y character

Genotypic correlation coefficient (r_g)

$$r_g = \frac{\sigma_{gxy}}{\sqrt{\sigma^2_{gx} \times \sigma^2_{gy}}}$$

Where,

σ_{gxy} = genotypic covariance between two characters x and y

σ^2_{gx} = genotypic variance of the x character

σ^2_{gy} = genotypic variance of the y character

3.3.3 Genetic diversity

Mahalanobis D^2 statistics

Mahalanobis D^2 statistics between two populations estimated on the basis of the 'p' characters is:

$$Dp^2 = \sum_{1}^{p} \sum_{1}^{p} 1\ W^{ij} (X_{i1} — X_{i2}) (X_{j1} — X_{j2})$$

Where,

W_{ij} = Variance -covariance matrix W^{ij} is the reciprocal of (W_{ij}), (i, j=1, 2…..p)

X_{i1} = Sample mean for i^{th} character for first sample

X_{ij} = Sample mean for i^{th} character for j^{th} sample. In the present study characters ($p_{1...16}$) were used to perform the above analysis. For conducting the D^2 analysis, the computer programme, W1NDOSTAT 8.0 cluster analysis was used.

3.4 Experiment-II: Characterization of melon (*Cucumis melo* L.) accessions using molecular markers

3.4.1 Collection of leaf material

Young, fresh, disease and insect free leaves from all ninety-six melon accessions were used for DNA extraction. Leaf samples were collected in butter papers and placed in ice containers while transferring from field to laboratory. These were stored in deep freezer at -80^oC for DNA isolation and SSR marker studies.

3.4.2 Buffers and solutions

The procedure of preparation of solutions and buffers used in the present

investigation was done as per protocols by Sambrook *et al* (1989).

3.4.3 Genomic DNA isolation

DNA extraction procedure as proposed by Doyle and Doyle (1989) was used with some minor modifications like treatment with polyvinyl pyrrolidone to remove the polyphenols thereby preventing their interaction with DNA and yielding high quality DNA**.** The different steps that were followed are as under:

Step 1: Two gram of leaves was crushed using pre chilled mortar and pestle in the presence of liquid nitrogen. Thorough crushing of leaves was done before adding extraction buffer. 20 mg of PVP per liter of CTAB buffer (Polyvinyl pyrrolidone) was added to each sample during the grinding step.

Step 2: The powder was transferred to a 50 ml polypropylene tube and 15 ml of pre warmed (65^0C) CTAB buffer was added. The contents were mixed well by vigorous shaking and tubes were incubated at 65^oC for one hour in a water bath. Occasional mixing was performed during this period.

Step 3: 15 ml of chloroform: isoamyl alcohol (24:1) (v/v) was added and contents were mixed by inverting the tubes for 5 minute. Alternatively mechanical shaking was performed for further mixing for a period of 30 minutes at room temperature.

Step 4: Samples were centrifuged for 15 minutes at 10,000 rpm at room temperature so as to separate the phases.

Step 5: Supernatant (aqueous phase) was carefully pipetted out without disturbing the interface to another fresh 50 ml Falcon tube.

Step 6: Chilled isopropanol (10ml) was added to precipitate the DNA and kept in refrigerator for 15 minutes so as to precipitate the DNA.

Step 7: DNA was spooled out with a glass hook (the supernatant was discarded) and transferred to an Eppendorf tube.

Step 8: The Eppendorf tube containing DNA pellet was centrifuged at 10,000 rpm for 7 minutes at 4^oC so as to collect DNA at the bottom.

Step 9: The pellet was washed twice with 70% ethanol.

Step 10: The pellet was dissolved in 400 to 500 µl TE buffer (pH 8.0).

3.4.4 DNA quantification

The concentration and purity of DNA was checked by Agarose gel electrophoresis. Different steps followed were as:

Step1: 0.8 g of agarose was dissolved in 100 ml of 0.5X TBE electrophoresis buffer (Tris base –45mM, Boric acid- 45mM and EDTA- 1mM).

Step 2: The mixture was heated till the agarose dissolved completely i.e. when solution became transparent and clear. It was cooled down to 60°C with constant stirring. Ethidium bromide was added to a final concentration of 0.5µg/ ml of buffer.

Step 3: Agarose solution was then poured into an already prepared gel mould with combs and left for 20-30 min for solidification.

Step 4: DNA samples for loading were prepared by adding 2 µl loading dye (6X) (0.25% w/v bromophenol blue, 50 per cent glycerol in sterile water) to 8 µl DNA.

Step 5: DNA samples were loaded into wells with the help of micropipette. Along with the DNA samples, marker of known concentration (uncut λ DNA of 50 ng/ µl concentration) was also loaded.

Step 6: Gel was run for about 1-2 hours at voltage of 5 V/cm and visualized under UV transilluminator.

Step 7: DNA samples were photographed using photo gel documentation system. The intensity of fluorescence of each sample was compared with that of a standard marker (50bp) and then DNA concentration of each sample was ascertained.

Step 8: Quality of DNA samples was judged based on whether DNA formed a single high molecular weight band (good quality) or a smear (degraded/ poor quality).

The DNA was then diluted to a final concentration of 20ng/ µl.

3.4.6 Selection of SSR primers

For the present study, 30 SSR primer pairs (Chiba *et al,* 2003) were used. The SSR primers were synthesized through Integrated DNA Technologies Canada. The selected microsatellite markers along with their annealing temperature are presented in Table 2.

Table 2: The selected microsatellite markers.

	Locus	Primer sequence (5'- 3')		Annealing temp. (^{o}C)
		Forward	Reverse	
1	**ECM50**	TCAACCGTCTTCTCTCCACA	GTCATCGTTGAGTGCCAGAG	57
2	**ECM51**	TTCAAGCCTAGTTGTTTCTTGAT	TGTAATCGGTTGAGTAAACAGGA	58
3	**ECM61**	TTTCAAAAAGCGAACCAGCTA	TCGGACTCGATTACCAAACA	54
4	**ECM65**	ACGACCTTCTCCTCCTCCTC	ACCGATTGAAGGGTTGGATT	54
5	**ECM70**	TCCCTACCAATGAGGGGACT	TCAAACAAGA\TACATAGCCAATGAAA	57
6	**ECM80**	CGTCCCCTTGTTACTACCTCA	AAATCCTCCCTACATATATTATGCAAT	52
7	**ECM85**	AGGACAGCGGAGCTTTTCTT	TGAAATCGAAGTCCACTCTGAA	54
8	**ECM109**	CCCCCTTTTCTCCTTCTTCTT	GCTCTCATGGGAAACAGAGG	58
9	**ECM124**	GCGTCCTAAAAAGGGATAAGG	ATTTTCACAAAAGGGGGAGAG	55
10	**ECM125**	GGAAACGCAAAATCAGTGAG	CTGAACGTGGACGACATTTTT	55
11	**ECM129**	TCAGACTCCATTTCAGAGCCTA	CTTCAACCCCATTTTCTCACA	57
12	**ECM130**	CATTGGGAAAAAGGGTATGGA	CTGGCTCCTTCACATTGTTGT	55
13	**ECM133**	AAACATCAACACACACCCACA	TCAGCGACGGTCATCTATTTT	55
14	**ECM134**	TCTTTCCTCTGCAAATCCTTCT	TGCTAAAGCTACATGCTGTCCT	58

	Locus	Primer sequence (5'- 3')		Annealing temp. (^{o}C)
		Forward	Reverse	
15	**ECM178**	CATAGAGCATTTGCCGGAGT	TGAAAAGCTAGCATGGATTGG	55
16	**ECM182**	TTCTTCATAATTCTAAATTTTTCCATC	CCAGGTGGAAGTTTTGCTTC	54
17	**CMMS14-1**	CATTGCTACTATTGTCGTCGTTGCT	TTTCTTTCTTTTCCGTATCCATTTT	60
18	**CMMS1-3**	TTGAATGATTGGAGGGAAGATAACG	CAAATATTGATGGATTTAATATATT	46
19	**CMMS3-1**	AAATATAAGCAAACCAAAGTTGACC	CCGGGATATACGGACATACACACAC	60
20	**CMMS30-3**	TTCCCACCAGCCCAACGGACACACT	GAGATACAGAAACGACGACTAACCT	60
21	**CMMS33-1**	TGTAATAGGATGACCAAGGGGAGTT	TTCAGGAGCTACAACAAGATTTCAA	58
22	**CMMS004**	GCCCAACGGACACACTCACTCACAC	GAGGGAGTAAGAATAAGAAGAAGAA	58
23	**CMGA127**	GAACTAAGACTCTCCAATTAA	ATGTCCCTAACTGCCAAACATA	46
24	**CMGA128**	ATGAAGAAGGGATATTCAAAG	ACTCCATTGTTGCTAACCTTT	53
25	**CMTCN8**	CCTCCGCCACATATTACAAT	TTCATCTTGACACGTAAGAG	48
26	**CMCTN38**	TAAAACACTCTCGTGACTCC	GATCTGAGGTTGAAGCAAAG	55
27	**CMCTN21**	GCTGTAAAACGAAACGGAGA	CGATCTTCTTTATTCTTCGCC	55
28	**CMTC13**	TGGATGGATAAGGTGGTAAG	TTCCCCTAGTCGCTCTCT	46
29	**CMAG59**	TTGGGTGGCAATGAGGAA	ATATGATCTTCCATTTCCA	46
30	**CMMS35-4**	ACGGATACATCGAGGAGACTTCATG	GTCAGCTTCAACCCTTTACTTTTTC	60

3.4.7 PCR standardization and amplification

A mixture 20 µl of various PCR reagents, based on the stock and final concentration of different components (Table 3) was prepared as under

Table 3: Stock and final concentration of different components used in PCR

Components	Stock Conc.	Volume (µl)	Final Conc.
Water	---	8.9	- - -
PCR buffer	10X	2.0	1X
$MgCl_2$	25mM	1.6	1.5mM
dNTPs	1mM	4.0	200µM
Primer Forward	5µM	1.25	0.5µM
Primer Reverse	5µM	1.25	0.5µM
Taq Polymerase	5U/µl	0.2	1Unit
DNA template	20ng/µl	2	20ng
Total		20	

The reagents were mixed thoroughly in a 500 µl Eppendorf tube and vortexed for a few seconds. 18 µl of the above mixture was distributed to each PCR reaction tube and then 2.0 µl of DNA (concentration 20ng/ µl) was added to each tube. *In vitro* amplification using polymerase chain reaction (PCR) was performed in a 96 well microtiter plate in an M J Research PTC200 or Eppendorf Master Cycler using 40 ng of genomic DNA of each

genotype in a final volume of 20µl per reaction. The following polymerase chain reaction (PCR) profile was used : pre-denaturation for 2 min at 94°C, then 35 cycles each consisting of a denaturation step for 1 min, an annealing step for 1 min at a given annealing temperature (Table 2), and an extension step for 4 min at 72°C. The details are given in Table 4 as under:

Table 4: Temperature profile used in PCR

Step	Temperature (ºC)	Time (minutes)	No. of cycles
1. Initial denaturation	94.0	2	1
2. Denaturation	94.0	1	35
3. Annealing	46-60	1	
4. Elongation (Extension)	72.0	1	
5. Final Extension	72.0	4	1
6. Hold	4		

3.4.8 Electrophoresis of amplified DNA

To 20 µl of the amplified product, 3.0µl of 6X loading dye was added so as to make the final concentration of the loading buffer in the reaction samples to 1X. The PCR products were resolved on 2.5 per cent superfine resolution agarose (Amresco 30175 Solon Ind. PKWY, Solon, Ohio 44139) gel. The gel was prepared in 0.5X TBE buffer. Ethidium bromide was added at concentration of 0.5µg/ µl. 10 µl of sample was loaded onto each well and gel was run at 5V/ cm, visualized under UV light and photographed using UVP gel documentation system (Model GDS 7600). 50Kb ladder was used as a standard.

3.4.9 Scoring of SSR allele profile

The total number of alleles was recorded for each microsatellite marker in all the genotypes under study by giving the number to amplified alleles as 1, 2, 3 etc. Data matrices were prepared in which the presence of a band was coded as 1 (band present) and 0 (band absent) in a binary matrix. The lines that did not show any amplification were scored as null alleles.

3.4.10 Statistical analysis

Polymorphic information content (PIC) that provides an estimate of the discriminatory power of a locus or loci, by taking into account, not only the number of alleles that are expressed, but also relative frequencies of those alleles, was estimated using the following equation of Anderson *et al* (1993).

$$PIC = 1- \sum_{i=1}^{n} (P_{ij})^2$$

Where P_{ij} is the frequency of j^{th} allele in i^{th} primer and summation extends over 'n' patterns.

Genetic diversity among the parental lines was assessed based on SSR markers using software package NTSYS-PC version 2.02e.

3.4.11 Statistical analysis using NTSYS-PC version 2.02e

Numerical Taxonomic and Multivariate Analysis System (NTSYS-pc) version 2.02e (Rohlf, 1998) software programme was used to analyze molecular data. Data from 30 primers were used to estimate the similarity based on the number of shared amplified bands. Similarity was estimated using SIMQUAL function of NTSYS, which computes a variety of similarity coefficient for qualitative data (nominal data). Dendrogram, was constructed using UPGMA (Unweighted Pair Group Method using Arithmetic Averages) available in NTSYS.

3.4.12 Statistical analysis using DARwin 5 software package

Dissimilarity coefficients were estimated for allelic data generated by 30 SSR primer pairs by using DARwin 5 software (Perrier and Jacquemoud-Collet, 2006) as follows:

$$D_{ij} = 1 - \frac{1}{L}\sum_{i=1}^{L}\frac{m_l}{\pi}$$

Where, d_{ij} : dissimilarity between its i and j

L: Number of loci

π: Poloidy

m_l: number of matching alleles for locus l

Factorial Correspondence Analysis (FCA) was performed using neighbor joining on the basis of UPGMA (Unweighted Pair Group Method using Arithmetic Averages) to show multiple dimensions of each group and the accessions in a scattered plot

3.5 Experiment III: Reaction to diseases

3.5.1 Reaction to cucumber mosaic virus (CMV)

Artificial inoculation

Screening for CMV resistance was done under artificial inoculation in an insect-proof nethouse during September 2009 and 2010. Seeds were sown in polyethylene bags (18 x 12 cm) filled with a potting mixture of soil, farm yard manure and sand (1:1:1) with 10 bags per genotype. Mechanical sap inoculation was done with a pure isolate of CMV at two-true-leaf stage. Screening for virus incidence was done on individual plant basis 7 days after inoculation with a resistant to severe mosaic scale of Mayee *et al* (1976)

Inoculation procedures

The infected plants of melon showing symptoms like mosaic, mottling, blistering, puckering, leaf deformations, vein banding, vein clearing, serrated margins etc were collected from the field. The young leaves of all these infected plants were clipped off, thoroughly washed with tap water and then with distilled water to remove any kind of extraneous matter from leaves. Washed leaves were dried between the two folds of blotter paper and crushed in sterilized pestle and mortar using 0.01M phosphate buffer (pH 7.0) @ 1ml/g of leaf tissue. The extract thus obtained was filtered through a double layered muslim cloth. This sap was

applied gently and evenly on the upper surface of the healthy seedlings of melon with a swab of sterilized absorbent cotton wool using carborundum (Silicon carbide, 600 mesh) as an abrasive. To ensure uniform pressure, spread of the inoculum and to avoid injury, the leaves were supported from below by a piece of sterilized soft cardboard. The leaves thus inoculated were washed with a jet of water to remove excessive inoculum after inoculation. The plants were labelled and kept in insect- proof cages Daryono *et al* (2003).

3.4.5.2 Reaction to downy mildew disease

Screening for downy mildew resistance was done under natural epiphytotic conditions in the field thrice (during the growing season April-June 2009, 2010 and 2011) .When the downy mildew symptoms were conspicuous, 10 plants with 3 infected leaves per plant were randomly marked from each genotype for disease scoring. A 0-5 scale (Pan and More, 1996) was used for individual leaf scoring (0 = no symptom, 1 = less than 10 isolated spots, 2 = 10-20 isolated spots, 3 = more than 20 spots + patches, more than 30% leaf area affected, 4 = necrotic patches, 50% leaf area affected and 5 = necrotic patches, more than 50% leaf area affected) .

On the basis of scoring of 3 individual leaves per plant and 10 plants in each genotype, PDI was calculated for each genotype using the formula:

$$\text{PDI} = \frac{\text{Summation of grades}}{\text{No. of leaves x highest numerical rating}} \text{ x } 100$$

Using PDI values, the genotypes were grouped as immune (0.0%), highly resistant (0.1-25 .0%), resistant (25.1-40.0%), moderately resistant (40.1-60%), susceptible (60.1-100.0%).

CHAPTER – IV

RESULTS AND DISCUSSION

The experimental results obtained through statistical analysis have been presented under the following headings:

4.1 Characterization on the basis of morphological characters

4.2 Characterization on the basis of biochemical traits

4.3 Characterization on the basis of SSR markers

4.4 Characterization on the basis of reaction to diseases

4.1 Characterization on the basis of morphological characters

Analysis of variance revealed highly significant differences among all ninety-six genotypes of melon (Table 4.1) for all the characters observed viz., node at which first hermaphrodite flower appears, number of primary branches /vine, days from sowing to marketable maturity, days from sowing to last fruit harvest, number of fruits per vine, fruit weight (g), fruit length (cm), fruit breadth (cm), seed cavity length (cm), seed cavity breadth (cm), rind thickness (mm), total soluble solids content (%), titrable acidity content (%), ascorbic acid content (mg/100g of fresh fruit weight), dry matter content (%), shelf life (days). The results indicated the presence of adequate amount of variability in the germplasm under study. Mean value and range for each character under study are presented in Table 4.2. Mean performance of each genotype for each character is presented in Table 4.3, 4.4 and 4.5

4.1.1 Node at which first hermaphrodite flower appears

Early maturity is depicted by node at which first hermaphrodite flower appears, so genotypes bearing hermaphrodite flower at lower node are preferred. In the present study, node at which first hermaphrodite flower appears showed the significant variation. During the year 2009, it ranged from 1.90 to 5.15 with the overall mean of 3.03.The genotype MM-4013 was found to have minimum number of node (1.90) to bear the first hermaphrodite flower and was statistically at par with MM-4409 (2.00), MM-4243 (2.00), MM-3851 (2.00), MM-3956 (2.00), MM-4256 (2.00), MM-4067 (2.02), MM-3874 (2.03), MM-4098 (2.03), MM-4276 (2.04), MM-4303 (2.05), MM-4270 (2.05), MM-3895 (2.05) and MM-4278(2.06) while maximum number of node at which first hermaphrodite flower appears was observed in MM-4247 (5.15) and was statistically at par with MM-3982 (5.10), MM-3994 (5.05), MM-4030 (5.05), MM-4091 (5.05) and MM-5736 (5.00). In 2010, node at which first hermaphrodite flower appears varied from 2.00 to 5.45 with the overall mean of 3.13. The genotype MM-4278, MM-3833 and MM-4018 were found to have minimum number of node (2.00) to bear the first hermaphrodite flower and were significantly at par with MM-4270 (2.01), MM-3895 (2.03), MM-3884 (2.04) and MM-4098 (2.05). Pooled mean ranged from 2.00 to 5.15 with the overall mean of 3.08. The genotype MM-4013 was recorded to have minimum number of

Table 4.1: Analysis of variance for different characters in melon

Mean Sum of Squares																	
Source of variation	**d.f**	**Node at which first hermaphrodite flower appears**	**Number of primary branches per vine**	**Days from sowing to marketable maturity**	**Days from sowing to last fruit harvest**	**Number of fruits per vine**	**Fruit weight**	**Fruit length**	**Fruit breadth**	**Seed cavity length**	**Seed cavity breadth**	**Rind thickness**	**Total soluble solids content**	**Ascorbic acid content**	**Titrable acidity**	**Dry matter content**	**Shelf life**
Genotypes	95	3.14**	4.04**	28.68**	25.97**	0.58**	144619.00**	22.11**	2.30**	21.25**	1.84**	0.56**	23.69**	1115.41**	0.25**	3.338**	0.69**
Error	190	0.2832	0.536	4.38	9.41	0.40	1687.18	0.26	0.18	0.13	0.43	0.29	1.07	7.81	0.148	0.7395	0.27

**Significant at 1 % level of significance

Table 4.2: Range and mean of various marphological and biochemical characters of melon.

Sr. No.	Characters	Range			Mean		
		2009	2010	Pooled mean	2009	2010	Pooled mean
1	Node at which first hermaphrodite flower appears	1.90 to 5.15	2.00 to 5.45	2.00 to 5.25	3.03	3.13	3.08
2	Number of primary branches /vine	2.30 to 6.96	2.10 to 7.00	2.20 to 6.83	4.18	4.31.	4.24
3	Days from sowing to marketable maturity	77.85 to 89.75	79.05 to 90.72	78.48 to 89.43	84.07	83.71	83.89
4	Days from sowing to last fruit harvest	97.25 to 112.60	97.89 to 109.95	98.83 to 110.85	105.29	105.03	105.16
5	Number of fruits per vine	1.40 to 3.05	1.42 to 2.90	1.51 to 2.97	2.25	2.37	2.31
6	Fruit weight (g)	484.00 to 1465.20	430.00 to 1544.80	457.00 -1505.00	807.25	804.78	806.07
7	Fruit length (cm)	7.67 to 20.40	7.49 to 22.49	7.58 -21.32	10.78	10.86	10.82
8	Fruit breadth (cm)	7.20 to 12.58	7.04 to 13.92	7.12 to 12.75	10.79	10.78	10.80
9	Seed cavity length (cm)	5.75 to 17.40	5.40to 18.59	5.57 to 17.72	7.95	7.93	7.92
10	Seed cavity breadth (cm)	5.45 to 9.78	5.30 to 9.97	5.37 to 9.42	7.63	7.54	7.58
11	Rind thickness (mm)	1.45 to 3.68	1.50 to 3.60	1.47 to 3.60	2.31	2.40	2.39
12	Shelf life (days)	1.40 to 3.45	1.48 to 3.69	1.55 to 3.49	2.19	2.34	2.26
13	Total soluble solids content (%)	2.30 to 13.15	3.00 to 13.45	2.77 to 13.16	10.38	10.26	10.33
14	Ascorbic acid content (mg/ fresh 100 g of fruit weight)	7.90 to 37.49	8.10 to 40.05	8.23 to 38.77	23.08	23.44	23.26
15	Titrable acidity (g anhydrous citric acid/100ml of fruit juice)	0.06 to 0.40	0.06 to 0.37	0.07 to 0.37	0.11	0.12	0.11
16	Dry matter content (%)	7.95 to 15.08	8.14 to 13.50	8.15 to 13.53	9.51	9.62	9.56

Table 4.3: Mean performance of melon accessions for various morphological characters.

Sr. No.	Accession No..	Node at which first hermaphrodite flower appears			Number of primary branches per vine		
		2009	2010	Pooled mean	2009	2010	Pooled mean
1	MM-3833	2.20	2.00	2.10	3.25	3.75	3.50
2	MM-3837	2.35	2.75	2.55	4.16	4.94	4.55
3	MM-3839	2.10	2.30	2.20	4.73	4.27	4.50
4	MM-3843	2.48	2.32	2.40	3.35	3.65	3.50
5	MM-3849	2.05	2.15	2.10	3.50	3.80	3.65
6	MM-3850	2.50	2.28	2.39	4.22	4.02	4.12
7	MM-3851	2.00	2.30	2.15	2.40	2.46	2.43
8	MM-3855	5.10	4.80	4.95	6.40	6.50	6.45
9	MM-3856	3.05	2.85	2.95	5.00	4.40	4.70
10	MM-3857	2.14	2.36	2.25	4.00	4.30	4.15
11	MM-3858	2.52	2.78	2.65	4.76	4.20	4.48
12	MM-3859	2.43	2.17	2.30	3.98	3.42	3.70
13	MM-3860	2.92	2.78	2.85	4.00	3.40	3.70
14	MM-3864	2.19	2.09	2.14	3.92	3.38	3.65
15	MM-3866	4.04	4.26	4.15	6.44	6.86	6.65
16	MM-3868	2.10	2.20	2.15	3.62	3.38	3.50
17	MM-3874	2.03	2.25	2.14	3.60	4.00	3.80
18	MM-3881	2.43	2.07	2.25	4.40	4.24	4.32
19	MM-3884	2.20	2.04	2.12	4.00	4.14	4.07
20	MM-3885	3.22	3.48	3.35	2.78	2.48	2.63
21	MM-3887	4.48	4.72	4.60	6.81	6.45	6.63
22	MM-3889	4.83	4.67	4.75	6.55	6.85	6.70
23	MM-3901	4.00	3.70	3.85	4.15	3.75	3.95
24	MM-3903	4.48	4.82	4.65	6.60	7.00	6.80
25	MM-3909	3.05	2.85	2.95	4.44	4.00	4.22
26	MM-3917	2.22	2.38	2.30	3.93	4.21	4.07
27	MM-3947	2.07	2.43	2.25	4.00	3.60	3.80

Table 4.3 Contd.....

Sr. No.	Accession No.	Node at which first hermaphrodite flower appears			Number of primary branches per vine		
		2009	2010	Pooled mean	2009	2010	Pooled mean
28	MM-3955	2.20	2.40	2.30	4.05	4.35	4.20
29	MM-3956	2.00	2.20	2.10	4.11	4.50	4.30
30	MM-3961	2.06	2.24	2.15	4.03	4.27	4.15
31	MM-3962	4.50	4.80	4.65	6.07	6.65	6.36
32	MM-3963	2.08	2.32	2.20	3.75	3.25	3.50
33	MM-3965	2.25	2.35	2.30	3.88	4.12	4.00
34	MM-3966	3.05	3.65	3.35	2.72	2.48	2.60
35	MM-3968	3.55	4.11	3.83	4.05	3.85	3.95
36	MM-3973	2.08	2.46	2.27	3.77	3.23	3.50
37	MM-3974	4.80	4.94	4.87	5.88	6.03	5.95
38	MM-3976	3.82	3.38	3.60	3.70	4.20	3.95
39	MM-3977	3.65	3.15	3.40	3.10	3.70	3.40
40	MM-3979	2.18	2.80	2.49	4.00	4.46	4.23
41	MM-3980	2.60	3.16	2.88	4.90	4.20	4.55
42	MM-3981	3.28	2.92	3.10	5.00	5.34	5.17
43	MM-3982	5.10	4.90	5.00	6.38	6.62	6.50
44	MM-3983	2.63	3.27	2.95	4.06	4.38	4.22
45	MM-3985	2.05	2.03	2.04	3.18	3.82	3.50
46	MM-3986	2.16	2.54	2.35	3.47	3.73	3.60
47	MM-3994	5.05	4.75	4.90	6.13	6.49	6.31
48	MM-3998	4.80	5.20	5.00	6.96	6.70	6.83
49	MM-4002	4.50	5.00	4.75	6.10	6.70	6.40
50	MM-4003	2.10	2.60	2.35	4.00	3.60	3.80
51	MM-4004	5.10	5.05	5.15	6.19	5.95	6.07
52	MM-4005	4.68	5.12	4.90	6.49	6.83	6.66
53	MM-4013	1.90	2.10	2.00	4.05	4.75	4.40
54	MM-4018	2.20	2.00	2.10	4.25	4.35	4.30

Table 4.3 Contd.....

Sr. No.	Accession No.	Node at which first hermaphrodite flower appears			Number of primary branches per vine		
		2009	2010	Pooled mean	2009	2010	Pooled mean
55	MM-4021	2.15	2.29	2.22	4.40	4.14	4.27
56	MM-4026	2.33	2.17	2.25	3.90	4.30	4.10
57	MM-4030	5.05	4.65	4.85	6.25	6.79	6.52
58	MM-4057	4.50	5.00	4.75	6.46	6.00	6.23
59	MM-4059	3.75	3.35	3.55	3.33	3.83	3.58
60	MM-4063	2.07	2.63	2.35	3.95	4.25	4.10
61	MM-4065	3.37	3.59	3.48	3.20	3.80	3.50
62	MM-4066	3.00	2.50	2.75	3.43	3.99	3.71
63	MM-4067	2.02	2.68	2.35	4.15	3.65	3.90
64	MM-4068	2.57	2.93	2.75	4.00	4.60	4.30
65	MM-4091	5.05	5.45	5.25	2.89	3.17	3.03
66	MM-4098	2.03	2.05	2.04	4.05	4.55	4.30
67	MM-4243	2.00	2.24	2.12	3.97	4.41	4.19
68	MM-4247	5.15	5.05	5.10	5.15	5.65	5.40
69	MM-4248	2.05	2.25	2.15	4.24	3.96	4.10
70	MM.4250	2.10	2.50	2.30	3.28	3.72	3.50
71	MM-4251	2.23	2.57	2.40	3.37	3.63	3.50
72	MM-4252	3.65	3.41	3.53	3.20	3.90	3.55
73	MM-4253	2.06	2.24	2.15	3.88	3.34	3.61
74	MM-4256	2.00	2.30	2.15	4.07	4.33	4.20
75	MM-4267	4.90	5.20	5.10	5.12	5.68	5.40
76	MM-4268	2.40	2.90	2.65	4.02	3.40	3.71
77	MM-4270	2.05	2.01	2.03	4.00	4.14	4.07
78	MM-4271	3.15	3.89	3.52	3.23	3.83	3.53
79	MM-4276	2.04	2.40	2.22	3.53	3.77	3.65
80	MM-4277	3.80	3.10	3.45	3.92	3.48	3.70
81	MM-4278	2.06	2.00	2.03	4.02	4.32	4.17

Table 4.3 Contd.....

Sr. No.	Accession No.	Node at which first hermaphrodite flower appears			Number of primary branches per vine		
		2009	2010	Pooled mean	2009	2010	Pooled mean
82	MM-4279	3.36	3.94	3.65	3.22	3.80	3.51
83	MM-4282	3.10	2.46	2.78	4.86	4.54	4.70
84	MM-4283	2.10	2.18	2.14	4.44	4.00	4.22
85	MM-4305	2.05	2.35	2.20	4.05	4.41	4.23
86	MM-4342	2.43	2.17	2.30	3.98	4.32	4.15
87	MM-4409	2.00	2.30	2.15	3.28	3.92	3.60
88	MM-5736	5.00	4.70	4.85	6.07	6.53	6.30
89	AR Hale's	3.63	3.27	3.45	2.32	2.48	2.40
90	Dulce-B.B	4.00	3.50	3.75	2.62	2.38	2.50
91	Gulf Coast	4.00	3.70	3.85	2.30	2.10	2.20
92	Gulf Stream	3.32	3.80	3.56	3.24	2.92	3.08
93	Jucumba	3.15	3.55	3.35	2.45	2.40	2.42
94	Rocky Ford	3.08	3.52	3.30	2.34	2.38	2.36
95	Hannah's Choice	3.10	3.64	3.37	2.40	2.41	2.40
96	Chujuc	3.06	3.34	3.20	2.32	2.35	2.33
	CD (5%)	**0.19**	**0.27**	**0.21**	**0.37**	**0.31**	**0.0.28**
	CD (1%)	**0.25**	**0.35**	**0.27**	**0.48**	**0.40**	**0.36**

Table 4.3 Contd.....

Sr. No.	Accession No.	Days from sowing to marketable maturity			Days from sowing to last fruit harvest		
		2009	2010	Pooled mean	2009	2010	Pooled mean
1	MM-3833	78.60	83.60	81.10	103.40	107.70	105.55
2	MM-3837	80.50	84.34	82.42	97.25	100.41	98.83
3	MM-3839	80.36	84.78	82.57	102.25	107.51	104.88
4	MM-3843	82.08	79.50	80.79	106.40	103.20	104.80
5	MM-3849	86.88	80.96	83.92	104.65	101.95	102.97
6	MM-3850	85.79	84.05	84.92	107.20	105.02	106.11
7	MM-3851	80.13	86.33	83.23	104.55	100.99	102.77
8	MM-3855	86.40	88.55	87.47	101.25	106.15	103.70
9	MM-3856	80.50	82.16	81.33	99.40	101.20	100.30
10	MM-3857	80.07	80.35	80.21	104.00	105.94	104.97
11	MM-3858	83.21	80.45	81.83	100.95	97.89	99.42
12	MM-3859	82.00	83.40	82.70	103.25	106.01	104.63
13	MM-3860	86.20	83.96	85.08	107.95	105.51	106.73
14	MM-3864	84.28	82.50	83.39	103.88	101.38	102.63
15	MM-3866	86.76	89.50	88.13	104.80	108.34	106.57
16	MM-3868	83.53	79.33	81.43	107.35	102.25	104.80
17	MM-3874	79.54	81.12	80.33	104.25	106.81	105.53
18	MM-3881	83.01	80.67	81.84	105.05	103.75	104.40
19	MM-3884	83.43	79.77	81.60	105.97	103.77	104.87
20	MM-3885	84.54	82.50	83.52	106.25	104.69	105.47
21	MM-3887	85.00	85.90	85.45	104.90	106.70	105.80
22	MM-3889	87.79	86.33	87.06	104.45	105.55	104.50
23	MM-3901	85.71	81.75	83.73	109.25	107.91	108.58
24	MM-3903	85.92	86.00	85.96	102.56	105.00	103.78
25	MM-3909	80.15	82.35	81.25	98.07	100.95	99.51
26	MM-3917	86.52	82.72	84.62	104.90	106.50	105.70
27	MM-3947	77.85	79.11	78.48	100.70	103.50	102.10

Table 4.3 Contd.....

Sr. No.	Accession No.	Days from sowing to marketable maturity			Days from sowing to last fruit harvest		
		2009	2010	Pooled mean	2009	2010	Pooled mean
28	MM-3955	79.70	81.74	80.72	99.10	101.90	100.50
29	MM-3956	78.25	79.99	79.12	102.00	103.54	102.77
30	MM-3961	78.40	81.90	80.15	98.85	102.35	100.60
31	MM-3962	82.30	86.90	84.60	102.35	105.91	104.13
32	MM-3963	81.45	79.55	80.50	103.25	100.49	101.87
33	MM-3965	82.75	83.31	83.03	102.00	102.80	102.40
34	MM-3966	84.25	85.45	84.85	108.35	109.59	108.97
35	MM-3968	86.90	82.30	84.60	108.75	103.79	106.27
36	MM-3973	79.30	82.90	81.10	103.25	107.85	105.55
37	MM-3974	88.14	90.72	89.43	111.56	108.04	109.80
38	MM-3976	85.94	83.40	84.67	108.20	104.80	106.50
39	MM-3977	84.10	85.40	84.75	105.20	106.90	106.05
40	MM-3979	80.87	81.10	80.97	108.00	108.82	108.41
41	MM-3980	83.55	82.05	82.80	103.75	101.67	102.71
42	MM-3981	81.04	79.10	80.07	101.97	98.57	100.27
43	MM-3982	86.85	83.75	85.30	108.25	105.69	106.97
44	MM-3983	80.90	81.50	81.20	101.00	103.34	102.17
45	MM-3985	81.00	81.60	81.30	105.00	108.34	106.67
46	MM-3986	84.14	81.12	82.63	106.75	103.05	104.90
47	MM-3994	89.75	87.31	88.53	105.32	103.02	104.17
48	MM-3998	84.30	84.10	84.20	107.00	109.26	108.13
49	MM-4002	84.90	88.24	86.57	102.25	107.49	104.87
50	MM-4003	82.16	81.10	81.63	104.80	104.00	104.40
51	MM-4004	85.00	85.90	85.45	101.25	105.68	103.63
52	MM-4005	83.30	81.10	82.20	106.43	103.17	104.80
53	MM-4013	81.25	82.45	81.85	101.55	104.51	103.03
54	MM-4018	80.30	84.50	82.40	100.95	108.51	104.73

Table 4.3 Contd.....

Sr. No.	Accession No.	Days from sowing to marketable maturity			Days from sowing to last fruit harvest		
		2009	2010	Pooled mean	2009	2010	Pooled mean
55	MM-4021	80.65	83.15	81.90	102.55	103.71	103.13
56	MM-4026	80.00	81.04	80.52	101.75	102.65	102.20
57	MM-4030	88.98	85.72	87.35	101.25	103.73	102.49
58	MM-4057	87.96	85.20	86.58	108.50	103.90	106.20
59	MM-4059	84.66	80.90	82.78	110.75	105.69	108.22
60	MM-4063	80.10	82.50	81.30	107.51	109.95	108.73
61	MM-4065	86.54	85.00	85.77	108.00	107.00	107.50
62	MM-4066	86.48	83.70	85.09	109.35	105.45	107.40
63	MM-4067	79.90	80.36	80.13	102.10	105.40	103.75
64	MM-4068	83.00	80.00	81.50	104.95	101.79	103.37
65	MM-4091	84.90	85.96	85.43	105.25	108.39	106.82
66	MM-4098	85.00	82.10	83.55	106.25	107.41	106.83
67	MM-4243	81.00	82.58	81.79	101.33	104.87	103.10
68	MM-4247	83.66	81.90	82.78	107.77	105.27	106.52
69	MM-4248	83.06	82.00	82.53	106.00	102.30	104.15
70	MM.4250	80.45	83.75	82.10	102.00	103.74	102.87
71	MM-4251	84.10	85.50	84.80	105.00	107.26	106.13
72	MM-4252	84.00	86.90	85.45	104.02	107.10	105.56
73	MM-4253	80.00	82.92	81.46	100.93	104.33	102.63
74	MM-4256	83.44	80.10	81.77	105.40	103.46	104.43
75	MM-4267	85.49	84.05	84.77	106.00	107.04	106.52
76	MM-4268	85.14	83.70	84.42	108.33	105.79	107.06
77	MM-4270	81.80	81.00	81.40	102.35	99.91	101.13
78	MM-4271	86.70	83.90	85.30	105.42	101.12	103.27
79	MM-4276	83.60	83.00	83.30	105.66	104.20	104.93
80	MM-4277	86.46	83.70	85.08	109.25	106.41	107.83
81	MM-4278	84.84	82.10	83.47	102.14	98.22	100.18

Table 4.3 Contd.....

Sr. No.	Accession No.	Days from sowing to marketable maturity			Days from sowing to last fruit harvest		
		2009	2010	Pooled mean	2009	2010	Pooled mean
82	MM-4279	84.70	83.70	84.20	107.95	105.51	106.73
83	MM-4282	82.42	79.10	80.76	100.30	98.90	99.60
84	MM-4283	80.29	79.05	79.67	107.06	103.74	105.40
85	MM-4305	86.20	84.00	85.10	112.60	109.10	110.85
86	MM-4342	80.70	81.70	81.20	103.00	103.86	103.43
87	MM-4409	83.96	79.10	81.53	105.90	101.50	103.70
88	MM-5736	84.13	82.07	83.10	104.65	103.11	103.88
89	AR Hale's	87.26	84.88	86.07	107.42	101.52	104.47
90	Dulce-B.B	83.00	84.54	83.77	104.60	101.74	103.17
91	Gulf Coast	85.80	84.00	84.90	108.30	104.90	106.60
92	Gulf Stream	86.46	83.10	84.78	110.05	104.15	107.10
93	Jucumba	84.94	82.80	83.87	106.55	104.05	105.30
94	Rocky Ford	85.65	83.22	84.43	106.81	103.85	105.33
95	Hannah's Choice	81.36	84.10	82.73	104.32	107.68	106.00
96	Chujuc	81.73	85.36	83.73	102.99	107.15	105.07
	CD (5%)	**3.36**	**3.25**	**3.21**	**4.80**	**4.96**	**4.68**
	CD (1%)	**4.42**	**4.27**	**4.22**	**6.31**	**6.52**	**6.15**

Table 4.3 Contd.....

Sr. No.	Accession No.	Number of fruits per vine			Fruit weight (g)		
		2009	2010	Pooled mean	2009	2010	Pooled mean
1	MM-3833	2.05	2.23	2.14	691.20	630.20	660.70
2	MM-3837	2.18	2.52	2.35	600.10	641.24	620.67
3	MM-3839	2.10	2.48	2.29	695.25	635.09	665.17
4	MM-3843	2.30	2.20	2.25	620.10	701.40	660.75
5	MM-3849	2.26	2.40	2.33	610.40	586.26	598.33
6	MM-3850	2.18	2.38	2.00	600.20	590.30	595.25
7	MM-3851	2.18	2.30	2.24	600.50	634.50	617.50
8	MM-3855	1.40	1.96	1.68	1280.25	1319.75	1300.00
9	MM-3856	2.22	2.62	2.42	600.10	650.36	625.23
10	MM-3857	2.50	2.20	2.35	626.30	683.96	655.13
11	MM-3858	2.30	2.66	2.48	605.25	625.75	615.50
12	MM-3859	2.15	2.35	2.25	624.20	712.46	668.33
13	MM-3860	2.22	2.40	2.31	925.65	875.95	900.80
14	MM-3864	2.30	2.00	2.15	638.90	682.62	660.76
15	MM-3866	1.60	1.94	1.57	1465.20	1544.80	1505.00
16	MM-3868	2.12	2.38	2.25	640.20	661.20	650.70
17	MM-3874	2.10	2.66	2.38	730.25	650.89	690.57
18	MM-3881	2.64	2.20	2.42	556.81	615.30	585.91
19	MM-3884	2.66	2.50	2.58	730.32	678.00	704.16
20	MM-3885	2.52	2.88	2.70	923.26	1038.70	980.98
21	MM-3887	2.05	2.55	2.30	880.50	825.90	853.20
22	MM-3889	1.67	2.09	1.88	1399.05	1290.95	1345.00
23	MM-3901	2.40	2.50	2.45	1015.25	948.49	981.87
24	MM-3903	1.52	1.74	1.63	1355.15	1464.85	1410.00
25	MM-3909	2.03	2.53	2.28	600.12	631.60	615.86
26	MM-3917	2.50	2.54	2.52	730.18	650.92	690.55
27	MM-3947	2.00	2.36	2.18	681.10	640.70	660.90

Table 4.3 Contd.....

Sr. No.	Accession No.	Number of fruits per vine			Fruit weight (g)		
		2009	2010	Pooled mean	2009	2010	Pooled mean
28	MM-3955	2.10	1.90	2.00	691.04	619.90	655.47
29	MM-3956	2.18	2.33	2.25	687.21	650.25	668.73
30	MM-3961	2.05	2.33	2.19	645.13	683.21	664.17
31	MM-3962	2.15	2.25	2.20	820.25	903.15	861.70
32	MM-3963	2.05	1.95	2.00	680.09	648.07	664.08
33	MM-3965	2.22	2.58	2.40	690.70	629.70	660.20
34	MM-3966	2.58	2.30	2.44	900.47	820.25	860.36
35	MM-3968	2.35	2.45	2.40	930.25	960.41	945.33
36	MM-3973	2.10	2.36	2.23	702.65	630.75	666.70
37	MM-3974	1.95	2.05	2.00	848.04	800.30	824.17
38	MM-3976	2.44	2.50	2.47	877.25	935.55	906.40
39	MM-3977	2.34	2.50	2.42	900.10	961.10	930.60
40	MM-3979	2.33	2.13	2.23	580.10	600.40	590.05
41	MM-3980	2.08	2.38	2.23	598.25	629.55	613.90
42	MM-3981	2.50	2.10	2.30	629.99	600.35	615.17
43	MM-3982	2.18	2.00	2.09	795.30	825.54	810.42
44	MM-3983	2.05	2.35	2.20	634.91	600.15	617.53
45	MM-3985	2.20	2.60	2.40	679.55	725.59	702.57
46	MM-3986	2.07	2.05	2.06	660.30	700.24	680.27
47	MM-3994	2.38	2.52	2.45	830.25	872.67	851.46
48	MM-3998	2.06	2.22	2.14	909.36	828.30	868.83
49	MM-4002	2.00	1.84	1.92	1405.25	1524.75	1465.00
50	MM-4003	2.32	2.48	2.40	720.70	680.30	700.50
51	MM-4004	2.40	2.53	2.46	838.65	905.35	872.00
52	MM-4005	2.52	2.38	2.45	904.70	820.30	862.50
53	MM-4013	2.05	2.27	2.16	554.17	610.83	582.50
54	MM-4018	2.10	2.40	2.25	699.68	637.70	668.69

Table 4.3 Contd.....

Sr. No.	Accession No.	Number of fruits per vine			Fruit weight (g)		
		2009	2010	Pooled mean	2009	2010	Pooled mean
55	MM-4021	2.10	2.50	2.30	689.85	630.15	660.00
56	MM-4026	2.18	2.66	2.42	720.30	661.40	690.85
57	MM-4030	1.80	1.76	1.78	1415.70	1344.30	1380.00
58	MM-4057	2.10	1.70	1.90	1315.25	1254.75	1285.00
59	MM-4059	2.34	2.50	2.25	891.10	912.30	901.70
60	MM-4063	2.25	2.55	2.40	605.25	645.25	625.25
61	MM-4065	2.10	1.90	2.00	980.70	1023.86	1002.28
62	MM-4066	2.38	2.42	2.40	880.25	920.15	900.20
63	MM-4067	2.15	2.59	2.37	640.70	679.70	660.20
64	MM-4068	2.06	2.58	2.32	600.25	627.09	613.67
65	MM-4091	2.12	2.52	2.32	889.84	840.90	865.37
66	MM-4098	3.05	2.90	2.97	484.00	430.00	457.00
67	MM-4243	2.10	2.48	2.29	705.33	665.01	685.17
68	MM-4247	2.40	2.12	2.26	900.30	840.30	870.30
69	MM-4248	2.20	2.00	2.10	630.25	680.35	655.30
70	MM.4250	2.05	2.15	2.10	678.71	640.15	659.43
71	MM-4251	2.33	2.07	2.20	620.78	700.72	660.75
72	MM-4252	2.56	2.31	2.43	870.90	929.70	900.30
73	MM-4253	2.20	2.60	2.40	720.15	661.83	690.99
74	MM-4256	2.05	2.29	2.17	705.33	684.95	695.14
75	MM-4267	2.43	2.17	2.30	900.88	840.78	870.83
76	MM-4268	2.20	2.14	2.17	890.30	930.10	910.20
77	MM-4270	2.10	2.03	2.06	712.70	684.24	698.47
78	MM-4271	2.50	2.34	2.42	1020.15	1093.31	1056.73
79	MM-4276	2.15	2.61	2.38	640.15	700.65	670.40
80	MM-4277	2.49	2.81	2.65	900.15	931.55	915.85
81	MM-4278	2.12	2.28	2.20	705.95	661.51	683.73

Table 4.3 Contd.....

Sr. No.	Accession No.	Number of fruits per vine			Fruit weight (g)		
		2009	2010	Pooled mean	2009	2010	Pooled mean
82	MM-4279	2.32	2.62	2.47	971.75	905.25	938.50
83	MM-4282	2.13	2.33	2.23	600.15	625.13	612.64
84	MM-4283	2.08	2.52	2.30	659.27	721.33	690.30
85	MM-4305	2.58	2.22	2.40	679.15	703.25	691.20
86	MM-4342	2.50	2.12	2.31	740.88	670.12	705.50
87	MM-4409	2.33	2.57	2.45	700.25	666.57	683.41
88	MM-5736	2.33	2.14	2.13	910.89	820.77	865.83
89	AR Hale's	1.52	1.50	1.51	1082.59	1030.25	1056.42
90	Dulce-B.B	1.64	1.42	1.53	1025.20	946.04	985.62
91	Gulf Coast	1.89	1.67	1.78	1070.23	1129.77	1100.58
92	Gulf Stream	1.60	2.02	1.81	1110.24	1070.26	1090.25
93	Jucumba	2.00	1.72	1.86	920.15	980.87	950.51
94	Rocky Ford	1.96	1.50	1.73	1115.20	1025.80	1070.50
95	Hannah's Choice	2.00	2.00	2.00	1109.86	1057.14	1083.50
96	Chujuc	1.49	1.61	1.55	905.35	974.99	940.17
	CD (5%)	**0.29**	**0.32**	**0.26**	**64.24**	**65.73**	**58.68**
	CD (1%)	**0.38**	**0.42**	**0.34**	**84.53**	**86.50**	**77.22**

Table 4.3 Contd.....

Sr. No.	Accession No.	Fruit length (cm)			Fruit breadth (cm)		
		2009	2010	Pooled mean	2009	2010	Pooled mean
1	MM-3833	10.05	9.55	9.80	10.30	9.90	10.10
2	MM-3837	10.18	10.42	10.30	9.57	9.81	9.69
3	MM-3839	10.30	9.90	10.10	11.43	11.03	11.23
4	MM-3843	9.50	10.00	9.75	9.72	10.22	9.97
5	MM-3849	9.68	9.46	9.57	10.16	9.96	10.06
6	MM-3850	10.20	10.00	10.10	10.44	10.23	10.34
7	MM-3851	10.45	10.66	10.54	11.18	11.39	11.28
8	MM-3855	18.82	19.22	19.02	11.50	11.80	11.65
9	MM-3856	10.70	10.90	10.80	10.24	10.46	10.35
10	MM-3857	10.57	10.77	10.67	9.96	10.16	10.06
11	MM-3858	9.02	9.22	9.12	9.90	10.11	10.01
12	MM-3859	9.00	9.50	9.25	9.70	10.10	9.90
13	MM-3860	10.68	10.38	10.53	11.45	11.15	11.30
14	MM-3864	10.26	10.50	10.38	10.73	10.97	10.85
15	MM-3866	20.15	22.49	21.32	11.58	13.92	12.75
16	MM-3868	9.70	9.90	9.80	10.53	10.77	10.65
17	MM-3874	9.87	9.63	9.75	11.19	10.95	11.07
18	MM-3881	9.55	9.76	9.67	9.70	9.94	9.82
19	MM-3884	10.15	9.95	10.05	11.69	11.51	11.60
20	MM-3885	9.87	10.27	10.07	11.55	11.95	11.75
21	MM-3887	11.31	11.05	11.18	10.98	10.72	10.85
22	MM-3889	19.48	19.08	19.28	11.82	11.42	11.62
23	MM-3901	10.28	9.96	10.12	11.36	11.04	11.20
24	MM-3903	19.40	21.50	20.45	11.76	13.72	12.74
25	MM-3909	10.60	10.74	10.67	11.29	11.45	11.37
26	MM-3917	9.95	9.55	9.75	10.30	10.70	10.50
27	MM-3947	10.00	9.60	9.80	11.00	10.60	10.80

Table 4.3 Contd.....

Sr. No.	Accession No.	Fruit length (cm)			Fruit breadth (cm)		
		2009	2010	Pooled mean	2009	2010	Pooled mean
28	MM-3955	10.45	10.15	10.30	10.26	9.86	10.06
29	MM-3956	9.80	9.60	9.70	11.05	10.65	10.85
30	MM-3961	9.97	10.17	10.07	11.08	11.38	11.23
31	MM-3962	10.33	10.69	10.51	11.08	11.28	11.18
32	MM-3963	9.82	9.58	9.70	11.02	9.72	9.87
33	MM-3965	9.81	9.21	9.51	10.80	10.40	10.60
34	MM-3966	10.35	9.85	10.10	11.95	11.55	11.75
35	MM-3968	10.15	10.31	10.23	11.13	11.33	11.23
36	MM-3973	10.10	9.50	9.80	10.95	10.40	10.65
37	MM-3974	10.42	10.18	10.30	11.12	10.92	11.02
38	MM-3976	10.00	10.20	10.10	11.25	11.55	11.40
39	MM-3977	10.41	10.65	10.53	10.85	11.15	11.00
40	MM-3979	9.44	10.04	9.74	9.50	10.00	9.75
41	MM-3980	9.65	9.85	9.75	10.07	10.19	10.13
42	MM-3981	12.27	12.13	12.20	12.58	12.48	12.53
43	MM-3982	11.44	11.60	11.52	12.20	12.40	12.30
44	MM-3983	10.70	10.50	10.60	11.46	11.30	11.38
45	MM-3985	9.80	10.10	9.95	10.80	11.00	10.90
46	MM-3986	9.43	10.03	9.73	10.25	10.75	10.50
47	MM-3994	11.32	11.72	11.52	12.45	12.75	12.60
48	MM-3998	11.57	10.97	11.27	11.08	10.58	10.83
49	MM-4002	20.40	21.60	21.00	12.00	12.50	12.25
50	MM-4003	10.28	10.12	10.20	11.70	11.50	11.60
51	MM-4004	10.30	10.90	10.60	10.85	11.35	11.10
52	MM-4005	13.00	12.60	12.80	11.00	10.70	10.85
53	MM-4013	9.50	9.64	9.57	9.60	9.70	9.65
54	MM-4018	10.40	10.10	10.25	9.97	9.77	9.87

Table 4.3 Contd.....

Sr. No.	Accession No.	Fruit length (cm)			Fruit breadth (cm)		
		2009	2010	Pooled mean	2009	2010	Pooled mean
55	MM-4021	9.32	8.98	9.15	10.80	10.50	10.65
56	MM-4026	10.00	9.50	9.75	10.59	10.19	10.39
57	MM-4030	19.77	18.97	19.37	11.96	11.26	11.61
58	MM-4057	20.00	19.40	19.70	11.38	10.82	11.10
59	MM-4059	12.20	12.32	12.26	12.02	12.12	12.07
60	MM-4063	9.68	9.46	9.57	9.84	9.66	9.75
61	MM-4065	9.50	9.70	9.60	10.18	10.36	10.27
62	MM-4066	10.24	10.82	10.53	10.97	11.47	11.22
63	MM-4067	9.00	9.14	9.07	9.95	10.05	10.00
64	MM-4068	10.60	10.70	10.65	10.64	10.76	10.70
65	MM-4091	10.39	9.99	10.19	11.16	10.84	11.01
66	MM-4098	7.67	7.49	7.58	7.20	7.04	7.12
67	MM-4243	10.78	10.48	10.63	10.85	10.61	10.73
68	MM-4247	10.00	9.50	9.75	10.55	10.15	10.35
69	MM-4248	9.73	10.03	9.88	10.42	10.64	10.53
70	MM.4250	9.83	9.57	9.70	10.99	10.75	10.87
71	MM-4251	10.45	10.85	10.65	11.68	11.32	11.50
72	MM-4252	12.00	12.34	12.17	12.04	12.36	12.20
73	MM-4253	10.70	10.08	10.39	11.13	10.57	10.85
74	MM-4256	10.71	10.49	10.60	10.38	10.22	11.30
75	MM-4267	10.05	9.49	9.77	10.60	10.10	10.35
76	MM-4268	10.62	11.12	10.87	11.02	11.42	11.22
77	MM-4270	10.00	9.10	9.55	10.05	9.25	9.65
78	MM-4271	8.63	9.43	9.03	9.30	10.00	9.65
79	MM-4276	9.06	10.06	9.56	9.55	10.45	10.00
80	MM-4277	10.24	10.84	10.53	11.07	11.57	11.32
81	MM-4278	9.60	9.00	9.30	11.01	10.39	10.70

Table 4.3 Contd.....

Sr. No.	Accession No.	Fruit length (cm)			Fruit breadth (cm)		
		2009	2010	Pooled mean	2009	2010	Pooled mean
82	MM-4279	12.60	11.60	12.10	12.58	11.82	12.20
83	MM-4282	11.00	11.24	11.12	12.04	12.24	12.14
84	MM-4283	10.00	10.80	10.40	10.75	11.45	11.10
85	MM-4305	10.30	10.90	10.60	10.83	11.37	11.10
86	MM-4342	10.52	9.62	10.07	11.00	10.20	10.60
87	MM-4409	10.06	9.10	9.58	10.65	9.75	10.20
88	MM-5736	10.22	9.42	9.82	10.71	10.01	10.36
89	AR Hale's	10.00	10.50	10.25	10.38	10.68	10.60
90	Dulce-B.B	9.57	9.33	9.45	9.65	9.40	9.52
91	Gulf Coast	10.05	9.35	9.70	10.38	9.50	10.35
92	Gulf Stream	10.37	9.87	10.17	9.98	9.42	9.70
93	Jucumba	10.15	10.27	10.21	10.35	10.40	10.37
94	Rocky Ford	9.32	8.84	9.08	9.87	9.43	9.65
95	Hannah's Choice	9.40	8.90	9.15	9.95	9.49	9.72
96	Chujuc	9.42	8.82	9.12	9.48	8.92	9.20
	CD (5%)	**0.79**	**0.83**	**0.75**	**0.66**	**0.68**	**0.60**
	CD (1%)	**10.3**	**1.09**	**0.98**	**0.86**	**0.89**	**0.78**

Table 4.3 Contd.....

Sr. No.	Accession No.	Seed cavity length (cm)			Seed cavity breadth (cm)		
		2009	2010	Pooled mean	2009	2010	Pooled mean
1	MM-3833	7.20	7.00	7.10	7.25	7.05	7.15
2	MM-3837	7.58	7.82	7.70	6.78	7.02	6.90
3	MM-3839	7.00	6.60	6.80	8.10	7.70	7.90
4	MM-3843	6.25	6.75	6.50	6.15	6.65	6.40
5	MM-3849	6.77	6.58	6.67	7.15	6.94	7.05
6	MM-3850	7.56	7.35	7.46	7.60	7.39	7.50
7	MM-3851	7.39	7.60	7.50	7.85	8.05	7.95
8	MM-3855	15.52	15.82	15.67	7.70	8.10	7.90
9	MM-3856	7.42	7.58	7.50	7.51	7.69	7.60
10	MM-3857	7.92	8.08	8.00	7.34	7.50	7.42
11	MM-3858	6.38	6.56	6.47	6.93	7.13	7.03
12	MM-3859	6.02	6.40	6.22	6.41	6.59	6.50
13	MM-3860	7.42	7.18	7.30	8.07	7.67	7.87
14	MM-3864	7.32	7.52	7.42	7.54	7.78	7.66
15	MM-3866	16.25	18.59	17.42	7.63	9.97	8.80
16	MM-3868	6.68	6.92	6.80	7.08	7.32	7.20
17	MM-3874	6.49	6.25	6.37	7.92	7.68	7.80
18	MM-3881	6.68	6.92	6.80	6.71	6.95	6.83
19	MM-3884	7.73	7.51	7.62	8.61	8.39	8.50
20	MM-3885	7.04	7.44	7.24	8.35	8.75	8.55
21	MM-3887	8.60	8.34	8.47	7.66	7.40	7.53
22	MM-3889	16.07	15.67	15.87	7.90	7.50	7.70
23	MM-3901	7.75	7.45	7.60	8.34	8.06	8.20
24	MM-3903	15.25	17.21	16.23	7.53	9.53	8.53
25	MM-3909	7.29	7.43	7.36	7.85	7.99	7.92
26	MM-3917	7.57	7.17	7.37	7.80	7.40	7.60
27	MM-3947	6.96	6.55	6.75	7.55	7.15	7.35

Table 4.3 Contd.....

Sr. No.	Accession No.	Seed cavity length (cm)			Seed cavity breadth (cm)		
		2009	2010	Pooled mean	2009	2010	Pooled mean
28	MM-3955	7.35	6.95	7.15	7.27	6.97	7.12
29	MM-3956	6.80	6.40	6.60	7.60	7.40	7.50
30	MM-3961	7.45	7.15	7.30	8.30	8.10	8.20
31	MM-3962	7.60	7.40	7.50	7.69	8.05	7.87
32	MM-3963	6.65	6.35	6.50	7.40	7.20	7.30
33	MM-3965	6.72	6.32	6.52	7.61	6.99	7.30
34	MM-3966	7.45	7.05	7.25	8.55	8.05	8.30
35	MM-3968	7.00	6.80	6.90	7.89	8.05	7.97
36	MM-3973	7.35	6.85	7.10	7.60	7.00	7.30
37	MM-3974	7.50	7.30	7.40	8.52	8.28	8.40
38	MM-3976	7.25	7.55	7.40	8.31	8.11	8.21
39	MM-3977	7.28	7.58	7.43	7.69	7.93	7.81
40	MM-3979	6.31	6.81	6.56	6.40	7.00	6.70
41	MM-3980	6.54	6.66	6.60	6.64	6.84	6.74
42	MM-3981	9.20	9.10	9.15	9.49	9.45	9.42
43	MM-3982	8.31	8.49	8.40	8.62	8.78	8.70
44	MM-3983	7.56	7.40	7.48	8.01	7.81	7.91
45	MM-3985	6.91	7.11	7.01	7.68	7.98	7.83
46	MM-3986	6.87	7.37	7.12	7.30	7.90	7.60
47	MM-3994	8.27	8.57	8.42	9.11	9.51	9.31
48	MM-3998	8.81	8.31	8.56	7.88	7.28	7.58
49	MM-4002	17.40	18.04	17.72	8.03	8.63	8.33
50	MM-4003	7.75	7.55	7.65	8.31	8.15	8.23
51	MM-4004	7.38	7.88	7.63	8.20	8.80	8.50
52	MM-4005	9.62	9.32	9.47	7.73	7.33	7.53
53	MM-4013	6.55	6.65	6.60	6.60	6.76	6.68
54	MM-4018	7.34	7.10	7.22	6.65	6.35	6.50

Table 4.3 Contd.....

Sr. No.	Accession No.	Seed cavity length (cm)			Seed cavity breadth (cm)		
		2009	2010	Pooled mean	2009	2010	Pooled mean
55	MM-4021	6.75	6.45	6.60	8.29	7.95	8.12
56	MM-4026	7.27	6.87	7.07	7.85	7.35	7.60
57	MM-4030	16.00	15.30	15.65	8.28	7.48	7.88
58	MM-4057	16.85	16.29	16.57	7.84	7.24	7.54
59	MM-4059	9.20	9.30	9.25	8.93	9.08	9.01
60	MM-4063	6.49	9.31	6.40	6.81	6.59	6.70
61	MM-4065	6.77	6.95	6.86	6.93	7.13	7.03
62	MM-4066	7.65	8.15	7.90	7.70	8.32	8.01
63	MM-4067	6.57	6.67	6.62	5.95	6.10	6.03
64	MM-4068	7.62	7.78	7.70	7.30	7.40	7.35
65	MM-4091	7.92	7.62	7.77	8.24	7.82	8.03
66	MM-4098	5.90	5.74	5.82	5.45	5.30	5.37
67	MM-4243	7.82	7.58	7.70	7.92	7.62	7.77
68	MM-4247	7.21	6.81	7.01	7.65	7.15	7.40
69	MM-4248	6.81	7.01	6.91	7.25	7.55	7.40
70	MM.4250	6.77	6.53	6.65	7.55	7.29	7.42
71	MM-4251	7.66	7.34	7.50	8.50	8.10	8.30
72	MM-4252	9.14	9.46	9.30	9.78	9.12	8.95
73	MM-4253	7.70	7.14	7.42	7.76	7.16	7.46
74	MM-4256	7.74	7.58	7.66	8.02	7.82	7.92
75	MM-4267	6.74	6.24	6.49	7.29	6.73	7.01
76	MM-4268	8.00	7.62	7.81	8.19	7.69	7.94
77	MM-4270	6.75	5.95	6.35	7.13	6.23	6.68
78	MM-4271	6.29	6.99	6.64	6.20	7.00	6.60
79	MM-4276	6.05	6.95	6.50	6.52	7.00	7.03
80	MM-4277	6.97	7.47	7.22	7.70	8.30	8.00
81	MM-4278	7.59	6.99	7.30	7.71	7.11	7.41

Table 4.3 Contd.....

Sr. No.	Accession No.	Seed cavity length (cm)			Seed cavity breadth (cm)		
		2009	2010	Pooled mean	2009	2010	Pooled mean
82	MM-4279	9.35	8.57	8.96	9.48	8.32	8.90
83	MM-4282	8.40	8.60	8.50	8.68	8.92	8.80
84	MM-4283	6.97	7.67	7.32	8.37	8.17	7.77
85	MM-4305	7.03	7.57	7.30	7.50	8.10	7.80
86	MM-4342	7.90	7.10	7.50	7.75	6.85	7.30
87	MM-4409	7.59	6.65	7.12	7.68	6.68	7.18
88	MM-5736	7.25	6.55	6.90	7.60	6.80	7.20
89	AR Hale's	6.55	6.85	6.70	6.88	7.18	7.03
90	Dulce-B.B	5.82	5.73	5.77	5.98	5.79	5.88
91	Gulf Coast	6.60	6.00	6.30	6.93	6.10	6.51
92	Gulf Stream	6.97	6.48	6.72	6.58	6.52	6.55
93	Jucumba	6.85	7.07	6.96	6.95	7.10	7.02
94	Rocky Ford	6.87	6.43	6.65	6.88	6.40	6.64
95	Hannah's Choice	7.01	6.55	6.78	6.95	6.45	6.70
96	Chujuc	5.75	5.40	5.57	5.80	5.50	5.65
	CD (5%)	**0.59**	**0.56**	**0.51**	**0.29**	**0.37**	**0.33**
	CD (1%)	**0.77**	**0.73**	**0.67**	**0.38**	**0.48**	**0.43**

Table 4.3 Contd.....

Sr. No.	Accession No.	Rind thickness (mm)			Shelf life (days)		
		2009	2010	Pooled mean	2009	2010	Pooled mean
1	MM-3833	2.00	2.20	2.10	2.00	2.50	2.25
2	MM-3837	2.25	2.55	2.40	2.00	1.90	1.95
3	MM-3839	2.00	2.40	2.20	3.00	2.00	2.50
4	MM-3843	1.98	2.13	2.05	1.50	2.00	1.75
5	MM-3849	2.30	2.46	2.38	1.75	2.35	2.05
6	MM-3850	2.40	2.56	2.48	2.05	2.55	2.30
7	MM-3851	2.26	2.10	2.18	2.00	2.30	2.15
8	MM-3855	1.70	1.80	1.75	2.00	2.00	2.00
9	MM-3856	2.15	2.55	2.35	2.31	1.95	2.13
10	MM-3857	2.20	2.00	2.10	2.00	2.50	2.25
11	MM-3858	2.30	2.64	2.47	2.00	2.00	2.00
12	MM-3859	2.54	2.42	2.48	1.80	2.26	2.03
13	MM-3860	2.60	2.84	2.72	2.15	2.35	2.25
14	MM-3864	2.49	2.75	2.62	2.00	2.06	2.03
15	MM-3866	2.05	2.15	2.10	1.76	2.00	1.88
16	MM-3868	2.00	2.00	2.00	1.50	2.50	2.00
17	MM-3874	2.32	2.58	2.45	2.00	1.60	1.80
18	MM-3881	2.35	2.47	2.41	1.95	2.20	2.07
19	MM-3884	2.55	2.69	2.62	2.00	2.00	2.00
20	MM-3885	3.05	2.91	2.98	2.90	3.30	3.10
21	MM-3887	1.60	1.70	1.65	2.00	1.70	1.85
22	MM-3889	2.05	1.95	2.00	1.85	2.15	2.00
23	MM-3901	2.09	1.97	2.03	2.87	3.13	3.00
24	MM-3903	2.10	1.70	1.90	1.90	2.18	2.04
25	MM-3909	2.17	2.43	2.30	1.55	1.97	1.76
26	MM-3917	2.30	2.60	2.45	1.50	1.90	1.70
27	MM-3947	2.20	2.40	2.30	2.05	2.65	2.35

Table 4.3 Contd.... .....

Sr. No.	Accession No.	Rind thickness (mm)			Shelf life (days)		
		2009	2010	Pooled mean	2009	2010	Pooled mean
28	MM-3955	2.32	2.48	2.40	2.50	2.00	2.25
29	MM-3956	2.56	2.60	2.58	2.10	2.40	2.25
30	MM-3961	2.50	2.70	2.60	2.00	1.60	1.80
31	MM-3962	2.15	2.35	2.25	2.10	2.30	2.20
32	MM-3963	1.90	2.14	2.02	2.00	1.50	1.75
33	MM-3965	2.33	2.47	2.40	2.00	2.00	2.00
34	MM-3966	3.06	2.90	2.98	2.80	3.40	3.10
35	MM-3968	2.10	2.32	2.21	3.00	3.50	3.25
36	MM-3973	2.20	2.26	2.23	2.15	2.49	2.32
37	MM-3974	1.90	1.70	1.80	2.00	1.76	1.88
38	MM-3976	2.45	2.75	2.60	2.85	3.15	3.00
39	MM-3977	2.33	2.51	2.42	2.20	3.00	2.60
40	MM-3979	2.30	2.48	2.39	2.00	2.54	2.27
41	MM-3980	2.30	2.34	2.32	1.90	2.10	2.00
42	MM-3981	2.37	2.63	2.50	2.00	2.00	2.00
43	MM-3982	2.00	1.80	1.90	2.00	2.48	2.24
44	MM-3983	2.15	2.45	2.30	1.50	2.00	1.75
45	MM-3985	1.95	2.05	2.00	2.50	2.64	2.57
46	MM-3986	1.87	2.13	2.00	2.00	1.80	1.90
47	MM-3994	2.00	1.70	1.85	2.15	1.75	1.95
48	MM-3998	1.68	1.62	1.65	2.00	1.84	1.92
49	MM-4002	1.98	2.22	2.10	2.00	2.00	2.00
50	MM-4003	2.58	2.82	2.70	1.75	2.25	2.00
51	MM-4004	1.45	1.50	1.47	2.00	1.70	1.85
52	MM-4005	1.52	1.58	1.55	1.60	2.10	1.85
53	MM-4013	2.40	2.46	2.43	2.15	2.45	2.30
54	MM-4018	2.12	2.24	2.18	1.75	2.35	2.05

Table 4.3 Contd....

Sr. No.	Accession No.	Rind thickness (mm)			Shelf life (days)		
		2009	2010	Pooled mean	2009	2010	Pooled mean
55	MM-4021	2.38	2.22	2.30	3.00	2.30	2.65
56	MM-4026	2.40	2.50	2.45	1.72	1.48	1.60
57	MM-4030	2.10	1.80	1.95	2.00	1.84	1.92
58	MM-4057	2.00	2.20	2.10	2.06	2.00	2.03
59	MM-4059	2.38	2.62	2.50	3.11	2.85	2.98
60	MM-4063	2.40	2.36	2.38	2.00	2.40	2.20
61	MM-4065	2.97	3.17	3.07	2.90	3.16	3.03
62	MM-4066	2.49	2.75	2.62	2.00	2.50	2.25
63	MM-4067	2.4	2.58	2.50	3.00	2.50	2.75
64	MM-4068	2.33	2.47	2.40	1.75	2.15	1.95
65	MM-4091	2.00	2.30	2.15	2.00	2.20	2.10
66	MM-4098	2.05	2.15	2.10	2.10	2.60	2.35
67	MM-4243	2.30	2.44	2.37	1.66	1.74	1.70
68	MM-4247	1.98	1.66	1.82	2.30	2.00	2.15
69	MM-4248	2.00	2.12	2.06	2.00	1.60	1.80
70	MM.4250	2.05	1.85	1.95	1.40	1.70	1.55
71	MM-4251	1.70	1.90	1.80	1.50	2.00	1.75
72	MM-4252	2.30	2.40	2.35	3.10	2.86	2.98
73	MM-4253	2.38	2.46	2.42	2.00	1.70	1.85
74	MM-4256	2.25	2.49	2.37	2.30	1.80	2.05
75	MM-4267	1.75	1.85	1.80	2.30	2.00	2.15
76	MM-4268	2.40	2.90	2.65	2.15	2.35	2.25
77	MM-4270	2.33	2.47	2.40	2.10	2.50	2.30
78	MM-4271	2.70	2.80	2.75	2.80	2.90	2.85
79	MM-4276	2.18	2.38	2.28	1.85	2.21	2.03
80	MM-4277	2.58	2.72	2.65	3.00	2.90	2.95
81	MM-4278	2.00	2.24	2.12	1.75	2.25	2.00

Table 4.3 Contd.... ...

Sr. No.	Accession No.	Rind thickness (mm)			Shelf life (days)		
		2009	2010	Pooled mean	2009	2010	Pooled mean
82	MM-4279	2.46	2.30	2.38	2.50	3.10	2.80
83	MM-4282	2.41	2.25	2.33	1.50	2.00	1.75
84	MM-4283	2.45	2.75	2.60	2.20	2.86	2.53
85	MM-4305	2.32	2.42	2.37	2.40	1.80	2.10
86	MM-4342	2.25	2.35	2.30	1.85	2.15	2.00
87	MM-4409	2.10	2.30	2.20	2.10	2.70	2.40
88	MM-5736	1.76	1.60	1.68	2.00	2.20	2.10
89	AR Hale's	3.29	3.15	3.22	3.45	3.53	3.49
90	Dulce-B.B	3.39	3.51	3.45	2.90	3.40	3.15
91	Gulf Coast	3.26	3.42	3.34	3.00	3.34	3.17
92	Gulf Stream	3.46	3.10	3.28	3.19	3.50	3.34
93	Jucumba	3.30	3.40	3.35	3.00	3.20	3.10
94	Rocky Ford	3.60	3.40	3.50	3.00	3.20	3.10
95	Hannah's Choice	3.30	3.44	3.37	2.97	3.17	3.07
96	Chujuc	3.68	3.60	3.64	3.21	3.69	3.45
	CD (5%)	**0.30**	**0.22**	**0.26**	**0.32**	**0.27**	**0.25**
	CD (1%)	**0.39**	**0.28**	**0.34**	**0.42**	**0.35**	**0.32**

node (2.00) to bear the first hermaphrodite flower and was significantly at par with MM-3833 (2.10), MM-3849 (2.10) and MM-3956 (2.10). However, maximum number of node at which first hermaphrodite flower were found in MM-4091 (5.15) and MM-4004 (5.15) and was significantly at par with MM-4247 (5.10), MM-4267 (5.10), MM-3982 (5.00) and MM-3998 (5.00).

4.1.2 Number of primary branches per vine

Number of primary branches per vine is an important character, which indicates the ideotype of plant. The results showed that sufficient variation existed for this character. During the year 2009, it varied from 2.30 to 6.96 with the overall mean of 4.18. The lowest number of branches per vine was observed in Gulf Coast (2.30) which was statistically at par with Rocky Ford (2.50), Dulce-B.B (2.50), Chujuc (2.32), AR Hale's (2.32) Hannah's Choice (2.40) and Jucumba (2.45) whereas, the highest number of primary branches per vine were found in MM-3998 (6.96) and was statistically at par with MM-3887 (6.81) and MM-3903 (6.60). However, in 2010 number of primary branches per vine ranged from 2.10 to 7.00 with the overall mean of 4.31. The lowest number of branches per vine was recorded in Gulf Coast (2.10) and was statistically at par with Chujuc (2.35), Rocky Ford (2.38), Dulce-B.B (2.38), Jacumba (2.40) and Hannah's Choice (2.41). However, the highest number of primary branches per vine was shown by MM-3903 (7.00) and was statistically at par with MM-3866 (6.86) 3889 (6.85), MM-4005 (6.83), and MM-4030 (6.79). Pooled mean revealed significant difference among genotypes with average value ranging from 2.20 to 6.83 with over all mean of 4.24.The lowest number of branches per vine was shown by in Gulf Coast (2.20) and was statistically at par with Chujuc (2.35), Rocky Ford (2.36), AR Hale's (2.40), Hannah's Choice (2.40) and Jucumba (2.42) while, the highest number of primary branches per vine were found in MM-3998 (6.83) which was statistically at par with MM-3903 (6.80) and MM-4005 (6.66). The variability in number of branches per vine was also reported by Prasad *et al* (2004), Dhillon *et al* (2007), Dhillon *et al* (2009), Fergany *et al* (2011) and Roy *et al* (2011).

4.1.3 Days from sowing to marketable maturity.

Early maturity is desirable in muskmelon to earn more profit. During 2009 it varied from 77.85 to 89.75 with the overall mean of 84.07. Lesser number of days from sowing to marketable maturity was observed in MM-3947 (77.85) and was statistically at par with MM-3956 (78.25), MM-3961 (78.40). MM-3833 (78.60), MM-3973 (79.30) and MM- 3874 (79.54), while more number of days from sowing to marketable maturity was found in MM-3994 (89.75) which was statistically at par with MM-4030 (88.98), MM-3974 (88.14), MM-4057 (87.96) and MM-3889 (87.79). In the year 2010, days from sowing to marketable maturity varied from 79.05 to 90.72 with the overall mean of 83.71. Lesser number of days from sowing to marketable maturity was recorded in MM-4283 (79.05) and was statistically at par with MM-4404 (79.10), MM-4282 (79.10), MM-3981 (79.10), MM-3947 (79.11), MM-

3868 (79.33) and MM-3843 (79.50). Pooled mean revealed that genotypes differ significantly from each other. The average ranged from 78.48 to 89.43 with the overall mean 83.89. Lesser number of days from sowing to marketable maturity was shown by MM-3947 (78.48) and was statistically at par with MM-3956 (79.12) and MM-4283 (79.67). However, more number of days from sowing to marketable maturity was found in MM-3974 (89.43) and was statistically at par with MM-3994 (88.53) and MM-4030 (87.35). The results are in consonance with those of Rakhi and Rajamony (2005), Lotti *et al* (2008) and Fergany *et al* (2011)

4.1.4 Days from sowing to last fruit harvest

There were significant differences among genotypes for days from sowing to last fruit harvest. During 2009, it varied from 97.25 to 112.60 with the overall mean of 105.29. Maximum number of days from sowing to last fruit harvest was observed in MM-4305 (112.60) which was statistically at par with MM-3974 (111.56), MM-4059 (110.75), MM-Gulf Stream (110.05), MM-4066 (109.35) and MM-3901 (109.25) while minimum days from sowing to last fruit harvest were found in MM-3837 (97.25) and was statistically at par with MM-3909 (98.07), MM-3961 (98.85), MM-3955 (99.10) and MM-3856 (99.40). For the year 2010, it ranged from 97.89 to 109.95 with the overall mean of 105.03. Maximum number of days from sowing to last fruit harvest was recorded in MM-4063 (109.95) which was statistically at par with MM-3966 (109.54), MM-3998 (109.26), MM-4305 (109.10), MM-(108.39) and MM-3866 (108.34), However, minimum days from sowing to last fruit harvest were observed in MM-3858 (97.89) and was statistically at par with MM-4278 (98.22), MM-3981 (98.57), MM-4282 (98.90) and MM-4270 (99.91).The pooled mean for days from sowing to last fruit harvest it ranged from 98.83 to 110.85 with the overall mean 105.16. Maximum number of days from sowing to last fruit harvest was shown by MM-4305 (110.85) which was statistically at par with MM-3974 (109.80), MM-3966 (108.97), MM-4063 (108.73) and MM-3901 (108.58). However, minimum days from sowing to last fruit harvest was found in MM-3837 (98.83) which was statistically at par with MM-3858 (99.42), MM-3909 (99.51) and MM-4282 (99.60).

4.1.5 Number of fruits per vine

It is an important yield contributing character. Number of fruits per vine in the year 2009 ranged from 1.40 to 3.05 with the overall mean of 2.25. The maximum number of fruits per vine were observed in MM-4098 (3.05) followed by MM-3884 (2.66) and MM-3881 (2.64), whereas minimum number of fruits per vine were recorded in MM-3855 (1.40) which was statistically at par with Chujuc (1.49), AR Hale's (1.52), MM-3903 (1.52) and Gulf Stream (1.60). While in the year 2010, number of fruits per vine varied from 1.42 to 2.90 with the overall mean of 2.37. The maximum number of fruits per vine was found in MM-4098 (2.90) which was statistically at par with MM-4277 (2.81), MM-3858 (2.66) and MM-3874

(2.66) However, minimum number of fruits per vine was recorded in Dulce-B.B (1.42) which was statistically at par with AR Hale's (1.50), Rocky Ford (1.50), Chujuc (1.61), and Gulf Coast (1.67). Pooled mean ranged from 1.51 to 2.97 with the overall mean of 2.37. The maximum number of fruits per vine was shown by MM-4098 (2.98) which was statistically at par with MM-3885 (2.70) and MM-4277 (2.65), whereas minimum number of fruits per vine was observed in AR Hale's (1.51) which was statistically at par with Dulce-B.B (1.53), Chujuc (1.55), MM-3866 (1.57), MM-3903 (1.63) and MM-3855 (1.68). The results are in conformity with those of Prasad *et al* (2004), Dhillon *et al* (2007), Dhillon *et al* (2009) and Fergany *et al* (2011).

4.1.6 Fruit weight (g)

In the present investigation fruit weight showed the considerable variation during both the years. For year 2009, it ranged from 484.00 to 1465.20 g with the overall mean of 807.25 g. The maximum fruit weight was observed in MM-3866 (1465.20g) and was statistically at par with MM-4030 (1415.70 g), MM-4002 (1405.25 g) and MM-3889 (1399.05 g). However, minimum fruit weight was recorded in MM- 4098 (484.00g) and was followed by MM-4013 (554.17 g) and MM-3881 (556.81 g). In the year 2010 fruit weight ranged from 430.00 to 1544.80 g with the overall mean of 804.78 g. The maximum fruit weight was found in MM-3866 (1544.80 g) and was statistically at par with MM-4002 (11524.75 g) whereas, minimum fruit weight was shown by MM- 4098 (430.00 g) and was followed by MM-3849 (586.26 g) and MM-3850 (590.30 g). The pooled mean showed significant variation (457.00 -1505.00 g) with overall mean of 806.07g. The maximum fruit weight was observed in MM-3866 (1505.00g) and was statistically at par with MM-4002 (1465.00 g) while minimum fruit weight was found in MM-4098 (457.00 g). Similar results were also reported by Dhillon *et al* (2007), Lotti *et al* (2008), Dhillon *et al* (2009), Dwivedi *et al* (2010) and Fergany *et al* (2011).

4.1.7 Fruit length (cm)

The genotypes under study possessed a large amount of variability for this character. In the year 2009, it varied from 7.67 to 20.40 cm with the overall mean of 10.78. Maximum fruit length was observed in MM-4002 (20.40 cm), which was statistically at par with MM-3866 (20.15cm), MM-4057 (20.00 cm), MM-3889 (19.48 cm) and MM-3903 (19.40cm). Genotype MM-4098 (7.67cm) had minimum fruit length followed by MM-4271 (8.63 cm). During the year 2010, fruit length varied from 7.49 to 22.49 cm with the overall mean of 10.86 cm. Largest fruit length was found in MM-3866 (21.32cm), which was statistically at par with MM-4002 (21.60 cm) and MM-3903 (21.50 cm). The lowest fruit length was recorded in MM-4098 (7.49cm) followed by Chujuc (8.82 cm) and Rocky Ford (8.84 cm). However, the pooled mean showed significant variation (7.58-21.32 cm) with overall mean of 10.82. Maximum fruit length was shown by MM-3866 (21.32 cm) which was statistically at

par with MM-4002 (21.00cm) and MM-3903 (20.45cm). Genotype MM-4098 (7.58 cm) had minimum fruit length followed by MM-4271 (9.03cm). Rakhi and Rajamony (2005), Lotti *et al* (2008), Ohashi *et al* (2009) and Dwivedi *et al* (2010) also observed significant variation in fruit length.

4.1.8 Fruit breadth (cm)

There were significant differences among genotypes under study for fruit breadth. In the year 2009, fruit breadth varied from 7.20 to 12.58 cm with overall mean of 10.79 cm. The maximum fruit breadth was recorded in MM-3981 (12.58cm) and MM-4279 (12.58cm) which were statistically at par with MM-3866 (12.45cm) and MM-3982 (12.20cm). However, minimum fruit breadth was observed in MM-4098 (7.20cm) followed by MM-4271 (9.30cm). During the year 2010, fruit breadth varied from 7.04 to 13.92 with overall mean of 10.78 cm. The maximum fruit breadth was found in MM-3994 (13.92cm) which were statistically at par with MM-3903(13.72cm) while, minimum fruit breadth was shown by MM-4098 (7.04cm) followed by Chujuc (8.92cm). The pooled mean varied from 7.12 to 12.75 cm with overall mean of 10.80 cm. The maximum fruit breadth was found in MM-3994 (12.75cm) which was statistically at par with MM-3903 (12.74cm) and MM-3866 (12.60cm). However, minimum fruit breadth was observed in MM-4098 (7.12cm) followed by Chujuc (9.20cm) and Dulce-B.B (9.52). The variability in fruit breadth was also reported by Rakhi and Rajamony (2005), Lotti *et al* (2008), Ohashi *et al* (2009) and Dwivedi *et al* (2010).

4.1.9 Seed cavity length (cm)

There were significant differences among all genotypes for seed cavity length. Seed cavity length during the year 2009 varied from 5.75 to 17.40 cm with over all mean of 7.95 cm. The longest seed cavity was found in MM-4002 (17.40cm), which was statistically at par with MM-4057 (16.85cm), the shortest seed cavity length was observed in Chujuc (5.75cm) and was statistically at par with with Dulce-B.B (5.82cm). During the year 2010, seed cavity length varied from 5.40 to 18.59 cm with over all mean of 7.93 cm. Maximum seed cavity length was observed in MM-3866 (18.59cm) which was statistically at par with MM-4002 (18.04cm), the minimum seed cavity length was shown by Chujuc (5.40cm) and was statistically at par with Dulce-B.B (5.73cm) and MM-4098 (5.72cm). Pooled mean ranged from 5.57 to 17.72 cm with over all mean of 7.92 cm. Genotype MM-4002 had longest seed cavity length (17.72cm) which was statistically at par with MM-3866 (17.42cm) while the genotype Chujuc had shortest seed cavity length (5.57cm) which was statistically at par with Dulce- B.B (5.77cm) (Plate 1).

4.1.10 Seed cavity breadth (cm)

Seed cavity breadth during the year 2009 showed considerable variation from 5.45 to 9.78 cm with overall mean of 7.63 cm. Maximum seed cavity breadth was observed in MM-4252 (9.78 cm) and was statistically at par with MM-4279 (9.48 cm) and MM-3981 (9.49 cm)

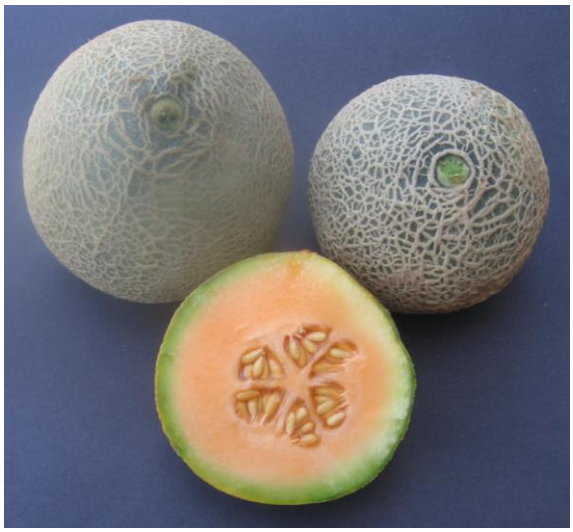
while minimum seed cavity breadth was found in MM-4098 (5.45cm) followed by Chujuc (5.80cm) and Dulce-B.B (5.98cm). During the year 2010, seed cavity breadth showed considerable variation from 5.30 to 9.97cm with overall mean of 7.54cm. The longest seed cavity breadth was recorded in MM-3866 (9.97cm) and was statistically at par with MM-3994 (9.51cm) and MM-3981 (9.45cm) while minimum seed cavity breadth was found in MM-4098 (5.30cm) followed by Chujuc (5.50cm) and Dulce-B.B (5.79cm). However, pooled mean varied from 5.37 to 9.42 cm with over all mean of 7.58 cm. Maximum seed cavity breadth was shown by MM-3981 (9.42cm) and was statistically at par with MM-3994 (9.31cm) whereas minimum seed cavity breadth was found in MM-4098 (5.37cm) followed by Chujuc (5.65cm) and Dulce-B.B (5.88cm) (Plate 1).

4.1.11 Rind thicknesses (mm)

Thickness of rind is important for long shelf life because of less damage to fruit skin caused by bruises during transportation. During the year 2009 it varied from 1.45 to 3.68 mm with over all mean of 2.31 mm. Genotype Chujuc had the thickest rind (3.60mm) and was statistically at par with Dulce-B.B (3.51mm), Hannaha's Choice (3.44mm), Gulf Coast (3.42mm), Rocky Ford (3.40mm) and Jucumba (3.40mm), whereas the minimum rind thickness was recorded in MM-4004 (1.50mm) and is statistically at par with MM-4005 (1.52mm), MM-3887 (1.60mm) and MM-3998 (1.68mm). In the year 2010, rind thickness ranged from 1.50 to 3.60 mm with over all mean of 2.40 mm. The maximum rind thickness was found in Chujuc (3.60mm) and was statistically at par with Dulce-B.B (3.51mm), Hannaha's Choice (3.44mm), Gulf Coast (3.42mm), Rocky Ford (3.40mm) and Jucumba (3.40mm) while minimum rind thickness was recorded in MM-4004(1.50mm) and was statistically at par with MM-4005 (1.58mm), MM-5736 (1.60mm) and MM-4247 (1.66mm). In the pooled mean rind thickness ranged from 1.47 to 3.60 mm with mean value of 2.39 mm. Genotype Chujuc had the thickest rind (3.64mm) (Plate 2a) and was statistically at par with Rocky Ford (3.50mm), Dulce-B.B (3.45mm), Hannaha's Choice (3.37mm), Jucumba (3.35mm) and Gulf Coast (3.34mm), whereas the thinnest rind was observed in MM-4004 (1.47mm) and is statistically at par with MM-4005 (1.55mm), MM-3887 (1.65mm) and MM-3998 (1.65mm).

4.1.12 Shelf life

During the year 2009, shelf life varied from 1.40 to 3.45 days with over all mean of 2.19 days. The maximum shelf life was found in AR Hale's (3.45) which was statistically at par with Chujuc (3.21), Gulf Stream (3.00), Gulf Coast (3.00), Jucumba (3.00) and Rocky Ford (3.00). However, the lowest shelf life was recorded in MM-4250 (1.40) and was statistically at par with MM-3843 (1.50), MM-3868 (1.50), MM-3917 (1.50), MM-3983 (1.50) and MM-3909 (1.55). In the year 2010, shelf life ranged from 1.48 to 3.69 with over all mean of 2.34. The maximum shelf life was found in Chujuc (3.69) which was statistically at



Chujuc

Dulce-B.B

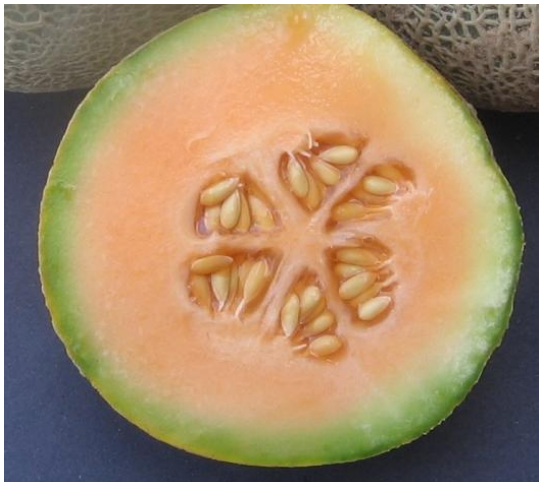
MM-3994

MM-3982

MM-3955

MM-3866

Plate 1: Variation in seed cavity size



Chujuc

Dulce-B.B

MM-4005

MM-4004

Plate 2a: Variation in rind thickness

MM-4002

Elliptical

MM-3979

Flattened

MM-4253

Globular

Plate 2b: Variation in fruit shape

par with AR Hale's (3.53), Gulf Stream (3.50) and Dulce-B.B (3.40) while the lowest shelf life was recorded in MM-4026 (1.48) and was statistically at par with MM-3963 (1.50), MM-3961 (1.60) and MM-3874 (1.60). Pooled mean also showed significant variation with average ranged from 1.55 to 3.49 days with overall mean of 2.26. The maximum shelf life was found in AR Hale's (3.49) which was statistically at par with Chujuc (3.45), Gulf Stream (3.34), and Gulf Coast (3.17). However, the lowest shelf life was recorded in MM-4250 (1.55) and was statistically at par with MM-4026 (1.60), MM-3917 (1.70) and MM-3843 (1.75).

4.1.13 Fruit shape

Large variability was observed among the genotypes for fruit shape viz., globular, flattened and elliptical. Out of 96 accessions, sixty-one accessions (63.54%) had globular fruit shape and twenty-nine accessions (30.20%) had flattened type fruit shape and elliptical type fruit shape was found in six accessions (Plate 2b). Similar findings have been reported by Dhillon *et al* (2007), Fergany *et al* (2011) and Roy *et al* (2011).

4.1.14 Fruit skin primary colour

Great variability was observed among genotypes for fruit skin primary colour viz., white, cream, light yellow, yellow, light orange, orange, brown and green. Twenty-five accessions (26.04%) had orange fruit skin primary colour, two accessions (2.08%) had light orange fruit skin primary colour, twenty-six accessions (27.08%) had brown fruit skin primary colour, twenty-one accessions (21.87%) had yellow fruit skin primary colour, two accessions (2.08%) had light yellow fruit skin primary colour, two accessions (2.08%) had cream fruit skin primary colour, six accessions (6.25%) had white fruit skin primary colour and twelve accessions (12.50%) had green fruit skin primary colour (Plate 3a). Similar results were also found by Lotti *et al* (2008) and Fergany *et al* (2011).

4.1.15 Fruit skin secondary colour

Wide variability was observed among genotypes for fruit skin secondary colour viz., white, cream, light yellow, orange, brown and green while some accessions had no secondary colour. Among total accessions thirty accessions (31.25%) had cream fruit skin secondary colour, nine accessions (9.37%) had white fruit skin secondary colour, six accessions (6.25) had orange fruit skin secondary colour, four accessions (4.16%) had brown fruit skin secondary colour, eight accessions (8.33%) had green fruit skin secondary colour and thirty-nine accessions (40.62) had no fruit skin secondary colour (Plate 3a).

4.1.16 Stem shape

Genotypes were grouped into two classes viz., rounded and angular stem shape. Most of the accessions viz., seventy-two (75% of total) had angular stem shape and twenty-four accessions (25% of total) had rounded stem shape.

Table 4.4: Brief morphological description of different melon accessions studied.

Sr. No.	Accession No.	Stem shape	Stem pubescence	Leaf margins	Fruit skin primary colour	Fruit skin secondary colour	Fruit shape	Netting
1	MM-3833	Rounded	Present	Unifid	Orange	Cream	Globular	Non-netted
2	MM-3837	Angular	Present	Multifid	Orange	Cream	Flattened	Non-netted
3	MM-3839	Angular	Present	Multifid	Brown	Cream	Flattened	Non-netted
4	MM-3843	Angular	Present	Bifid	Cream	Brown	Globular	Non-netted
5	MM-3849	Rounded	Present	Unifid	Orange	Cream	Globular	Non-netted
6	MM-3850	Angular	Present	Bifid	Yellow	-	Globular	Non-netted
7	MM-3851	Rounded	Present	Multifid	Orange	White	Globular	Non-netted
8	MM-3855	Angular	Present	Bifid	White	-	Elliptical	Non-netted
9	MM-3856	Angular	Present	Unifid	White	Light yellow	Globular	Non-netted
10	MM-3857	Rounded	Present	Unifid	Yellow	-	Globular	Non-netted
11	MM-3858	Angular	Present	Bifid	Brown	Cream	Flattened	Non-netted
12	MM-3859	Rounded	Present	Multifid	Orange	Cream	Globular	Non-netted
13	MM-3860	Angular	Present	Multifid	Yellow	Green	Globular	Netted
14	MM-3864	Rounded	Present	Bifid	Brown	White	Flattened	Non-netted
15	MM-3866	Rounded	Present	Unifid	Yellow	Cream	Elliptical	Non-netted
16	MM-3868	Angular	Present	Bifid	White	Orange	Globular	Non-netted
17	MM-3874	Rounded	Present	Unifid	Brown	-	Flattened	Non-netted
18	MM-3881	Angular	Present	Bifid	Yellow	-	Globular	Non-netted
19	MM-3884	Angular	Present	Unifid	Brown	Cream	Globular	Non-netted
20	MM-3885	Angular	Present	Multifid	Brown	Cream	Globular	Netted
21	MM-3887	Angular	Present	Unifid	Yellow	-	Flattened	Non-netted
22	MM-3889	Angular	Present	Unifid	White	Brown	Elliptical	Non-netted
23	MM-3901	Rounded	Present	Bifid	Green	-	Flattened	Netted
24	MM-3903	Angular	Present	Unifid	Cream	Brown	Elliptical	Non-netted
25	MM-3909	Angular	Present	Unifid	yellow	green	Flattened	Non-netted
26	MM-3917	Rounded	Present	Unifid	Brown	White	Flattened	Non-netted

Table 4.4: Contd.....

Sr. No.	Accession No.	Stem shape	Stem pubescence	Leaf margins	Fruit skin primary colour	Fruit skin secondary colour	Fruit shape	Netting
27	MM-3947	Angular	Present	Multifid	Brown	Cream	Globular	Non-netted
28	MM-3955	Rounded	Present	Unifid	Orange	Cream	Globular	Non-netted
29	MM-3956	Rounded	Present	Unifid	Brown	White	Globular	Non-netted
30	MM-3961	Rounded	Present	Multifid	Brown	Cream	Globular	Non-netted
31	MM-3962	Angular	Present	Unifid	Yellow	-	Globular	Non-netted
32	MM-3963	Angular	Present	Unifid	Brown	White	Flattened	Non-netted
33	MM-3965	Angular	Present	Bifid	Orange	Cream	Flattened	Non-netted
34	MM-3966	Angular	Present	Bifid	Brown	-	Flattened	Netted
35	MM-3968	Angular	Present	Multifid	Orange	-	Globular	Netted
36	MM-3973	Angular	Present	Bifid	Yellow	Green	Flattened	Non-netted
37	MM-3974	Angular	Present	Unifid	Yellow	Orange	Globular	Non-netted
38	MM-3976	Angular	Present	Unifid	Green	-	Globular	Netted
39	MM-3977	Angular	Present	Bifid	Green	-	Globular	Netted
40	MM-3979	Angular	Present	Unifid	Orange	Cream	Flattened	Non-netted
41	MM-3980	Rounded	Present	Bifid	Orange	Cream	Globular	Non-netted
42	MM-3981	Angular	Present	Multifid	Orange	Cream	Globular	Non-netted
43	MM-3982	Angular	Present	Unifid	Yellow	-	Globular	Non-netted
44	MM-3983	Angular	Present	Bifid	Yellow	Orange	Flattened	Non-netted
45	MM-3985	Angular	Present	Multifid	Orange	Cream	Globular	Non-netted
46	MM-3986	Angular	Present	Bifid	Orange	-	Globular	Non-netted
47	MM-3994	Angular	Present	Bifid	Orange	-	Flattened	Non-netted
48	MM-3998	Angular	Present	Multifid	Brown	Green	Flattened	Non-netted
49	MM-4002	Angular	Present	Multifid	Cream	Yellow	Elliptical	Non-netted
50	MM-4003	Angular	Present	Bifid	Orange	Cream	Flattened	Non-netted
51	MM-4004	Angular	Present	Unifid	Light orange	-	Globular	Non-netted
52	MM-4005	Angular	Present	Unifid	Yellow	-	Globular	Non-netted

Table 4.4: Contd.....

Sr. No.	Accession No.	Stem shape	Stem pubescence	Leaf margins	Fruit skin primary colour	Fruit skin secondary colour	Fruit shape	Netting
53	MM-4013	Angular	Present	Bifid	Light yellow	Orange	Globular	Non-netted
54	MM.4018	Rounded	Present	Multifid	Brown	White	Globular	Non-netted
55	MM-4021	Angular	Present	Unifid	Brown	White	Flattened	Non-netted
56	MM-4026	Angular	Present	Bifid	Yellow	-	Globular	Non-netted
57	MM-4030	Angular	Present	Unifid	orange	Cream	Elliptical	Non-netted
58	MM-4057	Angular	Present	Unifid	Orange	Cream	Elliptical	Non-netted
59	MM-4059	Rounded	Present	Unifid	White	-	Flattened	Netted
60	MM-4063	Angular	Present	Multifid	Light yellow	-	Flattened	Non-netted
61	MM-4065	Angular	Present	Multifid	Brown	Green	Flattened	Netted
62	MM-4066	Angular	Present	Unifid	Brown	Cream	Globular	Netted
63	MM-4067	Rounded	Present	Multifid	Brown	Cream	Globular	Non-netted
64	MM-4068	Angular	Present	Unifid	Brown	Cream	Flattened	Non-netted
65	MM-4091	Rounded	Present	Unifid	Light orange	Green	Globular	Non-netted
66	MM-4098	Angular	Present	Multifid	Yellow	-	Globular	Non-netted
67	MM-4243	Rounded	Present	Unifid	Brown	White	Globular	Non-netted
68	MM-4247	Angular	Present	Bifid	Yellow	Green	Globular	Non-netted
69	MM-4248	Rounded	Present	Unifid	Yellow	Orange	Globular	Non-netted
70	MM.4250	Angular	Present	Unifid	Yellow	Orange	Flattened	Non-netted
71	MM-4251	Rounded	Present	Unifid	Yellow	Green	Globular	Non-netted
72	MM-4252	Angular	Present	Bifid	Orange	Cream	Globular	Netted
73	MM.4253	Angular	Present	Unifid	Brown	Cream	Globular	Non-netted
74	MM-4256	Angular	Present	Bifid	Green	-	Globular	Netted
75	MM-4267	Angular	Present	Unifid	Yellow	-	Globular	Non-netted
76	MM-4268	Angular	Present	Multifid	Yellow	-	Flattened	Non-netted
77	MM-4270	Angular	Present	Unifid	Orange	Cream	Globular	Non-netted
78	MM-4271	Angular	Present	Bifid	Brown	Cream	Globular	Netted

Table 4.4: Contd.....

Sr. No.	Accession No.	Stem shape	Stem pubescence	Leaf margins	Fruit skin primary colour	Fruit skin secondary colour	Fruit shape	Netting
79	MM-4276	Angular	Present	Bifid	Orange	-	Flattened	Non-netted
80	MM-4277	Angular	Present	Unifid	Brown	-	Globular	Netted
81	MM-4278	Angular	Present	Bifid	Orange	Cream	Flattened	Non-netted
82	MM-4279	Angular	Present	Bifid	Brown	Cream	Globular	Netted
83	MM-4282	Angular	Present	Bifid	Orange	Cream	Globular	Non-netted
84	MM-4283	Rounded	Present	Unifid	Brown	White	Flattened	Non-netted
85	MM-4305	Rounded	Present	Unifid	Orange	-	Globular	Non-netted
86	MM-4342	Angular	Present	Bifid	Orange	Cream	Flattened	Non-netted
87	MM-4409	Rounded	Present	Unifid	Orange	Cream	Globular	Non-netted
88	MM-5736	Angular	Present	Unifid	Orange	-	Globular	Non-netted
89	AR Hale’s	Angular	Present	Multifid	Green	-	Globular	Netted
90	Dulce-B.B	Angular	Present	Multifid	Green	-	Globular	Netted
91	Gulf Coast	Angular	Present	Multifid	Green	-	Globular	Netted
92	Gulf Stream	Angular	Present	Multifid	Green	-	Globular	Netted
93	Jucumba	Angular	Present	Multifid	Green	-	Globular	Netted
94	Rocky Ford	Angular	Present	Multifid	Green	-	Globular	Netted
95	Hannah’s Choice	Angular	Present	Multifid	Green	-	Flattened	Netted
96	Chujuc	Angular	Present	Multifid	Green	-	Globular	Netted

4.1.17 Stem pubescence

No variation was found in stem pubescence. In all the accessions stem pubescence was present.

4.1.18 Leaf margin

Genotypes were grouped into unifid, bifid and multifid on the basis of leaf margin. Fourty-one accessions (42.70%) possessed unifid leaf margins and twenty-eight accessions (29.16%) possessed bifid leaf margins whereas twenty-seven accessions (28.12 %) possessed multifid leaf margins (Plate 3b).

4.1.19 Netting

Genotypes were classed into netted and non-netted on the basis of presence or absence of netting on the rind. Most of the accessions viz., seventy-three (76.04% of total) were non-netted, while twenty-three accessions (23.95% of total) were netted.

Significant variability existed in the germplasm as indicated by highly significant differences among accessions for all the traits, which could be used for improvement of the crop through selection.

In melon, earliness is very important as market prices for early crop are more giving higher net returns to the cultivator. Therefore, it is imperative to evolve early genotypes. However, nodes at which the first hermaphrodite flowers appear and days from sowing to first fruit harvest give a fair indication of earliness. The genotypes MM-4278, MM-3833, MM-4018, MM-4270, MM-3895, MM-3884 and MM-4098 had minimum number of node to bear the first hermaphrodite flower. Lesser number of days from sowing to first fruit harvest were observed in MM-3956 (79.12) and MM-4283 (79.67). Genotypes possessing early maturity can be used in the breeding programme to transfer this trait to the adapted cultivars.

The fruit yield is a complex trait. The direct selection for this trait is not usually effective. Number of fruits per vine, average fruit weight, number of primary branches per vine are the important component traits of fruit yield in melon (Taha *et al*, 2003). Selection based on these traits may be effective for improving the complex trait of fruit yield. The most desirable genotypes which combine yield contributing traits such as maximum number of fruits per vine (MM-4098, MM-3885, MM-4277, MM-3884 and MM-3881), average maximum fruit weight (MM-3866, MM-3855 and MM-3903), maximum number of primary branches per vine (MM-3998, MM-3903 and MM-4005, MM-3866 MM-3889) should be utilized in breeding programme for improving this trait.

Fruit shape is a desirable trait in melon. Fruit shape in melon influences flesh area percentage and flesh to cavity ratio (More *et al,* 1987). Globular shape being most preferred one because it gives high flesh recovery per volume. In the present study, wide variability was observed among the genotypes for fruit shape. Most of the accessions(63.54%) had globular shape.

Plate 3a: Variation in fruit skin primary and secondary colour

Unifid **Bifid** **Multifid**

Plate 3b: Variation in leaf margin

Flesh thickness is one of the important parameters in melon. Flesh thickness is related to both fruit size and seed cavity size. Selection of genotypes having fruits with high flesh thickness is an important objective of melon breeding. High flesh thickness is usually correlated with small seed-cavity (Taha *et al,* 2003). Small seed cavity is an important objective in melon breeding. The shortest seed cavity length along with minimum seed cavity breadth was observed in Chujuc and Dulce-B.B. These genotypes can be crossed with indigenous types to recombine good quality and adaptability of local types.

Conspicuous external colour of melon attracts the consumers. Fruit flesh colour is important not only for consumer's acceptability but also in case of aroma and flavour (Burger *et al,* 2003). Large variability was observed among genotypes for fruit skin primary colour and secondary colour viz., white, cream, light yellow, yellow, light orange, orange, brown and green.

Netting of the fruit enhances its quality and shelf life. It serves as a protection against mechanical injury, both pre and post harvest management. (Keiserman-Keren *et al,* 2004). Genotypes exhibited wide variability for this character. 76.04% of the genotypes were non-netted while 23.95% genotypes were netted.

4.2 Characterization on the basis of biochemical traits

Observation recorded for biochemical characters in case of ninety-six accessions are presented in Table 4.5.

4.2.1 Total soluble solids content (%)

Total soluble solids content during the year 2009, varied from 2.30 to 13.15 with overall mean of 10.38. The highest total soluble solid content was found in Rocky Ford (13.15) which was statistically at par with AR Hale's (12.90), Chujuc (12.87), MM- 4013 (12.86), MM-4283 (12.74), MM-4063 (12.66) and MM-3856 (12.61) while genotype MM-3887 had the lowest total soluble solids content (2.30) which was statistically at par with MM-4005 (2.49), MM-3998 (2.68), MM- 4247 (3.00), MM-4267 (3.30), MM-3994 (3.80). During the year 2010, total soluble solids content varied from 3.00 to 13.45 with overall mean of 10.26. Maximum total soluble solid content was found in Chujuc (13.45) which was statistically at par with MM- 4253 (13.14) and MM-3837 (13.05) while genotype MM-3887 and MM-3998 had lowest total soluble solids content (3.00) which were statistically at par with MM-4005 (3.05), MM-3982 (3.20),MM- 3994 (3.20), MM-5739 (3.68) and MM-4267 (3.70). The pooled mean ranged from 2.77 to 13.16 with mean value of 10.33. The highest total soluble solid content was found in Chujuc (13.16) which was statistically at par with Rocky Ford (12.86) and Dulce-B.B (12.74) while genotype MM-4005 had lowest total soluble solids content (2.77) which was statistically at par with, MM-3998 (2.84), MM-3887 (2.90), MM- 3994 (3.50), MM-4247 (3.50) and MM-4267 (3.50). The variability in total

Table 4.5: Mean performance of melon accessions for various biochemical traits.

Sr. No.	Accession No.	Total soluble solids content (%)			Ascorbic acid content (mg/100g of fruit weight)		
		2009	2010	Pooled mean	2009	2010	Pooled mean
1	MM-3833	10.05	12.15	11.10	22.52	18.08	20.30
2	MM-3837	11.95	13.05	12.50	26.48	30.60	28.54
3	MM-3839	12.00	11.50	11.75	19.84	18.90	19.37
4	MM-3843	10.98	10.30	10.64	25.75	28.81	27.28
5	MM-3849	12.06	12.94	12.50	26.60	24.40	25.50
6	MM-3850	12.34	11.50	11.92	19.70	20.96	20.33
7	MM-3851	9.50	8.96	9.23	21.70	18.70	20.20
8	MM-3855	9.51	9.03	9.27	17.00	17.76	17.38
9	MM-3856	12.61	11.95	12.28	30.25	27.25	28.75
10	MM-3857	12.08	11.06	11.57	26.00	26.50	26.25
11	MM-3858	12.02	12.42	12.22	26.94	28.10	27.52
12	MM-3859	12.06	11.60	11.83	26.05	26.51	26.28
13	MM-3860	12.14	11.52	11.83	23.30	25.00	24.15
14	MM-3864	12.00	12.60	12.30	31.10	25.30	28.20
15	MM-3866	8.30	7.90	8.10	14.90	16.00	15.45
16	MM-3868	11.33	10.88	11.10	28.40	26.20	27.30
17	MM-3874	11.70	11.96	11.83	26.00	26.86	26.43
18	MM-3881	12.26	11.50	11.88	20.30	26.24	23.27
19	MM-3884	11.68	12.00	11.84	20.54	24.62	22.58
20	MM-3885	10.28	8.98	9.63	27.00	27.86	27.43
21	MM-3887	2.30	3.00	2.90	9.12	8.10	8.61
22	MM-3889	8.65	9.01	8.83	18.90	19.46	19.18
23	MM-3901	11.90	12.18	12.04	27.01	23.05	25.03
24	MM-3903	7.05	8.09	7.57	19.90	20.30	20.10
25	MM-3909	10.05	10.25	10.15	25.00	26.54	25.77
26	MM-3917	12.02	11.60	11.81	28.13	25.95	27.04
27	MM-3947	11.02	11.84	11.43	21.40	17.46	19.43

Table 4.5 Contd.....

Sr. No.	Accession No.	Total soluble solids content (%)			Ascorbic acid content (mg/100g of fruit weight)		
		2009	2010	Pooled mean	2009	2010	Pooled mean
28	MM-3955	11.73	10.93	11.33	20.05	20.55	20.30
29	MM-3956	12.30	13.00	12.65	19.50	21.26	20.38
30	MM-3961	12.20	11.70	11.95	23.12	25.64	24.38
31	MM-3962	4.40	3.90	4.15	12.00	13.34	12.67
32	MM-3963	9.27	10.05	9.66	26.01	25.05	25.53
33	MM-3965	12.49	11.55	12.02	22.06	18.40	20.23
34	MM-3966	9.05	10.15	9.60	23.90	25.10	24.50
35	MM-3968	11.95	12.11	12.03	28.00	24.80	26.40
36	MM-3973	11.70	10.90	11.30	21.95	22.65	22.30
37	MM-3974	4.00	4.22	4.11	8.00	8.90	8.45
38	MM-3976	10.06	9.00	9.53	25.96	24.70	25.33
39	MM-3977	10.65	11.05	10.85	22.20	24.60	23.40
40	MM-3979	11.43	12.01	11.72	20.15	22.39	21.27
41	MM-3980	12.00	11.06	11.53	26.05	26.89	26.47
42	MM-3981	12.30	12.70	12.50	26.30	22.50	24.40
43	MM-3982	4.00	3.20	3.60	9.10	9.40	9.25
44	MM-3983	10.50	9.80	10.15	25.00	27.94	26.47
45	MM-3985	10.05	10.35	10.20	24.04	25.02	24.53
46	MM-3986	11.84	10.90	11.37	26.64	24.30	25.47
47	MM-3994	3.80	3.20	3.50	7.90	8.56	8.23
48	MM-3998	2.68	3.00	2.84	14.30	16.28	15.29
49	MM-4002	7.50	8.10	7.80	15.03	16.09	15.56
50	MM-4003	11.55	12.05	11.80	25.84	23.10	24.47
51	MM-4004	4.00	3.40	3.70	11.60	11.02	11.31
52	MM-4005	2.49	3.05	2.77	16.74	12.50	14.62
53	MM-4013	12.86	12.00	12.43	26.98	25.70	26.34
54	MM-4018	12.05	11.61	11.83	24.80	27.76	26.28

Table 4.5 Contd.....

Sr. No.	Accession No.	Total soluble solids content (%)			Ascorbic acid content (mg/100g of fruit weight)		
		2009	2010	Pooled mean	2009	2010	Pooled mean
55	MM-4021	11.60	12.50	12.05	29.30	25.20	27.25
56	MM-4026	11.52	10.88	11.20	18.50	19.76	19.13
57	MM-4030	7.43	8.03	7.73	14.30	16.16	15.23
58	MM-4057	9.60	9.00	9.30	14.05	16.75	15.40
59	MM-4059	12.21	11.15	11.68	24.00	24.60	24.30
60	MM-4063	12.66	11.04	11.85	23.10	25.34	24.22
61	MM-4065	10.22	9.00	9.61	23.98	25.08	24.53
62	MM-4066	12.10	11.50	11.80	22.90	25.40	24.15
63	MM-4067	12.05	12.79	12.42	24.10	24.78	24.44
64	MM-4068	12.90	11.80	12.35	28.10	24.96	26.53
65	MM-4091	4.60	3.96	4.28	10.95	11.69	11.32
66	MM-4098	10.98	12.02	11.50	24.00	25.38	24.69
67	MM-4243	12.00	11.32	11.66	28.70	26.10	27.40
68	MM-4247	3.00	4.00	3.50	10.10	11.04	10.57
69	MM-4248	12.00	10.80	11.40	25.69	22.05	23.87
70	MM-4250	9.25	10.05	9.65	24.56	26.00	25.28
71	MM-4251	10.90	11.36	11.13	22.70	25.64	24.17
72	MM-4252	12.24	10.90	11.57	26.78	23.88	25.33
73	MM-4253	12.18	13.14	12.66	23.70	25.14	24.42
74	MM-4256	12.02	11.58	11.80	25.15	27.51	26.33
75	MM-4267	3.30	3.70	3.50	8.15	9.21	8.68
76	MM-4268	12.01	10.93	11.47	23.05	23.91	23.48
77	MM-4270	11.96	12.78	12.37	24.95	27.59	26.27
78	MM-4271	10.71	11.03	10.87	26.00	26.74	26.37
79	MM-4276	11.53	12.55	12.04	25.40	27.80	26.60
80	MM-4277	12.05	10.95	11.50	26.50	27.76	27.13
81	MM-4278	12.34	11.80	12.07	25.01	25.45	25.23

Table 4.5 Contd.....

Sr. No.	Accession No.	Total soluble solids content (%)			Ascorbic acid content (mg/100g of fruit weight)		
		2009	2010	Pooled mean	2009	2010	Pooled mean
82	MM-4279	11.30	11.70	11.50	23.70	26.70	25.20
83	MM-4282	11.90	12.24	12.07	23.23	27.63	25.43
84	MM-4283	12.74	11.80	12.27	22.00	23.06	22.53
85	MM-4305	12.02	11.18	11.60	18.15	20.79	19.47
86	MM-4342	11.03	10.30	10.70	23.98	27.02	25.50
87	MM-4409	10.60	10.20	10.40	25.00	26.76	25.88
88	MM-5736	4.02	3.68	3.85	13.74	14.76	14.25
89	AR Hale's	12.90	12.10	12.50	37.49	40.05	38.77
90	Dulce-B.B	12.58	12.90	12.74	33.00	36.06	34.53
91	Gulf Coast	12.02	12.65	12.33	35.58	34.80	35.19
92	Gulf Stream	11.90	12.60	12.25	34.73	31.75	33.24
93	Jucumba	12.40	11.60	12.00	32.90	33.96	33.43
94	Rocky Ford	13.15	12.57	12.86	36.25	34.05	35.15
95	Hannah's Choice	11.70	11.34	11.52	34.00	34.30	34.15
96	Chujuc	12.87	13.45	13.16	35.25	37.75	36.50
	CD (5%)	**1.60**	**1.66**	**1.52**	**4.48**	**4.36**	**4.30**
	CD (1%)	**2.10**	**2.18**	**2.00**	**5.82**	**5.73**	**5.65**

Table 4.5 Contd.....

Sr. No.	Accession No.	Titrable acidity (g anhydrous citric acid/100ml fruit juice)			Dry matter content (%)		
		2009	2010	Pooled mean	2009	2010	Pooled mean
1	MM-3833	0.11	0.07	0.09	9.00	9.90	9.45
2	MM-3837	0.07	0.09	0.08	8.90	9.30	9.20
3	MM-3839	0.08	0.08	0.08	9.25	9.05	9.15
4	MM-3843	0.11	0.09	0.10	11.05	9.85	10.45
5	MM-3849	0.10	0.06	0.08	9.45	8.85	9.15
6	MM-3850	0.11	0.07	0.09	10.70	9.10	9.90
7	MM-3851	0.07	0.09	0.08	12.10	9.10	10.60
8	MM-3855	0.10	0.14	0.12	15.08	11.98	13.53
9	MM-3856	0.07	0.09	0.08	9.00	9.40	9.20
10	MM-3857	0.06	0.10	0.08	7.95	8.35	8.15
11	MM-3858	0.08	0.08	0.08	9.24	9.00	9.12
12	MM-3859	0.07	0.09	0.08	9.60	8.90	9.25
13	MM-3860	0.09	0.11	0.10	10.90	11.66	11.28
14	MM-3864	0.08	0.06	0.07	10.00	9.50	9.75
15	MM-3866	0.10	0.14	0.12	9.00	9.90	9.45
16	MM-3868	0.06	0.08	0.07	9.85	11.05	10.45
17	MM-3874	0.09	0.09	0.09	9.54	8.90	9.22
18	MM-3881	0.06	0.10	0.08	9.00	10.10	9.55
19	MM-3884	0.11	0.09	0.10	9.30	8.14	8.72
20	MM-3885	0.08	0.12	0.10	12.00	12.90	12.45
21	MM-3887	0.30	0.18	0.24	13.10	13.50	13.30
22	MM-3889	0.19	0.13	0.16	10.10	10.82	10.46
23	MM-3901	0.10	0.08	0.09	11.50	11.00	11.25
24	MM-3903	0.20	0.16	0.18	8.95	9.85	9.40
25	MM-3909	0.12	0.10	0.11	9.10	8.60	8.85
26	MM-3917	0.08	0.08	0.08	8.70	9.18	8.94

Table 4.5 Contd.....

Sr. No.	Accession No.	Titrable acidity (g anhydrous citric acid/100ml fruit juice)			Dry matter content (%)		
		2009	2010	Pooled mean	2009	2010	Pooled mean
27	MM-3947	0.11	0.09	0.10	9.30	9.60	9.45
28	MM-3955	0.07	0.11	0.09	10.00	9.50	9.75
29	MM-3956	0.10	0.06	0.08	8.90	10.00	9.45
30	MM-3961	0.09	0.09	0.09	8.50	9.50	9.00
31	MM-3962	0.24	0.30	0.27	8.50	9.00	8.75
32	MM-3963	0.11	0.09	0.10	9.80	9.10	9.45
33	MM-3965	0.07	0.09	0.08	9.00	9.46	9.23
34	MM-3966	0.14	0.10	0.12	8.98	10.16	9.57
35	MM-3968	0.08	0.08	0.08	10.80	11.94	11.37
36	MM-3973	0.11	0.07	0.09	10.24	9.00	9.62
37	MM-3974	0.29	0.27	0.28	9.05	9.85	9.45
38	MM-3976	0.09	0.15	0.12	10.70	12.50	11.60
39	MM-3977	0.10	0.10	0.10	11.46	11.00	11.23
40	MM-3979	0.13	0.09	0.11	9.50	10.10	9.80
41	MM-3980	0.07	0.09	0.08	9.00	9.30	9.15
42	MM-3981	0.08	0.08	0.08	9.50	10.00	9.75
43	MM-3982	0.27	0.35	0.31	10.51	8.95	9.73
44	MM-3983	0.08	0.10	0.09	10.00	9.60	9.80
45	MM-3985	0.10	0.12	0.11	9.00	9.54	9.27
46	MM-3986	0.07	0.11	0.09	9.10	9.80	9.45
47	MM-3994	0.27	0.37	0.33	10.90	9.84	10.37
48	MM-3998	0.40	0.32	0.36	10.86	10.10	10.48
49	MM-4002	0.18	0.14	0.16	11.05	10.38	10.71
50	MM-4003	0.11	0.09	0.10	9.90	8.70	9.30
51	MM-4004	0.34	0.31	0.32	11.20	9.60	10.40
52	MM-4005	0.39	0.33	0.36	12.00	12.70	12.35

Table 4.5 Contd.....

Sr. No.	Accession No.	Titrable acidity (g anhydrous citric acid/100ml fruit juice)			Dry matter content (%)		
		2009	2010	Pooled mean	2009	2010	Pooled mean
53	MM-4013	0.08	0.12	0.10	9.10	8.46	8.78
54	MM-4018	0.08	0.10	0.09	10.20	9.64	9.92
55	MM-4021	0.09	0.07	0.08	8.88	9.82	9.35
56	MM-4026	0.08	0.10	0.09	9.00	8.54	8.77
57	MM-4030	0.15	0.11	0.13	10.70	10.10	10.40
58	MM-4057	0.10	0.14	0.12	10.79	9.85	10.32
59	MM-4059	0.06	0.10	0.08	9.25	9.65	9.45
60	MM-4063	0.08	0.08	0.08	8.92	10.02	9.47
61	MM-4065	0.11	0.15	0.13	10.10	9.30	9.70
62	MM-4066	0.07	0.09	0.08	11.00	11.36	11.18
63	MM-4067	0.08	0.08	0.08	8.75	9.79	9.27
64	MM-4068	0.07	0.11	0.09	8.90	9.50	9.20
65	MM-4091	0.29	0.35	0.32	9.10	10.20	9.65
66	MM-4098	0.08	0.08	0.08	9.00	8.14	8.57
67	MM-4243	0.06	0.10	0.08	9.02	9.88	9.45
68	MM-4247	0.29	0.21	0.25	9.00	8.50	8.75
69	MM-4248	0.07	0.11	0.09	10.90	10.00	10.45
70	MM.4250	0.14	0.10	0.12	9.30	9.60	9.45
71	MM-4251	0.09	0.09	0.09	9.90	11.00	10.45
72	MM-4252	0.06	0.10	0.08	9.10	10.20	9.65
73	MM-4253	0.09	0.07	0.08	8.77	9.69	9.23
74	MM-4256	0.08	0.12	0.10	9.96	8.50	9.23
75	MM-4267	0.28	0.36	0.32	10.00	9.50	9.75
76	MM-4268	0.07	0.11	0.09	11.60	10.10	10.85
77	MM-4270	0.10	0.06	0.08	9.34	8.50	8.92
78	MM-4271	0.09	0.09	0.09	9.37	10.69	10.03

Table 4.5 Contd.....

Sr. No.	Accession No.	Titrable acidity (g anhydrous citric acid/100ml fruit juice)			Dry matter content (%)		
		2009	2010	Pooled mean	2009	2010	Pooled mean
79	MM-4276	0.10	0.06	0.08	9.05	9.25	9.15
80	MM-4277	0.07	0.11	0.09	9.85	10.69	10.27
81	MM-4278	0.08	0.08	0.08	8.90	9.50	9.20
82	MM-4279	0.10	0.08	0.09	9.10	9.90	9.50
83	MM-4282	0.09	0.09	0.09	9.00	9.84	9.42
84	MM-4283	0.06	0.10	0.08	8.78	9.66	9.22
85	MM-4305	0.08	0.12	0.10	9.00	9.40	9.20
86	MM-4342	0.09	0.13	0.11	9.75	11.85	10.80
87	MM-4409	0.10	0.10	0.10	9.07	9.83	9.45
88	MM-5736	0.30	0.36	0.33	8.80	9.80	9.30
89	AR Hale's	0.10	0.06	0.08	11.14	10.30	10.72
90	Dulce-B.B	0.12	0.08	0.10	10.07	10.67	10.37
91	Gulf Coast	0.07	0.09	0.08	11.56	11.00	11.28
92	Gulf Stream	0.08	0.08	0.08	11.00	12.50	11.75
93	Jucumba	0.07	0.09	0.08	10.73	10.17	10.45
94	Rocky Ford	0.11	0.13	0.12	10.66	10.00	10.33
95	Hannah's Choice	0.10	0.10	0.10	10.95	9.65	10.30
96	Chujuc	0.09	0.07	0.08	9.72	9.00	9.36
	CD (5%)	**0.10**	**0.09**	**0.10**	**1.38**	**1.36**	**1.29**
	CD (1%)	**0.13**	**0.11**	**0.13**	**1.81**	**1.78**	**1.69**

soluble solids content was also found by Stepansky *et al* (1999b), Burger *et al* (2003), Burger *et al* (2004), Bianco and Pace (2006) (3.9% to 15.2%), Burger *et al* (2006), Lotti *et al* (2008) (4.8 to 14.8^{0}B) and Yi-San *et al* (2009) (2.8 to 11°B).

4.2.2 Ascorbic acid content (mg/100g of fresh fruit flesh)

Ascorbic acid content during the year 2009, varied from 7.90 to 37.49 with overall mean of 23.08.The genotype AR Hale's possessed the highest value of ascorbic acid (37.49) which was statistically at par with Rocky Ford (36.25), Gulf Coast (35.58), Chujuc (35.25) and Gulf Stream (34.73). However, the lowest ascorbic acid content was observed in MM-3994 (7.90) which was statistically at par with MM-3974 (8.00), MM-4267 (8.15) and MM-3982 (9.10). In the year 2010 ascorbic acid content varied from 8.10 to 40.05 with overall mean of 23.44.The genotype AR Hale's possessed the highest value of ascorbic acid content (40.05) which was statistically at par with Chujuc (37.75) and Dulce-B.B (36.06). However, the lowest ascorbic acid content was observed in MM-3887 (8.10) which was statistically at par with MM-3974 (8.90), MM-3994 (8.56), MM-4267 (9.21) and MM-3982 (9.40). The pooled mean ranged from 8.23 to 38.77 with mean value of 23.26. The highest value of ascorbic acid content was found in AR Hale's (38.77) which was statistically at par with Chujuc (36.50) and Rocky Ford (36.25). However, the lowest ascorbic acid content was observed in MM-3994 (8.23) which was statistically at par with MM-3974 (8.45), MM-3887 (8.61), MM-4267 (8.68) and MM-3982 (9.25). The results are in agreement with those of Burger *et al* (2004), Sharma and Lal (2004) (8.35 to 23.12mg/100g), Bianco and Pace (2006) (9 to 31 mg/100 gfw), Burger *et al* (2006), Dhillon *et al* (2007) (1.6 to 34.1 mg/ 100g of fresh fruit weight), Dhillon *et al* (2009) (0.5 to 12.9 mg/ 100g of fresh fruit weight) and Fergany *et al* (2011).

4.2.3 Titrable acidity (g anhydrous citric acid/100ml fruit juice)

Citric and malic acids are the two important organic acids found in the flesh of different melon varieties. The sugar/acid ratio determines the fruit flavour. During the year 2009, titrable acidity varied from 0.06 to 0.40 with overall mean of 0.11. The maximum titrable acidity was shown by MM-3998 (0.40) and was statistically at par with MM-4005 (0.39), MM-4004 (0.34) and MM-3887 (0.30), while genotype MM-3881, MM-4243, MM-4252 had lowest titrable acidity (0.06). During the year 2010, titrable acidity varied from 0.06 to 0.37 with overall mean of 0.12. The maximum titrable acidity was found in MM-3994 (0.37) and was statistically at par with MM-4267 (0.36), MM-5736 (0.36), MM-4091 (0.35), MM-4005 (0.33) and MM-3998 (0.32) while genotype MM-3849, MM-3864, MM-3956, MM-4270 and MM-4276 had lowest titrable acidity (0.06). In the pooled mean titrable acidity varied from 0.07 to 0.37 with overall mean of 0.11.The highest titrable acidity was shown by MM-3998 (0.36) and MM-4005 (0.36) and were statistically at par with MM-5736 (0.33), MM-3994 (0.33), MM-4267 (0.32) and MM-4091 (0.32), while the lowest titrable acidity was

found in MM-3864 (0.07) and MM-3868 (0.07). Variation in titrable acidity was also reported by Leach *et al* (1989), Artes *et al* (1993) (0.14% to 0.50%.), Pitrat *et al* (2000), Burger *et al* (2003), Burger *et al* (2004), Albuquerque *et al* (2006), Bianco and Pace (2006), Burger *et al* (2006), Dhillon *et al* (2007) (0.08 to 0.61%), Dhillon *et al* (2009) (0.03 to 0.65%) and Fergany *et al* (2011) (0.12 to 0.57%).

4.2.4 Dry matter content (%)

During the year 2009, dry matter content varied from 7.95 to 15.08 with overall mean of 9.51. The maximum dry matter content was observed in MM-3855 (15.08%) and was statistically at par with MM-3887 (13.10%), MM-3851 (12.10%) and MM-4005 (12.00) while the lowest dry matter was recorded in MM-3857(7.95%) and was statistically at par with MM-3961 (8.50), MM-3962 (8.50), MM-3917 (8.70), MM-4253 (8.77) and MM-4283 (8.78). For the year 2010, dry matter content varied from 8.14% to 13.50% with overall mean of 9.62. The highest dry matter content was observed in MM-3887 (13.50%) and was statistically at par with MM-3885 (12.90%), MM-4005 (12.70%) and Gulf Stream (12.50%). However, the lowest dry matter was found in MM-3884 (8.14) and MM-4098 (8.14) and was statistically at par with MM-3857 (8.35%), MM-4013 (8.46%), MM-4247 (8.50%) and MM-4256 (8.50%). Pooled mean for dry matter content varied from 8.15 to 13.53 with overall mean of 9.56. The maximum dry matter content was observed in MM-3855 (13.53%) and was statistically at par with MM-3887 (13.30%) and MM-405 (12.35%). However the lowest dry matter was recorded in MM-3857 (8.15%) and was statistically at par with MM-3884 (8.35), MM-3962 (8.75), MM-4247 (8.75) and MM-4026 (8.77) and MM-3909 (8.85). Similar results were also observed by Sharma and Lal (2004) (6.63 to 11.17%).

Fruit quality is determined primarily by sweetness and a major component of this is total soluble solids content. The main sugar responsible for sweetness is sucrose and it is one of the most important quality traits. (Burger *et al*, 2006). The highest TSS content was found Chujuc (13.16%) which was statistically at par with Rocky Ford (12.86%) and Dulce-B.B (12.74%)

In sweet melons organic acids play a little role in determining their quality, which is determined by sweetness alone (Yamaguchi *et al*, 1977). Sweet melon cultivars have low acid level, while non-sweet melons possess relatively high acidity (Pitrat *et al*, 2000). These high acidic groups do not accumulate high levels of sugar which is characteristic of the sweet melon groups, though the combination of high sugar and high acid level can be obtained (Burger *et al*, 2003) and present a new melon flavour. In *Cucumis melo*, citrate was reported as major acid. Citric and malic acids are the most important organic acids found in the flesh of melon (Burger *et al*, 2003). The highest titrable acidity was observed in MM-4004, MM-4005, MM-3998, MM-5736 and MM-4091. Therefore, breeding efforts may be directed to develop recombinants with more total soluble solid content along with moderate acidity

Table 4.6: Desirable genotypes for various characters based on their mean values

Sr. No.	Characters	Genotypes
1	Node at which first hermaphrodite flower appears	MM-4013 (2.00), MM-3833 (2.10), MM-3849 (2.10), MM-3956 (2.10).
2	Number of primary branches /vine	MM-3998 (6.83), MM-3903 (6.80), MM-4005 (6.60)
3	Days from sowing to marketable maturity	MM-3947 (78.48), MM-3956 (79.12), MM-4283 (79.67)
4	Days from sowing to last fruit harvest	MM-4305 (110.85), MM-3974 (109.80), MM-3966 (108.97)
5	Number of fruits per vine	MM-4098 (2.90), MM-4277 (2.81), MM-3858 (2.66)
6	Fruit weight (g)	MM-3866 (155.00g), MM-4002 (1465.00g)
7	Fruit length (cm)	MM-4098 (7.58cm), MM-4271 (9.03)
8	Fruit breadth (cm)	MM-4098 (7.12cm), Chujuc (9.20cm), Dulce-B.B (9.52cm)
9	Seed cavity length (cm)	Chujuc (5.57cm), Dulce-B.B (5.77cm)
10	Seed cavity breadth (cm)	MM-4098 (5.37cm), Chujuc (5.65cm) and Dulce-B.B (5.88).
11	Rind thickness (mm)	Chujuc (3.64mm), Rocky Ford (3.50mm) and Dulce-B.B (3.45mm).
12	Total soluble solids content (%)	Chujuc (13.16%), Rocky Ford (12.86%)
13	Titrable acidity (g anhydrous citric acid/100 ml fruit juice)	MM-3998 (0.36), MM-4005 (0.36)
14	Ascorbic acid content (mg/100g of fruit weight	AR Hale's (38.77), Chujuc (36.50) and Rocky Ford (36.25)
15	Dry matter content (%)	MM-3855 (13.53%), MM-3887 (13.30%)
16	Shelf life (days)	AR Hale's (3.49), Chujuc (3.45), Gulf Stream (3.34)

levels producing a unique tasting melon.

Vitamin C (Ascorbic acid) present in melon is an important anti-oxidant. The genotypes AR Hale's, Chujuc, Gulf Coast, Dulce-B.B, Rocky Ford and Jucumba possessed relatively high value of ascorbic acid. These genotypes could be useful in melon breeding programme for enhancing ascorbic acid content.

The sensory and nutritional quality of fruit is made up of many attributes such as (sweetness, acidity, aroma, firmness, flesh colour and nutrients) that are developed mostly during the ripening phase. In climacteric fruit, such as the melon, the plant hormone ethylene is controlling most of the ripening processes (Giovannoni, 2001). Each sensory attribute is regulated at the molecular level by the expression of specific genes. Genetic studies have demonstrated that in *Cucumis melo* the climacteric character is dominant and controlled by two duplicate loci (Manriquez *et al*, 2006). In melon, an inverse relationship exists between the intensity of ethylene production and the duration of shelf-life (Zheng and Wolff, 2000). Melon with high and sharp climacteric ethylene production such as *cantalupensis* group have shorter shelf-life than *reticulatus group* which produce less ethylene (Manriquez *et al*, 2006). From the present investigation it was evident that genotypes belonging to *reticulatus group* such as AR Hale's, Chujuc, Gulf Stream and Gulf Coast have longer shelf life.

4.3 Components of variation and correlation coefficient

The phenotypic variation could represent only a rough estimate of the variation or magnitude of divergence present among different genotypes. The estimates of phenotypic and genotypic coefficients of variation are more reliable estimates of extent of genetic variability. As the estimates of phenotypic variability cannot differentiate between genetic and environmental effects, it is necessary to divide the phenotypic or observed variation into heritable (variation due to genotype) and environmental components. For this purpose, phenotypic and genotypic coefficients were computed and their estimates are presented in Table 4.7. A relative amount of variation for different characters can be judged by comparing the coefficients of genotypic and phenotypic variation.

Heritability is a measure of genetic relationship between parent and progeny and has been widely used in determining the degree to which a character may be transmitted from parents to offsprings. Knowledge of heritability for the character helps to estimate the genetic advance from selection. The results pertaining to heritability and percentage genetic advance are presented in Table 4.7.

Selection of a particular trait is made on the basis of phenotype, which is produced by interaction of genotype and environment. Genetic advance gives a good idea for actual position (Johnson *et al*, 1955).

4.3.1 Node at which first hermaphrodite flower appears

Node at which first hermaphrodite flower appears exhibited high phenotypic

Table 4.7: Estimates of Phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability (broad sense) and genetic advance for various characters in melon.

Sr. No.	Characters	Phenotypic coefficient of variation (PCV)	Genotypic coefficient of variation (GCV)	Heritability (%)	Genetic advance (%)
1	Node at which first hermaphrodite flower appears	33.45	33.00	92.34	67.08
2	Number of primary branches /vine	27.70	27.16	91.12	54.85
3	Days from sowing to marketable maturity	4.22	3.40	53.94	5.63
4	Days from sowing to last fruit harvest	3.68	2.24	36.96	2.80
5	Number of fruits per vine	19.14	17.30	81.78	32.24
6	Fruit weight (g)	37.98	37.62	94.09	69.25
7	Fruit length (cm)	25.17	24.72	91.48	50.03
8	Fruit breadth (cm)	8.55	7.63	79.66	14.03
9	Seed cavity length (cm)	27.55	27.08	91.58	54.82
10	Seed cavity breadth (cm)	12.28	11.86	90.26	23.59
11	Rind thickness (mm)	19.37	17.93	85.69	34.19
12	Total soluble solids content (%)	28.48	26.65	87.57	51.37
13	Titrable acidity (g anhydrous citric acid/100ml fruit juice)	22.15	21.05	80.05	42.06
14	Ascorbic acid content (mg/100g of fruit weight	28.40	25.73	82.11	48.04
15	Dry matter content (%)	13.29	9.76	64.86	14.77
16	Shelf life (days)	22.05	20.80	89.93	40.40

coefficient of variation (33.45%) and genotypic coefficient of variation (33.00%). The estimate of heritability was very high (92.34%) while genetic advance was also very high (67.08) for this trait. Similar results has been also reported by Nandpuri *et al* (1975), Kalloo *et al* (1983), Lal and Singh (1997), Pandey *et al* (2005) and Rakhi and Rajamony (2005)

4.3.2 Number of primary branches per vine

Number of primary branches per vine show high phenotypic coefficient of variation (27.70%) and genotypic coefficient of variation (27.160%). It also exhibited very high heritability (91.12%) and genetic advance was 54.85%.

4.3.3 Days from sowing to marketable maturity

Days from sowing to marketable maturity displayed low phenotypic coefficient of variation (4.22%) and genotypic coefficient of variation (3.40%). However, it showed moderate heritability (53.94%) and low genetic advance (5.63%). Low phenotypic coefficient of variation and genotypic coefficient of variation for days from sowing to first fruit harvest has also been reported by Swamy *et al* (1985), Dhaliwal *et al* (1996) and Lal and Singh (1997).

4.3.4 Days from sowing to last fruit harvest

Both phenotypic coefficient of variation (3.68%) and genotypic coefficient of variation (2.24%) were low for this trait. It also shows low heritability (36.96%) and low genetic advance (2.80%).

4.3.5 Number of fruits per vine

Number of fruits per vine show moderate phenotypic coefficient of variation (19.14%) and genotypic coefficient of variation (17.03%). However, it displayed high heritability (81.76%) while genetic advance was 32.24%. These results are in agreement with those of Nandpuri *et al* (1975), Kalloo *et al* (1983), Swamy *et al* (1985), Vijay (1987), Lal and Singh (1997) and Pandey *et al* (2005)

4.3.6 Fruit weight (g)

Fruit weight exhibited high phenotypic coefficient of variation (37.98%) and genotypic coefficient of variation (37.62%), whereas very high heritability (94.04%) and very high genetic advance (69.25%) were also observed for this trait. Similar findings have been reported by Swamy *et al* (1985), Vijay (1987), Lal and Singh (1997), Pandey *et al* (2005) Rakhi and Rajamony (2005), and Torkadi *et al* (2007). Higher heritability as well as higher genetic advance which indicated the role of additive gene effects in the expression of this character suggests genetic improvement through inbreeding and selection.

4.3.7 Fruit length (cm)

Fruit length showed high phenotypic coefficient of variation (25.17%) and genotypic coefficient of variation (24.72%). It depicted very high heritability (91.48%) and genetic advance was 50.03%. The results are in conformity with those of Chhonkar *et al* (1979),

Rakhi and Rajamony (2005) and Eduardo *et al* (2007).

4.3.8 Fruit breadth (cm)

Fruit breadth exhibited low phenotypic coefficient of variation 8.55% and genotypic coefficient of variation (7.63%), while it exhibited high heritability (79.66%) and low genetic advance (14.03%) Similar results were obtained by Rakhi and Rajamony (2005) and Eduardo *et al* (2007).

4.3.9 Seed cavity length (cm)

Seed cavity length showed high phenotypic coefficient of variation (27.55%) and genotypic coefficient of variation (27.08%). It also revealed very high heritability (91.58%) and high genetic advance (54.85%). The results are in conformity with those of Kalloo *et al* (1983)

4.3.10 Seed cavity breadth (cm)

Seed cavity breadth showed moderate phenotypic coefficient of variation (12.28%) and genotypic coefficient of variation (11.86%), while it shows very high heritability (90.26%) and genetic advance was 23.59%.

4.3.11 Rind thickness (mm)

Moderate phenotypic coefficient of variation (19.37%) and genotypic coefficient of variation (17.93%) was shown by this trait. However, it exhibited high heritability (85.69%) and genetic advance was 34.19%.

4.3.12 Total soluble solids content (%)

High phenotypic coefficient of variation (28.48%) and genotypic coefficient of variation (26.65%) were reported for this trait. However, it also exhibited high heritability (87.57%) and high genetic advance (51.37%). Results are in conformity with the findings of Chhonkar *et al* (1979) who reported high heritability (92.01) and high genetic advance (45.63%), Swamy *et al* (1985) they showed heritability (64.30%) and genetic advance (39.70), Vijay (1987) who reported heritability (75.77%) and high genetic advance (40.63%), Munshi and Verma (1998) and Pandey *et al* (2005) also reported high heritability and high genetic advance for this trait. The estimated high heritability coupled with high genetic advance indicated the presence of additive gene effects and efficacy of direct selection for this trait.

4.3.13 Titrable acidity (g anhydrous citric acid/100ml fruit juice)

High phenotypic coefficient of variation (22.15%) and genotypic coefficient of variation (21.05%) was shown by this trait, while it also exhibited high heritability (80.05%) and genetic advance was 42.06%. The results are in line with those of Swamy *et al* (1985),

4.3.14 Ascorbic acid content (mg/100g of fresh fruit flesh)

Ascorbic acid content showed high phenotypic coefficient of variation (28.04%) and genotypic coefficient of variation (25.73%), while it also shows high heritability (82.11%)

and genetic advance (48.04%). Similar results have been reported by Swamy *et al* (1985),

4.3.15 Dry matter content (%)

Moderate phenotypic coefficient of variation (13.29%) and low genotypic coefficient of variation (9.76%) was shown by this trait. However, it exhibited high heritability (64.86%) and low genetic advance (14.77%). The results are in agreement with those of Swamy *et al* (1985).

4.3.16 Shelf life

Shelf life exhibited high phenotypic coefficient of variation (22.05%) and genotypic coefficient of variation (20.08%). Heritability was 89.93% and genetic advance was 40.40%.

It was evident from the present investigation that fruit weight, node at which first hermaphrodite flower appears, fruit length, seed cavity length, number of primary branches per vine and total soluble solids content accounted for higher heritability as well as higher genetic advance which indicated the predominance of additive gene effect in the expression of these characters. Hence, the characters could be easily improved by simple selection. Moderate to high values of heritability coupled with moderate genetic advance was obtained for ascorbic acid content, rind thickness, titrable acidity, seed cavity breadth and shelf life indicating equal contribution of additive and non-additive gene effects. Hence, these characters could be partially improved by selection. Higher to moderate heritability estimates and low genetic advance were obtained for days from sowing to first fruit harvest, fruit breadth and dry matter content. The high heritability estimates obtained might be due to favourable effect of environment rather the genetic constitution and in such a situation there is little scope for improvement.

4.4 Correlation coefficients

In plant breeding, the degree of association of plant characters has always been useful for selection. The existence of association between different characters is usually determined by studying correlation existing between them. For this purpose, it is important to know the genetic correlation among different characters, which may provide information regarding the correlated response to selection.

Phenotypic and genotypic correlation coefficients between different characters based on pooled data of two years (2009 and 2010) are presented in Table 4.8.

4.4.1 Node at which first hermaphrodite flower appears

Node at which first hermaphrodite flower appears displayed positive and significant correlation with fruit weight (0.694 and 0.720) both phenotypic and genotypic level and with titrable acidity (0.625 and 0.739), it was highly significant at phenotypic and significant at genotypic level. However, it depicted negative and significant correlation with total soluble solid content (-0.755 and -0.810) both at phenotypic and genotypic level. These results corroborated the results of Taha *et al* (2003). Node at which first hermaphrodite flower

Table 4.8: Estimates of coefficients of correlation between different characters of melon.

Character		Node at which first hermaphrodite flower appears	Number of primary branches/ vine	Days from sowing to marketable maturity	Days from sowing to last fruit harvest	Number of fruiits per vine	Fruit weight (g)	Fruit length (cm)	Fruit breadth (cm)	Seed cavity length (cm)	Seed cavity breadth (cm)	Rind thickness (mm)	Total soluble solids content (%)	Titrable acidity (g anhydrous citric acid/100ml fruit juice)	Ascorbic acid content (mg/100 g of fruit weight)	Dry matter content (%)
Number of primary branches/ vine	P	0.576														
	G	0.590														
Days from sowing to marketable maturity	P	0.337	0.145													
	G	0.445	0.196													
Days from sowing to last fruit harvest	P	0.130	-0.073	0.335*												
	G	0.207	-0.078	0.453*												
Number of fruits per vine	P	-0.056	0.089	-0.043	0.072											
	G	-0.100	0.093	-0.081	0.158											
Fruit weight (g)	P	0.694*	0.300	0.325*	0.123*	-0.408*										
	G	0.720*	0.312	0.424*	0.201**	-0.479*										
Fruit length (cm)	P	0.517	0.602*	0.216	-0.047	-0.370*	0.744*									
	G	0.537	0.645**	0.277	-0.058	-0.440*	0.764*									
Fruit breadth (cm)	P	0.223	0.190	-0.154	-0.074	-0.066	0.281	0.430								
	G	0.264	0.231	-0.222	-0.169	-0.071	0.331	0.467								
Seed cavity length (cm)	P	0.517	0.567	0.242	-0.042	-0.409*	0.753*	0.955*	0.369*							
	G	0.531	0.586	0.300	-0.071	-0.478*	0.775*	0.981*	0.392*							
Seed cavity breadth (cm)	P	0.270	0.191	0.059	0.005	0.124	0.149	0.183	0.433*	0.206*						
	G	0.275	0.194	0.087	0.063	0.126	0.154	0.190	0.543*	0.217*						
Rind thickness (mm)	P	-0.251	-0.655*	0.032	0.055	-0.304*	0.081	-0.267	-0.150	-0.220*	-0.038					
	G	-0.281	-0.720*	0.054	0.091	-0.445*	0.082	-0.296	-0.151	-0.247*	-0.040					
Total soluble solids content (%)	P	-0.755*	-0.632*	-0.186	-0.110	-0.192	-0.290	-0.264	-0.154	-0.250*	-0.130*	0.516				
	G	-0.810*	-0.677*	-0.255	-0.159	-0.206	-0.329	-0.286	-0.177	-0.264*	-0.140*	0.616				
Titrable acidity (g anhydrous citric acid/100ml fruit juice)	P	0.625**	0.530	0.160	0.064	0.138	0.181	0.128	0.120	0.112	0.153*	-0.415	-0.744*			
	G	0.739*	0.632	0.193	0.210	0.196	0.218	0.153	0.142	0.133	0.187*	-0.527	-0.972*			
Ascorbic acid content (mg/100 g of fruit weight)	P	-0.526	-0.698*	-0.112	-0.066	-0.281*	-0.158	-0.323	-0.198	-0.289*	-0.163*	0.660*	0.726*	-0.607*		
	G	-0.594	-0.792*	-0.144	-0.155	-0.387*	-0.172	-0.369	-0.257	-0.332*	-0.187*	0.774*	0.872*	-0.760*		
Dry matter content (%)	P	-0.061	-0.161	0.008	0.023	0.084	0.602**	0.024	0.178	0.056	0.141*	0.007	0.111	-0.169	0.054	
	G	-0.039	-0.216	0.010	0.114	0.232	0.625**	0.043	0.184	0.062	0.213*	0.037	0.189	-0.236	0.068	
Shelf life (days)	P	0.119	-0.477	0.147	0.199*	-0.142	0.298	-0.168	-0.072	-0.134	0.058*	0.618*	0.243	-0.192	0.433*	0.108
	G	0.121	-0.520	0.216	0.350*	-0.218	0.329	-0.179	-0.073	-0.135	0.061**	0.695*	0.254	-0.224	0.479*	0.163

* Significant at 5% (CD 0.1153)
** Significant at 1 % (CD 0.1508)

appears showed positive and non-significant correlation with number of primary branches per vine (0.576 and 0.590), fruit length (0.517 and 0.537), seed cavity length (0.517 and 0.531), days from sowing to marketable maturity (0.337 and 0.445), seed cavity breadth (0.270 and 0.275), fruit breadth (0.223 and 0.264), days from sowing to last fruit harvest (0.130 and 0.207) and shelf life (0.119 and 0.121) both at phenotypic and genotypic level, respectively. Whereas it recorded negative and non-significant correlation with ascorbic acid content (-0.526 and -0.594), rind thickness (-0.251 and -0.281), number of fruits per vine (-0.056 and -0.100) and dry matter content (-0.061 and -0.039) both at phenotypic and genotypic level, respectively.

4.4.2 Number of primary branches per vine

Number of primary branches per vine exhibited positive and significant correlation with fruit length (0.602 and 0.645) at phenotypic and highly significant at genotypic level. Whereas it showed negative and significant correlation with ascorbic acid content (-0.698 and -0.792), rind thickness (-0.655 and -0.720) and total soluble solids content (-0.632 and -0.677) both at phenotypic and genotypic level, respectively. However, it displayed non-significant and positive correlation titrable acidity (0.530 and 0.632), seed cavity length (0.567 and 0.586), fruit weight (0.300 and 0.312), fruit breadth (0.190 and 0.231), days from sowing to marketable maturity (0.145 and 0.196), seed cavity breadth (0.191 and 0.194) and number of fruits per vine (0.089 and 0.093) both at phenotypic and genotypic level, respectively, while it recorded negative and non-significant correlation with shelf life (-0.477 and -0.520), dry matter content (-0.161 and -0.216) and days from sowing to last fruit harvest (-0.073 and -0.078) both at phenotypic and genotypic level, respectively.

4.4.3 Days from sowing to marketable maturity

Days from sowing to marketable maturity displayed positive and significant correlation with days from sowing to last fruit harvest (0.335 and 0.453) and fruit weight (0.325 and 0.424) both at phenotypic and genotypic level, while it exhibited positive and non-significant correlation with seed cavity length (0.242 and 0.300), fruit length (0.216 and 0.277), shelf life (0.147 and 0.216), titrable acidity (0.160 and 0.193), seed cavity breadth (0.059 and 0.087), rind thickness (0.032 and 0.054) and dry matter content (0.008 and 0.010) both at phenotypic and genotypic level, respectively. However, it depicted negative and non-significant correlation with total soluble solid content (-0.186 and -0.255), fruit breadth (-0.154 and -0.222), ascorbic acid content (-0.112 and -0.144) and number of fruits per vine (-0.043 and -0.081) both at phenotypic and genotypic level, respectively.

4.4.4 Days from sowing to last fruit harvest

Days from sowing to last fruit harvest revealed positive and significant correlation

with shelf life (0.199 and 0.350) both at phenotypic and genotypic level and with fruit weight (0.123 and 0.201) significant at phenotypic and highly significant at genotypic level, while it showed positive and non-significant correlation with number of fruits per vine (0.072 and 0.158), titrable acidity (0.064 and 0.210), dry matter content (0.023 and 0.114), rind thickness (0.055 and 0.091) and seed cavity breadth (0.005 and 0.063) both at phenotypic and genotypic level, respectively. However, it displayed negative and non-significant correlation with fruit breadth (-0.074 and -0.169), total soluble solids content (-0.110 and -0.159), ascorbic acid content (-0.066 and -0.155), seed cavity length (-0.042 and -0.071) and fruit length (-0.047 and -0.058) both at phenotypic and genotypic level, respectively.

4.4.5 Number of fruits per vine

Number of fruits per vine exhibited significant and negative correlation with fruit weight (-0.408 and -0.479), seed cavity length (-0.409 and -0.478), rind thickness (-0.304 and -0.445), fruit length (-0.370 and -0.440) and ascorbic acid content (-0.281 and -0.387) both at phenotypic and genotypic level, respectively. Taha *et al* (2003), Singh and Lal (2005) and Zalapa *et al* (2007) reported similar findings for this character. However, it displayed positive and non-significant correlation with dry matter content (0.084 and 0.232), titrable acidity (0.138 and 0.196) and seed cavity breadth (0.124 and 0.126) both at phenotypic and genotypic level, respectively. However, it showed negative and non-significant correlation with shelf life (-0.142 and -0.218), total soluble solid content (-0.192 and -0.206), fruit breadth (-0.066 and -0.071) both at phenotypic and genotypic level, respectively.

4.4.6 Fruit weight (g)

Estimation of correlation coefficients indicated that fruit weight had significant and positively correlated with seed cavity length (0.753 and 0.775) and fruit length (0.744 and 0.764) both at phenotypic and genotypic level, respectively and with dry matter content (0.602 and 0.625) highly significant at phenotypic and genotypic level, respectively. Similar results were reported by Singh and Ram (2003) and Pandey *et al* (2005), however, it recorded non-significant and positive correlation with fruit breadth (0.281 and 0.331), shelf life (0.298 and 0.329), titrable acidity (0.181 and 0.218), seed cavity breadth (0.149 and 0.154) and rind thickness (0.081 and 0.082) both at phenotypic and genotypic level, respectively. However, fruit weight depicted non-significant and negative correlation with total soluble solids content (-0.290 and -0.329) and ascorbic acid content (-0.158 and-0.172) both at phenotypic and genotypic level, respectively. Similar results were reported by Kaloo *et al* (1982), Swamy *et al* (1985), Swamy and Dutta (1991) and Mehta *et al* (2009).

4.4.7 Fruit length (cm)

Fruit length showed positive and significant correlation with seed cavity length (0.955 and 0.981) both at phenotypic and genotypic level. Similar results were found by Panday *et al* 2005, while, it displayed positive and non-significant correlation with fruit breadth (0.430 and 0.467), seed cavity breadth (0.183 and 0.190), titrable acidity (0.128 and 0.153) and dry matter content (0.024 and 0.043) both at phenotypic and genotypic level, respectively. However, it exhibited negative and non-significant correlation with ascorbic acid content (-0.323 and -0.369), rind thickness (-0.267 and -0.296), total soluble solids (-0.264 and -0.286) and shelf life (-0.168 and – 0.179) both at phenotypic and genotypic level, respectively.

4.4.8 Fruit breadth (cm)

Fruit breadth depicted positive and significant correlation with seed cavity breadth (0.433 and 0.543) and seed cavity length (0.369 and 0.392) both at phenotypic and genotypic level, while it exhibited positive and non-significant correlation with titrable acidity (0.120 and 0.142) and dry matter content (0.178 and 0.184) both at phenotypic and genotypic level, respectively. However, it revealed negative and non-significant correlation with ascorbic acid content (-0.198 and -0.257), total soluble solids content (-0.154 and -0.177), rind thickness (-0.150 and 0.151) and shelf life (-0.072 and-0.073) both at phenotypic and genotypic level, respectively.

4.4.9 Seed cavity length (cm)

Seed cavity length displayed significant and positive correlation with seed cavity breadth (0.206 and 0.217) both at phenotypic and genotypic level. However, it showed significant and negative correlation with ascorbic acid content (-0.289 and -0.332), total soluble solids content (-0.250 and -0.264) and rind thickness (-0.220 and -0.247) both at phenotypic and genotypic level, respectively, whereas it recorded non-significant and positive correlation with titrable acidity (0.112 and 0.133) and dry matter content (0.056 and 0.062) both at phenotypic and genotypic level, respectively. However, it exhibited non-significant and negative correlation with shelf life (-0.134 and -0.135) both at phenotypic and genotypic level, respectively.

4.4.10 Seed cavity breadth (cm)

Seed cavity breadth exhibited significant and positive correlation with dry matter content (0.141 and 0.213), titrable acidity (0.153 and 0.187) both at phenotypic and genotypic level and with shelf life (0.058 and 0.061) it showed significant at phenotypic and highly significant at genotypic level. However it depicted significant and negative correlation with ascorbic acid content (-0.163 and -0.187) and total soluble solids content (-0.130 and -

0.140) both at phenotypic and genotypic level, while it showed non-significant and negative correlation with rind thickness (-0.038 and -0.040) both at phenotypic and genotypic level.

4.4.11 Rind thicknesses (mm)

Rind thickness recorded positive and significant correlation with ascorbic acid content (0.660 and 0.774) and shelf life (0.618 and 0.695) both at phenotypic and genotypic level respectively, while it displayed positive and non-significant correlation with total soluble solids content (0.516 and 0.616) and dry matter content (0.007 and 0.037) both at phenotypic and genotypic level, respectively. However, it showed negative and non-significant correlation with titrable acidity (-0.415 and -0.527) both at phenotypic and genotypic level.

4.4.12 Total soluble solids content (%)

Total soluble solid content depicted positive and significant correlation with ascorbic acid (0.726 and 0.872) both at phenotypic and genotypic level. However, it displayed negative and significant correlation with titrable acidity (-0.744 and -0.972) both at phenotypic and genotypic level. Similar results have been reported by Burger *et al* (2004). While it exhibited positive and non-significant correlation with shelf life (0.243 and 0.254) and dry matter content (0.111 and 0.189) both at phenotypic and genotypic level, respectively.

4.4.13 Titrable acidity (g anhydrous citric acid/100ml fruit juice)

Titrable acidity showed significant and negative correlation with ascorbic acid content (-0.607 and -0.760) both at phenotypic and genotypic level. However, it exhibited negative and non-significant correlation with dry matter content (-0.169 and -0.236) and shelf life (-0.192 and -0.224) both at phenotypic and genotypic level, respectively.

4.4.14 Ascorbic acid content (mg/100g of fresh fruit flesh)

Ascorbic acid content reported positive and significant correlation with shelf life (0.433 and 0.479) both at phenotypic and genotypic level. However, it depicted positive and non-significant correlation with dry matter content (0.054 and 0.068) both at phenotypic and genotypic level.

The result of phenotypic and genotypic correlation coefficients between various characters indicated that the magnitude of genotypic correlation coefficient were slightly higher than their corresponding phenotypic correlation coefficients for all the characters, which may be ascribed to low environmental effect on these characters and indicating that there is strong inherent association between various characters under study (Choudhary *et al*, 2004). Melon (*Cucumis melo* L.) is an important member of family cucurbitaceae. The natural genetic variation for most of the yield attributes is considerable in this crop and there

is a need to broaden the genetic base of the new varieties. Correlation study between fruit weight and their relative contribution to yield will be of value in planning a melon breeding programme (Chhonkar *et al*, 1979)

Based on simple correlation fruit characters namely seed cavity length (0.753 and 0.775), fruit length (0.744 and 0.764), dry matter content (0.602 and 0.625) and fruit breadth (0.281 and 0.331) were found to be positively correlated with fruit weight. Therefore, it is obvious that fruit weight can be easily manipulated to the desired level through selection based on these characters. It was further noted that these characters were positively correlated among themselves also. This indicates that there is no hindrance in manipulating melon fruit size through breeding approaches. Given the negative correlation between fruit number per vine and average fruit weight, the development of genotypes capable of supporting moderate number of fruits along with maintaining commercially acceptable fruit size is desirable. Increasing the yield of melon through increasing the number of fruits alone with high TSS may be a challenge for breeder. Therefore, to increase fruit weight, seed cavity length, fruit length and fruit breadth can be used as selection indices.

Node at which first hermaphrodite flower appears and days from sowing to marketable maturity showed highly significant and positive correlation with fruit weight (0.694 and 0.720) and (0.325 and 0.424), respectively. As node at which first hermaphrodite flower appears and days from sowing to marketable maturity are characters of earliness, indicating association of fruit weight with these characters.

In melon, fruit quality assumes a great significance from consumers point of view. Though TSS did not show positive and significant correlation with the important traits the reason being large number of genotypes used and genetic divergence, but this trait is given utmost importance during selection in muskmelon. Thus, it could be concluded that although heavier fruits tend to have lower total soluble solids content but maintaining a desirable total soluble solids content with optimum fruit size should be objective of breeder (Singh and Ram, 2003).

Total soluble solids content displayed significant and positive correlation with ascorbic acid content both being important quality traits. Hence, selection for these traits would bring about an improvement in melon quality. However, total soluble solids content and ascorbic acid content exhibited significant and negative correlation with titrable acidity. From this investigation it was clear that high acid containing genotypes do not accumulate the high level of total soluble solids content and combination of high acid and high sugar does not appear to occur in these genotypes. This compliments the findings of Stepansky *et al* (1999b). However, independent genetic control of sugar and acid accumulation in sweet

melon has been demonstrated (Burger *et al*, 2003). Therefore, the combination of these two traits in melon opens up the possibility of breeding a unique tasting melon.

4.5 Clustering pattern based on D^2 analysis

Knowledge of genetic diversity of a crop and its quantitative assessment usually helps a plant breeder in choosing desirable parents for breeding programme. Geographic diversity in crop plants, very often fails to convey information about the genetic divergence. Therefore, it is worthwhile to use suitable tools like D^2 statistics (Mahalanobsis 1936) as a quantitative measure of genetic divergence.

4.5.1 Distribution of genotypes to different clusters

In the present study, D^2 analysis for sixteen traits, grouped the test genotypes into ten clusters (Table 4.9) with variable number of entries in each cluster indicating the presence of genetic diversity in the genotypes of present study. Cluster I contained maximum number of genotypes thirty-seven, cluster II with sixteen genotypes, cluster III with one genotype indicated an independent identity and importance due to the various unique characters possessed by the genotype, cluster IV with twelve genotypes, cluster V with four genotypes, cluster VI with thirteen genotypes, cluster VII with six genotypes, cluster VIII with three genotypes, cluster IX with two genotypes and cluster X with two genotypes. The formation of different clusters with variable number of entries in each cluster indicated diversity among genotypes. The genotypes from two countries or four agro-ecological zones were found to be scattered in different clusters, which suggested that a pattern of clustering of accessions was independent of their geographic origin. No parallelism was found between genetic and geographic diversity. This mixed grouping of genotypes from different origin in same cluster could be due to extensive utilization of a few donor species to develop melon genotypes across the world or due to unidirectional selection pressure practiced by the breeders in tailoring the promising cultivars. Similar results were reported by Prasad *et al* (2004) and Dhillon *et al* (2007).

4.5.2 Identification of diverse and desirable genotypes

Non-hierarchical cluster analysis was also performed in addition to grouping of genotypes into different clusters so as to identify the diverse and desirable genotypes in terms of inter cluster distance and mean performance of clusters for various characters, respectively. For this purpose intra and inter cluster distances (Table 4.10) and mean performance of each cluster for different traits was studied. The intra and inter cluster distances are pictorially represented in Figure 7.

The intra cluster distances ranged from 0.00 (cluster III) to 40.35 (cluster VIII) indicating that the genotypes in clusters have dissimilarity for morphological characters and

performance. The members of cluster IX and cluster III exhibited maximum divergence (inter-cluster distance 1028.24) followed by the members of cluster X and III (inter-cluster distance 938.21) and cluster IX and II (inter-cluster distance 876.17). However, the members of cluster VI and IV were least divergent (inter-cluster distance 66.05). The inter cluster distances were larger than the intra cluster distances indicating a wider genetic diversity between genotypes of clusters with respect to traits considered. Maximum inter-cluster distance indicates that genotypes falling in these clusters had wide diversity and can be used for hybridisation programme to get better recombinants in the segregating generations. Low levels of intra-cluster distances reveal narrow genetic variation within the cluster. Genotypes of same cluster may not provide desirable recombinants.

The cluster mean values for sixteen characters are presented in Table 4.11**.** The perusal of data indicated considerable differences for all the characters among clusters. It is inferred from the cluster means that each cluster has its uniqueness that separated it from other cluster. For example, cluster I was characterized by lowest mean value for days from sowing to marketable maturity (81.58) and titrable acidity (0.08 g anhydrous citric acid/100ml fruit juice). Genotypes belonging to the cluster II showed lowest mean value for days from sowing to last fruit harvest (102.65) and titrable acidity (0.08 g anhydrous citric acid/100ml fruit juice). However, cluster III includes the genotypes that produce highest mean value for number of fruits per vine (2.97), while it has lowest mean value for node at which first hermaphrodite flower appears (2.04), fruit weight (456.99g), fruit length (7.58cm), fruit breadth (7.12cm), seed cavity length (5.82cm), seed cavity breadth (5.37cm), titrable acidity (0.08 g anhydrous citric acid/100ml fruit juice) and dry matter content (8.56). Genotypes belonging to cluster IV displayed the highest mean value for days from sowing to last fruit harvest (106.56).

Genotypes belonging to cluster VI contained maximum mean value for node at which first hermaphrodite flower appears (4.82) and titrable acidity (0.29 g anhydrous citric acid/100ml fruit juice), while lowest mean value was found for rind thickness (1.89mm), total soluble solids content (4.02%), ascorbic acid content (12.13mg/100 g of fruit weight). Cluster VII was characterized by maximum mean value for days from sowing to marketable maturity (84.70), rind thickness (3.20mm), total soluble solids content (12.00 %), ascorbic acid content (33.80 mg/100 g of fruit weight) and shelf life (3.17 days), while the lowest mean value for number of primary branches/ vine (2.69). However, cluster VIII exhibited the highest mean value for dry matter content (11.43%), whereas cluster IX depicted highest mean value for fruit weight (1485.00g), fruit length (21.16), fruit breadth (12.50cm), seed cavity length (17.57cm) and seed cavity breadth (8.56cm), while the lowest mean value for

shelf life (1.94 days). Cluster X was characterized by the highest mean value for number of primary branches/ vine (6.61).

The knowledge of genetic divergence available in the germplasm has been successfully exploited for the selection of parents in many crop species as the concept of 'Genetic divergence' or 'Genetic distance' has been of vital utility in differentiating well defined populations.

In the present study, ninety-six genotypes of melon were classified into ten clusters with inter-cluster distance ranging from 66.05 (between cluster VI and IV) to 1028.24 (between cluster IX and cluster III). In this study, fruit weight showed significant difference for cluster means in cluster IX and cluster III as judged from the highest distance. Therefore, it may be suggested that crosses between these two clusters are likely to give new desirable recombinants. Crosses between cluster X and cluster III and cluster IX and cluster II, might be advantageous as they showed that genotypes found in one cluster were not close to those found in other cluster.

The importance of different plant characters in the inter-cluster divergence can be studied further by comparing cluster mean for different characters. Based on mean of the clusters, the donors for different characters could be selected from clusters. , cluster I for days from sowing to marketable maturity, cluster III for number of fruits per vine and lowest node at which first hermaphrodite flower appears, cluster VI for titrable acidity, cluster VII for rind thickness, total soluble solids content, ascorbic acid content and shelf life, cluster VIII for dry matter content, cluster IX for fruit weight, fruit length, fruit breadth and cluster X for number of primary branches per vine.

Crossing between individuals from clusters with maximum inter cluster distance may result in higher heterosis. However, it has been observed from various studies that crosses between genetically distant parents, show greater heterosis than crosses between closely related parents (Stuber *et al* 1992). The cluster comprising one genotype with specific valuable traits and other genotype falling in highly divergent group will help in broadening the existing genetic base of the crop.

Table 4.9: Clustering pattern of various accessions based on D^2 analysis.

Sr.No.	Cluster number	Number of genotypes in cluster	Genotypes
1	Cluster I	37	MM-3833, MM-3839 , MM-3843, MM-3857, MM-3859, MM-3864, MM-3868, MM-3874 , MM-3884, MM-3917, MM-3947, MM-3955, MM-3956, MM-3961, MM-3963, MM-3965, MM-3973, MM-3985, MM-3986, MM-4003, MM-4018, MM-4021, MM-4026, MM-4067, MM-4243, MM-4248, MM-4250, MM-4251, MM-4253, MM-4256, MM-4270, MM-4276, MM-4278, MM-4283, MM-4305, MM-4342, MM-4409.
2	Cluster II	16	MM-3837, MM-3849, MM-3850, MM-3851, MM-3856, MM-3858, MM-3881, MM-3909, MM-3979, MM-3980, MM-3981, MM-3983, MM-4013, MM-4063, MM-4068 , MM-4282
3	Cluster III	1	MM-4098
4	Cluster IV	12	MM-3860, MM-3968, MM-3976, MM-3977, MM-4059, MM-4066, MM-4252, MM-4268, MM-4277, MM-4279, Jucumba, Chujuc
5	Cluster V	4	MM-3885, MM-3901, MM-4065, Dulce-B.B
6	Cluster VI	13	MM-3887, MM-3962, MM-3966, MM-3974, MM-3982, MM-3994, MM-3998, MM-4004, MM-4005, MM-4091, MM-4247, MM-4267, MM-5736
7	Cluster VII	6	MM-4271, AR Hale’s, Rocky Ford, Gulf Stream, Hannah’s Choice, Gulf Coast
8	Cluster VIII	3	MM-3855, MM-3889, MM-4057
9	Cluster IX	2	MM-3866, MM-4002
10	Cluster X	2	MM-3903, MM-4030

Table 4.10: The Inter and Intra cluster (Underlined) average D^2 values and distances ($\sqrt{D^2}$) among melon accessions studied.

	Cluster I	**Cluster II**	**Cluster III**	**Cluster IV**	**Cluster V**	**Cluster VI**	**Cluster VII**	**Cluster VIII**	**Cluster IX**	**Cluster X**
Cluster I	20.60	66.411	218.25	245.04	312.67	182.36	401.37	635.09	810.11	720.07
Cluster II		17.48	152.26	311.10	378.73	248.28	467.42	701.15	876.17	786.13
Cluster III			0.00	463.12	530.76	400.07	619.44	853.22	1028.24	938.21
Cluster IV				24.14	68.11	66.05	156.60	390.33	565.30	475.28
Cluster V					15.38	132.42	89.17	322.86	497.78	407.77
Cluster VI						21.96	221.02	453.58	628.53	538.54
Cluster VII							23.82	234.80	409.48	319.52
Cluster VIII								40.35	175.06	85.14
Cluster IX									40.10	90.15
Cluster X										30.52

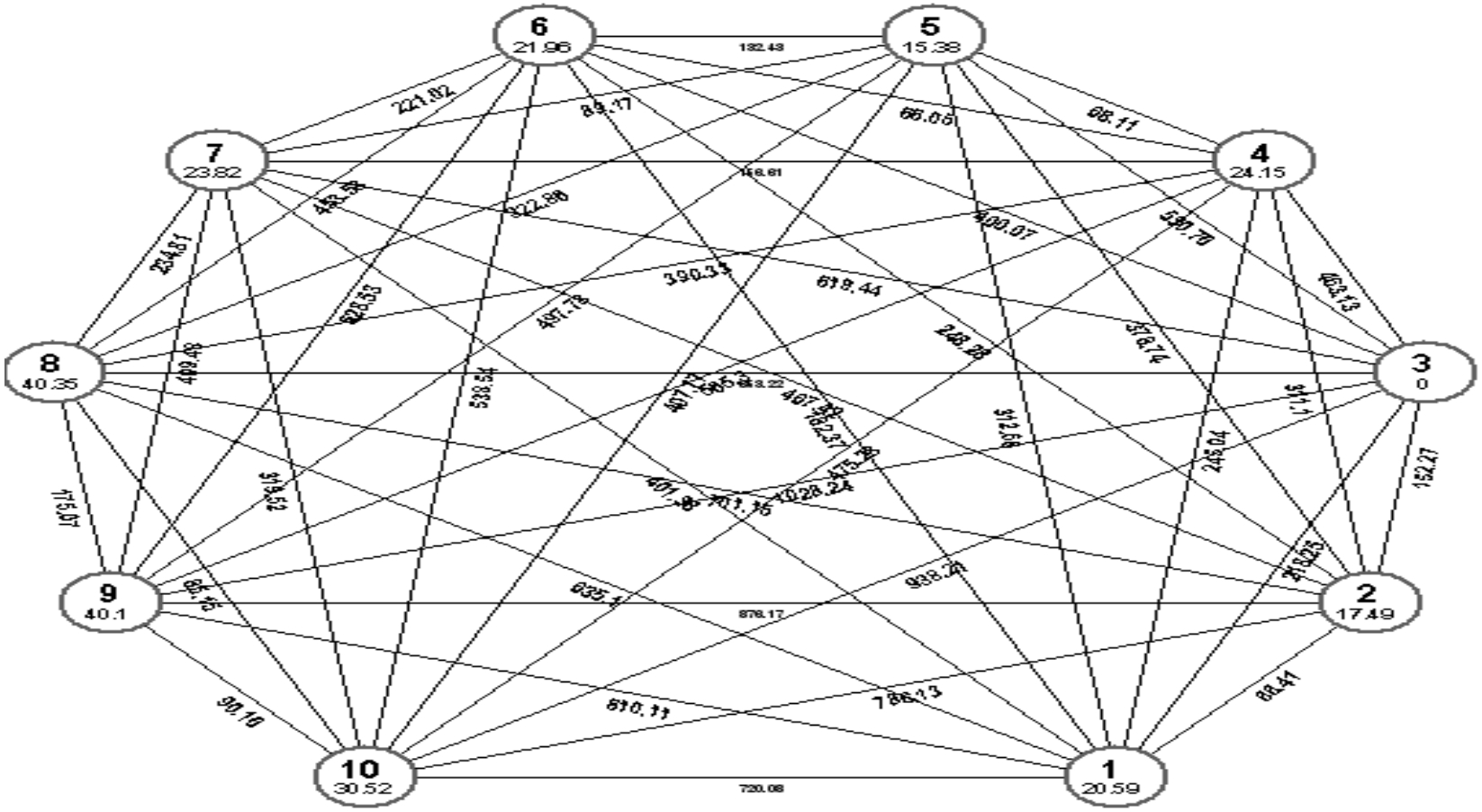


Figure 2: Genetic divergence ($\sqrt{D^2}$) among melon accessions.

Table 4.11: Mean performance of different clusters for evaluated morphological traits of melon accessions studied.

Characters	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII	Cluster IX	Cluster X
Node at which first hermaphrodite flower appears	2.20	2.58	2.04	3.31	3.60	4.82	3.50	4.81	4.45	4.75
Number of primary branches/ vine	3.90	4.25	4.30	3.45	3.14	5.69	2.69	6.45	6.52	6.61
Days from sowing to marketable maturity	81.58	81.96	83.54	84.47	84.19	85.08	84.70	87.03	87.35	86.65
Days from sowing to last fruit harvest	103.98	102.65	106.18	106.56	106.42	106.24	105.54	104.79	105.72	103.13
Number of fruits per vine	2.28	2.30	2.97	2.29	2.17	2.30	1.87	1.82	1.84	1.70
Fruit weight (g)	675.13	609.06	456.99	920.04	987.68	856.69	1076.33	1310.00	1485.00	1395.00
Fruit length (cm)	9.92	10.24	7.58	10.76	9.81	10.71	9.55	19.33	21.16	19.91
Fruit breadth (cm)	10.61	10.55	7.12	11.22	10.68	11.11	9.89	11.45	12.50	12.17
Seed cavity length (cm)	7.04	7.34	5.82	7.66	6.86	7.79	6.63	16.03	17.57	15.94
Seed cavity breadth (cm)	7.45	7.44	5.37	7.97	7.41	7.95	6.67	7.71	8.56	8.20
Rind thickness (mm)	2.29	2.37	2.10	2.66	2.88	1.89	3.20	1.95	2.10	1.92
Total soluble solids content (%)	11.53	11.72	11.50	11.56	10.97	4.02	12.00	9.13	7.95	7.65
Titrable acidity (g anhydrous citric acid/100ml fruit juice)	0.08	0.08	0.08	0.08	0.10	0.29	0.09	0.13	0.14	0.15
Ascorbic acid content (mg/100 g of fruit weight)	24.27	25.10	24.69	26.63	27.88	12.13	33.80	17.32	15.50	17.66
Dry matter content (%)	9.43	9.43	8.56	10.51	10.93	10.07	10.74	11.43	10.07	9.90
Shelf life (days)	2.07	2.03	2.35	2.82	3.07	2.10	3.17	2.01	1.94	1.97

4.6 Characterization on the basis of SSR markers

4.6.1 SSR marker analysis of melon germplasm

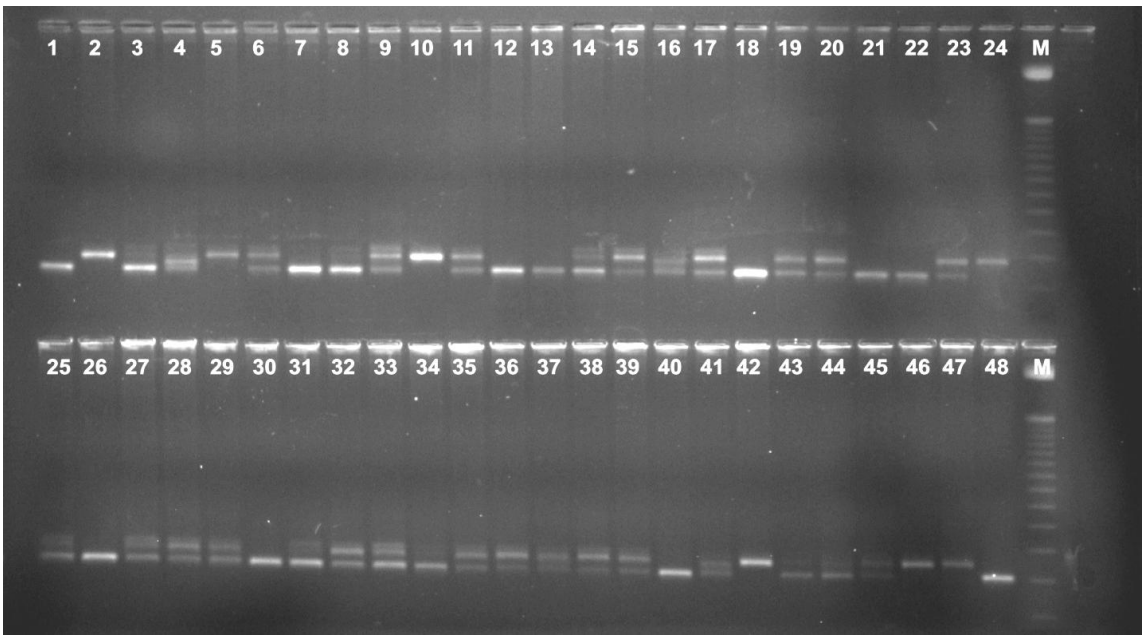
The summarized data of 30 SSR primers used for identification and evaluation of genetic diversity of 96 melon accessions is presented in Table 4.12. Out of 30 SSR primers used, 23 showed polymorphism among 96 melon accessions. The primer pairs (30) resulted in amplification of 67 alleles with an average of 2.23 alleles per locus. The highest number of alleles four was amplified by ECM 51. The variation in the number of alleles produced by SSR markers demonstrates heterozygosity in different alleles at a given locus in which the heterozygosity could reflect greatly the state of genetic variability (Plate 4a and 4b). All these amplified fragments produced different finger printing pattern that allowed all the varieties analysed to be distinguished. The average number of alleles per SSR marker reported herein (2.23) are in agreement with those of Lopez- Sese *et al* (2002) who found (2.4) alleles per locus and Tzitzikas *et al* (2009) who found 2.47 alleles per locus. The PCR amplification profile of SSR markers in ninety-six accessions for primer ECM 51 is shown in Plate 4.

4.6.2 Polymorphic Information Content (PIC)

The PIC values provide an estimate of the discriminating power of a marker by taking into account not only the number of alleles at a locus but also relative frequencies of those alleles in the genotypes. The data pertaining to polymorphic information content (PIC) values and the number of alleles detected for each of the 30 SSR markers are presented in Table 4.12. PIC values ranged from 0.42 (ECM124) to 0.74 (ECM51) with an average value of 0.57 across 96 melon genotypes. The results for highest PIC value (0.74) and average PIC value (0.57) are in agreement with previous studies of Chiba *et al* (2003) and Kong *et al* (2011) who reported a PIC value of 0.74 and 0.64, respectively. The PIC values of a primer vary with the crop and the set of the genotypes used. Lower PIC value may be the result of closely related genotypes and higher PIC values may be the result of diverse genotypes. Senior *et al* (1998) reported that marker loci with an average number of alleles running at equal frequencies will have the highest PIC values. The second reason for high PIC values could be due to differences in medium for resolving the amplified products (agarose gels vs. polyacrylamide gels) as reported by Smith *et al* (1997) who observed slightly higher average PIC value (0.62) when acrylamide gels were used for allele detection. In the present study, a high average value of polymorphism information content (PIC) was found indicating that this could be a valid tool for discrimination of melon genotypes.

Table 4.12: PIC value and number of alleles amplified by SSR markers

Sr. No.	Primer	No. of alleles amplified		Percent of polymorphism	PIC value
		Total	Polymorphic		
1	**CMTC13**	3	3	100	0.60
2	**CMAG59**	1	0	0	0.00
3	**CMCTN38**	3	3	100	0.65
4	**CMMS004**	1	0	0	0.00
5	**CMMS33-1**	3	3	100	0.65
6	**CMMS3-1**	3	3	100	0.65
7	**CMMS1-3**	2	2	100	0.46
8	**CMGA127**	2	2	100	0.44
9	**CMMS35-4**	3	3	100	0.62
10	**CMCGAN21**	3	3	100	0.67
11	**CMTCN8F**	1	0	0	0.00
12	**CMGA128**	2	2	100	0.49
13	**CMMS14-1**	2	2	100	0.48
14	**CMMS30-3**	1	0	0	0.00
15	**ECM51**	4	4	100	0.74
16	**ECM130**	3	3	100	0.66
17	**ECM182**	1	0	0	0.00
18	**ECM125**	3	3	100	0.62
19	**ECM65**	2	2	100	0.50
20	**ECM85**	1	0	0	0.00
21	**ECM109**	3	3	100	0.64
22	**ECM80**	1	0	0	0.00
23	**ECM129**	3	3	100	0.66
24	**ECM178**	3	3	100	0.66
25	**ECM61**	2	2	100	0.48
26	**ECM124**	2	2	100	0.42
27	**ECM70**	3	3	100	0.63
28	**ECM50**	2	2	100	0.50
29	**ECM133**	2	2	100	0.48
30	**ECM134**	2	2	100	0.46
Average		**2.23**			**0.57**



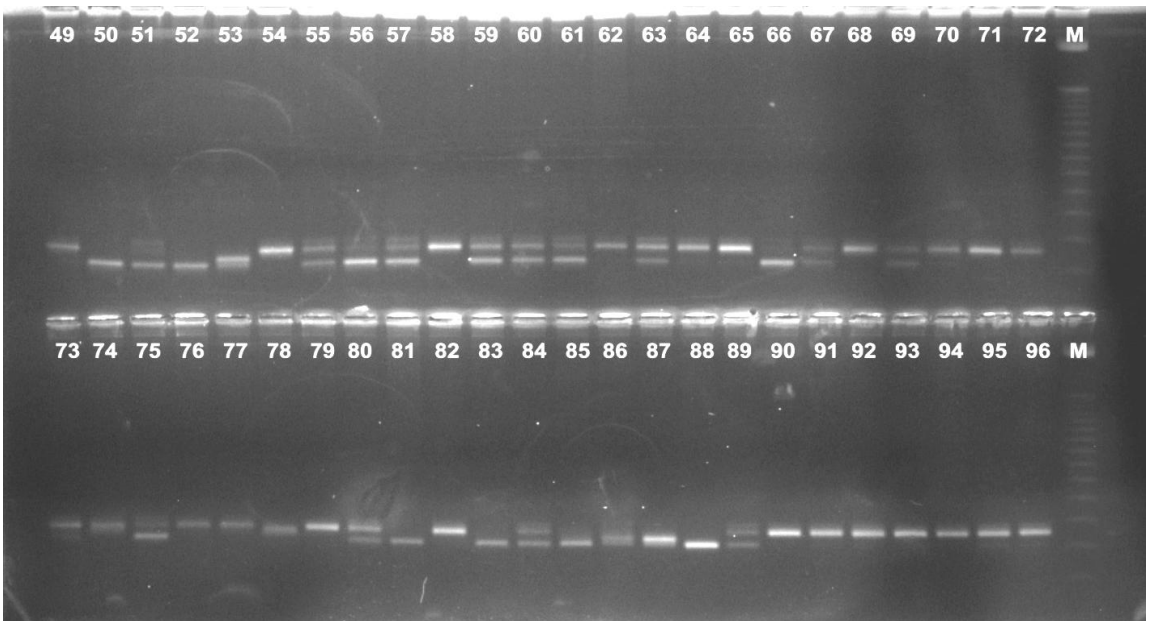


Plate 4: Amplification profile generated by primer ECM51 for 96 melon accessions where M = 50 bp DNA ladder

4.6.3 Similarity coefficient and cluster analysis based on molecular basis

The similarity coefficient based on DNA amplification of 96 melon genotypes using SSR primers was estimated by dice similarity coefficient. The dendrogram generated based on Unweighted Pair Group Method with Arithmetic Average (UPGMA) is depicted in Figure 3. Genetic similarity values between genotypes ranged from 0.25 to 0.80 as depicted in dendrogram. Factor Correspondence Analysis (FCA) was also done to visualize the relationship among melon accessions (Fig 4).

From the dendrogram (Fig 3), it is evident that the 96 melon genotypes studied in present experiment constituted three major clusters, I, II and III. There was a significant correlation between botanical groups and the clustering. Accessions belonging to *cantalupensis* except MM-3985 (79), MM-3903 (57) and MM-4030 (56) grouped together in cluster I. Accessions belonging to the *reticulatus* group, except MM-3968 (82) and MM-4268 (58) grouped together in cluster II and accessions belonging to the *momordica* group cluster together in cluster III. The largest cluster I consisted sixty genotypes and was further subdivided into sub groups IA, IB, IC, ID, IE and IF. Each subgroup is coalescing at different similarity coefficient. The subgroup IA comprises of twelve accessions. Among them MM-3833 and MM-3849 showed highest similarity coefficient of 0.66 between themselves. MM-3833 and MM-3849 were collected from same sub-zone (13.1) and had almost same stem shape, leaf margins, fruit skin primary colour, fruit skin secondary colour, fruit shape, number of fruits per vine, node at which the first hermaphrodite flower appears and fruit weight. Sub group IB consists of eight accessions. Among them MM-3979 and MM-3973 showed highest similarity coefficient of 0.68. These accessions were collected from same sub-zone (9.1). Both had almost same stem shape, fruit shape, skin primary colour, node at which the first hermaphrodite flower appears and fruit, number of fruits per vine, fruit length and dry matter content. Subgroup IC consists of seventeen accessions. Among them MM-3868 and MM-3881 showed highest similarity coefficient of 0.77. Both were collected from same sub-zone (13.1). Both have almost same stem shape, fruit shape, days from sowing to marketable maturity, days from sowing to last fruit harvest, fruit length and seed cavity length. Subgroup ID comprises of eleven accessions. Among them MM- 3986 and MM- 3843 showed highest similarity coefficient of 0.68. Both had almost same stem shape, leaf margins, fruit shape, number of primary branches per vine, fruit weight, fruit length and rind thickness. Subgroup IE comprises of seven accessions. Among them MM- 3851 and MM- 4067 showed highest similarity coefficient of 0.62 both had almost same leaf margins, fruit shape and stem shape and subgroup IF comprised five accessions. Among them MM- 4018 and MM- 4409 showed highest similarity coefficient of 0.65. Both were collected from same sub-zone (9.1) and these

had almost same stem shape, fruit shape, ascorbic acid content and dry matter content.

Cluster II consisted of twenty-four accessions and was further subdivided into IIA, IIB and IIC. The subgroup IIA comprised all eight reference accessions. Among them AR Hale's and Rocky Ford showed highest similarity coefficient of 0.78 between themselves. AR Hale's and Rocky Ford have almost same node at which the first hermaphrodite flower appears, number of primary branches per vine, fruit weight, seed cavity length, stem shape, leaf margins, fruit skin primary colour and stem shape. The subgroup IIB comprised ten accessions. Among them MM- 3885 and MM-3966 showed highest similarity coefficient of 0.80. Both were collected from same sub-zone (13.1). These have almost same stem shape, number of primary branches per vine, node at which the first hermaphrodite flower appears, fruit length, fruit breadth, fruit skin primary colour, rind thickness and shelf life. The subgroup IIC comprised six accessions. Among them MM-3976 and MM-3977 showed highest similarity coefficient of 0.79. These were collected from same sub-zone (9.1) and these have almost same stem shape, fruit shape, node at which the first hermaphrodite flower appears, number of fruits per vine and seed cavity length.

Cluster III consisted of twelve genotypes which had accessions belonging to the *momordica* group and were further subdivided into IIIA IIIB, IIIC and one un-clustered accession. The subgroup IIIA comprised three accessions. Among them MM-4004 and MM-4005 showed highest similarity coefficient of 0.78 among themselves. MM-4004 and MM-4005 were collected from same sub-zone (9.2). Both have almost same stem shape, leaf margins, fruit weight, titrable acidity and dry matter content. The subgroup IIIB comprised five accessions. Among them MM- 5736 and MM- 3974 showed highest similarity coefficient of 0.79 between themselves. Both have almost same stem shape, leaf margins, fruit shape and dry matter content. The subgroup IIIC comprised of three accessions. Among them MM-4091 and MM-4267 showed highest similarity coefficient of 0.77 between themselves. Both have almost same fruit shape, leaf margins node at which first hermaphrodite flower appears, number of fruits per vine and fruit weight. However, MM-3994 does not form group with any accession.

However, some accessions of *cantalupensis* and *reticulatus* were intermixed in cluster I and II. Two accessions (MM-3968 and MM-4268) of group *reticulatus* were grouped in cluster I together with group *cantalupensis*. Similarly three accessions (MM-3985, MM-3903 and MM-4030) of group *cantalupensis* were grouped in cluster II together with group *reticulatus.* Yi-San *et al* (2009) also observed intermixing of some of the melon accessions while analyzing genetic diversity in melon landraces using RAPD markers.

Factor Correspondence Analysis (FCA) was performed to visualize the relationship

among melon accessions (Fig 4). The first two principal components explained 21.92% and 9.13%, respectively. *Momordica* group which were clustered together in cluster III were also grouped closely in the right upper quadrant. Most of the melon accessions of cluster II were grouped closely in the left upper quadrant and those of cluster I appeared in the lower two quadrants. Therefore, it is concluded that grouping by UPGMA method could be well reproduced on a FCA.

The domestication of plants has 'resulted from long periods of intimate co evolution between plants and man'. However, the continued displacement of locally adapted landraces by elite cultivars constitutes genetic erosion of primary gene pool and support an exsitu conservation of genetic resources (Harlan, 1971). The identification and assessment of unique landrace gene pool to define their structure in relation to locally used elite germplasm allows for the breeding strategies for genetic conservation (Cowling *et al*, 2009). Analysis of plant diversity using molecular evaluation is useful for germplasm curators and plant geneticists and gives a solid historical reference data for future genetic studies aimed at assessing genetic erosion, exploration potential insitu conservation priorities. Only recently genetic diversity of melon has been critically assessed using a broad array of genetic markers (Garcia *et al*, 1998, Stepansky *et al*, 1999a, Mliki *et al*, 2001, Monforte *et al*, 2003).

The clustering of genotypes in the dendrogram of ninety-six melon accessions show significant relationship between botanical groups and clustering pattern viz., cluster I *cantalupensis*, clusterII *reticulatus* and clusterIII *momordica* grouping of accessions among themselves is in accordance with classification of melon (Pitrat *et al*, 2000). Also, these results support the previous reports on molecular variation in *C. melo* based on RAPDs and ISSRs (Stepansky *et al*, 1999a) and SSRs (Monforte *et al*, 2003). These results clearly demonstrated the distinction between sweet melon and non-sweet melon groups. The cluster separating the genotypes belonging to *cantalupensis* from the other is consistent with both the phenotypic and molecular data. Some of the clustering of genotypes was in agreement with morphological data but was not seen for all the genotypes under study. Perl-Treves *et al* (1985) also reported clear separation between sweet type (*cantalupensis*) and exotic type (*momordica*). Tzitzikas *et al* (2009) also observed that cultivars belonging to group *cantalupensis* clustered together. Dhillon *et al* (2007) also reported that accessions of *var momordica* grouped together and there was a separate cluster of the accessions of *var reticulatus*.

Clustering of genotypes besides being based on botanical relationship also depends on geographical origin. Many accessions with similar origin (region of cultivation) were closely related to each other e.g. in case of sub-cluster 1A, genotypes MM-3833 and MM-

3849 show maximum similarity with each other were collected from same sub-zone 13.1. Similarly in sub-group IB genotypes MM-3979 and MM- 3973 were collected from sub-zone 9.1.The highest similarity in whole dendrogram was shown by MM-3885 and MM-3966 in cluster IIB, were also collected from same sub-zone 13.1. The further support to this argument came from clustering of accessions belonging to *momordica* group in cluster III. Out of twelve accessions, eleven accessions cluster together. They were collected from same sub-zone 13.1 and only one *momordica* accession (MM-3994) showed highest level of variation from other *momordica* accessions which was collected from sub-zone 14.5. Thus, besides botanical relationship, geographical origin has also contributed towards genetic similarity. Lopez- Sese *et al* (2002) ruled out the possibility of a relationship between geographical location and diversity revealed by RAPD markers among Spanish melons.

All the eight reference accessions from USA used in the study viz., AR Hale's, Jucumba, Gulf Coast, Rocky Ford, Gulf Stream, Chujuc, Hannah's Choice and Dulce-B.B belonging to group *reticulatus* and grouped together in cluster II and shared similarity coefficient of 0.65 with sub-group IIB which included Indian melon accessions belonging to the group *reticulatus*. Reference accessions cluster together forming a genetically unique assemblage in sub-groups IIA. This observation on the basis of SSR analysis suggests that this germplasm shares genetic affinities with Indian melon accessions that could not have been predicted based on their geographic origin. Clustering of Indian and reference accessions suggested that either their Asiatic origin or independent domestication involving similar ancestors. India is considered as the primary center of diversity for melons (Robinson and Decker-Walters, 1997). Melons were transported from India to China (secondary center of diversity) and westward through south Asia, from the Middle East to Europe and then eventually to the America (Robinson and Decker-Walters, 1997).

Intermixing of some accessions of *cantalupensis* and *reticulatus* showed that the classification of melon groups mainly based on morphological characters does not necessarily correspond to genetic relationship shown by molecular analysis and may suggest genetic introgression among melon groups because of their out crossing nature. Intercrossing between *cantalupensis* or *reticulatus* with *momordica* was, however, not detected in this study. These results are in agreement with those of Monforte *et al* (2003) and Yi-San *et al* (2009).

Table 4.13: Sources of melon accessions with codes represented in dendrogram and FCA analysis

Sr. No.	Accession	Dendrogram / FCA Code	Zone	Sub Zone	Sub-Cluster
1	MM-3833 *C. melo* var. *cantalupensis*	1	13	13.1	IA
2	MM-4004 *C. melo* var. *momordica*	2	13	13.	IIIA
3	MM-3837 *C. melo* var. *cantalupensis*	3	13	113.	IA
4	MM-3917 *C. melo* var. *cantalupensis*	4	9	19.2	IA
5	MM-4005 *C. melo* var. *momordica*	5	13	13.1	IIIA
6	MM-3839 *C. melo* var. *cantalupensis*	6	13	13.1	IC
7	MM-3947 *C. melo* var. *cantalupensis*	7	9	9.2	IC
8	MM-4013 *C. melo* var. *cantalupensis*	8	9	9.1	ID
9	MM-3843 *C. melo* var. *cantalupensis*	9	13	13.1	ID
10	MM-3955 *C. melo* var. *cantalupensis*	10	14	14.5	IC
11	MM-4018 *C. melo* var. *cantalupensis*	11	9	9.1	IF
12	MM-3849 *C. melo* var. *cantalupensis*	12	13	13.1	IA
13	MM-3956 *C. melo* var. *cantalupensis*	13	14	14.5	ID
14	MM-4021 *C. melo* var. *cantalupensis*	14	9	9.1	IE
15	MM-3851 *C. melo* var. *cantalupensis*	15	13	13.1	IE
16	MM-3961 *C. melo* var. *cantalupensis*	16	14	14.5	IF
17	MM-4057 *C. melo* var. *cantalupensis*	17	9	9.1	ID
18	MM-3986 *C. melo* var. *cantalupensis*	18	9	9.1	ID
19	MM-4066 *C. melo* var. *reticulatus*	19	9	9.2	IIC

Sr. No.	Accession	Dendrogram / FCA Code	Zone	Sub Zone	Sub-Cluster
20	MM-3885 *C. melo* var. *reticulatus*	20	13	13.1	IIB
21	MM-3856 *C. melo* var. *cantalupensis*	21	13	13.1	ID
22	MM-4067 *C. melo* var. *cantalupensis*	22	9	9.2	IE
23	MM-4063 *C. melo* var. *cantalupensis*	23	9	9.2	IE
24	MM-4098 *C. melo* var. *cantalupensis*	24	13	13.1	IC
25	MM-4068 *C. melo* var. *cantalupensis*	25	9	9.2	IC
26	MM-4065 *C. melo* var. *reticulatus*	26	9	9.2	IIB
27	MM-3859 *C. melo* var. *cantalupensis*	27	13	13.1	IC
28	MM-3860 *C. melo* var. *reticulatus*	28	13	13.1	IIB
29	MM-4409 *C. melo* var. *cantalupensis*	29	9	9.1	IF
30	MM-3864 *C. melo* var. *cantalupensis*	30	13	13.1	IC
31	MM- 4091 *C. melo* var. *momordica*	31	13	13.1	IIIB
32	MM- 3866 *C. melo* var. *cantalupensis*	32	13	13.2	ID
33	MM- 3868 *C. melo* var. *cantalupensis*	33	13	13.1	IC
34	MM-3857 *C. melo* var. *cantalupensis*	34	9	9.2	IA
35	MM-4243 *C. melo* var. *cantalupensis*	35	4	4.3	IC
36	MM-5736 *C. melo* var. *momordica*	36	13	13.1	IIIB
37	MM-3874 *C. melo* var. *cantalupensis*	37	13	13.1	IA
38	MM-4247 *C. melo* var. *momordica*	38	13	13.1	IIIA

Sr. No.	Accession	Dendrogram / FCA Code	Zone	Sub Zone	Sub-Cluster
39	MM-3881 *C. melo* var. *cantalupensis*	39	13	13.1	IC
40	MM-4248 *C. melo* var. *cantalupensis*	40	9	9.2	IC
41	MM-4250 *C. melo* var. *cantalupensis*	41	9	9.2	IC
42	MM-3850 *C. melo* var. *cantalupensis*	42	13	13.1	IA
43	MM-3887 *C. melo* var. *momordica*	43	13	13.1	IIIB
44	MM-4251 *C. melo* var. *cantalupensis*	44	9	9.2	ID
45	MM-3858 *C. melo* var. *cantalupensis*	45	13	13.1	IB
46	MM- 3889 *C. melo* var. *cantalupensis*	46	13	13.1	IE
47	MM-4252 *C. melo* var. *reticulatus*	47	4	4.3	IIC
48	MM-3884 *C. melo* var. *cantalupensis*	48	13	13.1	IB
49	MM- 3901 *C. melo* var. *reticulatus*	49	9	9.2	IIB
50	MM-4253 *C. melo* var. *cantalupensis*	50	9	9.2	ID
51	MM-4059 *C. melo* var. *reticulatus*	51	9	9.1	IIB
52	MM-4256 *C. melo* var. *cantalupensis*	52	4	4.3	IB
53	MM- 4026 *C. melo* var. *cantalupensis*	53	9	9.1	IE
54	MM- 3909 *C. melo* var. *cantalupensis*	54	9	9.2	IB
55	MM-4267 *C. melo* var. *momordica*	55	13	13.1	IIIB
56	MM-4030 *C. melo* var. *cantalupensis*	56	9	9.1	IIC
57	MM-3903 *C. melo* var. *cantalupensis*	57	9	9.2	IIB

Sr. No.	Accession	Dendrogram / FCA Code	Zone	Sub Zone	Sub-Cluster
58	MM- 4268 *C. melo* var. *reticulatus*	58	13	13.1	IB
59	MM-3962 *C. melo* var. *momordica*	59	13	13.1	IIIB
60	MM-4270 *C. melo* var. *cantalupensis*	60	9	9.2	IC
61	MM-4276 *C. melo* var. *cantalupensis*	61	9	9.2	ID
62	MM-3963 *C. melo* var. *cantalupensis*	62	13	13.2	IA
63	MM-4271 *C. melo* var. *reticulatus*	63	9	9.2	IIB
64	MM-4277 *C. melo* var. *reticulatus*	64	9	9.2	IIB
65	MM- 4282 *C. melo* var. *cantalupensis*	65	9	9.2	IE
66	MM-4278 *C. melo* var. *cantalupensis*	66	9	9.2	IB
67	MM-3965 *C. melo* var. *cantalupensis*	67	14	14.5	IF
68	MM-4283 *C. melo* var. *cantalupensis*	68	9	9.2	IC
69	MM-4279 *C. melo* var. *reticulatus*	69	9	9.2	IIC
70	MM-3976 *C. melo* var. *reticulatus*	70	9	9.1	IIC
71	MM-3981 *C. melo* var. *cantalupensis*	71	9	9.1	IA
72	MM-3977 *C. melo* var. *reticulatus*	72	9	9.1	IIC
73	MM-4305 *C. melo* var. *cantalupensis*	73	9	9.2	IC
74	MM-3982 *C. melo* var. *momordica*	74	13	13.1	IIIB
75	MM-3973 *C. melo* var. *cantalupensis*	75	9	9.1	IB
76	MM-3983 *C. melo* var. *cantalupensis*	76	9	9.1	IA

Sr. No.	Accession	Dendrogram / FCA Code	Zone	Sub Zone	Sub-Cluster
77	MM-3974 *C. melo* var. *momordica*	77	13	13.1	IIB
78	MM-4342 *C. melo* var. *cantalupensis*	78	9	9.2	IC
79	MM-3985 *C. melo* var. *cantalupensis*	79	9	9.2	IIB
80	MM-3966 *C. melo* var. *reticulatus*	80	13	13.1	IIB
81	MM-3855 *C. melo* var. *cantalupensis*	81	13	13.1	ID
82	MM-3968 *C. melo* var. *reticulatus*	82	14	14.5	IF
83	MM-3998 *C. melo* var. *momordica*	83	13	13.1	IIIB
84	MM-3979 *C. melo* var. *cantalupensis*	84	9	9.1	IB
85	MM-4305 *C. melo* var. *cantalupensis*	85	9	9.2	IB
86	MM-3994 *C. melo* var. *momordica*	86	14	14.5	U.C.
87	MM-3980 *C. melo* var. *cantalupensis*	87	9	9.1	IA
88	MM-4003 *C. melo* var. *cantalupensis*	88	9	9.1	IC
89	AR Hale's *C. melo* var. *reticulatus*	89	USA		IIA
90	Dulce-B.B *C. melo* var. *reticulatus*	90			IIA
91	Gulf Coast *C. melo* var. *reticulatus*	91			IIA
92	Gulf Stream *C. melo* var. *reticulatus*	92			IIA
93	Jucumba *C. melo* var. *reticulatus*	93			IIA
94	Rocky Ford *C. melo* var. *reticulatus*	94			IIA
95	Hannah's Choice *C. melo* var. *reticulatus*	95			IIA
96	Chujuc *C. melo* var. *reticulatus*	96			IIA

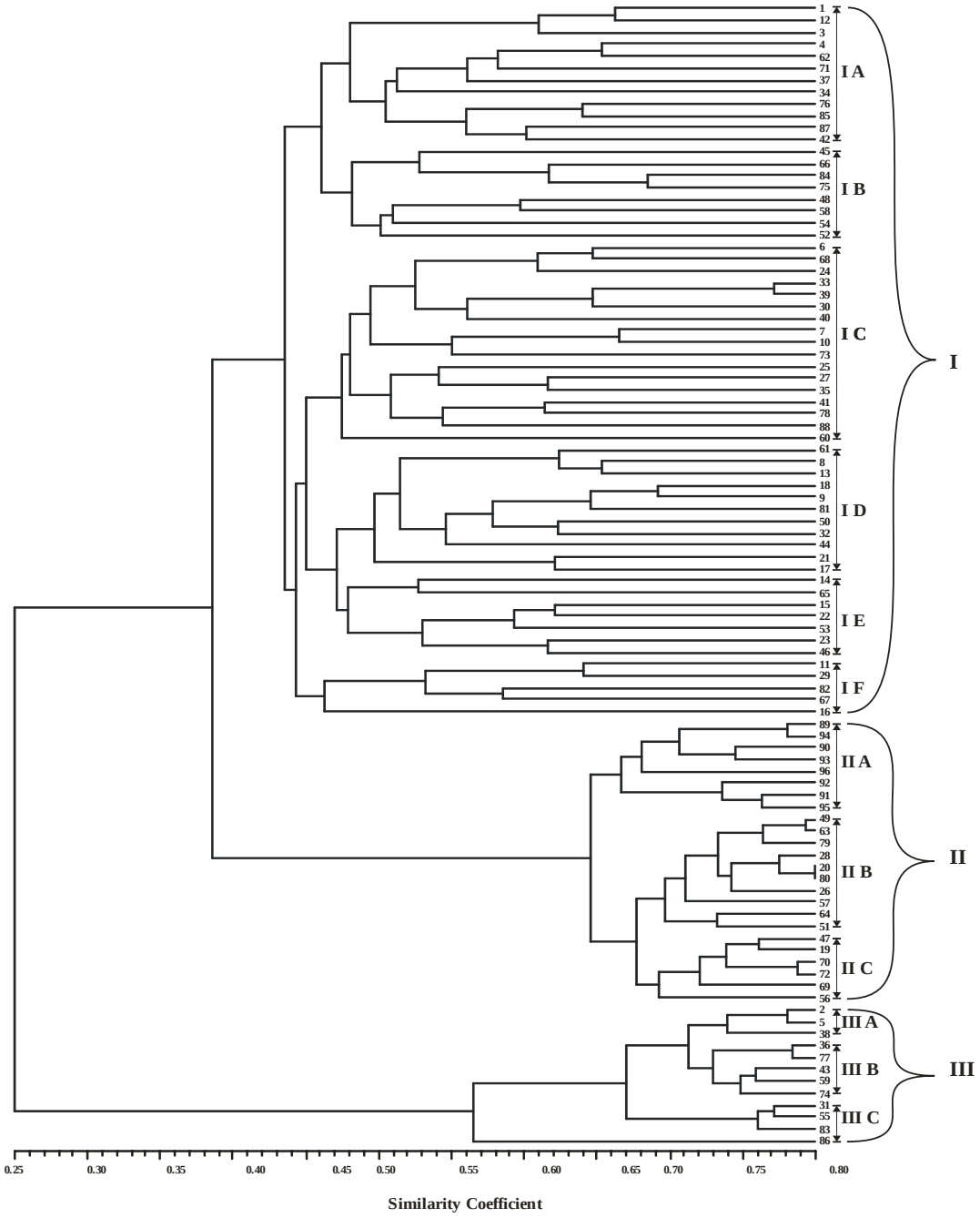


Fig 3: Dendrogram showing similarity coefficient of ninety-six melon accessions using computer software NTSYS.

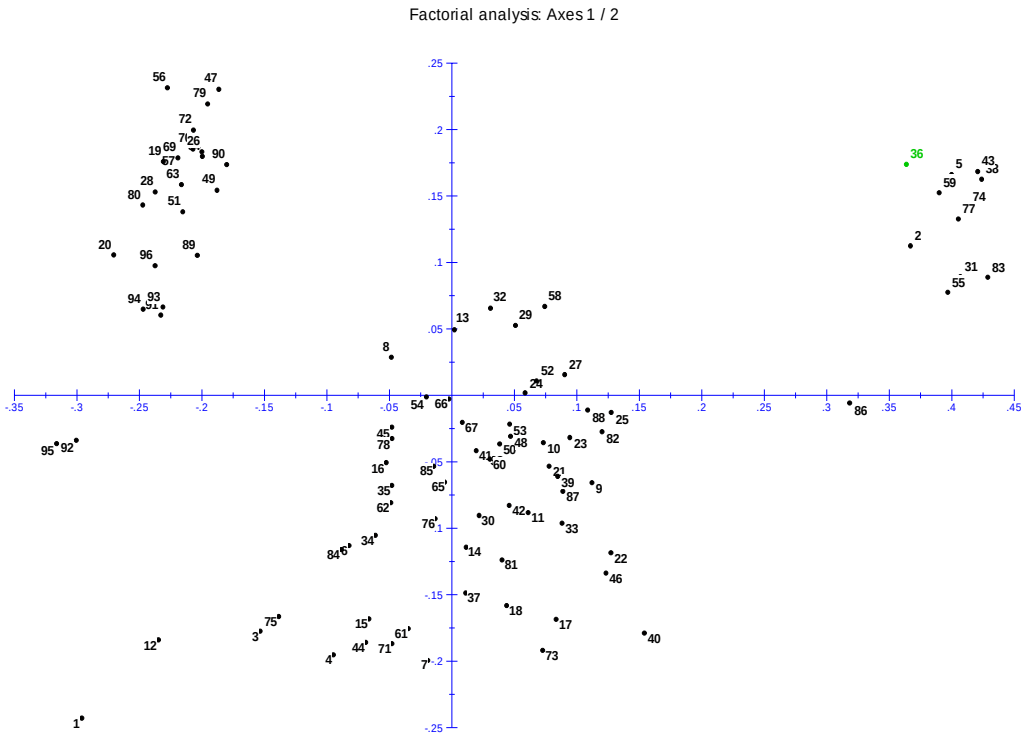


Fig 4: Factor Correspondence Analysis using molecular data for various melon accessions using computer software DARwin 5.0.

4.7 Clustering pattern based on D^2 and SSR marker analysis

The comparison of clusters based on D^2 analysis and SSR marker analysis indicated that the clustering pattern was different for the two approaches. The genotypes clustered in one group based on D^2 analysis were found to be scattered in different clusters by SSR markers analysis. Its reason could be that the molecular marker analysis revealed genetic diversity based on overall genetic constitution of the test material. The diversity based on the morphological traits is for a few traits of agronomic interest for which the germplasm is being subjected to intensive selection for long periods of time. The environmental influence could also affect the expression of these traits. The diversity assessment at molecular level represents a more realistic picture of overall genetic composition of the test material.

Further by increasing the number of markers covering the genome more widely more useful information can be obtained. However, the SSR markers have shown good potential in analyzing genetic diversity of melon.

4.8 Characterization on the basis of reaction to diseases

4.8.1 Reaction to cucumber mosaic virus (CMV)

The degree of infection on inoculated cotyledons and the development of systemic infection were evaluated under artificial condition during 2009 and 2010, in ninety-six melon accessions (including eight reference melon accessions)

Significant variation in resistance was found among ninety-six melon accessions tested during both the years under artificial condition (2009 and 2010) on the basis of variation in resistance ninety-six melon accessions were grouped into different categories (Table 4.14, 4.15, 4.16 and 4.17). During 2009, forty-nine accessions showed severe mosaic to CMV, twenty-two accessions showed mild mosaic to CMV, twenty-one accessions showed chlorosis to CMV, four accessions were free from CMV (MM-3974, MM-3982, MM-3994, MM-4067)

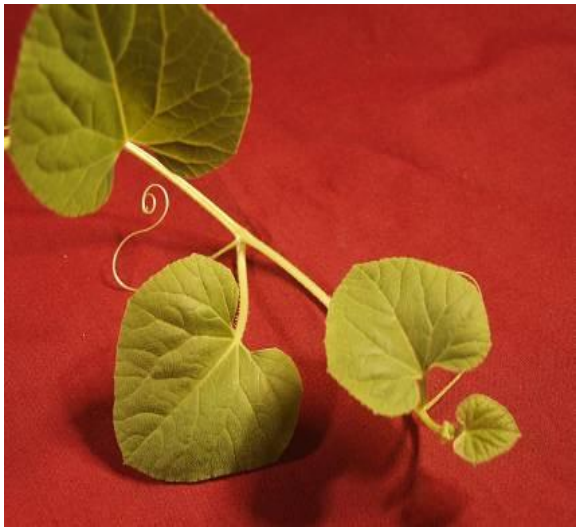
During 2010, sixty-six accessions showed severe mosaic to CMV, twenty-one accessions showed mild mosaic to CMV, five accessions showed chlorosis to CMV (MM-3884, MM-3917, MM-3966, MM-3979, MM-4068) and four accessions were free from CMV (MM-3974, MM-3982, MM-3994 and MM-4067)

Only four melon accessions (MM-3974, MM-3982, MM-3994, and MM-4067) showed complete resistance to CMV during both the years. On the other hand, none of the reference accessions inoculated with CMV showed resistance. Reaction of melon accessions under artificial inoculation is shown in plate 5.

Out of four melon accessions showing resistance to CMV, three (MM-3974, MM-3982 and MM-3994) accessions belong to group *momordica* and one accession (MM-4067) to group *cantalupensis*. It is known that snap melons are generally tolerant to CMV in conditions under which muskmelon genotypes are killed at four leaf stage and produce

Net house

SM-Severe mosaic



F-Free

MM- Mild mosaic

CH- Chlorosis

Plate 5: Reaction of melon accessions to CMV under artificial inoculation

reasonable yield (Dhillon *et al*, 2007). It would be interest to study the genetic control of CMV resistance in these four accessions to assess if other genes are involved and could be cumulated with those already described.

As we know CMV has been appearing in devastating form in recent years, the results of the present study would be of great help in strengthening the breeding programme to develop CMV resistant genotypes in melon and stabilizing the melon production and quality.

4.8.2 Reaction to downy mildew

Ninety-six melon accessions (including eight reference accessions) were screening for downy mildew resistance under natural epiphytotic conditions in the field thrice (during the growing season 2009, 2010 and 2011). Downy mildew had not occurred in natural epiphytotic condition during 2009 and 2010, However this occurred in natural epiphytotic condition during 2011 (Table 4.18). Perusal of the table out of ninety-six accessions screened for downy mildew. Percent Disease Index (PDI) for downy mildew ranged from 0.00 to 50.00%. Variation in resistance was found among ninety-six melon accessions on the basis of percent disease incidence. Ninety-six melon accessions were grouped into different categories (Table 4.19),

Table 4.14: Reaction of melon accession to CMV under artificial inoculation conditions during 2009

Sr. No.	Accession No.	No. of seedlings inoculated	No. of seedlings showing infection	Reaction category
1	MM-3833	10	5	SM
2	MM-3837	10	6	SM
3	MM-3839	10	1	CH
4	MM-3843	10	6	SM
5	MM-3849	10	5	SM
6	MM-3850	10	7	SM
7	MM-3851	10	5	SM
8	MM-3855	10	7	SM
9	MM-3856	10	5	SM
10	MM-3857	10	2	MM
11	MM-3858	10	2	MM
12	MM-3859	10	6	SM
13	MM-3860	10	7	SM
14	MM-3864	10	1	CH
15	MM-3866	10	2	MM
16	MM-3868	10	7	SM
17	MM-3874	10	6	SM
18	MM-3881	10	5	SM
19	MM-3884	10	2	MM

Sr. No.	Accession No.	No. of seedlings inoculated	No. of seedlings showing infection	Reaction category
20	MM-3885	10	5	SM
21	MM-3887	10	1	CH
22	MM-3889	10	1	CH
23	MM-3901	10	2	MM
24	MM-3903	10	2	MM
25	MM-3909	10	5	SM
26	MM-3917	10	1	CH
27	MM-3947	10	1	CH
28	MM-3955	10	7	SM
29	MM-3956	10	1	CH
30	MM-3961	10	2	MM
31	MM-3962	10	5	SM
32	MM-3963	10	5	SM
33	MM-3965	10	2	MM
34	MM-3966	10	2	MM
35	MM-3968	10	2	MM
36	MM-3973	10	7	SM
37	MM-3974	10	0	F
38	MM-3976	10	5	SM
39	MM-3977	10	1	CH
40	MM-3979	10	2	MM
41	MM-3980	10	2	MM
42	MM-3981	10	5	SM
43	MM-3982	10	0	F
44	MM-3983	10	1	CH
45	MM-3985	10	2	MM
46	MM-3986	10	5	SM
47	MM-3994	10	0	F
48	MM-3998	10	5	SM
49	MM-4002	10	6	SM
50	MM-4003	10	5	SM
51	MM-4004	10	1	CH
52	MM-4005	10	5	SM
53	MM-4013	10	1	CH
54	MM-4018	10	8	SM
55	MM-4021	10	5	SM
56	MM-4026	10	2	MM
57	MM-4030	10	9	SM
58	MM-4057	10	6	SM

Sr. No.	Accession No.	No. of seedlings inoculated	No. of seedlings showing infection	Reaction category
59	MM-4059	10	7	SM
60	MM-4063	10	1	CH
61	MM-4065	10	1	CH
62	MM-4066	10	2	MM
63	MM-4067	10	0	F
64	MM-4068	10	6	SM
65	MM-4091	10	7	SM
66	MM-4098	10	5	SM
67	MM-4243	10	5	SM
68	MM-4247	10	2	MM
69	MM-4248	10	2	MM
70	MM.4250	10	5	SM
71	MM-4251	10	6	SM
72	MM-4252	10	7	SM
73	MM-4253	10	5	SM
74	MM-4256	10	6	SM
75	MM-4267	10	3	MM
76	MM-4268	10	5	SM
77	MM-4270	10	6	SM
78	MM-4271	10	3	MM
79	MM-4276	10	2	MM
80	MM-4277	10	1	CH
81	MM-4278	10	1	CH
82	MM-4279	10	2	MM
83	MM-4282	10	3	MM
84	MM-4283	10	5	SM
85	MM-4305	10	1	CH
86	MM-4342	10	6	SM
87	MM-4409	10	1	CH
88	MM-5736	10	5	SM
89	AR Hale’s	10	1	CH
90	Dulce-B.B	10	6	SM
91	Gulf Coast	10	5	SM
92	Gulf Stream	10	2	MM
93	Jucumba	10	6	SM
94	Rocky Ford	10	2	MM
95	Hannah’s Choice	10	7	SM
96	Chujuc	10	3	SM

SM-Severe mosaic, MM- Mild mosaic, CH- Chlorosis, F-Free

Table 4.15: Reaction of melon accession to CMV under artificial inoculation condition during 2010

Sr.No.	Accession No.	No. of seedlings inoculated	No. of seedlings showing infection	Reaction category
1	MM-3833	10	7	SM
2	MM-3837	10	5	SM
3	MM-3839	10	5	SM
4	MM-3843	10	6	SM
5	MM-3849	10	5	SM
6	MM-3850	10	6	SM
7	MM-3851	10	6	SM
8	MM-3855	10	2	MM
9	MM-3856	10	7	SM
10	MM-3857	10	5	SM
11	MM-3858	10	5	SM
12	MM-3859	10	6	SM
13	MM-3860	10	2	MM
14	MM-3864	10	5	SM
15	MM-3866	10	7	SM
16	MM-3868	10	5	SM
17	MM-3874	10	5	SM
18	MM-3881	10	6	SM
19	MM-3884	10	1	CH
20	MM-3885	10	2	MM
21	MM-3887	10	5	SM
22	MM-3889	10	7	SM
23	MM-3901	10	3	MM
24	MM-3903	10	2	MM
25	MM-3909	10	8	SM
26	MM-3917	10	1	CH
27	MM-3947	10	3	MM
28	MM-3955	10	7	SM
29	MM-3956	10	2	MM
30	MM-3961	10	3	MM
31	MM-3962	10	5	SM
32	MM-3963	10	6	SM

Sr.No.	Accession No.	No. of seedlings inoculated	No. of seedlings showing infection	Reaction category
33	MM-3965	10	5	SM
34	MM-3966	10	1	CH
35	MM-3968	10	3	MM
36	MM-3973	10	10	SM
37	MM-3974	10	0	F
38	MM-3976	10	9	SM
39	MM-3977	10	2	MM
40	MM-3979	10	1	CH
41	MM-3980	10	5	SM
42	MM-3981	10	10	SM
43	MM-3982	10	0	F
44	MM-3983	10	5	SM
45	MM-3985	10	5	SM
46	MM-3986	10	2	MM
47	MM-3994	10	0	F
48	MM-3998	10	5	SM
49	MM-4002	10	7	SM
50	MM-4003	10	8	SM
51	MM-4004	10	3	MM
52	MM-4005	10	5	SM
53	MM-4013	10	5	SM
54	MM-4018	10	10	SM
55	MM-4021	10	3	MM
56	MM-4026	10	2	MM
57	MM-4030	10	7	SM
58	MM-4057	10	7	SM
59	MM-4059	10	9	SM
60	MM-4063	10	3	MM
61	MM-4065	10	5	SM
62	MM-4066	10	8	SM
63	MM-4067	10	0	F
64	MM-4068	10	1	CH
65	MM-4091	10	9	SM
66	MM-4098	10	2	MM

Sr.No.	Accession No.	No. of seedlings inoculated	No. of seedlings showing infection	Reaction category
67	MM-4243	10	5	SM
68	MM-4247	10	8	SM
69	MM-4248	10	8	SM
70	MM.4250	10	7	SM
71	MM-4251	10	10	SM
72	MM-4252	10	9	SM
73	MM-4253	10	7	SM
74	MM-4256	10	2	MM
75	MM-4267	10	5	SM
76	MM-4268	10	8	SM
77	MM-4270	10	5	SM
78	MM-4271	10	5	SM
79	MM-4276	10	2	MM
80	MM-4277	10	3	MM
81	MM-4278	10	5	SM
82	MM-4279	10	2	MM
83	MM-4282	10	5	SM
84	MM-4283	10	7	SM
85	MM-4305	10	6	SM
86	MM-4342	10	3	MM
87	MM-4409	10	5	SM
88	MM-5736	10	5	SM
89	AR Hale’s	10	5	SM
90	Dulce-B.B	10	8	SM
91	Gulf Coast	10	6	SM
92	Gulf Stream	10	7	SM
	Jucumba	10	8	SM
93	Rocky Ford	10	7	SM
94	Hannah’s Choice	10	5	SM
95	Chujuc	10	5	SM
96				

SM-Severe mosaic, MM- Mild mosaic, CH- Chlorosis, F-Free

Table 4.16: Grouping of melon accessions based on reaction to cucumber mosaic virus (CMV) during 2009

Sr. No.	Reaction to CMV	Accessions
1.	Severe mosaic	MM-3833, MM-3837, MM-3843, MM-3849, MM-3850, MM-3855, MM-3851, MM-3856, MM-3859, MM-3860, MM-3868, MM-3874, MM-3881, MM-3885, MM-3909, MM-3955, MM-3962 , MM-3963, MM-3973 ,MM-3976, MM-3981, MM-3986, MM-4002, MM-4003, MM-4005, MM-4018, MM-4021, MM-4030, MM-4057, MM-4059, MM-4068, MM-4091, MM-4098, MM-4243, MM-4250, MM-4251, MM-4252, MM-4253, MM-4256, MM-4268, MM-4270, MM-4283, MM-4342, MM-5736, Dulce-B.B, Gulf Coast, Jucumba, Hannah's Choice, Chujuc.
2.	Mild mosaic	MM-3866, MM-3857, MM-3858, MM-3884, MM-3901, MM-3903, MM-3961, MM-3966 MM-3968, MM-3965, MM-3979, MM-3980, MM-3985, MM-4066, MM-4026, MM-4247, MM-4248, MM-4267, MM-4271, MM-4276, MM-4279, MM-4282, Gulf Stream , Rocky Ford.
4.	Chlorosis	MM-3839, MM-3864, MM-3887, MM-3889, MM-3917, MM-3947, MM-3956, MM-3977, MM-3983, MM-4004, MM-4013, MM-4063 , MM-4065, MM-427, MM-4278, MM-4305, MM-4409, AR Hale's
5.	Free	MM-3974, MM-3982, MM-3994, MM-4067

Table 4.17: Grouping of melon accessions based on reaction to cucumber mosaic virus (CMV) during 2010

Sr. No.	Reaction to CMV	Accessions
1.	Severe mosaic	MM-3833, MM-3837, MM-3839, MM-3843, MM-3849, MM-3850, MM-3851, MM-3856, MM-3857, MM-3858, MM-3859, MM-3864, MM-3866, MM-3868, MM-3874, MM-3881, MM-3887, MM-3889, MM-3909, MM-3955, MM-3962, MM-3963, MM-3965 , MM-3973, MM-3976, MM-3980, MM-3981, MM-3983, MM-3985, MM-3998, MM-4002, MM-4003, MM-4005,, MM-4013, MM-4018, MM-4030, MM-4057, MM-4059, MM-4065, MM-4066, MM-4091, MM-4243, MM-4247, MM-4248, MM-4250, MM-4251, MM-4252, MM-4253, MM-4267, MM-4268, MM-4270, MM-4271, MM-4278, MM-4282, MM-4283, MM-4305, MM-4409, MM-5736, Dulce-B.B , Dulce-B.B , Gulf Coast, Gulf Stream, Jucumba, Rocky Ford, Hannah's Choice, Chujuc.
2.	Mild mosaic	MM-3855, MM-3860, MM-3885, MM-3901, MM-3903, MM-3947, MM-3956, MM-3961, MM-3968, MM-3977, MM-3986, MM-4004, MM-4021, MM-4026, MM-4063, MM-4098, MM-4256, MM-4276, MM-4277, MM-4279, MM-4342
3.	Chlorosis	MM-3884, MM-3917, MM-3966, MM-3979, MM-4068
4.	Free	MM-3974, MM-3982, MM-3994, MM-4067

Table 4.18: Reaction of melon accession to downy mildew under field condition during 2011

Sr. No.	Accession No.	PDI (%)	Reaction category
1	MM-3833	3.3	HR
2	MM-3837	5	HR
3	MM-3839	6.6	HR
4	MM-3843	3.3	HR
5	MM-3849	6.6	HR
6	MM-3850	8.3	HR
7	MM-3851	10	HR
8	MM-3855	3.3	HR
9	MM-3856	8.3	HR
10	MM-3857	5	HR
11	MM-3858	3.7	HR
12	MM-3859	8.3	HR
13	MM-3860	5.5	HR
14	MM-3864	3.3	HR
15	MM-3866	5	HR
16	MM-3868	3.3	HR
17	MM-3874	6.6	HR
18	MM-3881	5	HR
19	MM-3884	3.3	HR
20	MM-3885	6.6	HR
21	MM-3887	3.3	HR
22	MM-3889	4.7	HR
23	MM-3901	3.3	HR
24	MM-3903	5	HR
25	MM-3909	3.3	HR
26	MM-3917	42	MR
27	MM-3947	5	HR
28	MM-3955	4	HR
29	MM-3956	10	HR
30	MM-3961	3.3	HR
31	MM-3962	3.3	HR
32	MM-3963	6.6	HR

Sr. No.	Accession No.	PDI (%)	Reaction category
33	MM-3965	4.1	HR
34	MM-3966	5	HR
35	MM-3968	5	HR
36	MM-3973	3.3	HR
37	MM-3974	6.6	HR
38	MM-3976	50	MR
39	MM-3977	3.3	HR
40	MM-3979	6.6	HR
41	MM-3980	3.3	HR
42	MM-3981	5	HR
43	MM-3982	8.3	HR
44	MM-3983	0	I
45	MM-3985	30	R
46	MM-3986	6.6	HR
47	MM-3994	3.3	HR
48	MM-3998	5	HR
49	MM-4002	5	HR
50	MM-4003	3.3	HR
51	MM-4004	0	I
52	MM-4005	3.3	HR
53	MM-4013	10	HR
54	MM-4018	4	HR
55	MM-4021	6.6	HR
56	MM-4026	5	HR
57	MM-4030	5	HR
58	MM-4057	3.3	HR
59	MM-4059	10	HR
60	MM-4063	15	HR
61	MM-4065	5	HR
62	MM-4066	3.3	HR
63	MM-4067	6.6	HR
64	MM-4068	4	HR
65	MM-4091	3.3	HR

Sr. No.	Accession No.	PDI (%)	Reaction category
66	MM-4098	5	HR
67	MM-4243	3.3	HR
68	MM-4247	10	HR
69	MM-4248	8.3	HR
70	MM.4250	20	HR
71	MM-4251	6.6	HR
72	MM-4252	5	HR
73	MM-4253	3.3	HR
74	MM-4256	5	HR
75	MM-4267	5	HR
76	MM-4268	5	HR
77	MM-4270	3.3	HR
78	MM-4271	5	HR
79	MM-4276	16.6	HR
80	MM-4277	5	HR
81	MM-4278	10	HR
82	MM-4279	3.3	HR
83	MM-4282	5	HR
84	MM-4283	3.3	HR
85	MM-4305	11.6	HR
86	MM-4342	8.3	HR
87	MM-4409	3.3	HR
88	MM-5736	6.6	HR
89	AR Hale’s	30	R
90	Dulce-B.B	3.3	HR
91	Gulf Coast	4	HR
92	Gulf Stream	6.6	HR
	Jucumba	3.3	HR
93	Rocky Ford	5	HR
94	Hannah’s Choice	4.7	HR
95	Chujuc	3.3	HR
96			

I - Immune, HR - Highly Resistant, R - Resistant, MR - Moderately Resistant

Table 4.19: Grouping of melon accessions based on reaction to downy mildew under field condition during 2011

Sr. No.	Reaction to downy mildew	Accessions
1.	Moderately Resistant	MM-3917 and MM-3976
2.	Resistant	MM-3985 and AR Hale's
3.	Highly Resistant	MM-3833, MM-3837, MM-3839, MM-3843, MM-3849, MM-3850 MM-3851, MM-3855, MM-3856, MM-3857, MM-3858, MM-3859, MM-3860, MM-3864, MM-3866, MM-3868, MM-3874, MM-3881, MM-3884, MM-3885, MM-3887, MM-3889, MM-3901, MM-3903, MM-3909, MM-3947, MM-3955, MM-3956, MM-3961, MM-3962, MM-3963, MM-3965, MM-3966, MM-3968, MM-3973, MM-3974, MM-3976, MM-3977, MM-3979, MM-3980, MM-3981, MM-3982, MM-3985, MM-3986, MM-3994, MM-3998, MM-4002. MM-4003, MM-4005, MM-4013, MM-4018, MM-4021, MM-4026, MM-4030, MM-4057, MM-4059, MM-4063, MM-4065, MM-4066, MM-4067,MM-4068,MM-4091,MM-4098,MM-4243,MM-4247,MM-4248,MM-4250,MM-4251,MM-4252,MM-4253,MM-4256,MM-4267, MM-4268, MM-4270, MM-4271, MM-4276, MM-4277, MM-4278, MM-4279, MM-4282, MM-4283, MM-4305, MM-4342, MM-4409, MM-5736, Dulce-B.B, Gulf Coast, Gulf Stream, Jucumba, Rocky Ford, Hannah's Choice and Chujuc
4.	Immune	MM-3983 and MM-4004

two accessions MM-3917 and MM-3976 were moderately resistant (PDI 42 and 50% respectively), two accession AR Hale's and MM-3985 were resistant (PDI 30%), ninety genotypes were highly resistant and two accessions MM-3973 and MM-3983 were immune (PDI 0.00%). However, no genotype was found susceptible to downy mildew. Symptoms of downy mildew on melon leaves unde field conditions is shown in plate 6.

Downy mildew is one of the destructive diseases of melon. The control of this disease with fungicides, although necessary, often does not give satisfactory results. Environmental, economic and energy conservation concerns are placing increasing emphasis on the need for development of commercially acceptable, resistant cultivars (Thomas, 1992). Therefore breeding for resistance is the most effective way to control this disease (Helena *et al*, 2011). A high resistance in two accessions which showed immune response was found in this study. These accessions could be used to develop downy mildew resistant genotypes in melon. These findings compliment the results of Staub *et al* (1989) who have found high level of resistance to downy mildew in the accessions of Indian origin.

Four melon accessions viz., MM-3974, MM-3982, MM-3994, and MM-4067 were free from CMV infection under artificial condition and two accessions viz., MM-4004 and MM-3983 showed immune reaction to downy mildew. The results of this investigation is in agreement with previous findings which show that *momordica* group had resistance for CMV and downy mildew because one of two accessions (MM-4004) showing immune reaction to downy mildew belonged to group *momordica*. Similarly, among four accessions resistant to CMV three accessions (MM-3982, MM-3994, and MM-3974) belonged to group *momordica*. The accessions showing resistance or immunity were collected from sub-zone 13.1, so this sub-zone should be further explored for resistant genotypes. Most of these accessions which were free from CMV or exhibited immune reaction to downy mildew were collected from sub-zone 13.1. It is suggested that this zone may further be explored for more accessions possessing resistance to melon diseases.

In the present investigation, some accessions were more promising than others for different characters such as fruit weight, number of fruits per vine, number of days from sowing to marketable maturity, days from sowing to last fruit harvest, total soluble solids content, titrable acidity and reaction to disease. Nodes at which the first hermaphrodite flowers appear and days from sowing to first fruit harvest are indicators of earliness. The genotypes MM-4278, MM-3833, MM-4018, MM-4270, MM-3895, MM-3884 and MM-4098 had minimum number of node to bear the first hermaphrodite flower. However, lesser number of days from sowing to marketable maturity was present in MM-3956 (79.12 days) and MM-4283 (79.67 days) and these genotypes could be used for transferring earliness. The maximum expression for yield contributing characters such as number of fruits per vine, average fruit weight, numbers of primary branches per vine (Taha *et al*, 2003) were recorded in MM-4098,

Plate 6: Symptoms of downy mildew on melon leaves

MM-3866 and MM-3998, respectively. Small seed cavity which is a desirable trait in melon was noted in Chujuc and Dulce-B.B. These genotypes could be useful for the melon breeder for superior horticultural characters.

Total soluble solids content is an important quality trait in melon (Burger *et al*, 2006). The maximum TSS content was found in Chujuc. Titrable acidity is also an important quality trait in melon. Titrable acidity along with total soluble solids content determines melon flavour (Burger *et al*, 2003). The highest titrable acidity was present in case of MM-4004. The breeding efforts may be directed to develop inbred lines with more total soluble solid content along with moderate acidity levels producing a novel tasting melon. The genotype AR Hale's had possessed high level of ascorbic acid which is also a useful trait.

There was a close relationship between phenotypic and genotypic coefficient of variation in most of the traits indicating negligible effect of environmental factors (Choudhary *et al*, 2004). Heritability estimates had been found to be moderate to high for most of the characters indicating moderate to high transmissibility for these characters. Higher to moderate heritability estimates and low genetic advance were obtained for days from sowing to marketable maturity, fruit breadth and dry matter content. The high heritability estimates obtained might be due to favorable effect of environment rather the genetic constitution indicating little scope for improvement through selection.

Phenotypic and genotypic correlation coefficient of seed cavity length (0.753 and 0.775), fruit length (0.744 and 0.764) and fruit breadth (0.281 and 0.331) were positively correlated with fruit weight. Thus, fruit weight can be improved through selection based on these characters. However, there was recorded a negative correlation between fruit number per vine and average fruit weight. Increasing the yield of melon by increasing only the number of fruits/vine is not a suitable choice, other criterion could be fruit weight which has positive correlation with seed cavity length, fruit length and fruit breadth. Though TSS did not show positive and significant correlation with the important traits, the reason being large number of genotypes used in the study and genetic divergence.But this trait is given utmost importance during selection in muskmelon. Thus, it is suggested that although heavier fruits tend to have lower total soluble solids content but maintaining a desirable total soluble solids content with optimum fruit size should be objective of melon breeder (Singh and Ram, 2003).

D^2 and cluster analysis revealed that genetic diversity was not based on geographic diversity. Group constellation proved that the maximum inter-cluster distance occurred between cluster IX and cluster III, which indicated that genotypes falling in these clusters had maximum genetic variability and can be used in melon breeding programme to obtain superior recombinants in the segregating generations (Stuber *et al*, 1992).

The genetic diversity analysis on the basis of SSR markers grouped the genotypes into three major clusters. There was significant relationship between botanical groups and

clustering pattern viz., cluster I *cantalupensis*, cluster II *reticulatus* and cluster III *momordica*. Grouping of these accessions was in agreement with classification of melon given by Pitrat *et al* (2000). Clustering of genotypes besides based on botanical relationship also depends on geographical origin. Many accessions with similar origin (region of cultivation) were closely related to each other e.g. in case of sub-cluster 1A, genotypes MM-3833 and MM-3849 show maximum similarity with each other were collected from same sub-zone (13.1). Similarly, in sub-group IB genotypes MM-3979 and MM- 3973 were collected from sub-zone 9.1.The highest similarity in whole dendrogram was shown by MM-3885 and MM-3966 in cluster IIB, were also collected from same sub-zone (13.1). The further support to this argument came from clustering of accessions belonging to *momordica* group in cluster III. Out of twelve accessions, eleven accessions cluster together. They were collected from same sub-zone 13.1 and only one *momordica* accession (MM-3994) that showed highest level of variation from other *momordica* accessions was collected from sub-zone 14.5. Thus, besides botanical relation, geographical origin has also contributed towards genetic similarity. However, there was intermixing of some accessions of *cantalupensis* and *reticulatus*, which may suggest gene introgression among melon groups because of natural out crossing. Intercrossing between *cantalupensis* or *reticulatus* with *momordica* was not detected in this study. These results are in agreement with those of Monforte *et al* (2003) and Yi-San *et al* (2009). Factor Correspondence Analysis (FCA) was also done to visualize the relationship among melon accessions. The grouping by UPGMA method was reproduced on a FCA plot.

Four melon accessions viz., MM-3974, MM-3982, MM-3994, and MM-4067 were free from CMV infection under artificial conditions and two accessions viz., MM-4004 and MM-3983 showed immune reaction to downy mildew. This investigation is in agreement with the previous findings (Staub *et al*, 1989 and Dhillon *et al*, 2007) which show that *momordica* group has resistance to CMV and downy mildew because one of two accessions (MM-4004) showing immune response to downy mildew belonged to group *momordica*. Similarly, among four accessions resistant to CMV, three accessions (MM-3982, MM-3994, MM-3974) belonged to group *momordica*. Most of these accessions which were free from CMV or showed immune reaction to downy mildew were collected from sub-zone 13.1. It is suggested that this zone may further be explored for more accessions possessing resistance to melon diseases.

Implications of study in melon breeding

In this study clustering of genotypes on the basis of morphological characters showed genotypes from different countries or agro-ecological zones were found to be scattered in different clusters, which suggested that a pattern of clustering of accessions was independent of their geographic origin. The members of cluster IX and cluster III exhibited maximum divergence followed by the members of cluster X and III and cluster IX and II. These clusters

had wide diversity and can be used for hybridisation programme to get superior recombinants in the segregating generations. However, SSR analysis has provided the feasibility of developing genetically superior F_1 hybrids using genetically divergent accessions. Also SSR analysis suggested that reference accessions shared genetic affinities with Indian melon accessions that was not predicted based on their geographic origin which indicated the Asiatic origin of melon or independent domestication of melon in USA involving the ancestral types introduced from Asia. Four melon accessions free from CMV and two accessions showing immune reaction to downy mildew would be useful in strengthening the resistance breeding programme in melon and stabilizing the melon production in Punjab state.

CHAPTER – V

SUMMARY

The present investigation entitled "Analysis of genetic diversity of Indian melon (*Cucumis melo* L.) land races and its comparison with global reference melon populations" was conducted at Department of Vegetable Science and School of Agricultural Biotechnology, PAU Ludhiana, during the spring-summer seasons of year 2009 and 2010.

The eighty-eight accessions were collected from four agro-ecological regions (six sub regions) and eight reference accessions from USA. The genotypes were evaluated in a Randomized Block Design (RBD) with three replications. The genetic diversity was assessed using morpho-biochemical characters, SSR markers and on the basis of reaction to cucumber mosaic virus under artificial conditions and screening for downy mildew under field conditions.

For morphological characterization, the genotypes were evaluated for nineteen traits viz., node at which first hermaphrodite flower appears, number of primary branches per vine, days from sowing to marketable maturity, days from sowing to last fruit harvest, number of fruits per vine, fruit weight (g), fruit length (cm), fruit breadth (cm), seed cavity length (cm), seed cavity breadth (cm), rind thickness (mm), stem pubescence, stem shape, leaf margin, fruit shape, fruit skin primary colour, fruit skin secondary colour, netting, shelf life and for four biochemical traits viz., total soluble solids content (%), titrable acidity (g anhydrous citric acid/100ml fruit juice), ascorbic acid content (mg/100g of fruit weight) and dry matter content (%). Analysis of variance showed that mean square values were highly significant for all the characters. Number of fruits per vine ranged from1.51 to 2.97. Fruit weight exhibited wide range of variability (457.00 -1505.00g). A wide range of variation (2.77 to 12.97) was also observed in total soluble solids content. Titrable acidity varied from 0.07 to 0.37. However, there were narrow differences between magnitude of phenotypic and genotypic coefficients of variation for all the characters studied, indicating low environmental effect on expression of these characters, which implies that phenotypic variability is a reliable measure of genotypic variability. Highest phenotypic coefficient of variation was exhibited for fruit weight (37.98%), node at which first hermaphrodite flower appears (33.45%), while moderate phenotypic coefficient of variation was showed by total soluble solids content (28.48%), ascorbic acid content (28.40%), number of primary branches per vine (27.70%), seed cavity length (27.55%), fruit length (25.17%), titrable acidity (22.15%), rind thickness (19.37%), number of fruits per vine (19.14%), dry matter content (13.29%) and seed cavity breadth (12.28%). Further, fruit breadth (8.55%), days from sowing to marketable maturity (4.22%), days from sowing to last fruit harvest (3.68%) displayed comparatively low phenotypic coefficient of variation. Maximum genotypic coefficient of variation was observed in fruit

weight (37.62%) and node at which first hermaphrodite flower appears (33.00%), comparatively moderate genotypic coefficient of variation was recorded in case of number of primary branches per vine (27.16%), seed cavity length (27.08%), total soluble solids content (26.65%), ascorbic acid content (25.73%), fruit length (24.72%), titrable acidity (21.05%), shelf life (20.80%), rind thickness (17.93%), number of fruits per vine (17.30%), seed cavity breadth (11.86%). However, dry matter content (9.76%), fruit breadth (7.63%), days from sowing to marketable maturity (3.40%), days from sowing to last fruit harvest (2.24%) showed comparatively low genotypic coefficient of variation. A very high heritability estimates were observed for fruit weight (94.04%), node at which first hermaphrodite flower appears (92.34%), seed cavity length (91.58%), fruit length (91.48%) and number of primary branches per vine (91.12%), while high genetic advance was found for fruit weight (69.25%) and node at which first hermaphrodite flower appears (67.08%).

Number of fruits per vine exhibited significant and negative correlation with fruit weight, seed cavity length, rind thickness, fruit length and ascorbic acid content, whereas fruit weight had significant and positive correlation with seed cavity length, fruit length and dry matter content. However, rind thickness recorded positive and significant correlation with ascorbic acid content and shelf life. The total soluble solid content depicted positive and significant correlation with ascorbic acid content. However, it displayed negative and significant correlation with titrable acidity. Titrable acidity showed significant and negative correlation with ascorbic acid content, whereas ascorbic acid content recorded positive and significant correlation with shelf life. Days from sowing to marketable maturity displayed positive and significant correlation with days from sowing to last fruit harvest and fruit weight. However, days from sowing to last fruit harvest revealed positive and significant correlation with shelf life and fruit weight. Node at which first hermaphrodite flower appears displayed positive and significant correlation with fruit weight and titrable acidity. However, it depicted negative and significant correlation with total soluble solids content.

Mahalanobis D^2 based on 16 morphological traits allowed grouping of test genotypes into 10 clusters; cluster I was the largest comprising thirty-seven genotypes, cluster II with sixteen genotypes, cluster III with one genotype which indicated an independent identity due to its unique characters, cluster IV with twelve genotypes, cluster V with four genotypes, cluster VI with thirteen genotypes, cluster VII with six genotypes, cluster VIII with three genotypes, cluster IX with two genotypes and cluster X with two genotypes. The intra cluster distance ranged from 0.00 (cluster III) to 40.35 (cluster VIII) indicating that the genotypes in clusters have dissimilarity for morphological features. The members of cluster IX and cluster III exhibited maximum divergence (inter-cluster distance 1028.24) followed by the members of cluster X and III (inter-cluster distance 938.21) and cluster IX and II (inter-cluster distance 876.17).The members of cluster VI and IV were least divergent (inter-cluster distance 66.05).

The formation of different clusters with variable number of entries in each cluster indicated diversity among genotypes. The genotypes from different agro-ecological zones were found to be scattered in different clusters, which suggested that a pattern of clustering of accessions was independent of their geographic origin. Considering the genetic divergence and mean performance of genotypes in respect of various traits, genetically diverse genotypes were identified. Based on mean of the clusters, the donors for different characters could be selected from clusters such as cluster I for days from sowing to marketable maturity, cluster III for number of fruits per vine and lowest node number at which first hermaphrodite flower appears, cluster VI for titrable acidity, cluster VII for rind thickness, total soluble solids content, ascorbic acid content and shelf life, cluster VIII for dry matter content , cluster IX for fruit weight, fruit length, fruit breadth and cluster X for number of primary branches per vine. The inter cluster distances were larger than the intra cluster distances indicating a wider genetic diversity between genotypes of clusters with respect to traits studied. Therefore, superior recombinants can be obtained through hybridization between genotypes across the clusters.

For molecular characterization, thirty SSR markers were amplified through Polymerase Chain Reaction using primers. The amplified bands were recorded as 1 (band present) and 0 (band absent) in a binary matrix. Polymorphism Information Content (PIC) values for each SSR marker were determined. Cluster analysis of genotypes using binary data generated by microsatellite markers was conducted. All the 30 SSR markers revealed clear and consistent amplification profile but 23 primers showed polymorphic patterns and amplified a total of 67 alleles with an average of 2.23 alleles per locus. PIC value ranged from from 0.42 (ECM124) to 0.74 (ECM51) with an average value of 0.57 across 96 melon genotypes. The genotypes were grouped into three major groups (I, II and III). There was a significant correlation between botanical groups and the clustering. Accessions belonging to *cantalupensis* except MM-3985, MM-3903 and MM-4030 cluster together in cluster I. Accessions belonging to the *reticulatus* group except MM-3977 and MM-4268 cluster together in cluster II and accessions belonging to the *momordica* group cluster together in cluster III. The largest cluster I consisted of sixty genotypes and was further subdivided into sub groups IA, IB, IC, ID, IE and IF. Cluster II consisted of twenty-four accessions and was further subdivided into IIA, IIB and IIC. Cluster III consisted of twelve genotypes which had accessions belonging to the *momordica* group and was further subdivided into IIIA IIIB, IIIC and one un-clustered accession. Dendrogram showed overall similarity coefficient which ranged from 0.25 to 0.80. The lowest genetic similarity (0.25) was shown between group I and group III and maximum genetic similarity (0.80) was found between MM-3885 and MM-3966. All the 96 genotypes were analyzed for dissimilarity coefficient using computer software DARwin 5.0, for Factorial Correspondence Analysis (FCA). Factorialv

Correspondence Analysis plot thus obtained highly corresponds to the clustering observed using NTSYS indicating that the analysis was reliable. The results of this investigation exhibit the distinction between sweet melon and non-sweet melon groups. Clustering of genotypes besides being based on botanical relationship also depends on geographical origin. Many accessions with similar origin (region of cultivation) were closely related to each other e.g. in case of sub-cluster 1A, genotypes MM-3833 and MM-3849 show maximum similarity with each other were collected from same sub-zone 13.1. Similarly, in sub-group IB genotypes MM-3979 and MM- 3973 were collected from sub-zone 9.1.The highest similarity in whole dendrogram was shown by MM-3885 and MM-3966 in cluster IIB which were also collected from same sub-zone 13.1. The further support to this argument came from clustering of accessions belonging to *momordica* group in cluster III where out of twelve accessions, eleven accessions cluster together. They were collected from same sub-zone 13.1 and and only one *momordica* accession (MM-3994) showed highest level of variation from other *momordica* accessions was collected from sub-zone 14.5. Thus, besides botanical relationship geographical origin has also contributed towards genetic similarity. However, there was intermixing of some accessions of *cantalupensis* and *reticulatus* which may suggest genetic introgression among melon groups because of natural out-crossing. Intercrossing between *cantalupensis* or *reticulatus* with *momordica* was not detected in this study.

The eight reference accessions obtained from USA belonged to *reticulatus* group clustered together in sub-group IIA and shared similarity coefficient of 0.65 with sub-group IIB which included Indian melon accessions belonging to group *reticulatus*. Reference accessions cluster together forming a genetically unique assemblage in sub-groups IIA. The SSR marker analysis suggested that this germplasm shared genetic affinities with Indian melon accessions that could not be predicted based on their geographic origin. The clustering of reference accessions with Indian accessions indicated that genetic diversity of these has been conserved in India. It also infers either Asiatic origin or independent domestication involving of similar ancestors. Therefore, India is considered as the primary center of diversity for melons. Melons were transported from India to China (secondary center of diversity) and westward through south Asia, from the Middle East to Europe and then eventually to America.

Screening of all accessions for cucumber mosaic virus (CMV) under artificial condition was done during 2009 and 2010. Four melon accessions viz., MM-3974, MM-3982, MM-3994, and MM-4067 were free from CMV during both the years. However, none of the reference accessions inoculated with CMV showed resistance.

Melon accessions were screened for downy mildew resistance under natural epiphytotic conditions in the field during 2009, 2010 and 2011. Downy mildew did not appear in natural epiphytotic condition during 2009 and 2010, however, it was observed in natural

epiphytotic condition during 2011. On the basis of per cent disease incidence (PDI), two accessions, MM-3917 and MM-3976 were moderately resistant (PDI 42% and 50% respectively), two accession, AR Hale's and MM-3985 were resistant (PDI 30%), ninety accessions were highly resistant and two accessions, MM-3983 and MM-4004 were immune (PDI 0.00%). However, no genotype was found susceptible to downy mildew. It was observed that for identification of genotypes for downy mildew resistance artificial screening is pre-requisite.

This investigation supports the previous findings that *momordica* group possesses resistance for CMV and downy mildew because one of the two accessions (MM-4004) showing immune reaction to downy mildew belonged to group *momordica.* Similarly, out of four accessions resistant to CMV, three accessions, MM-3982, MM-3994 and MM-3974 belonged to group *momordica*. It was found that most of the accessions showing resistance or immunity to above mentioned diseases were collected from sub-zone 13.1. Therefore, this sub-zone should be explored further for genotypes possessing resistance to different biotic and abiotic stresses.

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