IDENTIFICATION OF BEST GENERAL COMBINING INBRED LINES AND THEIR HETEROTIC COMBINATIONS FOR SEED AND FRUIT QUALITY TRAITS AND RESISTANCE TO FUSARIUM WILT IN MUSKMELON (*Cucumis melo* L.)

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DEPARTMENT OF SEED SCIENCE AND TECHNOLOGY

UNIVERSITY OF AGRICULTURAL SCIENCES

BANGALORE

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BENGALURU JULY, 2022

Affectionately Dedicated

to

My Beloved Family and Friends

DEPARTMENT OF SEED SCIENCE AND TECHNOLOGY
UNIVERSITY OF AGRICULTURAL SCIENCES
BANGALORE

CERTIFICATE

This is to certify that the thesis entitled "**IDENTIFICATION OF BEST GENERAL COMBINING INBRED LINES AND THEIR HETEROTIC COMBINATIONS FOR SEED AND FRUIT QUALITY TRAITS AND RESISTANCE TO FUSARIUM WILT IN MUSKMELON (*Cucumis melo* L.)**" submitted by **Ms. RAMYA, M. J., ID. No. PALB 8103** for the award of the degree of **DOCTOR OF PHILOSOPHY** in **SEED SCIENCE AND TECHNOLOGY** to the University of Agricultural Sciences, Bangalore. This is a record of *bona-fide* research work done by her during the period of her study in this University, under my guidance and supervision and the thesis has not previously formed the basis for the award of any degree, diploma, associate-ship, fellowship or other similar titles.

Bengaluru
July, 2022

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IDENTIFICATION OF BEST GENERAL COMBINING INBRED LINES AND THEIR HETEROTIC COMBINATIONS FOR SEED AND FRUIT QUALITY TRAITS AND RESISTANCE TO FUSARIUM WILT IN MUSKMELON (*Cucumis melo* L.)

RAMYA, M. J.

ABSTRACT

The present investigation was undertaken at the department of Seed Science and Technology, GKVK, Bangalore in collaboration with Orbi Seeds International Pvt. Ltd., Bangalore, during Rabi 2019, Summer 2020 and Summer 2021 to identify the stable hybrids for seed and fruit quality traits in Musk melon. Five lines and twelve testers were used to make sixty hybrids in line × tester mating design. Hybrids developed were evaluated in randomized complete block design (RCBD) at research and development station of Orbi Seeds, Sira for seed and fruit quality traits. Among different lines, line-2 was identified as good general combiners for fruit diameter and seed quality traits, line-4 was a good general combiner for fruit weight. Line-1 was identified as good general combiner for TSS. Whereas, tester-1 was good general combiner for cavity size and most of seed quality traits. Tester-4 was identified as overall good general combiner status for all traits under consideration. Hybrids 1L × 4T found to have significant *sca* effects for smaller cavity size also for seedling vigour index-I and Seedling vigour index-II while 3L ×12 T and 5L × 1T for fruit weight and fruit diameter trait. Five hybrids and their parental genotypes of muskmelon were used for molecular screening of *Fom*-2 gene which imparts resistance to race-0 and race-1 of Fusarium wilt. Molecular validation was done with the gene specific marker *i.e. Fom*-2 gene R-408 (R allele). All the hybrids were found to carry resistance gene which was present the testers used for the study. Eventhough the female parent was found susceptible. SSR markers were also used for DNA fingerprinting for differentiation of parental lines. About ten primers were selected to test for polymorphism in five hybrids. Out of selected 10 primers, 5 showed polymorphism, while remaining five showed monomorphisms.

July, 2022

Department of Seed Science and Technology
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Major Advisor

ಉತ್ತಮವಾದ ಸಾಮಾನ್ಯ ಸಂಯೋಜನೆಯ ಪಿತೃತಳಿಗಳ ಗುರುತಿಸುವಿಕೆ ಮತ್ತು ಬೀಜ ಮತ್ತು ಹಣ್ಣಿನ ಗುಣಮಟ್ಟದ ಗುಣಲಕ್ಷಣಗಳಿಗಾಗಿ ಅವುಗಳ ಹೆಟಿರೋಟಿಕ್ ಸಂಯೋಜನೆಗಳು ಮತ್ತು ಕರಭೂಜದಲ್ಲಿ ಪ್ಯುಸೇರಿಯ ಸೊರಗು ರೋಗ ಪ್ರತಿರೋಧ (ಕ್ಯುಕ್ಯುಮಿಸ್ ಮೆಲೋ L.)

ರಮ್ಯಾ, ಎಂ. ಜೆ.

ಪ್ರಬಂಧದ ಸಾರಾಂಶ

ಪ್ರಸ್ತುತ ಕ್ಷೇತ್ರ ಪ್ರಯೋಗ ತನಿಖೆಯನ್ನು ಬೀಜ ವಿಜ್ಞಾನ ಮತ್ತು ತಂತ್ರಜ್ಞಾನ ವಿಭಾಗ, ಕೃವಿವಿ, ಜಿಕೆವಿಕೆ, ಬೆಂಗಳೂರು ಸಹಯೋಗದೊಂದಿಗೆ ಆರ್ಬಿ ಸೀಡ್ಸ್ ಇಂಟರ್‌ನ್ಯಾಶನಲ್ ಪ್ರೈವೇಟ್ ಲಿಮಿಟೇಡ್‌ನಲ್ಲಿ ಕೈಗೊಳ್ಳಲಾಯಿತು. ಚಳಿಗಾಲ ೨೦೧೯, ಬೇಸಿಗೆ ೨೦೨೦ ಮತ್ತು ಬೇಸಿಗೆ ೨೦೨೧ ರ ಕಾಲಾವಧಿಯಲ್ಲಿ ಕರಭೂಜ ಹಣ್ಣಿನ ಗುಣಮಟ್ಟದ ಗುಣಲಕ್ಷಣಗಳಿಗಾಗಿ, ಸ್ಥಿರವಾದ ಸಂಕರಣ ತಳಿಗಳನ್ನು ಗುತುತಿಸಲು ಲೈನ್ * ಪರೀಕ್ಷಕ ಸಯೋಗದಲ್ಲಿ ಅರವತ್ತು ಸಂಕರಣಗಳು ತಯಾರಿಸಲು ಐದು ಲೈನ್ ಮತ್ತು ಹನ್ನೆರಡು ಪರೀಕ್ಷಕಗಳನ್ನು ಬಳಸಲಾಯಿತು. ಅರವತ್ತು ಸಂಕರಣಗಳನ್ನು ಬೀಜ ಮತ್ತು ಹಣ್ಣಿನ ಗುಣಮಟ್ಟದ ಗುಣಲಕ್ಷಣಗಳಿಗಾಗಿ ಒಆರ್ಬಿ ಸೀಡ್ಸ್‌ನ ಸಂಶೋಧನಾ ಮತ್ತು ಅಭಿವೃದ್ಧಿ ಕ್ಷೇತ್ರದಲ್ಲಿ ಯಾದೃಚ್ಛಿಕ ಸಂಪೂರ್ಣ ತಾಕು ವಿನ್ಯಾಸದಲ್ಲಿ (ಆರ್‌ಸಿಬಿಡಿ) ಮೌಲ್ಯಮಾಪನ ಮಾಡಲಾಯಿತು. ಲೈನ್–೨ ಅನ್ನು ಹಣ್ಣಿನ ವ್ಯಾಸ ಮತ್ತು ಬೀಜದ ಗುಣಮಟ್ಟದ ಗುಣಲಕ್ಷಣಗಳಿಗೆ ಉತ್ತಮ ಸಾಮಾನ್ಯ ಸಂಯೋಜಕಗಳಾಗಿ ಗುರುತಿಸಲಾಗಿದೆ ಮತ್ತು ಲೈನ್–೪ ಹಣ್ಣಿನ ತೂಕಕ್ಕೆ ಉತ್ತಮ ಸಾಮಾನ್ಯ ಸಂಯೋಜಕವಾಗಿದೆ. ಲೈನ್–೧ ಅನ್ನು ಟಿಎಸ್‌ಎಸ್‌ಗಾಗಿ ಉತ್ತಮ ಸಾಮಾನ್ಯ ಸಂಯೋಜಕ ಎಂದು ಗುರುತಿಸಲಾಗಿದೆ. ಟೆಸ್ಟರ್–೧ ಅನ್ನು ಕುಹರದ ಗಾತ್ರ ಮತ್ತು ಹೆಚ್ಚಿನ ಬೀಜ ಗುಣಮಟ್ಟದ ಗುಣಲಕ್ಷಣಗಳಿಗೆ ಉತ್ತಮ ಸಾಮಾನ್ಯ ಸಂಯೋಜಕ ಎಂದು ಗುರುತಿಸಲಾಗಿದೆ. ಪರಿಗಣನೆಯಲ್ಲಿರುವ ಎಲ್ಲಾ ಗುಣಲಕ್ಷಣಗಳಿಗೆ ಟೆಸ್ಟರ್–೪ ಅನ್ನು ಒಟ್ಟಾರೆ ಉತ್ತಮ ಸಾಮಾನ್ಯ ಸಂಯೋಜಕ ಸ್ಥಿತಿ ಎಂದು ಗುರುತಿಸಲಾಗಿದೆ. ಸಂಕರಣ ಲೈನ್–೧*ಟೆಸ್ಟರ್–೪ ಸಣ್ಣ ಕುಹರದ ಗಾತ್ರಕ್ಕೆ ಗಮನಾರ್ಹವಾದ ಎಸ್‌ಸಿಎ ಪರಿಣಾಮಗಳನ್ನು ಹೊಂದಿದೆ ಎಂದು ಕಂಡುಬಂದಿದೆ ಮತ್ತು ಮೊಳಕೆ ಹುರುಪು ಸೂಚ್ಯಂಕ–೧, ಮೊಳಕೆ ಹುರುಪು ಸೂಚ್ಯಂಕ–೧೧, ಲೈನ್–೩*ಟೆಸ್ಟರ್–೧೨ ಹಾಗು ಲೈನ್–೫*ಟೆಸ್ಟರ್–೧ ರಲ್ಲಿ ಹಣ್ಣಿನ ತೂಕಕ್ಕೆ ಗಮನಾರ್ಹವಾದ ಎಸ್‌ಸಿಎ ಪರಿಣಾಮಗಳನ್ನು ಹೊಂದಿದೆ ಮತ್ತು ಹಣ್ಣಿನ ವ್ಯಾಸದ ಲಕ್ಷಣ ಐದು ಸಂಕರಣ ಮತ್ತು ಅವುಗಳ ಪೋಷಕರ ಜೀನೋಟೈಪ್ ಕರಭೂಜವನ್ನು *ಈಠಟ*–೨ ವಂಶವಾಹಿ ಆಣ್ವಿಕ ಮೌಲ್ಯೀಕರಣಕ್ಕೆ ಬಳಸಲಾಗಿದೆ. ವಂಶವಾಹಿಯ ನಿರ್ದಿಷ್ಟ ಮಾರ್ಕರ್ ಅಂದರೆ *ಈಠಟ*–೨ ವಂಶವಾಹಿ ಖ–೪೦೮ (ಆರ್ ಆಲೀಲ್) ನೊಂದಿಗೆ ಆಣ್ವಿಕ ಮೌಲ್ಯೀಕರಣವನ್ನು ಮಾಡಲಾಯಿತು. ಎಲ್ಲಾ ಸಂಕರಣ ತಳಿಗಳು ನಿರೋಧಕ ವಂಶವಾಹಿಯನ್ನು ಹೊಂದಿದ್ದವು. ಇದು ಅಧ್ಯಯನಕ್ಕೆ ಬಳಸಲಾದ ಪರೀಕ್ಷಕಗಳಲ್ಲಿ ಪ್ರಸ್ತುತವಾಗಿತ್ತು. ಡಿಎನ್‌ಎ ಫಿಂಗರ್‌ಪ್ರಿಂಟಿಂಗ್‌ಗಾಗಿ ಎಸ್‌ಎಸ್‌ಆರ್ ಮಾರ್ಕರ್‌ಗಳನ್ನು ಸಹ ಬಳಸಲಾಗಿದೆ. ಐದು ಸಂಕರಣ ತಳಿಗಳನ್ನು ಅವುಗಳ ಶುದ್ಧತೆಯನ್ನು ಪರೀಕ್ಷಿಸಲು ಎಸ್‌ಎಸ್‌ಆರ್ ಮಾರ್ಕರ್‌ಗಳ ೧೦ ಪ್ರೈಮರ್‌ಗಳನ್ನು ಬಳಸಲಾಗಿ ಅದರಲ್ಲಿ ೫ ಪ್ರೈಮರ್‌ಗಳು ಪಿತೃತಳಿಗಳನ್ನು ಪ್ರಾತ್ಯೇಕಿಸಲು ಬಹುರೂಪತೆಯನ್ನು ತೋರಿಸಿದವು.

ಜುಲೈ, ೨೦೨೨

ಬೀಜ ವಿಜ್ಞಾನ ಮತ್ತು ತಂತ್ರಜ್ಞಾನ ವಿಭಾಗ
ಜಿಕೆವಿಕೆ, ಕೃವಿವಿ, ಬೆಂಗಳೂರು

(ಪಿ. ಜೆ. ದೇವರಾಜು)
ಮುಖ್ಯ ಸಲಹೆಗಾರರು

CONTENTS

LIST OF TABLES

LIST OF FIGURES

LIST OF PLATES

LIST OF APPENDICES

I INTRODUCTION

Muskmelon (*Cucumis melo* L.; 2n = 2x = 24) is a warm season old-world cucurbit and economically important species of the Cucurbitaceae family. *Cucumis melo* extremely diverse for phenotypic traits and melons are cultivated in nearly all of the warmer regions of the world. Its short duration, high production potential and sweetness of the fruit (*i.e.*, sugar content), flavor or aroma, texture and phytonutrients provide it a commercial and desert fruit signature (Lester, 2008). Muskmelon is enormously good for health as it is rich in ascorbic acid, carotene, folic acid and potassium as well rich in a number of other human health bioactive compounds (Lester and Hodges, 2008). It is a rich source of dietary fiber, vitamins and minerals like calcium, phosphorus and iron (Pitrat, 2008). It is having magical health benefits therefore it is considered as a "wholesome food".

Muskmelon is cultivated in an area of 1.2 million ha with 29.5 million metric tonnes production and 24.9 tonnes ha^{-1} productivity. China is the largest producer with 50.04% share followed by Turkey (5.76%), Iran (4.98%), Egypt (3.54%) and India (3.49%). In India, it is cultivated in 47,000 ha with 8,78,000 MT production and productivity of 20 tonnes ha^{-1} (Anonymous, 2017). It is extensively cultivated in hot and dry areas of Uttar Pradesh, Punjab, Rajasthan, Madhya Pradesh, Bihar and Karnataka.

Since, ancient times muskmelon has been subjected to human selection and plant breeding efforts. There has been a substantial varietal improvement in muskmelon by using traditional breeding methods. Due to the presence of strong sexual incompatibility barriers at the interspecific and intergeneric levels, the genetic potential remains restricted for the development of new and enhanced melon cultivars (Robinson and Decker-Walters, 1999). Improvement in melon by traditional hybridisation is relatively slow and it is restricted to a narrow gene pool (Pitrat *et al.*, 1991).

The art of hybridisation came into existence along with heterosis. Hybrid vigour was first reported by Koelreuter (1763). The phenomenon has been exploited in many vegetable crops and large number of hybrids have been released for commercial cultivation. Hybrid cultivation is increasing day by day because of high yield. In

muskmelon, hybrids are preferred over variety due to their early maturity, high yielding potentiality, superior quality and high input response (Banga and Banga, 2000). Additionally, the development of F_1 hybrids in muskmelon is quite easy due to andromonoecious nature.

Therefore, selection of parents for the hybrids possessing desirable traits is most decisive and crucial step. Generally, parents are selected on the basis of *per se* performance, but due to various gene combinations may do not stand true. General combining ability is an average performance of an individual in a particular series of crosses.

The edaphic factors with interaction of genotype can help to arrive wide adaptability for breeding of stability or specific adaptability. A number of statistical methods have been developed to characterize production environments and reduce/predict the interaction between genotype × environment. A few important of these are joint regression (Eberhart and Russell, 1966; Perkins and Jinks, 1968), Additive Main Effects and Multiplicative Interaction (AMMI) model elaborated by Zobel *et al*. (1988) provides more insight on the patterns of genotypic responses to different environments.

Muskmelon exhibits a wide range of morphological, physiological and biochemical diversity (Eduardo *et al.* 2007). It is also prone to attack many diseases that affect the yield and quality of fruits. Indiscriminate use of pesticides to control diseases is a common practice at farmers field, which is a matter of concern for human health, environmental pollution and economics of the crop. Fusarium wilt, caused by *Fusarium oxysporum* f. sp. *melonis*, is one of the most difficult diseases to control primarily because the pathogen is soil-borne and remains viable in the soil as chlamydospores for decades. An effective control for this pathogen is through host resistance (Martyn and Gordon, 1996). It can cause upto 100% yield loss and, have been observed worldwide (Appel and Gordon 1995; Zitter 1999; Sherf and Macnab 1986).

A common method of artificial inoculation used to evaluate resistance to fusarium wilt is a time-consuming process and susceptible plants may escape detection (Burger *et al*., 2003). Thus, molecular markers tightly linked to fusarium wilt resistance genes are

highly valued in melon breeding. Currently, four races (0, 1, 2, and 1, 2) of the pathogen are defined by their capacity to incite disease in different varieties of melons. Resistance to race-1 is conferred by a single dominant gene *Fom*-2, gene also confer resistance to race 0 (Schreuder *et al*., 2000; Zink and Thomas, 1990).

Considering these aspects study was initiated with following objectives

1. To assess general combining ability of F_5 inbred lines for seed and fruit quality traits
2. To identify stable high yielding heterotic hybrids with desirable fruit quality traits
3. To identify hybrids resistant to Fusarium wilt using linked SSR markers
4. To fingerprint selected hybrids using SSR markers

II REVIEW OF LITERATURE

Literature related to the objectives of the present study has been comprehensively reviewed and presented under the following subheadings pertaining to seed and fruit quality traits in muskmelon.

2.1 Combining ability for seed and fruit quality traits

2.2 Heterosis for seed and fruit quality traits

2.3 Genotype by environment interactions and stability parameters

2.4 Screening for Fusarium wilt using linked markers

2.5 Fingerprinting of parental lines and hybrids

2.1 Combining ability for seed and fruit quality traits

The concept of combining ability for the evaluation of parents in a crossing programme is of immense importance. It has been extensively used to categorize the parental lines in their ability to transmit their desirable performance to hybrid combinations. Therefore, it helps the breeder in finding the best combiners which can be used in hybridization either to exploit heterosis or to combine favourable fixable genes. The common approach on the basis of *per se* performance does not necessarily lead to fruitful results (Allard, 1960). Combining ability analysis provides estimates of effects and variances. The concept of combining ability is well established in plant breeding since it distinguishes parental lines, provides means to understand the nature and magnitude of gene action involved in heterosis and also aids in designing breeding procedure. It was formulated by Sprague and Tatum (1942) in relation to single crosses of corn. General Combining Ability (GCA) is the average performance of a genotype in a series of cross combinations, estimated from the performance of F_1's from the crosses, whereas, specific combining ability (SCA) is used to designate those cases in which certain combinations do relatively better or worse than expected on the basis of average performance of genotypes involved. Griffing (1956) has shown the relationship between various heritable variance components of GCA and SCA variances. GCA variance is due to additive variance and

additive × additive interaction variance, while SCA variance is due to dominance variance and dominance × dominance variance components. Estimates of the variances due to GCA and SCA provide an appropriate diagnosis of the predominant role of additive or non-additive variances of gene in the inheritance of a trait.

Gurav *et al*. (2000) observed that Jam-e-Shahada was the best general combiner as it had produced significant *gca* effects for out of eight characters studied, indicating the need of its exploitation for yield heterosis. The combination Kavit × Bhang with the highest significant *sca* effects had recorded the highest heterosis over better parent and high per se performance for number of fruits and weight of fruit per vine in muskmelon.

Lal and Kaur (2002) assessed forty cross-combinations, involving the four female parents and ten male parents for combining ability effects. MS-1 and NDM-15 were found to be good combiners among females and males for fruit yield per vine and TSS content respectively. According to them, the best cross combinations generally involved with one of the best combing parents in muskmelon.

Al-Araby (2004) noticed both GCA and SCA were highly significant for stem length and number of leaves per plant in cucumber indicating that both additive and non-additive genetic variances were important for inheritance of these two traits. The ratio between the mean squares of GCA and SCA showed that, the non-additive gene effects were more important than additive ones in the inheritance of stem length, on contrary number of leaves per plant was governed mainly by additive gene effects.

Aravindakumar *et al*. (2005) studied forty-nine muskmelon hybrids involving seven lines and seven testers to determine the extent of heterosis and combining ability effects for earliness and growth parameters. Arka Jeet among the lines and IIHR -615-5-2 among the testers were good combiners for majority of the characters. The crosses Pusa Madhuras × IIHR-615-5-2 for days to first female flower opening, Pusa Sharbati × IIHR-352-14-1-9-1 for node at first female flower appeared, Kajri × IIHR-615-5-2 for days to first fruit harvest, Kajri × Durgapura Madhu for vine length and Punjab Sunehri × IIHR -616-2-3 for number of branches per vine were identified as good specific combiners.

Moon *et al*. (2006) studied twenty-eight F_1 hybrids of muskmelon and eight parents to investigate the extent of heterosis for different biochemical traits. Among all the parents Ravi had the highest TSS, total sugar and reducing sugar dominant alleles among parents for all the traits. DVRM-1 and Hara Madhu showed the highest values for carotenoid and ascorbic acid contents, respectively.

Jagtap (2010) conducted an experiment in 7×7 half diallel fashion in *kharif* 2008 and the resulting 21 hybrids along with 7 parents were evaluated in RBD with two replications during summer and *kharif*-2009, to study the heterosis and combining ability of F_1 and their parents. The studies on combining ability revealed that the parents Durgapura Selection (P2), Hara Madhu (P3), IVMM-3 (P4) and Punjab Sunehri (P7) were the good general combiners and have high gca effects for most of the characters during both the seasons.

Vasist *et al.* (2010) assessed twenty-eight cross combinations along with eight parental lines for their combining ability in muskmelon. Mean squares due to gca and sca were highly significant for the most of the characters. It indicated the importance of both additive and non-additive genetic components for characters under study. The parental line Hara Madhu was the best general combiner for total fruit yield per vine (0.17**), fruit weight (0.05**), number of fruits per vine (0.11*), TSS (0.52**) and fruit shape index (0.045**) and Punjab Rasila was the best general combiner for fruit/cavity ratio (0.16**), flesh thickness (0.105**), flesh proportion (0.018**) and node at which 1st female flower opens (-0.26**). The cross-combination MM-28 × IVMM-3 recorded highest SCA value for node at which 1st pistillate flower opens, number of fruits per vine and fruit weight whereas cross combination MM-28 × NDM- 21 exhibited best sca effects for total yield per vine. The results revealed the importance of heterosis breeding for effective utilization of non-additive genetic variance.

Glala *et al*. (2011) used six sweet melon (*Cucumis melo* var. *aegyptiacus*) inbred lines, utilized them in line × tester top crosses with three muskmelon (*Cucumis melo* var. *reticulatus*) inbred lines resulting in eighteen hybrids (F_1). The eighteen netted genotypes were evaluated in comparison with their respective parents during the hot summer season

of 2009. All genotypes (parents and hybrids) differed significantly from each other for all investigated traits. In terms of general combining ability (GCA), the three lines L1, L2 and L3 and two testers T1 and T3 were considered as good combining parents for simultaneous improvement of most of the yield and fruit quality traits. Significant effects were observed for both yield and fruit quality traits in the crosses L3×T2, L4×T1 and L5×T3 for yield traits and total soluble solids (TSS %), L2×T1 for both yield traits and fruit shape index and L2×T2 for main stem length (cm), average fruit weight (g) and flesh thickness (cm).

Mule *et al.* (2012) carried out experiment combining ability for fruit yield and its components traits on twenty-seven F1 hybrids of cucumber obtained from a Line × Tester method involving twelve diverse parents. Their results revealed that none of the parents was found good general combiners for all the traits consistently, however parents CCP-9, Gujarat local and SPP-44 were good combiner for fruit yield and its contributing traits.

Al-Hamdany (2013) crossed four varieties of melon in a complete diallel design. The results indicated that general combining ability was significant for all the studied characters except number of branches per plant and number of seeds per fruit, and that specific combining ability and reciprocal effects was significant for most studied characters. The results showed that general combining ability was higher than specific combining ability for number of nodes per first male flowering and fruit weight.

Shashikumar and Pitchaimuthu (2016) conducted combining ability analysis to understand the nature of gene action of quantitative traits and to identify promising parents for breeding programme in muskmelon. Six female and five male parents were crossed in line x tester mating fashion to produce thirty F_1 hybrids. Analysis of variance showed high magnitude of GCA over SCA variance indicating predominance of additive gene effects for all the traits. RM 43 and IIHR122 were the best general combiner for most of the quantitative traits. Strong phenotypic correlation between GCA and parent *per se* performance for all traits except for number of primary branches per vine and fruit yield per vine indicated the possibility of selection of traits at the level of parents.

Hassan *et al*. (2018) took six parental genotypes representing wide range of variability in most of the studied traits and crossed them in half diallel fashion. Seed crop grown during the summer seasons of 2015, 2016 and 2017, to study the important economical traits of muskmelon *viz*., fruit width, fruit length, flesh thickness, cavity diameter, total soluble solids, ascorbic acid content, carotenoids content, fruit weight, total yield/vine and fruit number/vine. A greater ratio of GCA/SCA than unity was detected for most studied traits, revealing that the inheritance of these traits was mainly controlled by additive gene effects. On the contrary, both TSS and ascorbic acid content traits, non-additive type of gene action seemed to be more prevalent. The cross 3M-637-D (P2) × 86E2143 (P4) was derived from low × high general combiner parents for total yield/vine and exhibited the highest mean yield, highest heterosis, highest sca effects for yield. They also showed, significant or highly significant desirable sca effects for 8 important traits.

Singh and Vasisht (2018) conducted a study to assess the extent of heterosis and combining ability of muskmelon in a half diallel mating design resulting forty-five F_1 hybrids. Both hybrids and inbred lines were evaluated for fourteen different characters during 2014-15 at PAU, Ludhiana. Among inbred lines, MS-5 and MM-311 were found to be the best general combiners for days to fruit maturity, fruit yield per plot and TSS content along with other important traits. Cross combinations *viz*., MS-5 × MM 308 and MS-5 × MM-304 were significantly better for days to fruit maturity, total fruit yield per plot and TSS content along with other important fruit traits over standard checks, Punjab Hybrid and Farmers' Glory.

Selim (2019) evaluated 36 hybrids resulting from 12 inbred lines and 3 testers in melon (*Cucumis melo* var. *ananas*) using line × tester mating design to determine heterosis, combining ability of yield and yield attributes.The results revealed highly significant mean squares for the studied traits. Inbred lines, Testers and line × tester interaction showed highly significant differences for the traits. The inbred line (T5) showed higher positive general combining ability (GCA) impact for all traits except early yield and fruit shape index (FSI). Among them four hybrids showed highly significant and significant SCA impacts of early yield, total yield, average fruit weight and TSS, respectively.

Badami *et al.* (2020) evaluated heterotic and combining ability effects in the diallel crosses of melon (*Cucumis melo* L.) for yield and quality-related traits. Seven melon genotypes were grown and crossed in a complete diallel fashion to produce F_1 hybrids and evaluated, 49 melon genotypes (7 parents + 42 F_1 hybrids). Analysis of variance revealed significant ($P \leq 0.01$) differences among the melon genotypes for harvest age, fruit flesh thickness, total soluble solids, fruit length and fruit diameter, merely significant differences ($P \leq 0.05$) for fruit weight. Combining ability analysis revealed that mean squares due to general combining ability (GCA) were significant for fruit diameter and mean squares due to specific combining ability (SCA) were significant for all traits. The parental genotypes PK-165, PK-464, and PK-669 exhibited the highest and desirable gca effects for yield and quality traits. Hence, these genotypes could be used to generate high-yielding hybrid/open-pollinated cultivars.

Neto (2020) evaluated yellow melon lines and hybrids. Yield and fruit quality traits were evaluated. Partial diallel analysis was carried out to estimate general combining ability and specific combining ability. The lines AF-02, LAM-02, and LAM-03 are the most promising as parents as they more frequently have favourable alleles. The most prominent hybrids in diallel analysis were AF-02 × LAM-02, AF-02 × LAM-03, AF-02 × LAM-04, and AF-03 × LAM-06.

2.2 Heterosis for seed and fruit quality traits

The exploitation of hybrid vigour in muskmelon has received greater importance on account of several advantages of hybrids over pure lines with response to better adaptability, marketable fruit yield and resistance to biotic and abiotic stresses. The superiority of F_1 hybrids over their parental genotypes is termed as heterosis. The phenomenon of heterosis in plants was recognized by Koelreuter (1763). Shull (1914) gave the term ‘Heterosis’ to the developmental stimulus resulting from the union of different gametes. Many scientists including Shull (1908 and 1914), East (1908), Bruce (1910) and Crow (1948) put forth hypothesis justifying the manifested effect of heterosis. The manifested effect of heterosis was called hybrid vigour. Hays and Jones (1916) were the first investigators to report heterosis in cucurbits.

Munshi and Verma (1997) studied six parental lines and fifteen F_1 hybrids of musk melon obtained from half diallel to investigate the extent of heterosis for yield and its contributing characters. They found Pusa Madhuras × Ravi, Pusa Sharbati × Pusa Madhuras and Pusa Madhuras × Hara Madhu to be three best performing F_1 hybrids for yield per plant, increased number of fruits and fruit weight. The best performing F_1 hybrid, Pusa Madhuras × Ravi, recorded 28.15% higher yield than the best commercial check Pusa Madhuras.

Mohanty and Mishra (1999) evaluated 8-parent half-diallel cross along with parents for heterotic manifestation of yield and yield components. Heterosis to the extent of 37.7, 28.6, 76.9, 142.9, 96.3, 48.9 and 188.7% over better parent and 52.1, 36.9, 89.6, 161.5, 109.9, 68.9 and 197.1% over mid-parent was recorded for vine length, number of primary branches, female flowers, fruits/plant, average fruit weight, flesh thickness and yield/plant respectively.

Gurav *et al*. (2000) studied heterosis and combining ability in muskmelon by using eight local and three improved collections in a half diallel set. They observed the combination Kavit × Bhang with the highest significant sca effects had recorded the highest heterosis over better parent and high *per se* performance for number of fruits and weight of fruits per vine.

Sulochanamma (2001) observed that the maximum heterobeltiosis (85.02%) for total yield by weight in muskmelon (*Cucumis melo* L.).

Lal and Kaur (2002) assessed 40 cross combinations among the four female parents and 10 male parents for their heterosis over better parents and two standard checks (Punjab Hybrid and MH-10) in muskmelon. They observed maximum heterosis for TSS content for the cross MS-1 × NDM-15.

Rajan *et al*. (2002) studied extent of heterosis in watermelon using ten lines and three testers. The cross combinations HW-1 × Arka Manik, Sel-B × Shipper, Durgapur Mitha × Shipper observed heterosis for traits *viz*., early picking, fruit yield per plant and total soluble solids.

Shamloul (2002) evaluated sixteen F_1 hybrids of sweet melon (*Cucumis melo* var. *aegyptiacus* L). The results indicated that the means of F_1 hybrids significantly exceeded the means of the mid-parents for all vegetative traits. The estimated amounts of heterosis for vegetative traits were 11.23, 25.80, and 4.74 % for length of plant, number of leaves per plant and leaf area/plant, respectively.

Choudhary *et al*. (2003) studied eight genetically diversed inbred lines, MS-1, RM-43, MHY-3, Punjab Sunehri, Jobner Local, Hara Madhu, Tonk Local and Durgapura Madhu, of muskmelon and were crossed in a diallel fashion, excluding reciprocals. The resulting twenty-eight F_1's, along with their parental lines, were grown during summer 2001 and heterosis for yield and its components was determined. Higher heterosis for number of fruits per plant (15.96 %) was noticed in the cross-Hara Madhu × Tonk Local over better parent and standard control. Significant heterosis for yield was observed in the crosses MS-1 × Hara Madhu (44.44 %), Jobner Local × Durgapura Madhu (38.65%) and Hara Madhu × Durgapura Madhu (35.90 %) over better parent.

Moon *et al*. (2003) studied the heterosis for yield and its characters in eight parental lines of muskmelon. Heterosis was recorded over the better parent and commercial check (Punjab hybrid) for node number to first female flower and days to first female flower opening and stated that appreciable heterosis was recorded over the better parent and commercial check for fruit weight and fruit diameter.

Al-Araby (2004) found in cucumber that heterosis over the mid-parents was highly significant with positive values for stem length. Heterosis based on the check hybrid was significant for stem length and number of leaves/plant, heterosis over the mid-parents was highly significant with positive values for number of nodes to first female flower and sex ratio. Meanwhile, it was highly significant with negative values for number of days to female flowering (50% flowering). Heterosis over the mid–parents was insignificant for number of male flowers / plant and number of female flowers/plant. Heterosis over the better parent was significant or highly significant with positive values for number of nodes to first female flower and sex ratio, while it was highly significant with negative values for

number of days to female flowering, number of female flowers/plant, and heterosis over the better parent was insignificant for number of male flowers/plant.

Aravindakumar *et al*. (2005) studied forty-nine hybrids involving seven lines and seven testers to determine the extent of heterosis for growth characters. Hybrid those showed maximum heterosis over desirable direction were Hara Madhu × IIHR-332 for vine length and Arka Jeet × IIHR-190-1-AB-6-1 for number of primary branches. Hybrid showed maximum heterosis over desirable direction were Pusa Madhuras × IIHR-615-5-2 for days to first female flower opening, Arka Jeet × IIHR-190-1-AB-6-1 for node at first female flower appeared, Kajari × IIHR-615-5-2 for days to first fruit harvest in muskmelon.

Souza *et al.* (2005) evaluated twelve triploid hybrids to estimate heterotic effects in watermelon (*Citrullus lanatus*). Tiffany, a triploid hybrid was used as standard check. Mid-parent heterosis effects was found as well as the standard cultivar ranging from negative to positive values attaining up to 300% prolificacy in some cases.

Sudhakar *et al*. (2005) studied heterosis in ten hybrids of cucumber. Heterosis was found better parent and mid parent for all the characters studied. The hybrids DC-1 × B-159 and VRC-11-2 × Bihar-10 were observed to be best hybrids for total fruit yield as they recorded heterosis over better parent (100.08 and 60.19%) and mid parent (140.66 and 71.29%). The high yielding F_1 hybrid DC-1 × B-159 and VRC-11-2 × Bihar-10 which recorded highest heterosis over better parent and mid parents.

Moon *et al*. (2006) studied twenty-eight F_1 hybrids of muskmelon and eight parents to investigate the extent of heterosis and suggested that the F_1 hybrid P2xP8 (Pusa Madhuras × Hara Madhu), which showed significantly higher heterosis over the top parent and commercial check for several quality characters with 44.54% and 15.89% higher yield, respectively, over the top parent Hara Madhu and commercial check Punjab Hybrid, may be recommended for commercial cultivation.

Iathet and Piluek (2006) in slicing melon (*Cucumis melo* var. *conomon*) found that heterobeltiosis was 12.71% for fruit number per plant, whereas heterosis for the total yield per plant was 8.20%. They also reported that the performance of the F_1 hybrid in terms of

fruit width, length and weight did not exceed that of the better parent or was equal to the mid-parent values.

Tomar and Bhalala (2006) investigated extent of heterosis in muskmelon hybrids obtained using half diallel design. Heterotic effects over the better parent were observed to be higher for number of the node on which first female flower appeared, fruits per plant, fruit weight, fruit yield per plant, moisture content and total soluble sugars in Environment-2 than in Environment-1. The hybrids AMM-01-18 × AMM-02-26, Hara Madhu × RM-50, AMM-00-25 × AMM-00-11 and AMM-01-18 × DM-1 were found to be high-yielding and heterotic in both the seasons studied.

Glala *et al*. (2011) used six sweet melon (*Cucumis melo* var. *aegyptiacus*) inbred lines, utilized them in line × tester top crosses with three muskmelon (*Cucumis melo* var. *reticulatus*) inbred lines resulting in 18 hybrids (F_1). Among the traits evaluated main stem length, Fruit thickness and net flesh percentage showed positive significant average heterobeltiosis, while number of branches, number of leaves, Average Fruit Weight, TSS and Fruit Shape Index manifested negative significant average heterobeltiosis for several crosses.

Mule *et al*. (2012) studied heterosis for fruit yield and its components in cucumber hybrids obtained from a Line x Tester method. The hybrids Pilibhit Local × K-90 followed by Sheetal × SPP-44 and Sheetal × CC-9 have exhibited higher heterobeltiosis for fruit yield and its component characters.

Yilmaz and Sai (2012) investigated the effect of heterosis for quantitative characteristics in fifty-three single, triple and double cross hybrids in muskmelon. They observed highest heterobeltiosis (184.23%) and heterosis (184.55%) for earliness by Special Combination (SC)-58 (G22 × C1) genotypes belonging to the single hybrid group. Superiority of the single hybrid group was observed both in total yield and in earliness of yield.

Shashikumar and Pitchaimuthu (2016) observed standard heterosis in ms-1 × IIHR 616, RM 43 × IIHR 718 and RM 43 × IIHR 121 among the 30 F_1 hybrids which out yielded

commercial check NS 910 with significantly larger fruits, significantly sweeter and earlier in picking.

Duradundi *et al*. (2018) undertaken an investigation to study the heterosis in muskmelon for growth, earliness and yield traits. The ten lines and three testers were sown and crossed in a line × tester mating system. Heterosis values were significant over better parent, best parent and over the commercial check in desirable direction in most crosses for growth, earliness and yield characters under consideration. The cross-involving KM-2 × PS exhibited maximum positive and significant heterosis over commercial check (56.96 %) for fruit yield per vine and fruit yield per hectare in muskmelon.

Hassan *et al*. (2018) took six parental genotypes representing wide range of variability in most of the studied traits and crossed in half diallel fashion. Evaluated during the three summer seasons of 2015, 2016 and 2017, to study the important economical traits of muskmelon. The maximum significant MP heterosis in desirable direction (112.4%) was recorded for ascorbic acid followed by total yield/vine (101.0%), number of fruits per vine (100%), TSS (65.3%), flesh thickness (62.1%), fruit weight (59.8%) and fruit length (53.6%). Heterobeltosis (over the best parent better, BP) was observed and the maximum significant manifestation was orderd as: Ascorbic acid (108%), number of fruits per vine (69.4%), both TSS (%) and cavity diameter (58.8%) and total yield per vine (49.8%).

2.3 Genotype by environment interactions and stability parameters

The adoption of melon hybrids by the productive sector necessitates a prior evaluation of the productivity, quality and shelf life of their fruits. Due to the different environmental conditions under which the hybrids are evaluated, an accentuated genotype-environmental interaction is expected to become apparent and likewise play important role in manifestation of phenotypic traits.

Dhakare and More (2008) evaluated fifty genotypes of muskmelon (*Cucumis melo* L.) were evaluated for stability in three consecutive environments. (*Rabi*, Summer and *Kharif*) They reported that mean sum of squares due to genotypes, when tested against G × E and pooled deviation were significantly high for all the traits. Similarly for

environmental variances, indicating genetic variability among the genotypes and environments were effective in influencing the performance of the genotypes except F:C ratio. The mean sum of squares due to G × E interaction, when tested against pooled deviation was highly significant for all the attributes. However, G × E (L) effects were found to be highly significant for all the attributes indicated that major components of differences in stability was due to both linear and non-linear components and the performance can be predicted over the environments except F:C ratio and fruit shape index. They found summer season suitable for expression of traits.

Venugopalan and Pitchaimuthu (2009) screened fourteen promising F1 hybrids of watermelon to identify stable hybrid(s) for a wide range for cultivation. They reported that two hybrids, *viz*., Arka Jyothi across the years and NS-295 were stable for a wide range for cultivation.

Oliveira *et al*. (2019) evaluated melon hybrids for yield, and soluble solids (SS) to determine the fruit's yield, quality and shelf life. They found predominance of the complex part of the genotype-environmental interaction for both yield and TSS content.

2.4 Screening for fusarium wilt using linked markers

Fusarium wilt is one of the most destructive diseases of muskmelon, which is an economically important disease worldwide causes yield losses in muskmelon growing areas. Using resistant genes and introgressing them into host is one of the most effective controlling measures to prevent Fusarium wilt.

Zheng and wolff (2000) screened for resistance to races 0 and 1 of Fusarium wilt, is conditioned by the dominant gene *Fom*-2. A RAPD fragment of 1.55 kb was amplified in resistant melon cultigens using a RAPD primer 596. They developed and tested SCAR marker for its segregation with the *Fom*-2 gene by using bulked segregant analysis and evaluated for its application in diverse melon cultigens. The results showed that the 1.4 kb SCAR marker was amplified from twenty-three out of thirty-six (64 %) resistant genotypes but from none of the thirty-one susceptible genotypes tested.

Burger *et al.* (2003) conducted marker assisted selection for fusarium resistance breeding using cleaved amplified polymorphic sequence (CAPS) and sequence characterized amplified region (SCAR) markers were compared using a single set of genotypes that included twenty-four melon accessions and breeding lines whose genotype regarding the *Fom-2* gene was well characterized. The practical value of the markers for discriminating a range of genotypes and clarifying the scoring of genotypes was also tested using a segregating breeding population which showed co-dominant SCAR markers to be useful in marker-assisted selection.

Sensoy *et al.* (2007) studied response to *Fusarium oxysporum* f. sp. *melonis* (*F.o.m.*) race 1 among seventy-nine *Cucumis melo* L. genotypes. Response was determined by using pathogenicity tests and RAPD markers (E07 and G17). They found that the marker E07 had higher success rate for detecting susceptible genotypes than that of G17.

Oumouloud *et al*. (2008) developed F_2 population derived from the 'Charentais-*Fom*-1' × 'TRG-1551' cross used in combination with bulked segregant analysis utilizing the random amplified polymorphic DNA (RAPD) markers, to develop molecular markers linked to the locus *Fom*-1. Four hundred decamer primers were screened to identify three RAPD markers (B17649, V01578, and V061092) linked to *Fom*-1 locus. Fragments amplified by primers B17649 and V01578 were linked in coupling phase to *Fom*-1, at 3.5 and 4 cM respectively, whereas V061092 marker was linked in repulsion to the same dominant resistant allele at 15.1 cM from the *Fom*-1 locus. These RAPDs were cloned and sequenced in order to design primers that would amplify only the target fragment. The derived sequence characterized amplified region (SCAR) markers SB17645 and SV01574 (645 and 574 bp, respectively) were present only in the resistant parent. The SV061092 marker amplified a band of 1092 bp only in the susceptible parent.

Tezuka *et al*. (2009) identified DNA markers tightly linked to *Fom-1* that could be used for marker assisted selection in breeding programs. First, they developed 125 F_2 plants derived from the cross between melon lines P11 (*fom-1fom-1*) and MR-1 (*Fom-1 Fom-1*). Using the F_2 population, we constructed a linkage map including fourteen SSR markers which had not been mapped previously. *Fom-1* was confirmed to be allocated to linkage

group-7. Then, they identified four AFLP markers using bulked segregant analysis. The AFLP marker TAG/GCC-470 was completely linked to *Fom- 1* and other three markers were mapped near *Fom-1*. TAG/GCC-470 and TCG/GGT-400 were respectively converted to STS and CAPS markers.

Oumouloud *et al*. (2012) used two sequence characterized amplified region (SCAR) markers, *Fom*2-R408 and *Fom*2-S342, were developed for *Fom*-2 resistant and susceptible alleles, respectively. These allele-specific PCR markers could be used as co-dominant markers when their primer pairs were combined in a multiplex PCR reaction. The specificity of these functional markers (FM) was validated on a set of twenty-seven genotypes representing several melon types. These FM markers are expected to enhance the reliability and cost effectiveness of marker-assisted selection for the *Fom*-2 gene in melon.

Gholizadegan and Seifi (2020) developed molecular markers for *Fom*-2 gene, which confers resistance to race-1 of Fusarium in muskmelon. After validation of the markers on a differential set of resistant and susceptible lines, they identified STS312 marker as the polymorphic and easy-to-score marker. Results suggested that resistance allele of *Fom*-2 gene is present in two landraces: Eyvankey and Mashhadi. These landraces can be used for resistance breeding in muskmelon.

Deol *et al*. (2021) Identified of new sources of resistance and did molecular mapping for Fusarium wilt resistance were conducted in a muskmelon inbred line KP4HM-15 with FW resistance introgressed from snapmelon. Inheritance studies in the F2 population derived from the cross Punjab Sunehri//KP4HM-15 indicated that FW resistance in KP4HM-15 is governed by a single dominant gene. Bulked segregant analysis was conducted to map the *Fom-5(t)* gene in KP4HM- 15 using 527 SSR primers. Four primer pairs, CMCTN35, DM0096, CSWCTT02, and ECM181, were found to show differential polymorphism in the resistant and susceptible bulks and were analysed in the whole of the population. Two SSR markers, DM0096 and CSWCTT02, mapped close to the *Fom-5(t)* gene at a genetic distance of 1.4 and 2.5 cM, respectively.

2.5 Fingerprinting of parental lines and hybrids

In melon (*Cucumis melo* L.), the grow-out test (GOT) has been traditionally used as a genetic purity test. However, this method is time-consuming, space-demanding, and associated with classification of the genotypes. Molecular markers have proved to be an efficient tool in genotyping analyses. Advancement of molecular biology has helped with identification of the DNA markers or molecular markers which can be effectually and proficiently employed for assessment of the genetic purity of hybrids at genomic level. The utilization of different types of molecular markers like Random Amplified Polymorphic DNA (RAPD), Amplified Fragment Length Polymorphism (AFLP), Sequence Tagged Microsatellite Site (STMS), Simple Sequence Repeats (SSR), Single Nucleotide Polymorphism (SNP) *etc.*, for testing the hybrid seed purity has been demonstrated in many crops (Yashitola *et al*., 2002).

Dongre *et al.* (2011) stated that SSR markers has significant importance for rapid assessment of hybrid and parental line seed purity.

Nandankumar *et al.* (2004) used Microsatellite markers for fingerprinting of hybrids, assessing variation within parental lines and testing the genetic purity of hybrid seed lot in rice. Ten sequence tagged microsatellite sites (STMS) markers were employed for fingerprinting eleven rice hybrids and their parental lines. Nine STMS markers were found polymorphic across the hybrids and produced unique fingerprint for the eleven hybrids. A set of four markers (RM 206, RM 216, RM 258 and RM 263) differentiated all the hybrids from each other, which can be used as referral markers for unambiguous identification and protection of these hybrids.

Fen *et al*. (2008) tested hybrid purity of melon (*Cucumis melo* L.) by polymerase chain reaction (PCR) assay based on simple sequence repeat (SSR) markers in two F_1 melon hybrids (‘Dongfangmi 1’ and ‘Dongfangmi 2’) and their parental lines. Twelve pairs of SSR primers for ‘Dongfangmi 1’ and three pairs for ‘Dongfangmi 2’ were selected. ‘Dongfangmi 1’ and ‘Dongfangmi 2’ were identified from their parental lines, and seven other uterine hybrid lines by multiplex primers MS48 + MS60 and MS4 + MS20, respectively.

Pallavi *et al.* (2011) screened fifty-eight primer pairs to identify the specific marker associated with each hybrid and parental lines. Hybrid KBSH-44 could be clearly identified by using ORS 309 and ORS 170, based on the banding pattern resolved on polyacrylamide gel (6%). ORS 309 amplified allele size at 250 bp was specific to female parent (CMS-17A) and 230 bp was specific to male parent (RHA 95-C-1). These two bands of allele size 230 and 250 bp were found only in hybrid KBSH-44. Another SSR primer ORS 170 was able to distinguish the hybrid KBSH-44 by amplifying allele of size 230 bp a female specific (CMS-17A) allele and 200 bp amplicon a male specific allele (RHA 95-C-1). SSR primer ORS 811 found specific to identify KBSH-53 and it amplified allele of size 270 bp in its female parent (CMS-53A) and allele size of 230 bp in its pollen parent (RHA 95-C-1). The hybrid has both the alleles from its parents at 270 and 230 bp.

Chethankumar *et al*. (2011) used thirty-five Simple Sequence Repeat (SSR) markers for distinguishing rice hybrids KRH-2 and DRRH-2 with their parents. Among them, 10 were found to be polymorphic. KRH-2 could be clearly identified by using RM206, RM234, and RM276, Similarly, DRRH-2 could be clearly identified by using RM234, RM228, and RM204.

Nataraj *et al.* (2016) identified SSR markers for hybrid purity testing in newly released hybrid rice KRH-4. In this study 25 simple sequence repeats (SSR) markers were employed. Among polymorphic primers RM202, RM204, RM219, RM216, RM1385, RM21, RM336, RM209, RM7279 and RM206 could clearly distinguish KRH-4 from its parental lines.

Nethra *et al.* (2016) used fifty-eight micro-satellite markers were for fingerprinting of two CMS, two restorer and sixteen cultivars of rice. Forty-eight markers were found polymorphic, out of which 28 amplified a specific or unique allele to twenty rice lines. In addition, with a set of eighteen unique polymorphic markers, KRH-4 and KRH-2 could be distinguished easily.

Lu *et al*. (2018), used genomic simple sequence repeat (SSR) markers were used to fingerprint the watermelon breeding lines, as well as the purity of their hybrid derivatives.

Fifty-five sets of SSR markers were employed in this study. Fourteen of these markers were polymorphic between the breeding lines and were used for assessing hybrid purity. Cross-checking assay validated nine SSR markers as informative SSR markers for purity detection of these hybrids. To confirm the accuracy and efficiency of these markers, their derived PCR products were further sequenced, and ClSSR09643, ClSSR18153 and ClSSR01623 were selected as high-efficiency SSR markers. Interestingly, SSR markers ClSSR09643 and ClSSR18153 were broadly applied for purity detection of more than two different hybrids, while SSR marker ClSSR01623 behaved as a specific marker for purity detection in this study. Genetic purity of six commercial watermelon hybrids was definitely evaluated using these SSR markers. Here, they elucidated the potential of nine SSR markers including three with higher breeding selection efficiency.

Kishore *et al*. (2020) used a total of ninty-six genome-wide single nucleotide polymorphism (SNP) markers to differentiate eighty-five melon F_1 hybrid plants from their parental lines of these, thirty-nine SNP markers showed polymorphism between the parents.

III MATERIAL AND METHODS

The material used to conduct the experiments and methodology employed to address the objectives of the present exploration and to test the framed hypothesis in the introduction chapter are presented in this chapter under the following heads.

1. Combining ability for seed and fruit quality traits
2. Heterosis for seed and fruit quality traits
3. Genotype by environment interactions and stability parameters
4. Screening of identified stable hybrids for fusarium wilt
5. Fingerprinting of parental lines and selected hybrids

3.1 Combining ability for seed and fruit quality traits

3.1.1 Experimental site

The investigation was carried out at Research and Development Station of Orbi Seeds International Pvt. Ltd., Yelahanka, Bangalore which is located at an altitude of 915 meters above mean sea level, 13^0 10 ″N latitude and 77^0 61″ E longitude.

3.1.2 Basic genetic material

The experimental material consisted of 5 lines and 12 testers contrasting for fruit and seed quality traits. These inbred lines were crossed in Line × Tester mating (Kempthorne, 1957) fashion during *Rabi* 2019 to develop 60 single cross hybrids.

3.1.3 Experimental Design

The present work was divided into two parts as follows

3.1.3.1 Method used to develop hybrids

1. Lines and Testers seeds were sown in portrays and kept in nursery. Fifteen days after sowing the seedlings were transplanted in the main field.
2. The planting ratio of 3:1 was maintained *i.e.*, for every 15 plants of lines, 5 plants of testers were planted.

3. After fifteen days of planting, the plants were pinched at apical portions to retain two lateral branches per plant.
4. Once the plants reached 5-6 internode stage emasculation was carried out and anthers were removed in andromonoecious lines. Both andromonoecious and monoecious lines were covered with butter paper covers to avoid cross contamination.
5. Male flower buds which were expected to open the next day were selected and removed from tester plants.
6. Male flowers from selected testers were stored in moist cloth overnight for the anthers to burst open.
7. Male flowers were then used for pollinating the emasculated female flowers in the morning hours between 7.00 to 9.00 am, labelling was done and covered using butter paper covers.
8. Fruits were ready for harvesting after 35-40 days of pollination.
9. At the attainment of physiological maturity, they were harvested and kept for post-harvest ripening for 3-4 days.
10. Seeds were extracted and kept for overnight for fermentation, washed and shade dried.

3.1.3.2 Evaluation of experimental material

3.1.3.2.1 Experimental site

The evaluation was carried out at Research and Development Station of Orbi Seeds International Pvt. Ltd., Ajjenahalli, Sira Taluk, Tumkur District, which is located at an altitude of 764 meters above mean sea level, 13^0 76 ″N latitude and 76^0 73″ E longitude.

3.1.3.2.2 Details of the experiment

Sixty single cross hybrids, their parents and check Akany from Bhalsar Seeds International were evaluated twice following RCBD with two replications (Cochran and Cox, 1957) during *Summer*- 2020 and *Kharif* 2020 at Research and Development Station of Orbi Seeds International Pvt. Ltd., Ajjenahalli, Sira Taluk, Tumkur District.

Plate 1: Carrying out emasculation in lines R&D Farm of Orbi Seeds International Pvt. Ltd, Bangalore

Plate 2: General view of the field plot for carrying out Line X Tester crossing programme

Plate 3: General view of hybrid evaluation plot at R&D Farm of Orbi Seeds International Pvt. Ltd, Ajjenahalli, Sira

Table 1a: List of Lines and Testers used in the study

Sl. No.	Lines (F)	Code	Sl. No.	Testers (M)	Code
1	ORBI-MG-1	L-1	1	ORBI-T1	T-1
2	ORBI-MG-2	L-2	2	ORBI-T2	T-2
3	ORBI-MG-3	L-3	3	ORBI-T3	T-3
4	ORBI-MG-4	L-4	4	ORBI-T4	T-4
5	ORBI-MG-5	L-5	5	ORBI-T5	T-5
			6	ORBI-T6	T-6
			7	ORBI-T7	T-7
			8	ORBI-T8	T-8
			9	ORBI-T9	T-9
			10	ORBI-T10	T-10
			11	ORBI-T11	T-11
			12	ORBI-T12	T-12

Observations recorded

For the present investigation, observations were recorded on five randomly selected plants from each hybrid, parents and checks for fruit and seed quality traits.

3.1.4 Yield and its component traits

The fruits were harvested at maturity, and the following data were recorded.

3.1.4.1 Fruit weight (g)

During the period of harvesting, randomly selected five matured fruits were weighed. It was pooled and then divided by five to take average fruit weight per genotype was expressed in grams.

3.1.4.2 Fruit diameter (cm)

The fruits which were selected for fruit weight were utilized for taking fruit diameter. Fruits were cut horizontally and with the help of an ordinary scale diameter was measured and expressed in centimetre.

Table 1b: List of single cross hybrids

Cross Combination	Hybrid Code	Cross Combination	Hybrid Code	Cross Combination	Hybrid Code	Cross Combination	Hybrid Code	Cross Combination	Hybrid Code
1L × 1T	20MG-01	2L × 1T	20MG-13	3L × 1T	20MG-25	4L × 1T	20MG-37	5L × 1T	20MG-49
1L × 2T	20MG-02	2L × 2T	20MG-14	3L × 2T	20MG-26	4L × 2T	20MG-38	5L × 2T	20MG-50
1L × 3T	20MG-03	2L × 3T	20MG-15	3L × 3T	20MG-27	4L × 3T	20MG-39	5L × 3T	20MG-51
1L × 4T	20MG-04	2L × 4T	20MG-16	3L × 4T	20MG-28	4L × 4T	20MG-40	5L × 4T	20MG-52
1L × 5T	20MG-05	2L × 5T	20MG-17	3L × 5T	20MG-29	4L × 5T	20MG-41	5L × 5T	20MG-53
1L × 6T	20MG-06	2L × 6T	20MG-18	3L × 6T	20MG-30	4L × 6T	20MG-42	5L × 6T	20MG-54
1L × 7T	20MG-07	2L × 7T	20MG-19	3L × 7T	20MG-31	4L × 7T	20MG-43	5L × 7T	20MG-55
1L × 8T	20MG-08	2L × 8T	20MG-20	3L × 8T	20MG-32	4L × 8T	20MG-44	5L × 8T	20MG-56
1L × 9T	20MG-09	2L × 9T	20MG-21	3L × 9T	20MG-33	4L × 9T	20MG-45	5L × 9T	20MG-57
1L × 10T	20MG-10	2L × 10T	20MG-22	3L × 10T	20MG-34	4L × 10T	20MG-46	5L × 10T	20MG-58
1L × 11T	20MG-11	2L × 11T	20MG-23	3L × 11T	20MG-35	4L × 11T	20MG-47	5L × 11T	20MG-59
1L × 12T	20MG-12	2L × 12T	20MG-24	3L × 12T	20MG-36	4L × 12T	20MG-48	5L × 12T	20MG-60

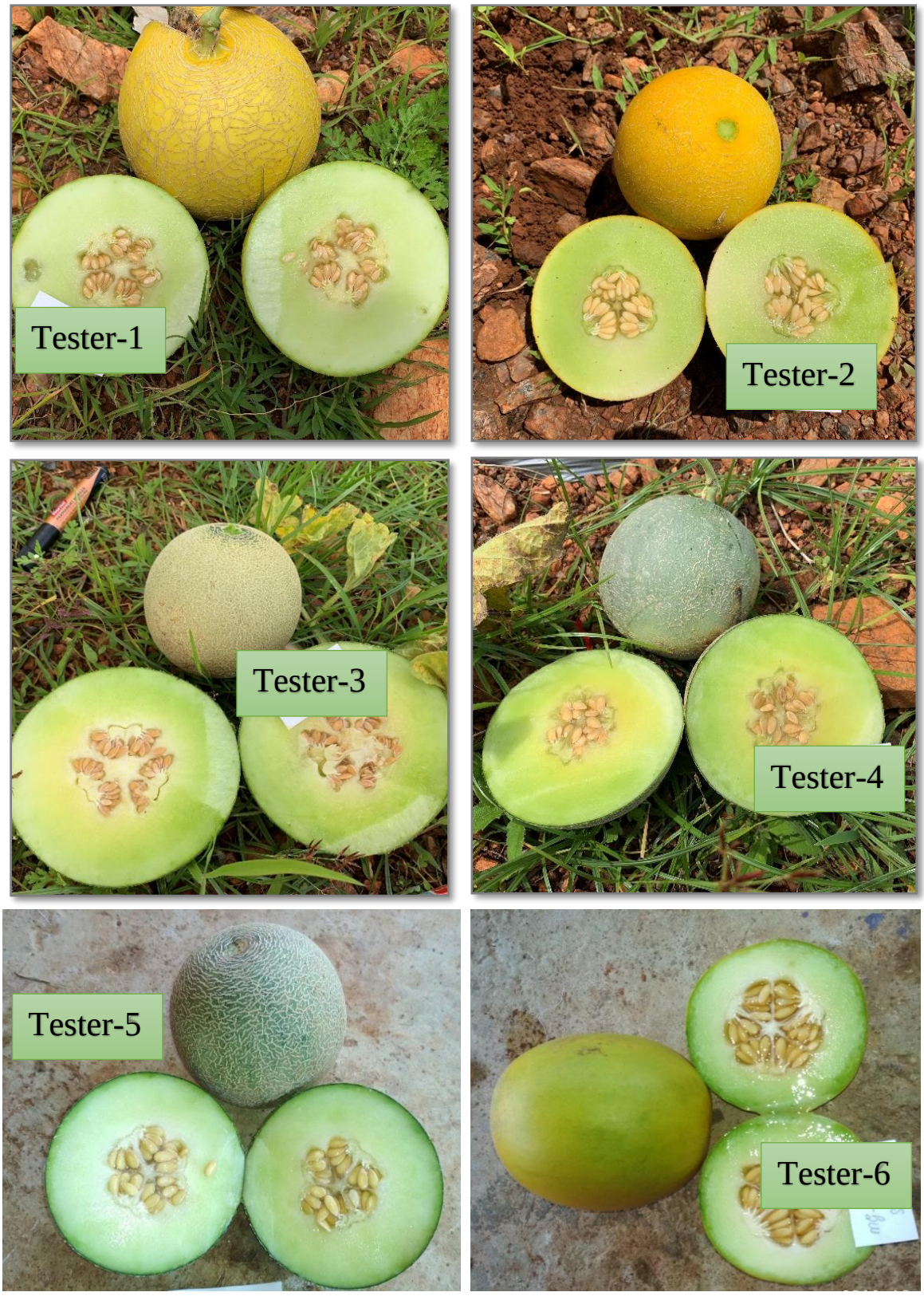


Plate 4a: Different testers used in the experiment

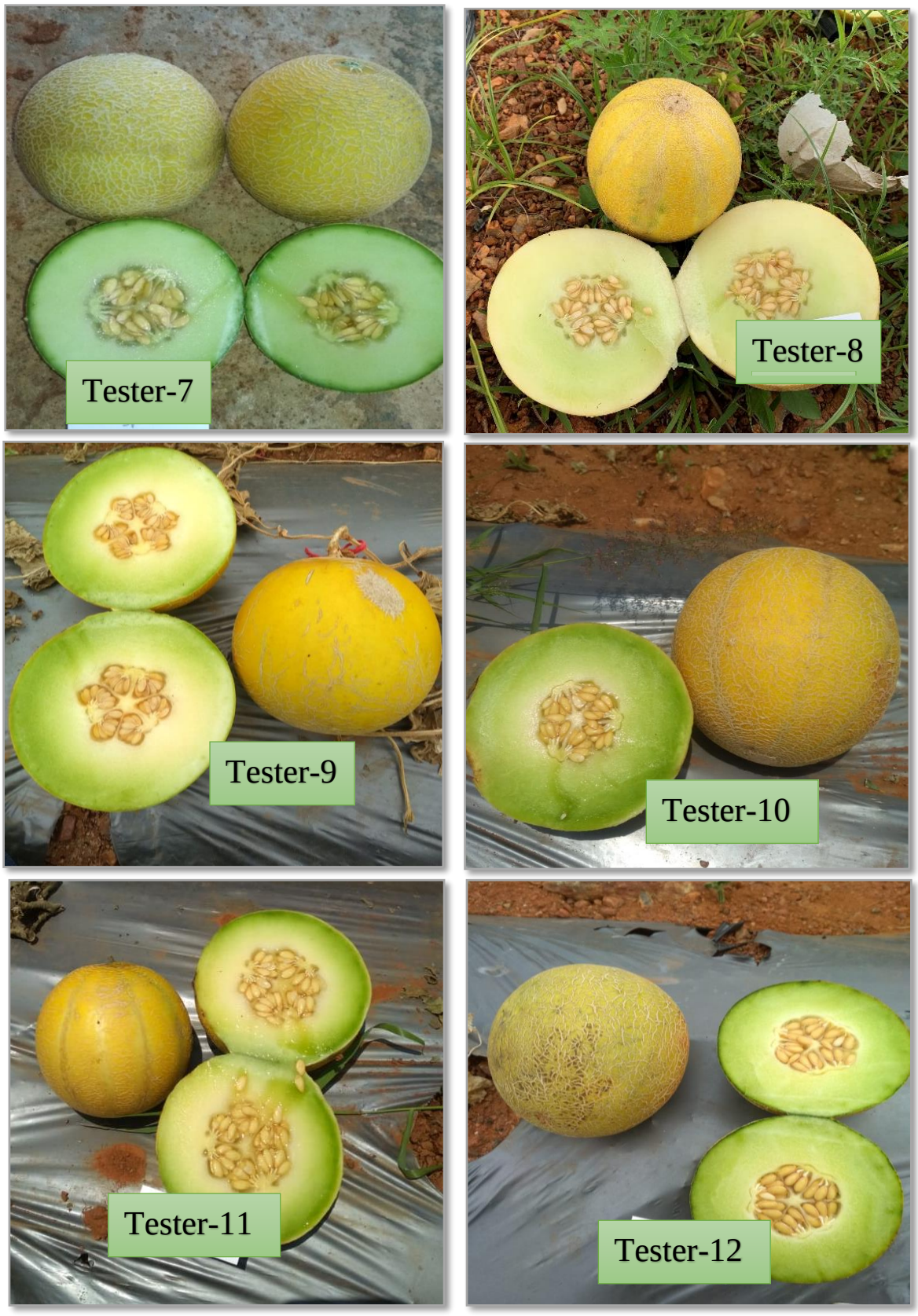
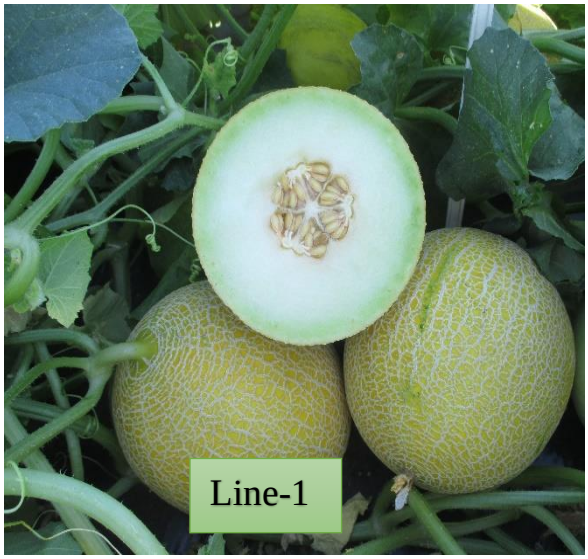
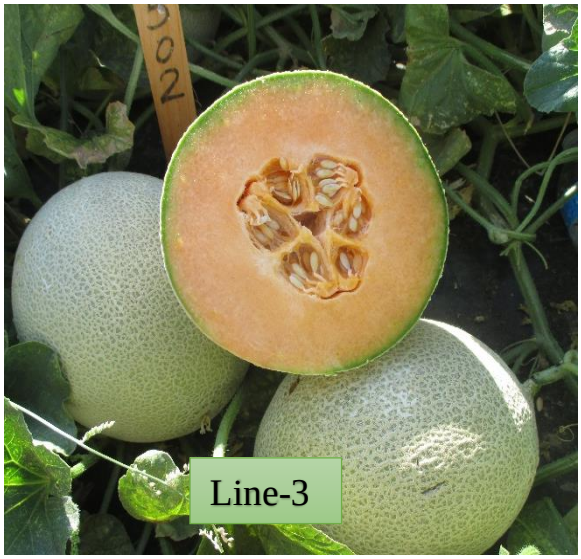


Plate 4b: Different testers used in the experiment





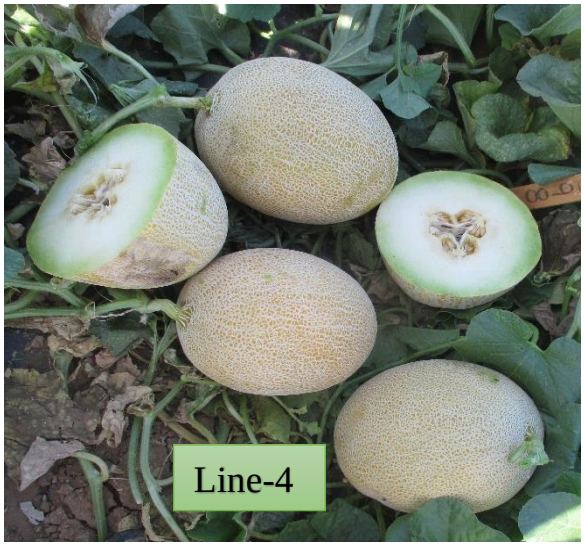


Plate 5: Different lines used in the experiment

3.1.4.3 Fruit cavity size (cm)

The fruits which were selected for fruit diameter were utilized for taking fruit cavity size. The average size of seed cavity was calculated expressed in centimetre.

3.1.4.4 TSS (º Brix)

The flesh of five ripe fruits used to measure fruit cavity were crushed separately and a drop of juice was placed on the Hand refractometer and mean value was taken.

3.1.5 Seed quality traits

3.1.5.1 Germination %

The germination test was conducted in the laboratory using between paper method as per ISTA rules (Anon., 2010). One hundred seeds in four replications were randomly drawn from each treatment. The rolled towels were incubated inside the germination chamber maintained at 90 per cent relative humidity and 25 ± 1°C. The evaluation of the germinated seedlings was done and germination was expressed in percentage.

$$\text{Seed germination (\%)} = \frac{\text{Number of normal seedlings}}{\text{Total number of seeds used for germination}} \times 100$$

3.1.5.2 Shoot length (cm)

Ten normal seedlings were randomly selected and shoot length was recorded from collar region to shoot apex and mean shoot length was calculated and expressed in centimeter.

3.1.5.3 Root length (cm)

Ten normal seedlings were randomly selected and root length was recorded from root tip to collar region and mean root length was calculated and expressed in centimeter.

3.1.5.4 Seedling fresh weight (mg)

Ten seedlings selected for seedling length measurement were used for recording seedling fresh weight. The mean seedling fresh weight was recorded and expressed in milligrams per seedling.

3.1.5.5 Seedling dry weight (mg)

Ten seedlings selected for seedling length measurement were used for recording seedling dry weight. Seedlings were dried in hot air oven maintained at 85 ± 2 ºC for 24 hours. The mean seedling dry weight was recorded and expressed in milligrams per seedling.

3.1.5.6 Seedling vigour index-I

The seedling vigour index was calculated as per the formula suggested by Abdul-Baki and Anderson (1972) and expressed as whole number for each treatment by using the formula,

$$\text{SVI} - \text{I} = Germination\ (\%)\ x\ Mean\ seedling\ length\ (cm)$$

3.1.5.7 Seedling vigour index-II

The seedling vigour index-II was calculated as per the formula suggested by Abdul-Baki and Anderson (1972) and expressed as whole number for each treatment by using the formula,

$$\text{SVI} - \text{II} = Germination\ (\%)\ x\ Mean\ seedling\ dry\ weight\ (mg)$$

3.1.6 Statistical analysis

3.1.6.1 Analysis of variance for parents and hybrids

The mean value of five random plants for all the mentioned characters recorded on parents and hybrids were utilised and variance due to different sources was established (Panse and Sukhatme, 1967). The model for ANOVA table adopted is given below.


Plate 6: Nursery and transplanting of hybrids for evaluation at R&D Farm of Orbi Seeds International Pvt. Ltd, Ajjenahalli, Sira


Plate 7: Visit by advisory committee members to hybrid evaluation plot at R&D Farm of Orbi Seeds International Pvt. Ltd, Ajjenahalli, Sira


Plate 8: Stable hybrid evaluation plot at R&D Farm of Orbi Seeds International Pvt. Ltd, Ajjenahalli, Sira (January-2021)

Table 2: ANOVA for parents and hybrids

S. No.	Source of variation	Degrees of freedom	Mean sum of squares
1	Replication	(r-1)	Mr
2	Treatment	(t-1)	Mt
a.	Parents	(m+f-1)	Mp
i.	Males (Testers)	(m-1)	Mm
ii.	Females (Lines)	(f-1)	Mf
iii.	Lines vs Testers	1	Mm Vs Mf
b.	Hybrids	(mf-1)	Mh
c.	Parents vs Hybrids	1	Mp Vs Mh
3	Error	(t-1)(r-1)	Me
4	Total	(mfr-1)	—

Where,

r = number of replications

t = number of genotypes/ entries / treatments

P = (m+f) = total no of parents

n = no. of hybrids

m = number of male parents

M= Mean of squares

f = number of female parents

e = Error

The mean of the character for different genotypes was subjected to L x T analysis and variance due to general combining ability (GCA) of parents and specific combining ability (SCA) of different cross combinations were worked out based on the procedure developed by Kempthorne (1957).

Table 3: Structure of ANOVA for combining ability

Source of variation	Df	MSS	Expected MSS
Replication	(r-1)		
Crosses	(mf-1)		
Lines	(f-1)	M1	σ_e^2 + r [cov (FS) - 2 cov (HS)] + rm cov (HS)
Testers	(m-1)	M2	σ_e^2 + r [cov (FS) - 2 cov (HS)] + rm cov (HS)
Line × tester	(f-1)(m-1)	M3	σ_e^2 + r [cov (FS) - 2 cov (HS)]
Error	(t-1)(r-1)	M4	σ_e^2
Total	(gr-1)		

Where,

r - number of replications

Cov (FS) - Covariance of full sibs

f - number of female parents

Cov (HS) - Covariance of half sibs

m - number of male parents

σ_e^2 = Variance due to error

3.1.6.1 Estimation of general and specific combining ability effects:

The following linear model was used to estimate general combining ability (GCA) and specific combining ability (SCA) effects:

$$Xij = \mu + gi + gj + Sij + eijk$$

Where,

μ = population mean

gi = gca effect of ith female parent

gj = gca effect of jth female parent

Sij = gca effect of ijth combination

Eijk = error associated with the observation Xijk

i= number of females

j= number of male parents

k= number of replications

3.1.6.2 The individual effects were estimated as follows:

1. General combining ability effects:

$$\text{(a) lines: Agi} = \frac{\text{xi} \ldots .}{\text{mr}} - \frac{\text{x} \ldots .}{\text{mfr}}$$

Where,

xi…= total of i^{th} female parent over all male parents and replications

x…= total of all hybrids over female and male parents

Agi = general combining ability effects of i^{th} line

$$\text{(b) Tester: gi} = \frac{\text{x.j}}{\text{r}} - \frac{\text{x} \ldots .}{\text{mfr}}$$

2. Specific combining ability effects:

$$\text{Sij} = \frac{\text{x.j}}{\text{r}} - \frac{X\text{I}}{\text{Mr}} - \frac{X\text{J}}{\text{fr}} + \frac{X \ldots}{\text{Mfr}}$$

Where,

Sij = specific combining ability effect of ijth combination

Xij = total of ijth combination over all the replications

3.1.6.3 The standard errors for testing the significance of GCA and SCA effects were estimated using the following formulae:

1. Standard error (SE) of g'is = √m4/mr

2. Standard error (SE) of g'js = √m4/fr

3. Standard error (SE) of g'ijs = √m4/r

3.2 Estimation of Heterosis:

The overall mean value for each parent or cross from the two replications for each character was considered for the estimation of heterosis. Heterosis was calculated as the per cent increase or decrease in the mean F1 performance over mid parent, better parent and standard check is as follows.

Data generated from the hybrids and parents on productivity *per se* traits were used to estimate the heterosis as suggested by Turner (1953) and Hayes *et al.* (1955).

$$\text{Heterosis over mid parent (\%)} = \frac{\overline{F_1} - \overline{MP}}{\overline{MP}} \times 100$$

$$\text{Heterosis over better parent (\%)} = \frac{\overline{F_1} - \overline{BP}}{\overline{BP}} \times 100$$

$$\text{Heterosis over standard check (\%)} = \frac{\overline{F_1} - \overline{SC}}{\overline{SC}} \times 100$$

Where,

Me = Error MSS in general ANOVA table

R = Number of replications

$\overline{F_1}$ = Mean value of hybrid

$\overline{MP}$ = Mean value of mid parent

$\overline{BP}$ = Mean value of better parent

$\overline{SC}$ = Mean value of standard check

3.2.1 Testing the significance of heterosis

Significance of heterosis is estimated by using the standard error. Testing the significance of the estimates of heterosis, are done by using the mean squares due to error (Me) and standard error from general ANOVA were used

$$\text{Standard error for heterosis} = \sqrt{\frac{(3Me)}{r}}$$

Where,

Me = Error MSS in general ANOVA table

R = Number of replications

$\overline{F_1}$ = Mean value of hybrid over replication

Significance of all the types of heterosis were determined by t test as follows

$$\text{'t' statistic for heterosis } = \frac{\overline{F_1} - \overline{H}}{SE(H)} \times 100$$

Where,

$\overline{F_1}$ = Mean value of hybrid over replication

$\overline{H_1}$ = Mean value of Heterosis

SE(H) = Standard error of heterosis

The calculated 't' statistic was compared with table 't' value at error degrees of freedom of ANOVA.

3.2.2 Overall status of the parents and crosses with respect to GCA, SCA and heterosis

Since yield component characters are correlated either positively or negatively, it is common to find gca and sca/heterosis for a particular parent and cross respectively, in the desirable direction for some characters and in the undesirable direction for some characters. The problem of ascertaining the status of a parent with respect to *gca* and *sca* /heterosis, respectively was determined following method suggested by Arunachalam and Bandhyopadyay (1979), which is slightly modified by Mohan Rao (2000).

3.2.3 Overall GCA status of parents, SCA and heterotic status of crosses

General combining ability effects and estimates of mid parent heterosis (MPH) of crosses were ranked by giving highest rank for the parent or the cross which manifested highest *gca* effects and *sca* effects or heterosis, respectively. This was reported for each character except for cavity size character ranking were given in a reverse order because smaller cavity parents / hybrids are preferred. The ranks obtained by parents/crosses were summed up across all the characters to arrive at a total score for each of the parent or cross.

Further, the mean of the total scores thus obtained was used as the final norm to ascertain the status of a parent or a cross for their *gca* and *sca* /heterosis. For the parents and crosses whose total rank exceeded the final norm were given as high (H) overall *gca* and *sca* / heterotic status, respectively.

3.3 Identification of stable hybrids

Stable performance of cultivars is very important to sustain the production and productivity of any crop. Stable performance of any cultivar depends on its ability to adapt to vagaries of environmental conditions. With this informative background, an investigation was undertaken to identify the stable hybrids in muskmelon.

3.3.1 Experimental site

The investigation was carried out at Research and Development Station of Orbi Seeds International Pvt. Ltd., Ajjenahalli, Sira Taluk, Tumkur District, during 2020-21 across three dates of sowing (Table 4).

Table 4: Experimental layout and different dates of sowing for stability analysis

	Details	
Material	5 superior hybrids + One checks	
Spacing	1.5 × 0.3 m	
Design	RCBD	
Location	Research and Development Station of Orbi Seeds International Pvt. Ltd, Ajjenahalli, Sira Taluk.	
Seasons	Date of Sowing	Date of Transplanting
	4th January 2021	18th January 2021
	1st February 2021	15th February 2021
	2nd March 2021	16th March 2021
Replications	Three	

3.3.2 Experimental material

Five hybrids were selected out of 60 hybrids evaluated during summer 2020 and *Kharif* 2020 and commercial check, constituted the experimental material. They were evaluated at Research and Development Station of Orbi Seeds International Pvt. Ltd., Ajjenahalli, Sira Taluk, following RCBD design with three replications across three different dates of sowing.

3.3.3 Observations recorded

Observations were recorded on five randomly selected plants on each entry in each replication quantitative traits by following the procedure as given in 3.1.1

3.3.4 Statistical Analysis

The mean data for each character recorded on five randomly selected plants of each hybrid from each replication was subjected to different statistical methods which are explained below.

3.3.4.1 Pooled analysis of variance

The data of fifteen single cross hybrids across four sowings and three replications were subjected to pooled analysis of variance as per Sundararajan *et al*. (1972) (Table 5). Analysis of variance was carried out for the traits under study to ascertain the significance of genotype by environment interactions by following two way ANOVA. Subsequently, the data was subjected to stability analysis (Eberhart and Russel, 1966).

Table 5: The structure of pooled analysis of variance (Sundararajan *et al*. 1972)

Source of variation	Degrees of freedom	Mean Sum of Squares	Expected MSS
Environment (e)	(e-1)	MSS(e)	-
Hybrids (h)	(h-1)	MSS(h)	$\sigma^2_e + \sigma^2_{he} + e\sigma^2_i + \sigma^2_i$
Hybrids × Environment	(e-1)(h-1)	MSS(he)	$\sigma^2_e + \sigma^2_{he}$
Pooled error	(he-1)	EMSS	σ^2_e

3.3.4.2 AMMI analysis

The combination of principal components analysis and analysis of variance in the AMMI model, along with prediction assessment, is a valuable approach for understanding genotype environment interaction (GEI) and obtaining better yield estimates. Stable performance of single cross hybrids were estimated by using AMMI model which combination of analysis of variance for the genotype and environment main effects with principal components analysis of the genotype environment interaction. It has proved useful for understanding the complex Genotype Environment Interaction (GEI). The results can be graphed in a useful bi-plot that shows both main and interaction effects for both the genotypes and environments. AMMI combines analysis of variance (ANOVA) (Table 6) into a single model with additive and multiplicative parameters.

Table 6: ANOVA Structure of AMMI model

Source of Variation	Degrees of freedom	Sum of Squares	Mean Sum of squares	F Ratio	% Variation
Hybrids (H)	H – 1	SS_H	MSS_H	MSS_H/ MSS_e	$(SS_H/ TSS) \times 100$
Environment (E)	E – 1	SS_E	MSS_E	MSS_E/ MSS_e	$(SS_E/TSS) \times 100$
Hybrids × Environment	(H-1) (E-1)	SS_{HE}	MSS_{HE}	MSS_{HE}/MSS_e	$(SS_{HE}/TSS) \times 100$
IPCA 1	G+E-1-2n	SS_{IPCA1}	MSS_{IPCA1}	MSS_{IPCA1}/MSS_e	$(SS_{IPCA1}/SS_{HE}) \times 100$
IPCA 2	G+E-1-2n	SS_{IPCA2}	MSS_{IPCA2}	MSS_{IPCA2}/ MSS_e	$(SS_{IPCA2}/SS_{HE}) \times 100$
Residual	(I-1) (E-10-{dfPCA 1+ dfPCA 2+-+PCAn}	SS_r	MSS_r	MSS_r/MSS_e	SS_r
Error		SS_e	MSS_e	MSS_e	SS_e

The model equation is-

$$Y_{ij} = \mu + g_i + e_i + \sum_{k=1}^{n} \lambda_k a_{ik} \gamma_{jk} + e_{ij}$$

Where,

Y_{ij} = Yield of the i^{th} genotype in the j^{th} environment is the grand mean

g_i and e_j = Genotype and environment deviations from the grand mean

λ_k = Eigen value of the PCA analysis axis k

α_{ik} and γ_{jk} = Genotype and environment principal component scores for axis k

N = Number of principal components retained in the model

e_{ij} = Error term

The interaction was explained in the form of a bi-plot display where, principal component analysis (PCA) scores are plotted against each other and it provides visual inspection and interpretation of the GEI components. Integrating genotypic stability statistics and bi-plot display enables genotypes to be grouped based on the similarity of their performance across the environments.

3.3.4.3 The GGE bi-plot criteria to interpret GEI

GGE-bi-plot, which is a combination of GGE concepts and AMMI bi-plot (Yan *et. al*., 2000) was used for visual interpretation of patterns of GEI. The GGE bi-plot is based on the following model.

$$\text{GEE} = Y_{ij} - Y_i = \lambda_1 \alpha_{i1} \gamma_{i1} + \lambda_2 \alpha_{i2} \gamma_{j2} + \varepsilon_{ij}$$

Where,

Y_{ij} = Trait mean of i^{th} inbred line in the j^{th} environment

Y_i = Trait mean of all the inbred lines in the j^{th} environment

λ_1 and λ_2 = Square root of eigen values of first and second IPC axes, 1 and 2

α_{i1} and α_{i2} = The scores of the first and second IPC, respectively, for the i^{th} inbred line

γ_{ij} and γ_{ij} = The first and second IPCs respectively for j^{th} environment

There are many ways to visualize a GGE bi-plot, but the polygon style of the biplot is most relevant (Segherloo *et al.*, 2010). Inbred line and environment interaction IPC 1 scores were plotted against their IPC 2 scores to visually identify accessions with specific/wide adaptation and similarity between inbred lines and environments. The inbred

lines that are more similar to each other in terms of their responses are more close to each other in the GGE bi-plot than those that are less similar. The inbred lines placed near origin of IPC 1 *vs* IPC 2 bi-plot are regarded as better adaptable across environments than those located far from the origin (Crossa *et al.*,1990). The inbred lines that are farther from bi-plot origin are connected with straight lines so that a polygon is formed with all other inbred lines contained within the polygon. A set of lines were drawn from the bi-plot origin perpendicular to each side of polygon. The perpendicular lines to the polygon sides divide the polygon into sectors, each having its own winning inbred line which is the vertex inbred line for that sector (Yan *et al*., 2000).

3.4 Molecular screening of melon germplasm for fusarium wilt

The study was conducted in the Molecular Laboratory, Orbi Seeds International Pvt. Ltd. Bangalore. DNA was isolated from preselected hybrids and their parental genotypes using Cetyl Trimethyl Ammonium Bromide (CTAB) method of extraction according to Murray and Thompson (1980). The designation of lines used in molecular screening was given in Table 1.

3.4.1 DNA Extraction

Total genomic DNA of all genotypes was extracted using CTAB method (Murray and Thomson 1980) as described below:

- The leaves of fourteen-day old seedlings of five hybrids and their parental lines raised in portrays were collected in early morning and sterilized with 70 per cent ethanol, weighed to 0.1g and were crushed with liquid nitrogen using clean pestle and mortar.
- The crushed leaf samples were transferred to autoclaved 1.5ml Eppendorf tubes and 1ml of CTAB buffer along with a pinch of poly vinyl pyrrolidone (PVP) and kept in hot water bath at 66ºC for about 30 minutes and then cooled to room temperature.
- The cooled Eppendorf tubes along with the homogenized solution were centrifuged at 4000rpm for 10 minutes and the supernatant was transferred to another centrifuge tube.

- Equal volume of chloroform: iso-amyl alcohol (24:1) *i.e.* wet chloroform was added to the supernatant and centrifuged again at 4000 rpm for 10 minutes. This step was repeated twice or thrice until clear supernatant was obtained.
- Once the clear supernatant was obtained, equal volume of chilled isopropanol was added and refrigerated at -20ºC overnight.
- The overnight refrigerated mixture was centrifuged at 8000 rpm for 10 minutes and the supernatant was discarded.
- The pellet obtained was washed by adding 20µl of ethanol and vertexing it mildly and then the ethanol was discarded and pellet was air dried.
- 20µl of TE buffer was added to the airdried pellet and was gently tapped to dissolve the DNA.
- It was then stored at -20 ºC for future work.

Table 7. Preparation of PCR mixture for amplification

Components	Stock Concentration	Volume (µl)	Final concentration
Doubled distilled water		6.7	
MgCl2	25 mM	1.5	1.5 mM
PCR buffer	5X	5.0	1.0X
dNTP mix	25 mM	0.5	0.25 mM
Primer Forward	10 mM	2.0	0.5 mM
Primer Reverse	10 mM	2.0	0.5 mM
Taq Polymerase	5 units/µl	0.3	1 unit
DNA Template	100ng/µl	2.0	200 ng
Total		**20 µl**	

3.4.2 Quantification of DNA by agarose gel electrophoresis

- The extracted DNA was quantified by using 0.8 per cent agarose gel. Before this the gel casting plate and comb was sterilized first using 70 per cent ethanol.
- The comb was then fitted to casting plate in a perfectly horizontal way.
- To prepare the gel, 0.8 g of agarose (0.8 g/ 100 ml) was weighed and 100 ml of 1x TBE buffer was added and the solution was heated in a microwave oven to melt the agarose.
- Once the agarose is completely melted, it was allowed to cool to 55-60 ºC.
- Ethidium bromide (0.5 mg/ml) was added to the cooled solution and mixed. This was then carefully poured to gel mould and rested to solidify.
- Once the gel has solidified, the combs were removed with care.
- This casted gel was immersed in electrophoresis unit with 1x TBE buffer to a depth of 1cm with care to place sample wells towards cathodes.
- 4 µl of the extracted DNA samples of Hybrids and their parents were pipetted on a para film and mixed with 4 µl of 10x loading dye by pipetting. The DNA well mixed with loading dye was then loaded to the gel.
- Once the samples were loaded, the gel was run at 80V/3W for 1.5 to 2 hours.
- The bands obtained were visualised using gel documentation system Quantum capt., Lab India and documented.
- Samples were then quantified using nanodrop for precision and consistency of the results.

3.4.3 PCR analysis

- In vitro amplification using Polymerase Chain Reaction (PCR) was performed in an Eppendorf Master Cycler for screening. PCR analysis was carried out using primers. PCR analysis was carried out in the reaction volume of 20µl. PCR reaction mixture and profile is given in Table 6 and Table 7, respectively.

- Allele specific primer *Fom*2-R408 (F: GAGAAATTTGCAATGGGTGG R: TTACACTATTATTGCTCAACTTGC) was used.
- Melting temperature for the primer used was 55 ºC and PCR was run for 36 cycles.

3.4.3.1 PCR Reaction mixture

Table 8. Temperature profile used in PCR

Step No.	Cycling conditions	Temperature	Time
I	Initial Denaturation	94ºC	2 min
II	Denaturation	94ºC	40 sec
III	Annealing	61ºC	1 min
IV	Extension	72ºC	1 min
V	Go to step II, III and IV		36 cycles
VI	Final extension	72ºC	10 min

3.4.4 Agarose gel electrophoresis of PCR products

Three per cent agarose gel was prepared by using electrophoresis grade agarose for required volume of 1x TBE buffer. After adding calculated quantity of agarose to the required quantity of 1x TBE buffer it was heated in microwave oven to dissolve the agarose and then cooled to 55ºC to 60ºC. Ethidium bromide (0.5µg/ml) was added to the gel. Then the gel was poured on to the casting tray with combs. The gel was allowed to set for a while. After the gel has solidified, the comb was removed and the gel was kept immersed in 1x TBE buffer in electrophoresis unit. Then the entire 15µl of PCR product mixed with 4µl of loading dye was loaded into the wells by pipetting. Also, a 100-base pair (bp) ladder was loaded as reference for size of PCR product along with samples. The gel was then run for about 2-3 hours at 80V. After the completion of run, the bands were visualized through gel documentation system Quantum Capt., Lab India and obtained bands were documented.

3.4.5 Screening of SSR markers for fusarium wilt

The obtained clear and unambiguous bands were studied to identify Fom2 allele within parental lines and hybrids. Scoring of bands obtained was made by comparing the bands to the ladder and then bands were analyzed.

3.5 Fingerprinting of parental lines and hybrids of selected hybrids

The study was conducted in the Molecular Laboratory, Orbi Seeds International Pvt. Ltd. Bangalore. DNA was isolated from genotypes using CTAB method of extraction. The designation of lines used in molecular screening was given in Table 1. Primers used are presented in appendix-I.

3.5.2 Plant Material

The leaf samples of fourteen-day old seedlings of five hybrids and their parental lines raised in portrays were used for isolation of DNA by following of CTAB method Murray and Thompson (1980). The DNA extracted, quantified and stored in step 3.4 was used for fingerprinting.

3.5.3 SSR Analysis

Table 9. Preparation of PCR mixture for amplification

Components of PCR reaction mixture	Volume/sample (15µl)
Template DNA	2.0
PCR Buffer	1.5
Primer (F-R)	1.5
dNTPs	0.75
Taq-Polymerase (3µl)	0.45
Sterile water	8.8
Grand Total	**15**

The used PCR components obtained from Bangalore Sigma Aldrich Ltd., Bangalore, India. The reaction mixture was mixed thoroughly and then PCR tubes were loaded in BioRAD thermal cycler.

Table 10. Reaction conditions for PCR amplification

Profile 1	95ºC for 5 minutes	Initial Denaturation
Profile 2	94ºC for 1 minute	Denaturation
Profile 3	47ºC to 58ºC for 1 minute	Annealing
Profile 4	72ºC for 2 minutes	Extension
Profile 5	72ºC for 8 minutes	Final extension
Profile 6	4ºC	Final hold
Profile 2, 3 and 4 were repeated for 38 cycles.		

Note: Annealing temperatures depend on the primer used

3.5.5 Analysis of SSR markers

- The forward and reverse SSR primers were used for PCR amplification of genomic DNA of hybrids and parental lines.
- 3 per cent agarose gel electrophoresis was performed for resolution of polymorphism.
- The banding pattern obtained was analysed.

3.5.6 Screening of SSR markers for polymorphism

The obtained clear and unambiguous bands were studied to record polymorphism of markers within parental lines and hybrids. The unique polymorphic markers and common polymorphic markers for five hybrids were identified by observing the banding pattern. Scoring of bands obtained was made by comparing the bands to the ladder and then bands were analysed for parental polymorphism for hybrids.

IV RESULTS AND DISCUSSION

In the conventional plant breeding approach, there are different ways and means involved in development of a hybrid *viz.*, utilization of genetically diversified population, which provides source for crop improvement. By making use of genetically diverse population and making selections with desirable traits for crop performance to adopt them for different environmental conditions, help us to use them in series of cross combinations to create a superior cultivar. To accomplish this, a breeding programme can effectively planned with prior knowledge of genetic makeup of the genotypes, for traits like fruit and seed quality. With the advancement of biometrical techniques, variation can be assessed along with precise performance of the genotype and effect of environment on the complex traits such as yield.

4.1 Combining ability for seed and fruit quality traits

4.1.1 General analysis of variance

4.1.2 Analysis of variance for combining ability

4.1.3 General combining ability effects among parents

4.1.4 Overall general combining ability effects

4.1.5 Specific combining ability effects among crosses

4.1.6 Overall specific combining ability effects

4.2 Heterosis for seed and fruit quality traits

4.2.1 Overall mid parent heterotic status

4.3 Genotype × environment interactions and stability parameters

4.4 Screening of selected hybrids for fusarium wilt using linked markers

4.5 Fingerprinting of selected parental line and hybrids

4.1 Combining ability for seed and fruit quality traits

4.1.1 General Analysis of variance

Success of a breeding programme rest upon information and utilization of diversified differences available among genotypes (parental lines) and its progeny for traits of importance. Variances due to genotypes (parents and hybrids) were significant for all the traits except total soluble solids. The mean sum of squares due to parents versus crosses was highly significant for yield attributes *viz*., fruit diameter and average single fruit weight except for total soluble solids and cavity size (Table 11). As evidenced by the significance of mean sum of squares due to crosses and among the parental genotypes resulted in crosses that were also significantly differed from each other. This was reflected by the presence of average heterosis as evidenced by the significance of parents versus crosses with single degree of freedom. The findings were in consistent with the findings of Gurav *et al*. (2000).

4.1.2 Analysis of variance for combining ability

The variance due to lines and their interactions differed significantly for majority of the characters (Table 12) according to the analysis of variance for combining ability.

Lines had significant effect on all the characters studied except for TSS and seedling dry weight. As such testers had no effect on the fruit quality traits studied but had significant effect on seed quality parameters except for seedling dry weight and seedling vigour-II. Mean sum of squares due to lines and lines × tester interaction were found significant for most of traits studied indicating both GCA and SCA variance to be equally cardinal in the inheritance of all the characters under investigation. Similar findings were reported by Shashikumar and Pitchaimuthu (2016).

4.1.3 General combining ability effects among parents

The general combining ability effects of lines and testers are presented in the Table 13. Identification of parents based on per se performance may not be reliable to make heterotic hybrids. GCA of parents for a particular trait would reflect in SCA of a specific cross combination due to its interactive effect. Hence selection of line/tester based on its *gca* effect has greater importance in planning a breeding programme.

Table 11. Analysis of variance for fruit and seed quality traits in Muskmelon

Source of Variation	Df	Fruit weight (g)	Cavity Size (cm)	Fruit Diameter (cm)	TSS (°Brix)	Germination (%)	Shoot Length (cm)	Root length (cm)	Seedling fresh weight (mg)	Seedling dry weight (mg)	SVI-I	SVI-II
Replication	1	8483.43	3.24	7.70	20.36*	3.14	0.001	0.02	1066.67	0.15	2076.93	3507.00
Genotypes (Parents+ Hybrids)	76	364916.088**	3.04**	15.44**	6.00	30.93**	1.39**	1.41**	21472.78**	3.16**	54196.65**	32189.26**
Parents	16	40779.466	0.66	0.21	0.75	7.61**	0.33**	0.34**	6501.08**	0.93**	10374.72**	6698.22**
Lines	4	59644.85	0.30	0.12	0.35	3.15	0.49**	0.47**	3322.52**	0.45**	9156.22**	2177.60*
Testers	11	2721.37	0.65	0.25	0.95	9.92**	0.18**	0.20**	350.78**	0.05	8190.63**	1296.04
Lines vs Testers	1	383956.94	2.18	0.24	0.14	0.03	1.28**	1.43**	86868.62**	12.53**	39273.82**	84202.77**
Parents vs Crosses	1	7038007.89**	2.67	321.21**	1.24	186.80**	32.95**	33.23**	1351872.92**	202.02**	1438302.59**	1841805.50**
Error	76	131202.32	1.63	5.09	4.32	2.06	0.01	0.01	664.82	0.05	1218.29	717.79
Total	153	246493.35	2.34	10.24	5.26	16.41	0.70	0.71	11003.43	1.60	27539.95	16368.91

*Significant at P=0.05; **Significant at P=0.01

Table 12. Analysis of variance for combining ability of fruit and seed quality traits in Muskmelon

Source of Variation	Df	Fruit weight (g)	Cavity Size (cm)	Fruit Diameter (cm)	TSS (^{0}Brix)	Germination (%)	Shoot Length (cm)	Root length (cm)	Seedling fresh weight (mg)	Seedling dry weight (mg)	SVI-I	SVI-II
Replicates	1	13356.30	3.69	8.50	9.63	6.07	0.004	0.008	1677.76	0.22	2421.46	5352.02
Crosses	59	339714.29**	3.69*	14.38**	7.51	34.61**	1.14**	1.16**	2983.75**	0.40	42621.14**	8430.63**
Line effect	4	2075815.44**	23.49**	78.33**	5.67	208.40**	15.87**	16.11**	13510.46**	2.11	477937.7**	28866.5**
Tester effect	11	101856.50	2.35	2.63	3.96	21.15	0.07	0.05	7944.43**	1.02	8171.28	11983.26*
Line × Tester effect	44	241351.36	2.23	11.51*	8.57*	22.18**	0.07**	0.08**	786.61	0.09	11659.37**	5684.70**
Error	59	163104.62	2.00	6.49	5.24	2.09	0.01	0.01	738.31	0.06	1267.25	771.89
Total	119	249409.01	2.85	10.42	6.40	18.25	0.57	0.058	1859.49	0.23	21780.14	4607.57

*Significant at P=0.05; **Significant at P=0.01

Fruit yield being a complex trait, expression of performance depends upon number of other contributing characters like fruit weight and fruit diameter. For these traits line-4 exhibited significant effect on fruit weight and fruit diameter trait which in turn results in increased yield. Testers as such had no significant effect on the fruit yield characters. The findings are in agreement with Lal and Kaur (2002) in Muskmelon.

Line-1 had negative significant effect on cavity size which is important for lesser cavity in hybrids, preferred by the consumers. However, it has significant positive effect on germination percentage of seed. Tester-1 had significant negative effect on cavity size (-1.38) which is preferable.

Tester-1 and line-2 had considerable effect on all the seed quality parameters studied except for germination percentage, whereas Tester-10 and Tester-12 had significant effect on germination percentage trait.

This indicates that though some parents are inferior, interaction among the lines and testers have contributed for the crosses to perform superiorly. It is appealing to note that line-2 is most promising for fruit weight and fruit diameter. The similar results were reported by Al-araby (2004) in Muskmelon.

4.1.4 Overall general combining ability status of parents (lines and testers) in Muskmelon

Overall *gca* status of parents is an important parameter. The results indicated that none of the parents found to be a promising combiner for all the traits, it is important to assess whether one parent is a good overall general combiner or not across the characters. In this context, a method suggested by Arunachalam and Bandopadhyay (1979) used in the present investigation to determine overall *gca* effects of a line or tester studied (Table 14). Across the traits studied, the line-2 was found to be high (H) overall general combiner as shown in the table. Line-3 and line-1 were found to be poor combiners. Fifty-eight per cent of testers T-1, T-2, T-4, T-5, T-9, T-10 and T-12 were found to be high general combiners and tester-7 was found to be poor combiner.

Table 13. General combining ability effects of lines and testers (parents) for seed and fruit quality traits in Muskmelon

Lines	Fruit weight (grams)	Cavity Size (cm)	Fruit Diameter (cm)	TSS (°Brix)	Germination (%)	Shoot Length (cm)	Root length (cm)	Seedling fresh weight (mg)	Seedling dry weight (mg)	SVI-I	SVI-II
Line-1	-388.17**	-1.57**	-1.90**	-0.20	4.86**	-0.63**	-0.63**	-29.73**	-0.35**	-25.78**	32.67**
Line-2	249.65**	-0.089**	1.29**	0.34	0.40	1.20**	1.21**	31.04**	0.40**	215.32**	40.47**
Line-3	-181.13**	-0.33	-1.94**	-0.40	-1.71**	0.48**	0.49**	-14.20**	-0.18**	51.38**	-38.15**
Line-4	316.45**	0.50	1.87**	-0.40	-0.88**	-0.49**	-0.49**	-1.27	-0.01	-98.48**	-13.21*
Line-5	3.2	0.51	0.67	0.67	-2.67**	-0.56**	-0.57**	14.16**	0.15**	-142.44**	-21.78**
SEm ±	82.43	0.28	0.52	0.46	0.29	0.02	0.02	5.26	0.04	7.12	5.46
CD at 95%	164.95	0.57	1.04	0.93	0.58	0.04	0.05	10.53	0.09	14.25	10.94
Testers											
Tester-1	-18.68	-1.38**	-1.08	-1.28	0.59	0.10**	0.08*	17.46*	0.28**	23.72*	32.73**
Tester-2	-84.98	-0.14	0.49	0.11	1.89**	0.06	0.08	-13.02	-0.18*	48.43**	9.09
Tester-3	-114.98	-0.11	0.16	-0.38	-0.008	0.05	0.05	-32.32**	-0.38**	9.92	-32.54**
Tester-4	125.41	0.12	0.37	-0.28	-0.30	0.06	0.05	58.92**	0.62**	4.99	48.95**
Tester-5	179.41	-0.04	0.72	-0.08	-0.04	-0.02	-0.01	7.29	0.09	-10.21	2.77
Tester-6	-111.48	-0.08	-0.03	-0.38	-1.70**	0.02	0.002	5.07	0.03	-29.69**	-19.14*
Tester-7	-130.38	0.02	-0.42	-0.08	-1.90**	0.05	0.03	-36.33**	-0.41**	-25.63*	-59.29**
Tester-8	-2.7	0.41	0.22	-0.28	-1.60**	-0.11**	-0.08*	-15.94	-0.13	-44.02**	-32.53**
Tester-9	40.71	0.17	0.34	0.21	-0.05	0.04	0.04	27.88**	0.31**	-2.23	20.29*
Tester-10	109.21	0.34	-0.16	0.51	2.59**	-0.006	-0.02	-5.66	-0.09	42.84**	25.90**
Tester-11	15.91	0.50	-0.63	0.81	-0.30	-0.10**	-0.09*	-31.11**	-0.35**	-22.65*	-33.69**
Tester-12	-7.38	0.18	0.06	1.11	1.69**	-0.15**	-0.13**	17.76*	0.17*	4.52	37.48**
SEm±	127.71	0.44	0.80	0.72	0.45	0.03	0.04	8.15	0.07	11.03	8.47
CD at 95%	255.15	0.89	1.61	1.44	0.90	0.07	0.08	16.31	0.14	22.08	16.95

*Significant at P=0.05; **Significant at P=0.01

Table 14. Overall general combining ability status of lines and testers in muskmelon

SI No	Lines	Total Rank	Overall GCA Status
1	Line-1	39	L
2	Line-2	17	**H**
3	Line-3	39	L
4	Line-4	32	H
5	Line-5	38	L
6	Tester-1	52	H
7	Tester-2	48	H
8	Tester-3	79	L
9	Tester-4	44	**H**
10	Tester-5	64	H
11	Tester-6	87	L
12	Tester-7	104	L
13	Tester-8	98	L
14	Tester-9	57	H
15	Tester-10	59	H
16	Tester-11	100	L
17	Tester-12	66	H

Final Norm for Lines: 33 **Final norm for Testers: 71.5**

H: Overall high combiner L: Overall low combiner

4.1.5 Estimates of specific combining ability effects among lines and testers in Muskmelon

The specific combining ability effects of top performing crosses are presented in Table 15 and Appendix VI. Out of sixty crosses, five cross combinations found to be significant and exhibited significant *sca* effects in the desirable direction. The cross 1L × 4T was the best specific combination for fruit cavity since it had negative effect. But it had positive effect on seedling vigour index-I and seedling vigour index-II.

The crosses 5L × 1T and 3L × 12T found considerably significant in desirable direction for fruit weight and fruit diameter. The cross combinations 1L × 5T and 2L × 1T were found significant for TSS content of the fruits.

The cross 3L × 12T found desirable combination from parents with low *gca* estimates, for fruit yield trait. This is an example of low × low type crossing creating hybrids with significant *sca* effects, implying that over dominance and epistasis is involved. Other cross combinations involving both parents being in high × high category or high × low *gca* effect. Such observations indicate the involvement of additive dominance type of interaction in the expression of quantitative traits.

Across cross combinations involving either one prominent and one poor combiner or from two poor combiners, there was high prevalence of non-additive gene action in these hybrids suggested that once the beneficial genes were to be identified, a hybrid development programme may improve even better. To take the advantage of this form of gene activity, the best breeding methodology to accumulate favorable genes through reciprocal recurrent selection. These results are in comparison with findings of Aravindakumar *et al*. (2005).

4.1.6 Overall specific combining ability (SCA) status of Muskmelon hybrids

It’s vital to find out whether a particular cross combination is superior or not across the qualities, and also it is crucial to find out parent’s overall general combining ability status. The overall SCA status of each cross was computed and tabulated (Table 16) summarises these findings.

Table 15. Estimates of specific combining ability effects in top performing hybrids for fruit quality traits in muskmelon

Crosses	Fruit weight (g)	Fruit cavity size (cm)	Fruit diameter (cm)	TSS (^{o}Brix)	Germination (%)	Shoot Length (cm)	Root length (cm)	Seedling fresh weight (mg)	Seedling dry weight (mg)	SVI-I	SVI-II
1L x 4T	-390.52	**-4.40****	-7.01**	-8.30**	5.43**	0.18*	0.12	8.69	0.08	120.75**	84.03**
1L x 5T	56.37	0.25	1.98	3.00*	-2.46*	-0.02	0.04	-8.57	0.01	-41.13	-30.29
2L x 1T	75.14	-0.12	-0.35	3.65*	-7.5	-0.30	-0.25	-64.32	-0.58	-197.48	-150.24
3L x 12T	**1171.33****	1.46	**6.13****	-1.19	-0.98	-0.21	-0.21	9.52	0.06	-52.34	-7.36
5L x 1T	**745.13****	0.53	**4.34****	-0.49	2.57*	-0.02	-0.07	22.70	0.11	38.08	43.91*
SEm ±	256.12	0.90	1.59	1.47	1.01	0.08	0.09	18.24	0.16	24.69	18.95
CD (0.05)	512.50	1.80	3.19	2.94	2.03	0.17	0.190	36.48	0.32	49.38	37.90

*Significant at P=0.05; **Significant at P=0.01

Overall status of a particular cross combination provides a holistic idea on its performance across yield and yield attributing characters. Forty three *percent* of crosses *i.e.*, 26 out of sixty hybrids had high (H) overall SCA, the remaining 34 crosses had low (L) overall SCA status across the traits. Similar reports were given by Singh and Vasist (2018).

4.1.6 Distribution of heterotic crosses in relation to overall *gca* status of parents and *sca* of crosses

It's important to determine whether hybrids possess higher *sca* and *gca* values across all characters and their distribution, the research findings are tabulated in Table 16. Out of 24 crosses belonging to high × high *gca* status 9 number of hybrid combination resulted in having High (H) overall *sca* status. 14 out of 24 crosses belonging to low × high *gca* status shown high overall *sca* status. 3 out of 6 crosses belonging to low × low *gca* status shown High overall *sca* for fruit quality traits. The results are on par with Hassan *et al.* (2018).

Table 16: Distribution of heterotic crosses in relation to overall *gca* status of parents and *sca* of crosses in Muskmelon

Parental *gca* status	No. of crosses under the category	Number of crosses with high (H) overall *sca* status	Conditional probability of given cross belonging to high *sca* status
H × H	24	9	0.34
H × L	6	0	0
L × H	24	14	0.53
L × L	6	3	0.11

4.1.7 Proportional contribution of lines, testers and their interaction to total hybrid

The proportional contribution of lines, testers and line X tester interaction for fruit quality traits is presented in the table 17. The results revealed that the percent contribution of hybrids (line X tester) was higher for all the yield traits studied such as fruit weight

(52.9), fruit cavity size (45.02), fruit diameter (59.67) and TSS (85.05). *Per cent* contribution from lines were more for shoot length (93.80), root length (93.81) and seedling vigour index-I (76.02).

Testers *per cent* contribution was more towards seedling fresh weight (49.64) and seedling dry weight (47.15).

Between lines and testers, lines had more contribution for fruit weight (41.4), fruit cavity size (43.10) and fruit diameter (36.91) except for TSS, where testers had more contribution.

The contribution of female and male interaction was higher than parents for all the traits studied which indicates dominance of non-additive gene action and interaction among diverse loci of parental lines. Neto (2020) reported similar findings in yellow melon for fruit yield and quality traits.

Table 17. Proportional contribution of lines, testers and line × tester interaction towards seed and fruit quality parameters (%)

Sl. No.	Character	Lines	Testers	Line X Tester
1	**Fruit weight (g)**	41.4	5.59	52.9
2	**Fruit cavity size (cm)**	43.10	11.86	45.02
3	**Fruit diameter (cm)**	36.91	3.40	59.67
4	**TSS (ºBrix)**	5.11	9.82	85.05
5	**Germination (%)**	40.81	11.39	47.79
6	**Shoot Length (cm)**	93.80	1.13	5.04
7	**Root Length (cm)**	93.81	0.88	5.29
8	**Seedling fresh weight (mg)**	30.69	49.64	19.66
9	**Seedling dry weight (mg)**	35.44	47.15	17.40
10	**Seedling vigour index-I**	76.02	3.57	20.40
11	**Seedling vigour index-II**	23.21	26.50	50.28

Table 18: Overall specific combining ability status of hybrids in relation to parental general combining ability in muskmelon

Lines	Line-1 (H)		Line-2 (H)		Line-3 (L)		Line-4 (H)		Line-5 (H)	
Testers	**Total score**	**Overall *sca* status**	**Total score**	**Overall *sca* status**	**Total score**	**Overall *sca* status**	**Total score**	**Overall *sca* status**	**Total score**	**Overall *sca* status**
Tester-1 (L)	256	H	286	H	244	H	297	H	157	H
Tester-2 (H)	525	L	494	L	359	L	361	L	355	L
Tester-3 (L)	132	H	355	L	261	H	237	H	453	L
Tester-4 (H)	247	H	208	H	443	L	370	L	175	H
Tester-5 (H)	192	H	403	L	340	L	314	H	407	L
Tester-6 (L)	340	L	338	L	353	L	333	H	265	H
Tester-7 (L)	273	H	404	L	364	L	425	L	413	L
Tester-8 (L)	261	H	292	H	259	H	362	L	125	H
Tester-9 (H)	479	L	334	H	377	L	257	H	454	L
Tester-10 (H)	329	H	353	L	356	L	390	L	477	L
Tester-11 (L)	478	L	252	H	432	L	356	L	295	H
Tester-12 (H)	247	H	442	L	383	L	368	L	393	L

Final Norm: 335.5

(H): High overall general combiner **(L): Low overall general combiner**

H: High overall specific combiner **L: Low overall specific combiner**

4.2 Heterosis over mid parent, better parent and checks for fruit and seed quality traits in muskmelon

Heterosis is the manifestation of hybrid vigour. The heterotic effect of hybrids is due to cumulative effect of divergent alleles from two contrasting parents. The present investigation involving seventeen parents (five lines and twelve testers) and their sixty hybrids were evaluated to determine the magnitude of heterosis over parental mean, better parent and standard check hybrid (Akany). Inclusion of a commercial hybrid as a standard check is desirable over a variety, as increase in yield over a prevailing hybrid that would enable detecting hybrids for large scale cultivation aiming at increased productivity.

Fruit weight and fruit diameter are important traits having a positive association with fruit yield. The highest significant positive heterosis for fruit weight and fruit diameter was recorded by 20MG-40 (182.13%), 20MG-49 (93.38%) for mid-parent heterosis, respectively (Table 19).

Highest significant positive heterosis for fruit weight and fruit diameter was recorded by 20MG-49 (148.58%) and 20MG-44 (86.96%) for better parent heterosis. A large number of crosses showed the significant heterosis in desirable direction for the traits attributing to fruit yield. The highest standard heterosis was exhibited by 20MG-35 (121.55%) for fruit weight and 20MG-44 (72%) for fruit diameter.

The highest negative heterosis was exhibited by 20MG-01 for fruit cavity trait which contributes to smaller seed cavity in hybrid. Its important to note that line-1 was used in most of the crosses which exhibited significant heterosis, which is a good combiner for seed cavity size. Germination *per cent*, 20MG-01 (13.33%), 20MG-12 (11.90%) and 20MG-04 (3.24%) were exhibited significant mid-parent, better-parent and standard heterosis, respectively. Shoot length and root length 20MG-23 exhibited significantly higher mid-parent (29.78%, 29.03%), Standard heterosis (2.99%, 2.94%) and significantly higher better-parent heterosis was reported in 20MG-35 (23.18%) for shoot length and 20MG-24 reported higher better parent heterosis (37.37%).

Table 19: Estimates heterosis for fruit and seed quality traits in Muskmelon

Characters	Mid parent heterosis	Better parent heterosis	Standard heterosis
Fruit weight (g)	20MG-40 182.13**	20MG-49 148.58**	20MG-35 121.15**
Fruit cavity size (cm)	20MG-01 -151.58*	20MG-01 -149.00*	20MG-01 -157.51*
Fruit diameter (cm)	20MG-49 93.38**	20MG-44 86.96**	20MG-44 72.00**
TSS (^{0}Brix)	20MG-60 42.86*	20MG-60 38.89	20MG-47 27.75
Germination (%)	20MG-01 13.33**	20MG-12 11.90**	20MG-04 3.24*
Shoot Length (cm)	20MG-23 29.78**	20MG-35 23.18**	20MG-23 2.99*
Root Length (cm)	20MG-23 29.03**	20MG-24 37.37**	20MG-23 2.94*
Seedling Fresh Weight (mg)	20MG-40 31.34**	20MG-52 29.53**	20MG-52 7.05**
Seedling Dry weight (mg)	20MG-52 34.77**	20MG-52 29.49**	20MG-16 6.51**
Seedling vigour index-I	20MG-24 36.40**	20MG-14 33.07**	20MG-14 -2.59
Seedling vigour index-II	20MG-04 42.24**	20MG-04 34.61**	20MG-04 6.81**

Significantly higher better-parent (29.53%) and standard heterosis (7.05%) was recorded by 20MG-52 and 20MG-40 recorded highest mid-parent (31.34%) heterosis. 20MG-52 recorded highest significant mid-parent (34.77%) and better-parent (29.49%) heterosis, whereas highest standard heterosis (6.51%) was recorded by 20MG-16.

Highest significant mid-parent (36.40%) heterosis for seedling vigour index-I was recorded by 20MG-24 and 20MG-14 recorded higher better parent and standard heterosis.

20MG-04 recorded significantly higher mid-parent (42.24 %), better-parent (34.61 %) and standard heterosis (6.81 %). Munshi and Verma (1997) and Mohanty and Mishra (1999) reported similar findings in muskmelon.

All the traits under consideration distinctly differed for heterosis and its range in desirable direction, which in-turn indicates that in different set of crosses, different pathways are responsible for realising heterotic effects. Considerably high heterotic effects in certain combination and low in the others revealed the nature of gene action and it varied with the genetic constitution of parental genotypes involved in the crosses. Nature and magnitude of heterosis as such help in identification of superior combinations to find better transgressive segregants.

The extent of heterosis over mid parent, better parent and standard checks varied across the cross combinations for fruit and seed quality traits. Increased yield being the ultimate objective in any of crop breeding programme; hence positive and significant heterosis for fruit traits is always required.

4.2.1 Overall heterotic status of crosses

In addition to determining the overall general combining ability status of parents and overall specific combining ability status of crosses, its important to determine the overall heterotic status of the crosses across fruit yield traits. The method explained by Mohan Rao (2000), which is the modified method of Arunachalam and Bandyopadhyay (1979), overall heterotic status of each cross was determined and results of the same are presented in Table 20.

By utilising the method, the hybrids were grouped into high and low mid-parent heterotic cross combinations, with final norm calculated 335.5. Nearly 46 *per cent* of the crosses *i.e.*, 28 hybrids manifested high (H) overall heterotic status. Line-1 and line-5 a high and low combiner, resulted in hybrids with significant heterosis in desirable direction over standard checks for the most of the traits.

Table 20. Overall heterotic status of hybrids in relation to parental general combining ability in muskmelon

Lines	Line-1 (H)		Line-2 (H)		Line-3 (L)		Line-4 (H)		Line-5 (H)	
Testers	**Total score**	**Overall heterotic status**	**Total score**	**Overall heterotic status**	**Total score**	**Overall heterotic status**	**Total score**	**Overall heterotic status**	**Total score**	**Overall heterotic status**
Tester-1 (L)	341	L	362	L	205	H	287	H	183	H
Tester-2 (H)	376	L	249	H	287	H	416	L	282	H
Tester-3 (L)	434	L	316	H	424	L	431	L	371	L
Tester-4 (H)	223	H	274	H	339	L	367	L	307	H
Tester-5 (H)	369	L	284	H	286	H	392	L	286	H
Tester-6 (L)	396	L	208	H	373	L	309	H	335	H
Tester-7 (L)	452	L	247	H	405	L	412	L	417	L
Tester-8 (L)	504	L	324	H	408	L	367	L	362	L
Tester-9 (H)	322	H	215	H	380	L	343	L	335	H
Tester-10 (H)	444	L	278	H	389	L	210	H	431	L
Tester-11 (L)	526	**L**	228	H	359	L	289	H	452	L
Tester-12 (H)	245	H	290	H	245	H	195	**H**	344	L

Final Norm: 335.5

(H): High overall general combiner **(L): Low overall general combiner**

H: High overall specific combiner **L: Low overall specific combiner**

4.2.2 Conditional probability of crosses with overall heterosis and specific combining ability in relation to their parental general combining ability for fruit traits in muskmelon

The *sca* effects represent dominance and epistatic gene action which is of vital importance in heterosis breeding. The highest probability of cross with high overall *sca* status belongs to the category of parents of a hybrids involving low overall combining female and high overall combining male for fruit quality traits. This indicated that parents involved in a cross with low general combining line and high general combining tester are desired for producing hybrids with desirable characteristics. On the other hand, the probability of crosses with high overall mid-parent heterotic status belonging to differential classes is distributed nearly equally. This indicates that irrespective of the parents involved in the cross whether a high combiner or low combiner heterotic crosses are reflected in all the categories of crosses equally indicating that parents used in the study are showing good dispersion of favourable alleles. This is deviating from the general trend that in most of crops where crosses involving parents with poor X poor *gca* parents found to show low heterosis and high X high combiners resulting in high heterotic crosses. Results (Table 20) showing a mere superiority of crosses falling under the category of high X high general combiners. These results are in consistence with Hassan *et al* (2018).

Table 21: Distribution of heterotic crosses in relation to parental *gca* status in muskmelon

Parental gca status	No. of crosses under the category	Number of crosses with high (H) overall heterotic status	Conditional probability of given cross belonging to high heterotic status
H × H	**24**	**14**	**0.50**
H × L	**6**	**3**	**0.35**
L × H	**24**	**10**	**0.10**
L × L	**6**	**1**	**0.03**

4.3 Genotype × environment interactions and stability parameters

The performance of genotypes often deviates in response to production environments represented by temporal (year-to-year) and spatial (location-to-location) variation resulting in significant crossover genotype × year and genotype × location interactions.

Table 22a: Summary of top five heterotic hybrids for fruit yield in muskmelon

Crosses	Fruit weight (g)		Fruit cavity size (cm)	
	Mean	Heterosis over check	Mean	Heterosis over check
		Akany		Akany
1L × 4T	-390.52	35.89	**-4.40****	-34.65
1L × 5T	56.37	47.48	0.25	-29.70
2L × 1T	75.14	114.37	-0.12	-14.85
3L × 12T	**1171.33****	150.91*	1.46	4.95
5L × 1T	**745.13****	148.58*	0.53	3.96
SEm ±	556.10*		1.20	
CD (0.05)	285.71		1.00	

*Significant at P=0.05; **Significant at P=0.01

Crop cultivars performing steadily across years are referred to as stable and across locations as adaptable from the commercial crop cultivation point of view. However, hybrids that show inconsistent performance across different environments due to genotype × environment interaction (GEI). Hence, it is important to categorize stable hybrids with consistent performance across different environments.

Genotype - environment interaction gives an opportunity to select the stable hybrid. Genotype environment interaction could be exploited by selecting for specific adaptation or by growing specific genotypes. But, from the farmer's point of view, location is considered a constant factor and genotype environment interaction effects are repeatable

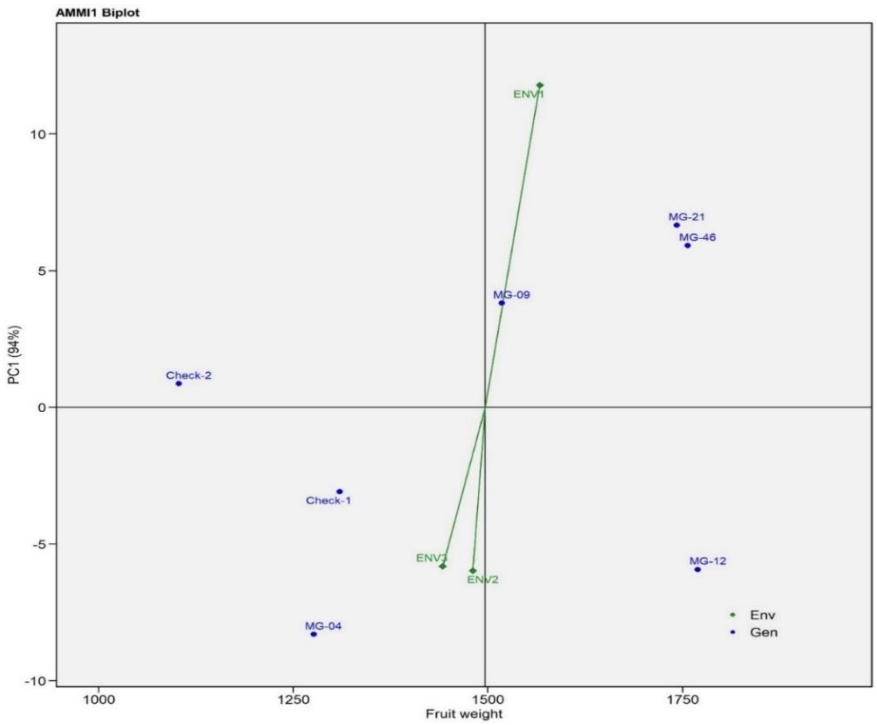


Fig. 1: Biplots showing patterns interactions for fruit weight of hybrids across different environments

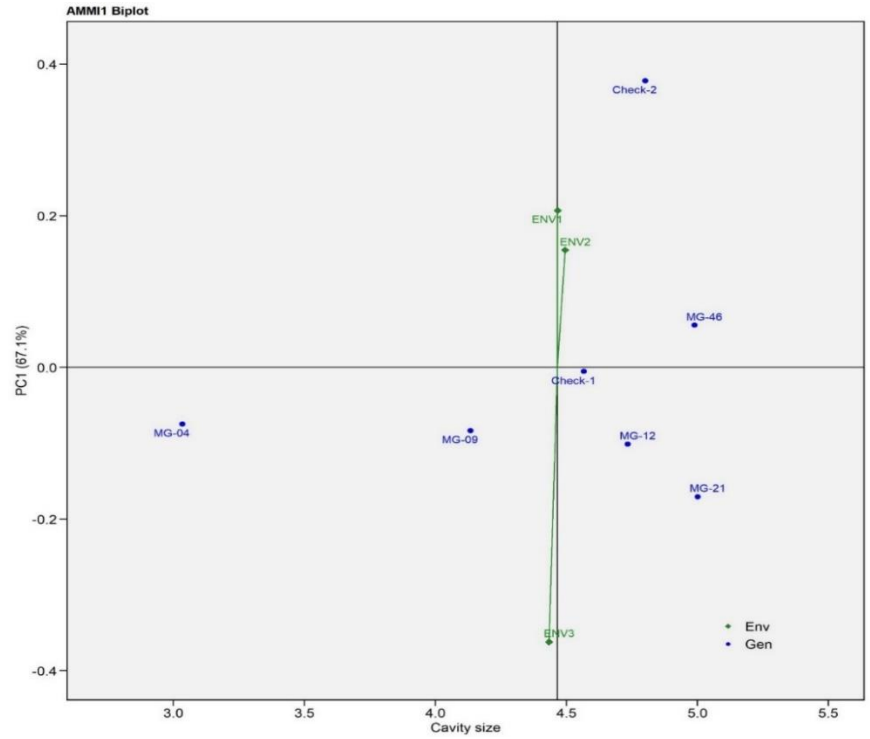


Fig. 2: Biplots showing patterns interactions for cavity size of hybrids across different environments

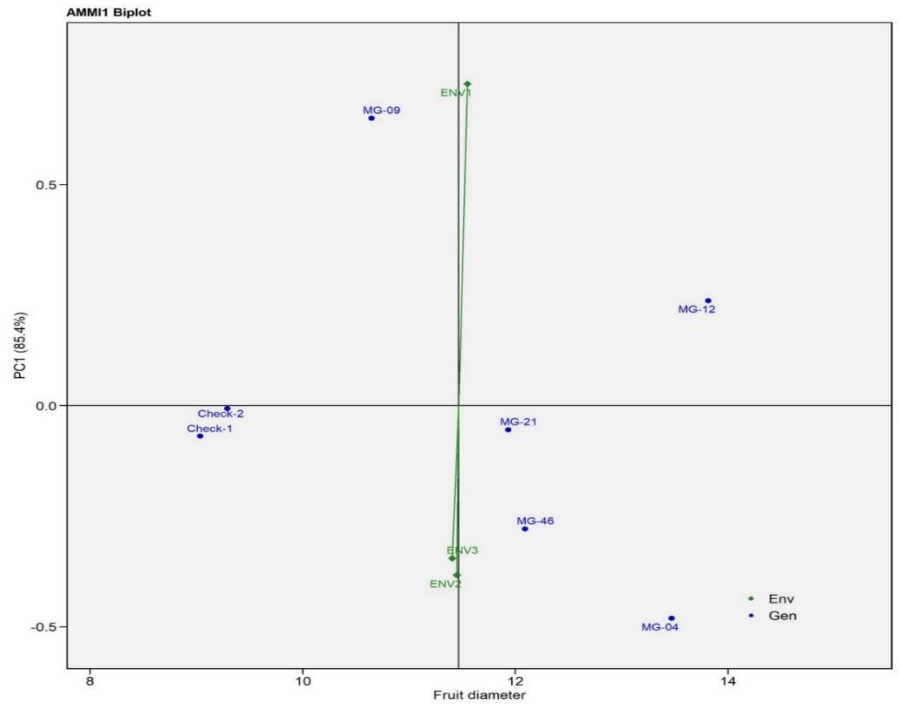


Fig. 3: Biplots showing patterns interactions for fruit diameter of hybrids across different environments

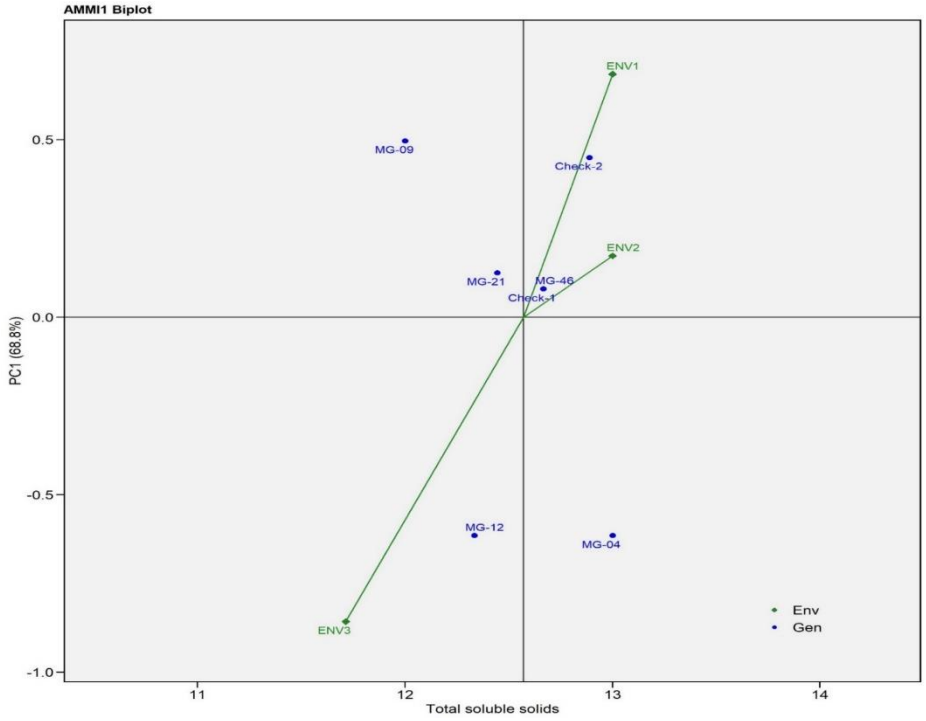


Fig. 4: Biplots showing patterns interactions for TSS of hybrids across different environments

in time. The genotypes developed under favourable environmental conditions may not perform the same in the unfavourable environmental conditions. Therefore, it is essential to identify those genotypes with specific/wide adapting to different locations by evaluating them under different environments as indicated by Venugopalan and Pitchaimuthu (2009) in watermelon.

Table 22b: Summary of top five heterotic hybrids for fruit yield in muskmelon

Crosses	Fruit diameter (cm)		TSS (ºBrix)	
	Mean	Heterosis over check	Mean	Heterosis over check
		Akany		Akany
1L × 4T	-7.01**	**59.42**	-8.30**	27.78
1L × 5T	1.98	59.09	**3.00***	27.76
2L × 1T	-0.35	46.75	**3.65***	27.78
3L × 12T	**6.13****	66.88*	-1.19	1.01
5L x 1T	**4.34****	83.12*	-0.49	16.67
SEm ±	3.56*		2.32	
CD (0.05)	1.80		1.61	

*Significant at P=0.05; **Significant at P=0.01

4.3.1 Detection of Genotype × Environment Interaction (GEI)

Advancement in breeding superior cultivars is assured with GEI as it confounds the manifestation of any genotype across environments and selection of superior performing genotypes (Magari and Kang, 1993). The AMMI extracts a large part of the GEI and efficiently analyses interaction patterns and captures a large portion of the genotype × environment interaction sum of squares clearly separating main and interaction effects.

The model often provides an agronomically meaningful interpretation of the data as this model effectively combines the additive parameters of univariate ANOVA with multiplicative parameters of principle component analysis (PCA) to characterize GEI.

The results of Additive Main effects and Multiplicative Interactions (AMMI) ANOVA (Table 23) indicated that, multi-location testing of 5 hybrids has not only shown significant genotypic effects except for total soluble solids. Significant effects of the environments in the expression of fruit weight was noticed. The AMMI analysis of variance revealed mean squares attributable to hybrid, location and hybrid × location (GLI) interaction were highly significant for all the traits except for cavity size. The results uphold the findings of earlier studies made by Oliveira *et al*. (2019).

Table 23: AMMI ANOVA for Fruit yield traits

Source of Variation	Degrees of Freedom	Avg. Single Fruit weight (g)	Cavity Size (cm)	Fruit Diameter (cm)	TSS (^{o}Brix)
		MSS	MSS	MSS	MSS
Environments	2	85522.42**	0.02	0.11	11.57
Rep (Env)	6	1833.09	0.005	0.075	1.57
Genotypes	6	662707.29**	4.37**	32.16**	1.05
G×E	12	11556.07**	0.014	0.18**	0.55**
PC1	7	18627.42	0.016	0.27	0.65
PC2	5	1656.19	0.011	0.06	0.41
Residual	36	1323.96	0.016	0.036	0.38
Total	74	60585.07	0.36	2.69	0.89

*Significant at P=0.05; **Significant at P=0.01

4.3.2 GGL bi-plot

Differences in hybrid stability and adaptability to environment can be qualitatively assessed using the bi-plot graphical representation that scatters the genotypes according to their interaction principal component (IPC) scores. Yan *et al*. (2000) proposed a standard bi-plot of genotype (G) + Genotype × environment (GE) based on a SREG (sites regression) model referred to GGE bi-plot.

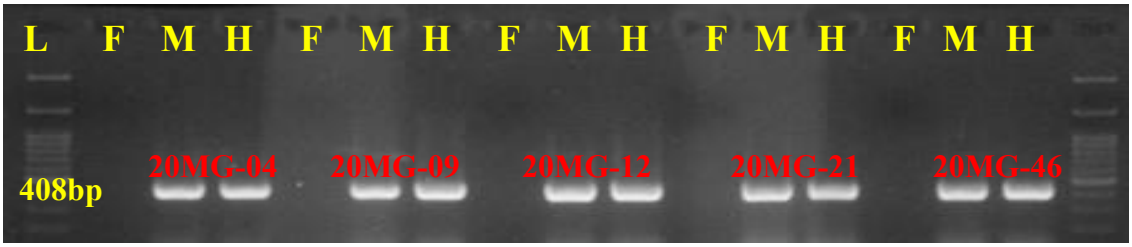


Plate 9: Screening of selected hybrids for *Fom*-2 gene imparting resistance to Fusarium wilt

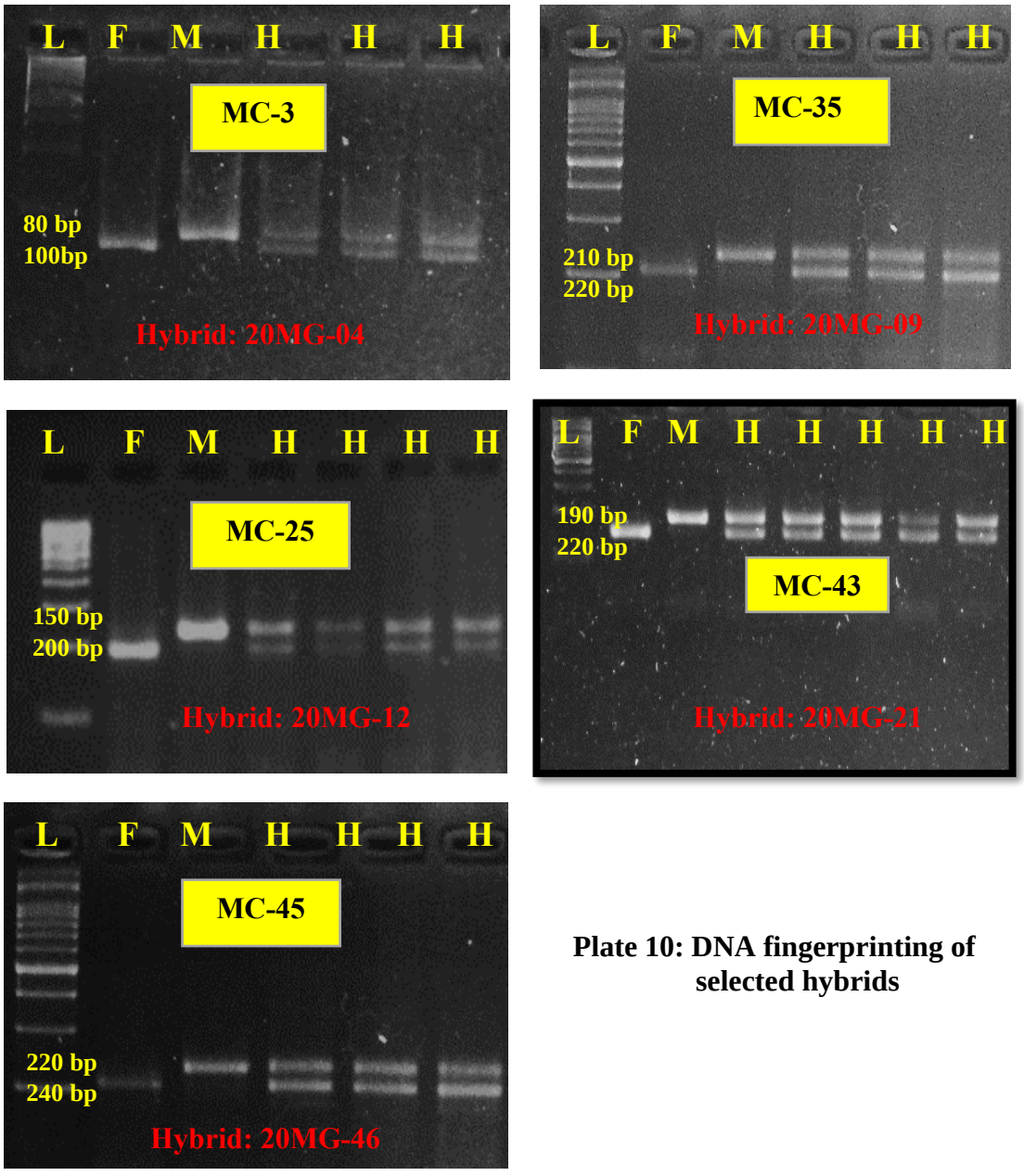


Plate 10: DNA fingerprinting of selected hybrids

It is a multivariate analytical tool that graphically displays interaction between each genotype and each environment in a two-dimensional bi-plot and allows visualization of the inter-relationship among environments, and the inter-relationship between genotypes and environments. GGE bi-plot is useful in displaying which-won-where pattern of the data that help to identify high-yielding and stable cultivars and discriminating representative test environments. Among different GGL bi-plots, polygon view of the bi-plot is the best way to visualize GEI patterns and help identify possible existence of different mega- environments (Yan *et al*., 2000). The overview of biplots analysis for fruit weight, fruit diameter, cavity size and total soluble solids are presented in Figure 1-4, respectively, representing genotypes adaptability to a specific environment and, it is further visualized by different patterns for selecting the genotypes for specific environments.

Hybrids located on the vertexes of the polygon performed either the best or the poorest in one or other test temporal and/or spatial environments as the longest distance mapped by them from the origin for the major fruit quality traits *viz*., fruit weight, fruit diameter, cavity size and total soluble solids are presented in Fig. 1-4.

The hybrid 20MG-21 was suitable for all three sowings for obtaining high fruit diameter, similarly hybrid 20MG-09 was suitable for fruit weight. 20MG-46 and 20MG-21 hybrid were stable for Total Soluble Solids across all three environments. Hybrid 20MG-12 was stable for cavity size.

4.4 Screening of identified stable hybrids for Fusarium wilt

The resistance gene *Fom*-2 provide resistance against race 0 and 1 of *Fusarium oxysporum* f. sp. *melonis*. Molecular marker linked with *Fom*-2 gene was used to screen 5 hybrids and their parental genotypes.

The DNA amplification and resistant allele had a single fragment size of 408 bp depicted presence of *Fom*-2 gene in all the male parents and hybrids used in the study (Plate 9).

FOM2R primer got amplified in all the parents indicating the presence of gene in all the testers and while the female was found susceptible as there was no amplification. Hybrids were all found resistant.

The molecular validation showed that *Fom*-2 resistant gene was present in all the hybrids and male testers used in the study. Resistant gene present in genotypes, can be further used in strengthening the resistance breeding programme against *Fusarium oxysporum* f. sp. *melonis*.

4.5 Fingerprinting of selected parental line and hybrids

The five hybrids selected were fingerprinted using microsatellite (SSR) markers. A set of 10 markers specific to muskmelon were used. Out of selected 10 primers, five showed polymorphic bands (Plate 10).

The primers MC3 and MC-35 were uniquely polymorphic to hybrid 20MG-04 and 20MG-09. The primer MC-3 gave a polymorphic band at 80 bp for female and 100bp for male whereas MC-35 produced a polymorphic band at 210 bp for female and 220 bp for male. The primer MC-25 gave polymorphic banding pattern for 20MG-12 at a molecular weight of 150 bp for female and 200bp for male and hybrid showing both 150 bp and 200 bp.

The primer MC-45 gave polymorphic banding pattern for 20MG-46 at a molecular weight of 220 bp for female, 240 bp for male and hybrid showing both 220 and 240 bp bands.

1L X 4T (20MG-04)

1L X 9T (20MG-09)

1L X 12T (20MG-12)

4L X 10T (20MG-46)

2L X 9T (20MG-21)

AKANY

Plate 11: Promising hybrids identified

V SUMMARY

The present investigation entitled 'Identification of best general combining inbred lines and heterotic combinations for seed and fruit quality traits and resistance to *Fusarium* wilt in musk melon (C*ucumis melo* L.)' was undertaken at the department of Seed Science and Technology, GKVK, Bangalore in collaboration with Orbi Seeds International Pvt. Ltd., Bangalore with the following objective:

1. To assess general combining ability of F_5 inbred lines for seed and fruit quality traits
2. To identify stable high yielding heterotic hybrids with desirable fruit quality traits
3. To identify hybrids resistant to *Fusarium* wilt using linked SSR markers
4. To fingerprint selected hybrids using SSR markers.

The salient findings of the investigation are summarized as follows

- The ANOVA for combining ability revealed that higher magnitude of GCA compared to SCA variance for all traits indicating the prevalence of additive genetic variance.
- The line-2 was identified as good general combiners for fruit diameter and seed quality traits and line-4 was good general combiner for fruit weight. The line-1 was identified as good general combiner for TSS. Tester-1 was identified as good general combiner for cavity size and most of seed quality traits. Tester-4 was identified as overall good general combiner status for all traits under consideration.
- The hybrids 1L × 4T found to have significant *sca* effects for smaller cavity size also for seedling vigour index-I and Seedling vigour index-II and 3L ×12 T and 5L × 1T had significant *sca* effects for fruit weight and fruit diameter trait.
- Significance of additive genetic variance, variance due to dominance effects of gene and proportion of dominance variance due to positive and negative effects of genes for fruit diameter and fruit weight.

- Significance of dominance genetic variance, dominance effects of gene and proportion of dominance variance due to positive and negative effects of genes for seed quality traits.
- The degree of dominance for most of the characters was more than unity, there by suggesting dominance component is relatively more important in the expression of traits and substantial improvement can be achieved by following bi parental mating or recurrent selection in segregating material along with conventional breeding methods.
- Negative significant heterosis recorded by hybrid 20MG-04 for cavity size indicated these hybrids exhibiting smaller cavity.
- The hybrids 20MG-46 and 20MG-20 were found stable for TSS across the three different dates of sowing.
- 5 hybrids and their parental genotypes of muskmelon were used for molecular screening of *Fom*-2 gene.
- Molecular validation was done with the gene specific marker *i.e. Fom*-2 gene R-408 (R allele). All the hybrids were carrying Resistance gene which was present the testers used for the study. While the female parent was found susceptible.
- SSR markers were also used for DNA fingerprinting. About 10 primers were selected to test for polymorphism in five hybrids. Out of selected 10 primers, 5 showed polymorphism, while remaining five showed monomorphism.
- The primers MC3 and MC-35 were uniquely polymorphic to hybrid 20MG-04 and 20MG-09. The primer MC-3 gave a polymorphic band at 80 bp for female and 100bp for male, whereas MC-35 produced a polymorphic band at 210 bp for female and 220 bp for male.
- The primer MC-25 gave polymorphic banding pattern for 20MG-12 at a molecular weight of 150 bp for female and 200bp for male and hybrid showing both 150 bp and 200 bp.
- The primer MC-45 gave polymorphic banding pattern for 20MG-46 at a molecular weight of 220 bp for female, 240 bp for male and hybrid showing both 220 and 240 bp bands.

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APPENDICES

Appendix-I: List of primers with their nucleotide sequences

Sl. No.	PRIMER		SEQUENCE (5' TO 3')
1	MC 3	F 5'-3'	TGGAATGGCAACTACACG
2		R 3'-5'	GGGGAGGCTGAAAGACTA
3	MC 33	F 5'-3'	GCTCTGCGTTTCATTCTTCA
4		R 3'-5'	TGAACCCTCAGACTCAAACTC
5	MC 45	F 5'-3'	GGAATTCAGGTGAACCTGACG
6		R 3'-5'	CCAGGAGGAAGAGGAACTGC
7	MC 73	F 5'-3'	CCCACATTGGTCTCAACAAG
8		R 3'-5'	AAAAAATTTGGCATTAGCTATAAAAA
9	MC 21	F 5'-3'	CAGAGGGGTGGTTCCTCTTT
10		R 3'-5'	CCACATGGATGATCGAGAGA
11	MC 35	F 5'-3'	CTAAATCACGCAAACCCATC
12		R 3'-5'	GAGCAAAAGACTGAGGAAAACT
13	MC 25	F 5'-3'	TTCCCATTCACAGATCACTCC
14		R 3'-5'	CCACCAAATTCAAGAACCCAC
15	MC 27	F 5'-3'	TTGGTTGTGGTGCTGAGTTC
16		R 3'-5'	GATGTAGGGGTTGGGTTGAT
17	MC 71	F 5'-3'	ACGACTCTTGGAAATCGGTC
18		R 3'-5'	TTTAGAAAAGAATCACGAAGAGAGC
19	MC 43	F 5'-3'	TAAAGAATCGGCCAGTTCGG
20		R 3'-5'	GGGGTTAGAGAAAATGAGAGGC

APPENDIX II: Means of sixty single cross hybrids for seed and fruit quality traits in muskmelon

Hybrid Combination	Fruit weight (g)	Cavity Size (cm)	Fruit Diameter (cm)	TSS (°Brix)	Germination (%)	Shoot Length (cm)	Root length (cm)	Seedling fresh weight (mg)	Seedling dry weight (mg)	SVI-I	SVI-II
20MG-01	366.000	2.45	1.45	1.00	93.50	8.55	8.70	1073.00	13.25	1612.80	1239.00
20MG-02	723.000	3.85	11.80	9.00	93.00	8.35	8.60	1023.20	12.55	1576.30	1166.90
20MG-03	666.500	3.65	11.55	11.00	90.50	8.25	8.40	1010.75	12.25	1506.85	1108.75
20MG-04	931.500	3.30	12.28	11.50	95.50	8.55	8.65	1113.70	13.50	1642.60	1289.20
20MG-05	1011.000	3.55	12.25	11.50	87.50	8.25	8.50	1044.80	12.90	1465.50	1128.70
20MG-06	698.500	4.10	10.85	8.50	88.50	8.25	8.45	1043.35	12.80	1477.90	1132.85
20MG-07	705.000	3.95	10.45	7.50	87.50	8.40	8.52	1010.50	12.25	1480.83	1071.75
20MG-08	681.000	4.10	9.80	8.00	86.00	8.15	8.30	1024.80	12.65	1414.85	1087.75
20MG-09	900.500	3.43	9.05	9.50	93.00	8.25	8.40	1088.90	13.20	1548.60	1227.80
20MG-10	852.000	3.60	8.25	9.00	90.50	8.05	8.30	1035.20	12.70	1479.75	1149.50
20MG-11	601.000	4.50	7.50	8.00	85.00	8.15	8.30	1010.70	12.25	1398.20	1041.10
20MG-12	1166.500	4.45	9.30	10.50	94.00	8.45	8.55	1074.10	13.10	1598.00	1231.30
20MG-13	1469.500	4.30	11.30	11.50	79.00	9.90	10.15	1060.00	13.25	1584.20	1046.50
20MG-14	1176.500	5.15	12.10	7.50	89.00	10.15	10.35	1117.85	13.55	1824.60	1206.00
20MG-15	1068.500	6.05	11.55	7.00	88.00	10.10	10.23	1105.60	13.65	1788.82	1201.25
20MG-16	1737.000	6.40	13.10	7.50	86.50	10.00	10.15	1146.70	13.90	1743.35	1202.20
20MG-17	2042.000	5.85	15.00	8.50	83.50	10.15	10.40	1096.55	13.45	1715.95	1123.20
20MG-18	1387.000	5.55	13.20	9.50	85.00	10.25	10.40	1130.30	13.70	1755.20	1164.40
20MG-19	1138.000	5.75	11.30	9.50	87.00	10.10	10.20	1109.80	13.70	1765.50	1192.10

Hybrid Combination	Fruit weight (g)	Cavity Size (cm)	Fruit Diameter (cm)	TSS (ºBrix)	Germination (%)	Shoot Length (cm)	Root length (cm)	Seedling fresh weight (mg)	Seedling dry weight (mg)	SVI-I	SVI-II
20MG-20	1374.000	6.75	12.20	8.00	87.00	10.15	10.40	1083.80	13.30	1787.90	1157.00
20MG-21	1692.500	5.90	14.05	11.00	87.50	10.25	10.45	1122.05	13.60	1811.10	1189.85
20MG-22	1582.000	5.35	13.45	11.50	85.50	10.30	10.43	1101.30	13.35	1772.55	1141.80
20MG-23	1191.000	6.05	12.55	10.00	86.00	10.35	10.50	1113.80	13.75	1793.15	1182.55
20MG-24	1098.500	6.55	13.10	8.00	87.00	9.95	10.20	1094.55	13.35	1753.10	1161.30
20MG-25	965.500	5.15	11.60	9.00	86.50	9.85	10.00	1092.40	13.40	1717.10	1158.80
20MG-26	769.000	3.30	8.35	9.00	87.50	9.65	9.75	1062.60	12.80	1697.80	1120.30
20MG-27	646.000	3.60	7.15	7.50	83.50	9.70	9.95	1010.30	12.40	1640.85	1035.30
20MG-28	647.500	4.30	7.35	8.50	83.00	9.35	9.55	1121.90	13.60	1569.00	1128.60
20MG-29	655.000	3.95	7.45	8.00	89.50	9.25	9.38	1084.85	13.15	1666.97	1176.90
20MG-30	704.500	3.90	7.95	8.00	79.00	9.45	9.60	1052.90	13.00	1505.00	1026.90
20MG-31	701.000	3.70	7.70	8.50	81.50	9.65	9.80	1008.97	12.38	1585.25	1008.43
20MG-32	673.500	4.40	7.40	9.00	82.50	9.20	9.45	1056.05	12.80	1538.70	1055.95
20MG-33	778.000	4.80	8.40	9.00	79.50	9.40	9.55	1081.60	13.35	1506.45	1061.20
20MG-34	1357.500	6.05	11.75	7.00	86.00	9.25	9.35	1068.40	12.95	1599.60	1113.75
20MG-35	2169.500	6.55	15.00	8.00	82.50	9.30	9.55	1010.45	12.40	1555.30	1022.95
20MG-36	1720.000	5.30	13.85	9.00	84.50	9.05	9.25	1088.90	13.20	1546.20	1115.50
20MG-37	1218.500	5.40	12.85	7.50	85.50	8.45	8.57	1110.85	13.55	1455.70	1158.65
20MG-38	1391.500	5.55	13.35	8.50	83.00	8.20	8.35	1044.60	12.90	1373.90	1071.00
20MG-39	1581.500	4.75	13.90	8.50	82.00	8.25	8.40	1049.70	12.65	1365.15	1037.05
20MG-40	1824.000	5.70	12.95	6.50	78.50	8.55	8.80	1125.00	13.80	1362.05	1083.20

Hybrid Combination	Fruit weight (g)	Cavity Size (cm)	Fruit Diameter (cm)	TSS (°Brix)	Germination (%)	Shoot Length (cm)	Root length (cm)	Seedling fresh weight (mg)	Seedling dry weight (mg)	SVI-I	SVI-II
20MG-41	1540.500	5.40	12.60	7.00	82.00	8.35	8.50	1095.15	13.28	1381.75	1088.47
20MG-42	1318.000	5.40	13.85	7.00	83.50	8.55	8.65	1084.80	13.15	1436.20	1098.10
20MG-43	1629.500	6.60	14.45	7.00	82.50	8.60	8.85	1014.30	12.53	1439.55	1033.20
20MG-44	1700.000	6.50	15.05	8.00	84.00	8.35	8.55	1063.35	13.05	1419.50	1096.05
20MG-45	1488.000	5.70	14.55	8.50	80.00	8.55	8.67	1113.85	13.50	1377.92	1079.80
20MG-46	1699.000	5.05	12.80	11.00	92.50	8.95	9.10	1056.90	13.05	1669.65	1207.05
20MG-47	1190.000	4.55	10.90	11.50	90.50	8.30	8.55	1043.55	12.65	1525.05	1144.90
20MG-48	1177.500	4.40	12.55	9.50	91.50	8.25	8.40	1092.40	13.40	1523.40	1226.40
20MG-49	1704.000	5.25	14.60	10.50	86.00	8.45	8.55	1130.15	13.70	1462.00	1178.40
20MG-50	1332.000	6.00	14.10	10.50	84.50	8.65	8.90	1065.70	13.00	1482.75	1098.95
20MG-51	1279.500	5.95	13.90	8.00	83.50	8.65	8.85	1041.10	12.85	1461.10	1072.60
20MG-52	1304.000	5.50	13.40	8.50	82.50	8.55	8.68	1166.40	14.05	1421.13	1159.25
20MG-53	1465.500	5.60	13.55	8.50	83.00	8.55	8.70	1094.17	13.42	1431.90	1114.30
20MG-54	1151.500	5.20	11.20	9.00	83.00	8.30	8.45	1093.10	13.25	1390.40	1099.70
20MG-55	991.500	4.70	11.20	11.00	79.50	8.20	8.32	1053.80	12.78	1313.85	1015.75
20MG-56	1374.500	4.90	13.90	9.50	80.00	8.25	8.40	1071.35	13.23	1332.10	1058.25
20MG-57	1161.500	5.60	12.90	7.00	85.00	8.45	8.70	1112.10	13.65	1457.90	1160.50
20MG-58	872.500	6.25	10.15	8.00	86.00	8.10	8.25	1088.95	13.20	1405.85	1135.10
20MG-59	745.000	5.45	8.10	10.50	82.00	8.05	8.15	1045.00	12.90	1328.20	1057.70
20MG-60	617.500	4.80	8.45	12.50	79.00	8.20	8.45	1117.95	13.55	1315.10	1070.60

APPENDIX-III: Mid Parent heterosis for sixty single cross hybrids for seed and fruit quality traits in muskmelon

Hybrid Combination	Fruit weight (g)	Fruit cavity size (cm)	Fruit diameter (cm)	TSS (^{0}Brix)	Germination (%)	Shoot Length (cm)	Root length (cm)	Seedling fresh weight (mg)	Seedling dry weight (mg)	SVI-I	SVI-II
20MG-01	-41.39	-151.58 **	-81.47 **	-111.11 **	13.33 **	11.40 **	10.83 **	22.18 **	22.97 **	26.02 **	39.22 **
20MG-02	23.38	-18.52	48.43	5.88	12.39 **	7.40 **	7.50 **	16.11 **	16.74 **	20.85 **	31.05 **
20MG-03	8.95	-27.36	39.16	15.79	8.06 **	6.11 **	5.66 **	15.78 **	15.02 **	14.43 **	24.27 **
20MG-04	47.04	-29.79	56.37 *	21.05	12.68 **	9.27 **	8.46 **	28.06 **	26.17 **	22.60 **	42.24 **
20MG-05	58.40	-21.55	50.77	24.32	7.36 **	6.80 **	6.92 **	18.70 **	19.44 **	14.90 **	28.00 **
20MG-06	10.61	-9.89	30.72	-10.53	7.27 **	8.20 **	7.99 **	20.94 **	21.62 **	16.03 **	30.26 **
20MG-07	15.01	-4.82	28.62	-21.05	5.11 **	10.89 **	10.18 **	17.30 **	15.57 **	16.19 **	21.37 **
20MG-08	9.09	-3.53	20.25	-17.95	2.38	8.31 **	7.79 **	16.84 **	18.22 **	10.61 **	21.01 **
20MG-09	36.70	-19.41	11.38	5.56	9.73 **	7.49 **	7.01 **	24.26 **	22.79 **	17.63 **	34.83 **
20MG-10	33.91	-16.28	0.30	0.00	6.16 **	6.27 **	6.41 **	17.75 **	18.41 **	12.81 **	25.82 **
20MG-11	-3.61	7.14	-9.09	-13.51	1.80	9.76 **	8.85 **	16.37 **	15.29 **	11.27 **	17.29 **
20MG-12	80.85	6.59	11.04	16.67	13.60 **	15.75 **	14.57 **	23.22 **	22.14 **	30.83 **	38.58 **
20MG-13	89.25	-11.34	48.20	35.29	-2.47	20.36 **	21.38 **	16.14 **	19.10 **	17.90 **	16.14 **
20MG-14	59.42	6.74	56.13	-6.25	9.54 **	21.92 **	21.59 **	22.07 **	22.07 **	33.36 **	33.77 **
20MG-15	39.90	18.05	42.59	-22.22	6.99 **	21.32 **	20.83 **	21.82 **	24.09 **	29.56 **	32.98 **
20MG-16	121.13 **	33.33	71.24 *	-16.67	3.90 *	19.40 **	19.59 **	26.82 **	25.79 **	24.19 **	31.03 **
20MG-17	158.40 **	26.49	89.27 **	-2.86	4.38 **	22.66 **	22.90 **	19.88 **	20.63 **	28.12 **	25.79 **
20MG-18	77.03	19.35	62.96 *	5.56	4.94 **	25.38 **	24.74 **	25.97 **	25.98 **	31.22 **	32.19 **
20MG-19	48.76	35.29	42.59	5.56	6.42 **	24.31 **	23.64 **	23.86 **	25.11 **	31.91 **	33.31 **
20MG-20	77.00	55.17	53.46	-13.51	5.45 **	25.70 **	26.64 **	18.89 **	20.36 **	33.13 **	27.14 **
20MG-21	108.76 *	35.63	77.29 **	29.41	5.11 **	24.62 **	24.96 **	23.19 **	22.52 **	31.21 **	29.09 **

Hybrid Combination	Fruit weight (g)	Fruit cavity size (cm)	Fruit diameter (cm)	TSS (°Brix)	Germination (%)	Shoot Length (cm)	Root length (cm)	Seedling fresh weight (mg)	Seedling dry weight (mg)	SVI-I	SVI-II
20MG-22	100.70 *	21.59	67.60 *	35.29	2.09	26.77 **	25.41 **	20.54 **	20.54 **	28.86 **	23.47 **
20MG-23	53.58	40.70	55.90 *	14.29	4.88 **	29.78 **	29.03 **	23.34 **	25.28 **	35.80 **	31.58 **
20MG-24	37.83	53.22	60.24 *	-5.88	7.08 **	26.75 **	27.90 **	20.78 **	20.54 **	36.40 **	29.08 **
20MG-25	20.95	0.49	53.64	0.00	4.85 **	27.51 **	26.98 **	25.76 **	26.12 **	33.54 **	32.09 **
20MG-26	1.22	-35.29	8.79	5.88	5.74 **	23.32 **	21.50 **	21.91 **	20.75 **	29.57 **	27.64 **
20MG-27	-17.76	-33.33	-10.90	-21.05	-0.30	23.96 **	24.76 **	17.01 **	18.10 **	24.03 **	17.71 **
20MG-28	-19.79	-15.27	-2.97	-10.53	-2.06	18.73 **	19.37 **	30.44 **	28.91 **	16.57 **	26.29 **
20MG-29	-19.33	-19.39	-5.10	-13.51	9.82 **	18.97 **	17.55 **	24.61 **	23.47 **	30.07 **	35.42 **
20MG-30	-12.51	-20.81	-0.93	-15.79	-4.24 **	23.13 **	22.29 **	23.41 **	25.30 **	17.59 **	19.83 **
20MG-31	-10.90	-18.23	-1.91	-10.53	-2.10	26.56 **	26.25 **	18.44 **	18.42 **	23.79 **	15.86 **
20MG-32	-15.60	-4.86	-6.03	-7.69	-1.79	21.45 **	22.33 **	21.73 **	21.33 **	19.72 **	19.15 **
20MG-33	-6.55	3.78	7.01	0.00	-6.19 **	21.68 **	21.27 **	24.80 **	25.94 **	13.91 **	18.19 **
20MG-34	67.59	29.41	47.80	-22.22	0.88	21.31 **	19.49 **	22.86 **	22.46 **	21.38 **	23.62 **
20MG-35	172.12 **	43.17	88.09 **	-13.51	-1.20	24.41 **	24.84 **	17.64 **	18.38 **	23.18 **	16.92 **
20MG-36	110.08 *	16.48	70.99 *	0.00	2.11	23.13 **	23.54 **	26.30 **	24.82 **	25.96 **	27.37 **
20MG-37	91.14	3.35	70.76 *	-14.29	4.59 **	10.10 **	9.58 **	28.41 **	27.23 **	14.95 **	33.03 **
20MG-38	132.30 *	6.73	74.51 *	3.03	1.22	5.47 **	4.70 **	20.33 **	21.41 **	6.42 **	22.90 **
20MG-39	153.14 **	-13.64	73.75 **	-8.11	-1.20	6.11 **	5.99 **	22.07 **	20.19 **	4.73 *	18.76 **
20MG-40	182.13 **	10.14	71.52 *	-29.73	-6.55 **	9.27 **	10.69 **	31.34 **	30.50 **	2.68	22.06 **
20MG-41	136.55 *	8.00	61.02 *	-22.22	1.55	8.09 **	7.26 **	26.30 **	24.36 **	9.47 **	26.15 **
20MG-42	104.50	7.46	73.13 *	-24.32	2.14	12.13 **	10.90 **	27.68 **	26.44 **	13.95 **	29.08 **
20MG-43	160.30 **	42.70	84.66 **	-24.32	0.00	13.53 **	14.75 **	19.56 **	19.57 **	14.14 **	19.57 **

Hybrid Combination	Fruit weight (g)	Fruit cavity size (cm)	Fruit diameter (cm)	TSS (°Brix)	Germination (%)	Shoot Length (cm)	Root length (cm)	Seedling fresh weight (mg)	Seedling dry weight (mg)	SVI-I	SVI-II
20MG-44	166.77 **	37.57	91.72 **	-15.79	0.90	10.96 **	11.40 **	23.08 **	23.40 **	12.14 **	24.56 **
20MG-45	121.51 *	20.63	85.94 **	-2.86	-4.76 **	11.40 **	10.86 **	29.04 **	27.06 **	5.74 *	21.10 **
20MG-46	161.69 **	5.76	61.51 *	25.71	9.47 **	18.15 **	17.04 **	22.04 **	23.11 **	28.59 **	34.91 **
20MG-47	86.96	-2.67	37.11	27.78	9.37 **	11.78 **	12.50 **	22.00 **	20.48 **	22.66 **	31.80 **
20MG-48	78.95	-5.38	55.42 *	8.57	11.59 **	13.01 **	12.94 **	27.23 **	26.42 **	26.10 **	41.04 **
20MG-49	170.58 **	4.48	93.38 **	20.00	5.20 **	10.82 **	10.14 **	30.83 **	30.48 **	16.30 **	37.24 **
20MG-50	125.29 *	20.00	83.71 **	27.27	3.05 *	11.97 **	12.48 **	22.94 **	24.11 **	15.69 **	27.92 **
20MG-51	107.37	12.26	73.21 **	-13.51	0.60	11.97 **	12.56 **	21.25 **	23.86 **	12.90 **	24.59 **
20MG-52	104.15	10.55	76.90 *	-8.11	-1.79	9.97 **	9.98 **	36.37 **	34.77 **	7.89 **	32.48 **
20MG-53	127.74 *	16.67	72.61 *	-5.56	2.79	11.40 **	10.65 **	26.37 **	27.55 **	14.29 **	31.02 **
20MG-54	80.84	7.77	39.56	-2.70	1.53	9.57 **	9.21 **	28.85 **	29.27 **	11.14 **	31.17 **
20MG-55	60.37	6.21	42.68	18.92	-3.64 *	8.97 **	8.82 **	24.40 **	23.73 **	4.95 *	19.25 **
20MG-56	118.35 *	8.29	76.51 **	0.00	-3.90 *	10.37 **	10.34 **	24.18 **	26.86 **	6.02 *	21.98 **
20MG-57	74.92	23.76	64.33 *	-20.00	1.19	10.82 **	12.08 **	29.03 **	30.31 **	12.69 **	31.98 **
20MG-58	36.01	36.61	27.67	-8.57	1.78	7.64 **	6.97 **	25.92 **	26.32 **	9.06 **	28.65 **
20MG-59	18.49	21.79	1.57	16.67	-0.91	9.15 **	8.13 **	22.35 **	24.64 **	7.64 **	23.52 **
20MG-60	-5.04	7.87	4.32	42.86	-3.66 *	13.10 **	14.58 **	30.40 **	29.67 **	9.71 **	24.90 **
SEm±	313.69	1.10	1.95	1.80	1.24	0.10	0.11	22.32	0.20	30.22	23.20
CD at 95%	627.69	2.21	3.90	3.60	2.48	0.21	0.23	44.68	0.40	60.48	26.79

*Significant at P=0.05; **Significant at P=0.01

APPENDIX-IV: Better Parent heterosis for sixty single cross hybrids for seed and fruit quality traits in muskmelon

Hybrid Combination	Fruit weight (g)	Fruit cavity size (cm)	Fruit diameter (cm)	TSS (^{o}Brix)	Germination (%)	Shoot length (cm)	Root length (cm)	Seedling fresh weight (mg)	Seedling dry weight (mg)	SVI-I	SVI-II
20MG-01	-45.78	-149.00 **	-82.42 **	-110.53 **	11.31 **	6.21 **	6.10 **	15.47 **	16.23 **	22.54 **	29.37 **
20MG-02	7.11	-22.22	43.03	-5.26	10.71 **	1.21	1.18	10.11 **	10.09 **	15.46 **	21.84 **
20MG-03	-1.26	-34.23	38.32	15.79	7.74 **	0.00	0.00	8.77 **	7.46 **	8.38 **	15.77 **
20MG-04	38.00	-32.65	48.79	21.05	11.70 **	2.40	2.37	19.85 **	18.42 **	14.36 **	34.61 **
20MG-05	49.78	-21.98	48.48	21.05	4.17 *	1.23	1.19	12.43 **	13.16 **	12.08 **	17.86 **
20MG-06	3.48	-10.87	29.94	-10.53	5.36 **	3.77 *	3.68 *	12.28 **	12.28 **	13.33 **	18.29 **
20MG-07	4.44	-12.22	26.67	-21.05	4.17 *	7.01 **	6.90 **	8.74 **	7.46 **	13.42 **	11.91 **
20MG-08	0.89	-8.89	18.79	-20.00	2.38	5.16 **	5.06 **	10.28 **	10.96 **	7.61 **	13.58 **
20MG-09	33.41	-23.89	9.70	0.00	8.77 **	2.48	2.44	17.18 **	15.79 **	11.45 **	28.20 **
20MG-10	26.22	-20.00	0.00	-5.26	4.62 **	2.55	2.47	11.40 **	11.40 **	7.22 **	20.03 **
20MG-11	-10.96	0.00	-9.09	-15.79	1.19	7.95 **	7.10 **	8.77 **	7.46 **	10.11 **	8.71 **
20MG-12	72.81	-1.11	9.41	10.53	11.90 **	15.75 **	14.00 **	15.59 **	14.91 **	28.52 **	28.57 **
20MG-13	50.10	-14.00	43.95	35.29	-2.47	17.86 **	19.06 **	6.18 *	9.50 **	15.54 **	6.79 *
20MG-14	20.17	4.04	54.14	-11.76	9.20 **	20.83 **	21.41 **	11.98 **	11.98 **	33.07 **	23.06 **
20MG-15	9.14	9.01	38.32	-26.32	5.39 **	20.24 **	19.94 **	10.75 **	12.81 **	28.66 **	22.58 **
20MG-16	77.43	30.61	66.88 *	-21.05	1.17	19.05 **	19.06 **	14.87 **	14.88 **	21.38 **	22.67 **
20MG-17	108.58 *	24.47	87.50 **	-5.56	3.09	20.83 **	21.99 **	9.84 **	11.16 **	25.15 **	14.61 **
20MG-18	41.68	18.09	58.08	0.00	4.94 **	22.02 **	21.99 **	13.22 **	13.22 **	28.01 **	18.82 **
20MG-19	16.24	22.34	41.25	0.00	5.45 **	20.24 **	19.65 **	11.17 **	13.22 **	28.76 **	21.64 **
20MG-20	40.35	43.62	51.55	-20.00	3.57 *	20.83 **	21.99 **	8.56 **	9.92 **	30.39 **	18.06 **
20MG-21	72.88	25.53	75.62 *	29.41	2.34	22.02 **	22.58 **	12.40 **	12.40 **	30.34 **	21.41 **

Hybrid Combination	Fruit weight (g)	Fruit cavity size (cm)	Fruit diameter (cm)	TSS (°Brix)	Germination (%)	Shoot length (cm)	Root length (cm)	Seedling fresh weight (mg)	Seedling dry weight (mg)	SVI-I	SVI-II
20MG-22	61.59	13.83	64.02 *	35.29	-1.16	22.62 **	22.29 **	10.32 **	10.33 **	28.44 **	16.51 **
20MG-23	21.65	28.72	52.12	11.11	3.61 *	23.21 **	23.17 **	11.57 **	13.64 **	30.78 **	20.67 **
20MG-24	12.21	39.36	54.12	-5.88	6.75 **	18.45 **	19.65 **	9.64 **	10.33 **	27.86 **	18.50 **
20MG-25	-5.57	-1.90	50.65	-5.26	2.98	22.36 **	21.95 **	20.03 **	20.72 **	30.47 **	24.29 **
20MG-26	-24.79	-37.14	8.44	-5.26	4.17 *	16.97 **	14.71 **	16.76 **	15.32 **	24.36 **	20.17 **
20MG-27	-36.82	-35.14	-14.37	-21.05	-0.60	17.58 **	18.45 **	11.01 **	11.71 **	18.02 **	11.05 **
20MG-28	-36.67	-18.10	-4.55	-10.53	-2.92	11.98 **	13.02 **	23.27 **	22.52 **	9.24 **	21.06 **
20MG-29	-35.94	-24.76	-6.87	-15.79	6.55 **	13.50 **	11.61 **	19.20 **	18.47 **	27.48 **	26.24 **
20MG-30	-31.10	-25.71	-4.79	-15.79	-5.95 **	18.87 **	17.79 **	15.69 **	17.12 **	15.41 **	10.15 **
20MG-31	-31.44	-29.52	-3.75	-10.53	-2.98	22.93 **	22.88 **	10.86 **	11.49 **	21.42 **	8.17 **
20MG-32	-34.13	-16.19	-8.07	-10.00	-1.79	18.71 **	19.62 **	16.04 **	15.32 **	17.02 **	13.26 **
20MG-33	-23.91	-8.57	5.00	-5.26	-7.02 **	16.77 **	16.46 **	18.84 **	20.27 **	8.42 **	13.83 **
20MG-34	32.76	15.24	43.29	-26.32	-0.58	17.83 **	15.43 **	17.39 **	16.67 **	15.91 **	19.46 **
20MG-35	112.18 **	24.76	81.82 *	-15.79	-1.79	23.18 **	23.23 **	11.03 **	11.71 **	22.48 **	9.72 **
20MG-36	68.22	0.95	62.94 *	-5.26	0.60	22.30 **	22.52 **	19.65 **	18.92 **	23.15 **	19.65 **
20MG-37	73.82	-0.92	67.97 *	-16.67	3.64 *	4.97 **	4.57 **	23.02 **	21.52 **	10.61 **	25.97 **
20MG-38	98.50	1.83	74.51 *	-5.56	0.61	-0.61	-1.76	15.68 **	15.70 **	0.64	16.44 **
20MG-39	125.61 *	-14.41	66.47 *	-10.53	-1.80	0.00	0.00	16.25 **	13.45 **	-1.81	12.75 **
20MG-40	160.20 **	4.59	69.28 *	-31.58	-8.19 **	2.40	4.14 *	24.58 **	23.77 **	-5.17 *	17.76 **
20MG-41	119.76 *	-0.92	57.50	-22.22	-0.61	2.45	1.19	21.28 **	19.06 **	5.67 *	18.34 **
20MG-42	88.02	-0.92	65.87 *	-26.32	1.21	7.55 **	6.13 **	20.13 **	17.94 **	10.13 **	19.38 **
20MG-43	132.45 *	21.10	80.63 *	-26.32	0.00	9.55 **	10.97 **	12.33 **	12.33 **	10.26 **	12.33 **

Hybrid Combination	Fruit weight (g)	Fruit cavity size (cm)	Fruit diameter (cm)	TSS (°Brix)	Germination (%)	Shoot length (cm)	Root length (cm)	Seedling fresh weight (mg)	Seedling dry weight (mg)	SVI-I	SVI-II
20MG-44	142.51 *	19.27	86.96 **	-20.00	0.00	7.74 **	8.23 **	17.76 **	17.04 **	7.96 **	19.16 **
20MG-45	112.27	4.59	81.87 *	-5.56	-6.43 **	6.21 **	5.79 **	23.35 **	21.08 **	-0.83	17.40 **
20MG-46	142.37 *	-7.34	56.10	22.22	6.94 **	14.01 **	12.35 **	17.04 **	17.04 **	20.98 **	31.23 **
20MG-47	69.76	-16.51	32.12	27.78	9.04 **	9.93 **	10.32 **	15.56 **	13.45 **	20.10 **	24.47 **
20MG-48	67.97	-19.27	47.65	5.56	10.91 **	13.01 **	12.75 **	20.97 **	20.18 **	25.20 **	33.33 **
20MG-49	148.58 *	3.96	89.61 **	16.67	4.24 *	4.97 **	4.27 *	25.50 **	26.27 **	11.09 **	31.66 **
20MG-50	94.31	18.81	83.12 *	16.67	2.42	4.85 **	4.71 **	18.35 **	19.82 **	8.61 **	22.78 **
20MG-51	86.65	7.21	66.47 *	-15.79	0.00	4.85 **	5.36 **	15.61 **	18.43 **	5.09 *	19.84 **
20MG-52	90.23	8.91	74.03 *	-10.53	-3.51 *	2.40	2.66	29.53 **	29.49 **	-1.06	29.52 **
20MG-53	113.79	10.89	69.38 *	-5.56	0.61	4.91 **	3.57 *	21.51 **	23.73 **	9.51 **	24.50 **
20MG-54	67.98	2.97	34.13	-5.26	0.61	4.40 **	3.68 *	21.39 **	22.12 **	6.62 *	22.86 **
20MG-55	44.64	-6.93	40.00	15.79	-3.64 *	4.46 **	4.39 *	17.02 **	17.74 **	0.63	13.49 **
20MG-56	100.51	-2.97	72.67 *	-5.00	-4.76 **	6.45 **	6.33 **	18.97 **	21.89 **	1.31	18.23 **
20MG-57	69.44	10.89	61.25	-22.22	-0.58	4.97 **	6.10 **	23.50 **	25.81 **	4.92	29.66 **
20MG-58	27.28	23.76	23.78	-11.11	-0.58	3.18 *	1.85	20.93 **	21.66 **	1.87	26.82 **
20MG-59	8.68	7.92	-1.82	16.67	-1.20	6.62 **	5.16 **	16.05 **	18.89 **	4.60	18.17 **
20MG-60	-9.92	-4.95	-0.59	38.89	-4.24 *	12.33 **	13.80 **	24.15 **	24.88 **	9.64 **	19.61 **
SEm±	362.21	1.27	2.25	2.07	1.43	0.12	0.13	25.78	0.23	34.90	26.79
CD at 95%	724.79	2.55	4.51	4.16	2.87	0.24	0.26	51.59	0.46	69.84	53.60

*Significant at P=0.05; **Significant at P=0.01

APPENDIX-V: Standard heterosis for sixty single cross hybrids for seed and fruit quality traits in muskmelon

Hybrid Combination	Fruit weight (g)	Fruit cavity size (cm)	Fruit diameter (cm)	TSS (^{0}Brix)	Germination (%)	Shoot length (cm)	Root length (cm)	Seedling fresh weight (mg)	Seedling dry weight (mg)	SVI-I	SVI-II
20MG-01	-46.61	-148.51 **	-81.17 *	-111.11 **	1.08	-14.93 **	-14.71 **	-1.52	1.53	-13.89 **	2.65
20MG-02	5.47	-23.76	53.25	0.00	0.54	-16.92 **	-15.69 **	-6.09 *	-3.83 *	-15.84 **	-3.33
20MG-03	-2.77	-27.72	50.00	22.22	-2.16	-17.91 **	-17.65 **	-7.24 **	-6.13 **	-19.55 **	-8.14 **
20MG-04	35.89	-34.65	59.42	27.78	3.24 *	-14.93 **	-15.20 **	2.21	3.45	-12.30 **	6.81 **
20MG-05	47.48	-29.70	59.09	27.78	-5.41 **	-17.91 **	-16.67 **	-4.11	-1.15	-21.76 **	-6.49 **
20MG-06	1.90	-18.81	40.91	-5.56	-4.32 **	-17.91 **	-17.16 **	-4.24	-1.92	-21.10 **	-6.15 **
20MG-07	2.84	-21.78	35.71	-16.67	-5.41 **	-16.42 **	-16.42 **	-7.26 **	-6.13 **	-20.94 **	-11.21 **
20MG-08	-0.66	-18.81	27.27	-11.11	-7.03 **	-18.91 **	-18.63 **	-5.95 *	-3.07	-24.46 **	-9.88 **
20MG-09	31.36	-32.18	17.53	5.56	0.54	-17.91 **	-17.65 **	-0.06	1.15	-17.32 **	1.72
20MG-10	24.29	-28.71	7.14	0.00	-2.16	-19.90 **	-18.63 **	-4.99 *	-2.68	-21.00 **	-4.77 *
20MG-11	-12.33	-10.89	-2.60	-11.11	-8.11 **	-18.91 **	-18.63 **	-7.24 **	-6.13 **	-25.35 **	-13.75 **
20MG-12	70.17	-11.88	20.78	16.67	1.62	-15.92 **	-16.18 **	-1.42	0.38	-14.68 **	2.01
20MG-13	114.37	-14.85	46.75	27.78	-14.59 **	-1.49	-0.49	-2.72	1.53	-15.42 **	-13.30 **
20MG-14	71.63	1.98	57.14	-16.67	-3.78 *	1.00	1.47	2.59	3.83 *	-2.59	-0.09
20MG-15	55.87	19.80	50.00	-22.22	-4.86 **	0.50	0.25	1.47	4.60 *	-4.50 *	-0.48
20MG-16	153.39 *	26.73	70.13 *	-16.67	-6.49 **	-0.50	-0.49	5.24 *	6.51 **	-6.92 **	-0.40
20MG-17	197.88 **	15.84	94.81 **	-5.56	-9.73 **	1.00	1.96	0.64	3.07	-8.39 **	-6.95 **
20MG-18	102.33	9.90	71.43 *	5.56	-8.11 **	1.99	1.96	3.74	4.98 **	-6.29 **	-3.53
20MG-19	66.01	13.86	46.75	5.56	-5.95 **	0.50	0.00	1.85	4.98 **	-5.74 **	-1.24
20MG-20	100.44	33.66	58.44	-11.11	-5.95 **	1.00	1.96	-0.53	1.92	-4.55 *	-4.15
20MG-21	146.90 *	16.83	82.47 *	22.22	-5.41 **	1.99	2.45	2.98	4.21 *	-3.31	-1.42

Hybrid Combination	Fruit weight (g)	Fruit cavity size (cm)	Fruit diameter (cm)	TSS (⁰Brix)	Germination (%)	Shoot length (cm)	Root length (cm)	Seedling fresh weight (mg)	Seedling dry weight (mg)	SVI-I	SVI-II
20MG-22	130.78 *	5.94	74.68 *	27.78	-7.57 **	2.49 *	2.21	1.07	2.30	-5.37 **	-5.41 *
20MG-23	73.74	19.80	62.99	11.11	-7.03 **	2.99 *	2.94 *	2.22	5.36 **	-4.27 *	-2.03
20MG-24	60.25	29.70	70.13 *	-11.11	-5.95 **	-1.00	0.00	0.45	2.30	-6.40 **	-3.79
20MG-25	40.85	1.98	50.65	0.00	-6.49 **	-1.99	-1.96	0.26	2.68	-8.33 **	-4.00
20MG-26	12.18	-34.65	8.44	0.00	-5.41 **	-3.98 **	-4.41 **	-2.48	-1.92	-9.36 **	-7.19 **
20MG-27	-5.76	-28.71	-7.14	-16.67	-9.73 **	-3.48 **	-2.45	-7.28 **	-4.98 **	-12.40 **	-14.23 **
20MG-28	-5.54	-14.85	-4.55	-5.56	-10.27 **	-6.97 **	-6.37 **	2.96	4.21 *	-16.23 **	-6.50 **
20MG-29	-4.45	-21.78	-3.25	-11.11	-3.24 *	-7.96 **	-8.09 **	-0.44	0.77	-11.00 **	-2.50
20MG-30	2.77	-22.77	3.25	-11.11	-14.59 **	-5.97 **	-5.88 **	-3.37	-0.38	-19.65 **	-14.92 **
20MG-31	2.26	-26.73	0.00	-5.56	-11.89 **	-3.98 **	-3.92 **	-7.40 **	-5.17 **	-15.37 **	-16.46 **
20MG-32	-1.75	-12.87	-3.90	0.00	-10.81 **	-8.46 **	-7.35 **	-3.08	-1.92	-17.85 **	-12.52 **
20MG-33	13.49	-4.95	9.09	0.00	-14.05 **	-6.47 **	-6.37 **	-0.73	2.30	-19.57 **	-12.08 **
20MG-34	98.03	19.80	52.60	-22.22	-7.03 **	-7.96 **	-8.33 **	-1.95	-0.77	-14.60 **	-7.73 **
20MG-35	216.48 **	29.70	94.81 **	-11.11	-10.81 **	-7.46 **	-6.37 **	-7.26 **	-4.98 **	-16.96 **	-15.25 **
20MG-36	150.91 *	4.95	79.87 *	0.00	-8.65 **	-9.95 **	-9.31 **	-0.06	1.15	-17.45 **	-7.58 **
20MG-37	77.75	6.93	66.88 *	-16.67	-7.57 **	-15.92 **	-15.93 **	1.95	3.83 *	-22.28 **	-4.01
20MG-38	102.99	9.90	73.38 *	-5.56	-10.27 **	-18.41 **	-18.14 **	-4.13	-1.15	-26.65 **	-11.27 **
20MG-39	130.71 *	-5.94	80.52 *	-5.56	-11.35 **	-17.91 **	-17.65 **	-3.66	-3.07	-27.12 **	-14.08 **
20MG-40	166.08 **	12.87	68.18 *	-27.78	-15.14 **	-14.93 **	-13.73 **	3.25	5.75 **	-27.28 **	-10.26 **
20MG-41	124.73 *	6.93	63.64	-22.22	-11.35 **	-16.92 **	-16.67 **	0.51	1.72	-26.23 **	-9.82 **
20MG-42	92.27	6.93	79.87 *	-22.22	-9.73 **	-14.93 **	-15.20 **	-0.44	0.77	-23.32 **	-9.03 **
20MG-43	137.71 *	30.69	87.66 *	-22.22	-10.81 **	-14.43 **	-13.24 **	-6.91 **	-4.02 *	-23.14 **	-14.40 **

Hybrid Combination	Fruit weight (g)	Fruit cavity size (cm)	Fruit diameter (cm)	TSS (^{0}Brix)	Germination (%)	Shoot length (cm)	Root length (cm)	Seedling fresh weight (mg)	Seedling dry weight (mg)	SVI-I	SVI-II
20MG-44	147.99 *	28.71	95.45 **	-11.11	-9.19 **	-16.92 **	-16.18 **	-2.41	0.00	-24.21 **	-9.20 **
20MG-45	117.07	12.87	88.96 **	-5.56	-13.51 **	-14.93 **	-14.95 **	2.23	3.45	-26.43 **	-10.54 **
20MG-46	147.85 *	0.00	66.23 *	22.22	0.00	-10.95 **	-10.78 **	-3.00	0.00	-10.86 **	0.00
20MG-47	73.60	-9.90	41.56	27.78	-2.16	-17.41 **	-16.18 **	-4.23	-3.07	-18.58 **	-5.15 *
20MG-48	71.77	-12.87	62.99	5.56	-1.08	-17.91 **	-17.65 **	0.26	2.68	-18.67 **	1.60
20MG-49	148.58 *	3.96	89.61 **	16.67	-7.03 **	-15.92 **	-16.18 **	3.72	4.98 **	-21.95 **	-2.37
20MG-50	94.31	18.81	83.12 *	16.67	-8.65 **	-13.93 **	-12.75 **	-2.19	-0.38	-20.84 **	-8.96 **
20MG-51	86.65	17.82	80.52 *	-11.11	-9.73 **	-13.93 **	-13.24 **	-4.45	-1.53	-21.99 **	-11.14 **
20MG-52	90.23	8.91	74.03 *	-5.56	-10.81 **	-14.93 **	-14.95 **	7.05 **	7.66 **	-24.13 **	-3.96
20MG-53	113.79	10.89	75.97 *	-5.56	-10.27 **	-14.93 **	-14.71 **	0.42	2.87	-23.55 **	-7.68 **
20MG-54	67.98	2.97	45.45	0.00	-10.27 **	-17.41 **	-17.16 **	0.32	1.53	-25.77 **	-8.89 **
20MG-55	44.64	-6.93	45.45	22.22	-14.05 **	-18.41 **	-18.38 **	-3.29	-2.11	-29.86 **	-15.85 **
20MG-56	100.51	-2.97	80.52 *	5.56	-13.51 **	-17.91 **	-17.65 **	-1.67	1.34	-28.88 **	-12.33 **
20MG-57	69.44	10.89	67.53 *	-22.22	-8.11 **	-15.92 **	-14.71 **	2.06	4.60 *	-22.16 **	-3.86
20MG-58	27.28	23.76	31.82	-11.11	-7.03 **	-19.40 **	-19.12 **	-0.06	1.15	-24.94 **	-5.96 **
20MG-59	8.68	7.92	5.19	16.67	-11.35 **	-19.90 **	-20.10 **	-4.09	-1.15	-29.09 **	-12.37 **
20MG-60	-9.92	-4.95	9.74	38.89	-14.59 **	-18.41 **	-17.16 **	2.60	3.83 *	-29.79 **	-11.30 **
SEm±	362.21	1.27	2.25	2.07	1.43	0.12	0.13	25.78	0.23	34.90	26.79
CD at 95%	724.79	2.55	4.51	4.16	2.86	0.25	0.268	51.59	0.46	69.84	53.60

*Significant at P=0.05; **Significant at P=0.01

APPENDIX-VI: Estimates of specific combining effects (sca) in crosses for fruit and seed quality traits in muskmelon

Hybrid Combination	Fruit weight (g)	Fruit cavity size (cm)	Fruit diameter (cm)	TSS (⁰Brix)	Germination (%)	Shoot length (cm)	Root length (cm)	Seedling fresh weight (mg)	Seedling dry weight (mg)	SVI-I	SVI-II
20MG-01	-390.53	-4.40	-7.01	-8.30	2.533 *	0.142	0.140	9.451	0.178	72.224 **	50.052 *
20MG-02	32.78	0.66	1.76	0.30	0.733	-0.018	0.045	-9.859	-0.052	11.014	1.592
20MG-03	6.28	0.43	1.84	2.80	0.133	-0.108	-0.130	-3.009	-0.153	-19.921	-14.918
20MG-04	30.88	-0.16	2.36	3.20	5.433 **	0.182 *	0.120	8.691	0.087	120.759 **	84.032 **
20MG-05	56.38	0.26	1.98	3.00	-2.467 *	-0.028	0.040	-8.574	0.018	-41.131	-30.293
20MG-06	34.78	0.85	1.34	0.30	-0.167	-0.078	-0.025	-7.809	-0.023	-9.256	-4.218
20MG-07	60.18	0.59	1.33	-1.00	-0.967	0.042	0.020	0.756	-0.118	-10.386	-25.173
20MG-08	-91.43	0.35	0.03	-0.30	-2.767 **	-0.038	-0.085	-5.339	0.003	-57.976 *	-35.928
20MG-09	84.58	-0.08	-0.84	0.70	3.133 **	-0.098	-0.120	14.931	0.097	33.989	51.292 **
20MG-10	-32.43	-0.08	-1.13	-0.10	-2.467 *	-0.248 **	-0.150	-5.219	0.008	-79.946 **	-32.618
20MG-11	-190.13	0.66	-1.41	-1.40	-5.067 **	-0.048	-0.075	-4.269	-0.183	-95.996 **	-81.418 **
20MG-12	398.68	0.93	-0.25	0.80	1.933	0.302 **	0.215 *	10.251	0.138	76.624 **	37.602
20MG-13	75.14	-0.12	-0.36	3.66	-7.508 **	-0.342 **	-0.257 **	-64.324 **	-0.585 **	-197.480 **	-150.244 **
20MG-14	-151.56	-0.51	-1.14	-1.74	1.192	-0.052	-0.053	24.016	0.185	18.210	32.896
20MG-15	-229.56	0.36	-1.36	-1.74	2.092 *	-0.092	-0.152	31.066	0.485 **	20.950	69.786 **
20MG-16	198.54	0.47	-0.01	-1.34	0.892	-0.202 *	-0.227 *	-19.084	-0.275	-19.595	-10.764
20MG-17	449.54	0.09	1.53	-0.54	-2.008	0.038	0.092	-17.599	-0.195	-31.785	-43.589 *
20MG-18	85.44	-0.17	0.49	0.76	0.792	0.088	0.077	18.366	0.115	26.940	19.536
20MG-19	-144.66	-0.08	-1.02	0.46	2.992 **	-0.092	-0.152	39.281 *	0.570 **	33.185	87.381 **
20MG-20	-36.26	0.53	-0.77	-0.84	2.692 *	0.128	0.167	-7.114	-0.110	73.970 **	25.526
20MG-21	238.74	-0.08	0.96	1.66	2.092 *	0.068	0.082	-12.694	-0.265	55.385 *	5.546

Hybrid Combination	Fruit weight (g)	Fruit cavity size (cm)	Fruit diameter (cm)	TSS (°Brix)	Germination (%)	Shoot length (cm)	Root length (cm)	Seedling fresh weight (mg)	Seedling dry weight (mg)	SVI-I	SVI-II
20MG-22	59.74	-0.80	0.87	1.86	-3.008 **	0.168	0.128	0.106	-0.105	-28.250	-48.114 *
20MG-23	-237.96	-0.26	0.44	0.06	0.392	0.318 **	0.278 **	38.056 *	0.555 **	57.850 *	52.236 **
20MG-24	-307.16	0.56	0.35	-2.24	-0.608	-0.032	0.017	-30.074	-0.375 *	-9.380	-40.194 *
20MG-25	1.93	1.95	3.19	1.91	2.117 *	0.321 **	0.315 **	13.324	0.159	99.353 **	40.687 *
20MG-26	-128.27	-1.14	-1.64	0.51	1.817	0.161	0.070	14.014	0.029	55.343 *	25.827
20MG-27	-221.27	-0.87	-2.51	-0.49	-0.283	0.221 *	0.295 **	-18.986	-0.171	36.908	-17.533
20MG-28	-460.17	-0.41	-2.52	0.41	-0.483	-0.139	-0.105	1.364	0.019	-30.012	-5.733
20MG-29	-506.67	-0.59	-2.77	-0.29	6.117 ***	-0.149	-0.210 *	15.949	0.099	83.173 **	88.742 **
20MG-30	-166.27	-0.60	-1.51	0.01	-3.083 **	0.001	0.000	-13.786	0.009	-59.327 *	-39.333 *
20MG-31	-150.87	-0.91	-1.37	0.21	-0.383	0.171	0.170	-16.296	-0.161	16.868	-17.663
20MG-32	-305.97	-0.60	-2.32	0.91	0.317	-0.109	-0.060	10.384	-0.016	-11.297	3.107
20MG-33	-244.97	0.05	-1.44	0.41	-3.783 ***	-0.069	-0.095	-7.896	0.079	-85.332 **	-44.473 *
20MG-34	266.03	1.12	2.42	-1.89	-0.383	-0.169	-0.225 *	12.454	0.089	-37.267	2.467
20MG-35	1171.33	1.46	6.14	-1.19	-0.983	-0.019	0.050	-20.046	-0.201	-16.067	-28.733
20MG-36	745.13	0.53	4.35	-0.49	-0.983	-0.219 *	-0.210 *	9.524	0.069	-52.347 *	-7.363
20MG-37	-242.65	1.37	0.62	0.41	0.283	-0.100	-0.128	18.847	0.136	-12.180	15.595
20MG-38	-3.35	0.28	-0.46	0.01	-3.517 **	-0.310 **	-0.348 **	-16.913	-0.044	-118.690 **	-48.415 *
20MG-39	216.65	-0.55	0.42	0.51	-2.617 *	-0.250 **	-0.273 **	7.487	-0.094	-88.925 **	-40.725 *
20MG-40	218.75	0.16	-0.74	-1.59	-5.817 **	0.040	0.127	-8.463	0.046	-87.095 **	-76.075 **
20MG-41	-118.75	0.03	-1.44	-1.29	-2.217 *	-0.070	-0.103	13.322	0.051	-52.185 *	-24.625
20MG-42	-50.35	0.07	0.57	-0.99	0.583	0.080	0.032	5.187	-0.014	21.740	6.925
20MG-43	280.05	1.16	1.56	-1.29	-0.217	0.100	0.202 *	-23.898	-0.184	21.035	-17.830

Hybrid Combination	Fruit weight (g)	Fruit cavity size (cm)	Fruit diameter (cm)	TSS (°Brix)	Germination (%)	Shoot length (cm)	Root length (cm)	Seedling fresh weight (mg)	Seedling dry weight (mg)	SVI-I	SVI-II
20MG-44	222.95	0.67	1.51	-0.09	0.983	0.020	0.022	4.757	0.061	19.370	18.265
20MG-45	-32.55	0.11	0.89	-0.09	-4.117 **	0.060	0.012	11.427	0.056	-63.990 *	-50.815 **
20MG-46	109.95	-0.71	-0.35	2.11	5.283 **	0.510 **	0.507 **	-11.973	0.016	182.650 **	70.825 **
20MG-47	-305.75	-1.37	-1.78	2.31	6.183 **	-0.040	0.032	0.127	-0.124	103.550 **	68.275 **
20MG-48	-294.95	-1.20	-0.77	0.01	5.183 **	-0.040	-0.078	0.097	0.096	74.720 **	78.595 **
20MG-49	556.10	1.20	3.56	2.33	2.575 *	-0.021	-0.070	22.703	0.113	38.083	43.910 *
20MG-50	250.40	0.71	1.48	0.93	-0.225	0.219 *	0.285 **	-11.257	-0.117	34.123	-11.900
20MG-51	227.90	0.63	1.61	-1.08	0.675	0.229 *	0.260 **	-16.557	-0.067	50.988 *	3.390
20MG-52	12.00	-0.06	0.91	-0.68	-0.025	0.119	0.085	17.493	0.123	15.943	8.540
20MG-53	119.50	0.21	0.70	-0.88	0.575	0.209 *	0.180	-3.097	0.028	41.927	9.765
20MG-54	96.40	-0.15	-0.89	-0.08	1.875	-0.091	-0.085	-1.957	-0.087	19.902	17.090
20MG-55	-44.70	-0.76	-0.50	1.63	-1.425	-0.221 *	-0.240 *	0.158	-0.107	-60.703 *	-26.715
20MG-56	210.70	-0.95	1.55	0.33	-1.225	-0.001	-0.045	-2.687	0.063	-24.067	-10.970
20MG-57	-45.80	0.00	0.43	-2.68	2.675 *	0.039	0.120	-5.767	0.033	59.948 *	38.450 *
20MG-58	-403.30	0.47	-1.81	-1.98	0.575	-0.261 **	-0.260 **	4.633	-0.007	-37.188	7.440
20MG-59	-437.50	-0.49	-3.39	0.23	-0.525	-0.211 *	-0.285 **	-13.867	-0.047	-49.337	-10.360
20MG-60	-541.70	-0.82	-3.68	1.93	-5.525 **	-0.011	0.055	10.203	0.073	-89.618 **	-68.640 **
SEm ±	285.71	1.00	1.80	1.61	1.01	0.08	0.09	18.24	0.16	24.69	18.95
CD (0.05)	556.10*	1.20	3.56*	2.32	2.033	0.172	0.190	36.482	0.328	49.386	37.908

*Significant at P=0.05; **Significant at P=0.01

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Combining Ability for Seed and Fruit Quality Traits using Line x Tester Analysis in Muskmelon (*Cucumis melo* L.)

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ABSTRACT

Muskmelon (*Cucumis melo* L.) five female lines and twelve testers were used to produce sixty F_1 hybrids using line x tester design. Four economic characters fruit weight, fruit diameter, cavity size and total soluble solids were analysed along with seed quality traits. The analysis of variance indicated significant variability among all the genotypes for all the traits except for TSS. The combining ability analysis revealed that general combining ability effects and specific combining ability effects were significant for fruit weight and fruit diameter. Among cross combinations, L-3 x T-11, L-3 x T-12 and L-5 x T-1exhibited maximum specific combining ability for fruit weight and diameter traits and these hybrid combinations were also found statistically superior over commercial check.

Keywords : Muskmelon, Lines, Testers, Combining ability

MUSKMELON, a member of genus *Cucumis* and family Cucurbitaceae is grown in temperate, sub-tropical and tropical regions of the world. It's short duration, high production potential and sweet taste provide a commercial and dessert fruit signature. It is a rich source of dietary fibre, vitamins and minerals like calcium, phosphrous and iron (Pitrat, 2008). It is enormously good for health as it is rich in ascorbic acid, carotene, folic acid and potassium as well as a number of other health bioactive compounds (Lester and Hodges, 2008). It is having magical health benefits therefore it is considered as a 'wholesome food'.

Muskmelon is cultivated on 1.2 million ha area with 29.5 million MT production with productivity of 24.9 tonnes ha^{-1}. China is being the largest producer with 50.04 per cent share followed by Turkey (5.76%), Iran (4.98%), Egypt (3.54%) and India (3.49%). In India, it is cultivated on 47,000 ha with 8,78,000 MT production with productivity of 20 tonnes ha^{-1} (Anonymous, 2017). It is extensively cultivated in hot and dry areas of Uttar Pradesh, Punjab, Rajasthan, Madhya Pradesh, Bihar and Karnataka.

The art of hybridisation came into existence along with heterosis. Hybrid vigour was first reported by Koelreuter (1763). In vegetables the phenomenon has been exploited in many crops and large number of hybrids has been released for commercial cultivation, along with improvement in yield, biotic and abiotic stress. Hybrid cultivation is increasing day by day because of hybrid development techniques. In muskmelon, hybrids are preferred over varieties due to their early maturity, high yield potential, superior quality and high input efficiency (Banga and Banga, 2000). Additionally, the development of F_1 hybrids in muskmelon is quite easy due to their andromonoecious nature. Therefore, selection of parents for the hybrids possessing desirable traits is most decisive and crucial step. Generally, parents are selected on basis of *per se* performance, but due to various gene combinations may does not stand true.

The extent of heterosis over mid parent, better parent and standard checks varies across the cross combinations for fruit and seed quality traits. Increased yield being the ultimate objective in any of crop breeding programme; hence positive and significant heterosis for fruit traits is always required.

MATERIAL AND METHODS

The present investigations were conducted during 2019- 2020 in the Research and Development station

of Orbi Seeds International Pvt. Ltd., Bangalore. The experimental materials comprised five inbred lines, twelve testers and 1 standard check. The crosses were made during *rabi* season of 2019. The hermaphrodite flowers from the designated female lines were emasculated one day before opening of the flowers during evening hours, emasculated flowers were covered at bud stage with white parchment/ butter paper bags after removing anthers to avoid out-crossing. Male flower buds which were about to open the next day morning were removed and covered in a moist cloth and stored. The emasculated flowers were used for crossing in the next morning. The male flowers collected on the previous day evening were removed from moist cloth and emasculated flowers were pollinated with the pollens of the desired freshly opened male flowers. After pollination, each pollinated flower was tagged and again covered with parchment paper bag to prevent cross contamination.

Simultaneously each parent was selfed. Selfing was done by bagging the hermaphrodite flowers in the evening and these were pollinated by taking pollens from covered male flowers of the same plant and tagged with different colour thread to avoid confusion while harvesting.

F_1 seeds were collected from the female plants after the fruits reaches maturity. They were kept for overnight for fermentation, washed the next morning and dried to 8-10 per cent moisture levels.

Nursery was prepared by sowing the F_1 seeds of each entry in portrays and kept covered with polythene cover to protect the emerging seedlings from low temperatures. When the seedlings attained two to three leaf stage, irrigation was withheld for one day prior to transplanting to harden the seedlings. The seedlings were then transplanted in the evening hours in the experimental field after removing from portrays at Sira (Tumkur Dist.) location during Summer 2020 in RBD with two replications with the spacing of 45cm x 2m. Since the location is suitable for evaluating the hybrids. Twelve plants from each entry transplanted under each replication.

TABLE 1

List of lines and testers used for the study

Lines	Code	Testers	Code
ORBI-MG-1	L-1	ORBI-T1	T-1
ORBI-MG-2	L-2	ORBI-T2	T-2
ORBI-MG-3	L-3	ORBI-T3	T-3
ORBI-MG-4	L-4	ORBI-T4	T-4
ORBI-MG-5	L-5	ORBI-T5	T-5
		ORBI-T6	T-6
		ORBI-T7	T-7
		ORBI-T8	T-8
		ORBI-T9	T-9
		ORBI-T10	T-10
		ORBI-T11	T-11
		ORBI-T12	T-12

Data were recorded on five plants in each replication and analysed using line x tester analysis by Kempthorne (1957) using WINDOSTAT *ver* 9.1 at the Department of Genetics and Plant Breeding, UAS, GKVK, Bengaluru. Economic heterosis was estimated over a check Akany from Bhalsar Seeds International Pvt. Ltd. for fruit weight (g), fruit diameter (cm), cavity size (cm) and total soluble solids (TSS °Brix), Germination per cent, Shoot length (cm), Root Length (cm), Seedling vigour index-I and Seedling vigour index-II.

RESULTS AND DISCUSSION

Success of a breeding programme rests upon utilization of variability available among genotypes (parental lines) and its progeny for traits of importance. Variances due to genotypes (parents and hybrids) were significant for all the traits except total soluble solids. The mean sum of squares due to parents versus crosses was highly significant for yield attributes *viz.,* fruit diameter and average single fruit weight except for total soluble solids and cavity size (Table 2) Similar results were seen by Kamdi *et al.* (2011) in sorghum for grain yield. As evidenced by the significance of mean sum of squares due to crosses, the significant differences among the parental genotypes resulted in crosses that were also

TABLE 2
Analysis of variance for combining ability of seed and fruit quality traits

Source of variation	Degrees of freedom	Fruit weight (g)	Fruit cavity size (cm)	Fruit diameter (cm)	TSS (p Brix)	Germination (%)	Shoot Length (cm)	Root length (cm)	SVI-I	SVI-II
Replication	1	8483.43	3.24	7.70	20.36 *	3.14	0.001	0.02	2076.93	3507.00
Genotypes	76	364916.088 **	3.04 **	15.44 **	6.00	30.93 **	1.39 **	1.41 **	54196.65 **	32189.26 **
Lines (5) + Testers (12)	16	40779.466	0.66	0.21	0.75	7.61 **	0.33 **	0.34 **	10374.72 **	6698.22 **
Lines	4	59644.85	0.30	0.12	0.35	3.15	0.49 **	0.47 **	9156.22 **	2177.60 *
Testers	11	2721.37	0.65	0.25	0.95	9.92 **	0.18 **	0.20 **	8190.63 **	1296.04
Lines vs Testers	1	383956.94	2.18	0.24	0.14	0.03	1.28 **	1.43 **	39273.82 **	84202.77 **
Parents vs Crosses	1	7038007.89 **	2.67	321.21 **	1.24	186.80 **	32.95 **	33.23 **	1438302.59 **	1841805.50**
Crosses	59	339714.29 **	3.69 *	14.38 **	7.51	34.61 **	1.14 **	1.16 **	477937.7 **	28866.5 **
Line effect	4	2075815.44 **	23.49 **	78.33 **	5.67	208.40 **	15.87 **	16.11 **	8171.28	11983.26 *
Tester effect	11	101856.50	2.35	2.63	3.96	21.15	0.07	0.05	11659.37 **	5684.70 **
Line x Tester effect	44	241351.36	2.23	11.51 *	8.57 *	22.18 **	0.07 **	0.08 **	477937.7 **	28866.5 **
Error	76	131202.32	1.63	5.09	4.32	2.06	0.01	0.01	1218.29	717.79
Total	153	246493.35	2.34	10.24	5.26	16.41	0.70	0.71	27539.95	16368.91

*Significant at P=0.05; **Significant at P=0.01

significantly different from each other. This was reflected by the presence of average heterosis as evidenced by the significance of parents versus crosses with single degree of freedom. The findings are consistent with the findings of Gurav *et al*. (2000).

The variance due to lines and their interaction was significant for majority of the characters according to the analysis of variance for combining ability. Lines had significant effect on all the characters studied except for TSS and seedling dry weight. Kumar and Gowda (2016) recorded similar findings in tomato for fruit shelf life.

As such testers had no effect on the fruit quality traits studied but had significant effect on seed quality parameters except on seedling vigour-II. Mean sum of squares due to lines and lines x tester interaction were found significant for most of traits studied indicating both GCA and SCA variance to be equally cardinal in the inheritance of all the characters under investigation.

The general combining ability effects of lines and testers are presented in the Table 3. Identification of parents based on *per se* performance may not be reliable to make heterotic hybrids, GCA of parents for a particular trait would reflect in SCA of a specific cross combination due its interactive effect. Hence selection of line/ tester based on its GCA effect has greater importance in planning a breeding programme.

Fruit yield being a complex trait, expression of this depends upon number of other contributing characters like fruit weight and fruit diameter. For these traits line-4 exhibited significant effect on fruit weight and fruit diameter which in turn results in increased yield. Testers as such had no significant effect on the fruit yield characters. The findings are in agreement with Lal and Kaur (2002).

Line-1 had negative significant effect on cavity size which is important for smaller cavity in hybrid which is preferable by the consumers and also had significant effect on germination percentage of seed. Tester-1 had significant negative effect on cavity size (-1.38) which is preferable. Tester-1 and line-2 had

TABLE 3

General combining ability effects of lines and testers (parents) for seed and fruit quality traits in Muskmelon

Lines	Fruit weight (grams)	Cavity Size (cm)	Fruit Diameter (cm)	TSS (p Brix)	Germination (%)	Shoot Length (cm)	Root length (cm)	SVI-I	SVI-I
Line-1	-388.17 **	-1.57 **	-1.90 **	-0.20	4.86 **	-0.63 **	-0.63 **	-25.78 **	32.67 **
Line-2	249.65 **	-0.089 **	1.29 **	0.34	0.40	1.20 **	1.21 **	215.32 **	40.47 **
Line-3	-181.13 **	-0.33	-1.94 **	-0.40	-1.71 **	0.48 **	0.49 **	51.38 **	-38.15 **
Line-4	316.45 **	0.50	1.87 **	-0.40	-0.88 **	-0.49 **	-0.49 **	-98.48 **	-13.21 *
Line-5	3.2	0.51	0.67	0.67	-2.67 **	-0.56 **	-0.57 **	-142.44 **	-21.78 **
SEm =	82.43	0.28	0.52	0.46	0.29	0.02	0.02	7.12	5.46
CD at 95%	164.95	0.57	1.04	0.93	0.58	0.04	0.05	14.25	10.94
Testers									
Tester-1	-18.68	-1.38 **	-1.08	-1.28	0.59	0.10 **	0.08 *	23.72 *	32.73 **
Tester-2	-84.98	-0.14	0.49	0.11	1.89 **	0.06	0.08	48.43 **	9.09
Tester-3	-114.98	-0.11	0.16	-0.38	-0.008	0.05	0.05	9.92	-32.54 **
Tester-4	125.41	0.12	0.37	-0.28	-0.30	0.06	0.05	4.99	48.95 **
Tester-5	179.41	-0.04	0.72	-0.08	-0.04	-0.02	-0.01	-10.21	2.77
Tester-6	-111.48	-0.08	-0.03	-0.38	-1.70 **	0.02	0.002	-29.69 **	-19.14 *
Tester-7	-130.38	0.02	-0.42	-0.08	-1.90 **	0.05	0.03	-25.63 *	-59.29 **
Tester-8	-2.7	0.41	0.22	-0.28	-1.60 **	-0.11 **	-0.08 *	-44.02 **	-32.53 **
Tester-9	40.71	0.17	0.34	0.21	-0.05	0.04	0.04	-2.23	20.29 *
Tester-10	109.21	0.34	-0.16	0.51	2.59 **	-0.006	-0.02	42.84 **	25.90 **
Tester-11	15.91	0.50	-0.63	0.81	-0.30	-0.10 **	-0.09 *	-22.65 *	-33.69 **
Tester-12	-7.38	0.18	0.06	1.11	1.69 **	-0.15 **	-0.13 **	4.52	37.48 **
SEm =	127.71	0.44	0.80	0.72	0.45	0.03	0.04	11.03	8.47
CD at 95%	255.15	0.89	1.61	1.44	0.90	0.07	0.08	22.08	16.95

*Significant at P=0.05; **Significant at P=0.01

significant effect on all the seed quality parameters studied except for germination percentage. Tester-10 and Tester-12 had significant effect on germination percentage trait. This indicates that though some parents are inferior, interaction among the lines and testers has contributing for the crosses to perform superiorly. It is appealing to note that line-2 is most promising for fruit weight and fruit diameter. The similar results were reported by Al-araby (2004) and Choudhary *et al*. (2006) in Muskmelon.

The specific combining ability effects of top performing crosses are presented in Table 4. Out of sixty crosses which five cross combinations found to be significant and exhibited significant SCA effects in the desirable direction. The cross 1L x 4T was the best specific combination for fruit cavity (negative effect) and positive SCA effect for seedling vigour index-I and seedling vigour index-II.

The crosses 5L x 1T and 3L x 12T found to be significant in desirable direction for fruit weight and fruit diameter. The cross combinations 1L x 5T and 2L x 1T was found significant for TSS.

Few hybrids were result of cross between either one prominent and one poor combiner or from two poor combiners. The high prevalence of non-additive gene action in these hybrids suggested that once the beneficial genes were to be identified, a hybrid development programme may improve even better. To take the advantage of this form of gene activity, the best breeding activity to accumulate favorable genes through reciprocal recurrent selection. These results are in comparison with findings of aravindakumar *et al.* (2005).

It was observed that the cross combination 3L x 11T, 3L x 12T and 5L x 1T had significantly higher SCA values for fruit weight and fruit diameter traits. Cross

TABLE 4

Estimates of specific combining ability effects in top performing hybrids for seed and fruit quality traits in muskmelon

Crosses	Fruit weight (g)	Fruit cavity size (cm)	Fruit diameter (cm)	TSS (° Brix)	Germination (%)	Shoot Length (cm)	Root length (cm)	SVI-I	SVI-I
1L x 4T	-390.52	-4.40 **	-7.01 **	-8.30 **	5.43 **	0.18 *	0.12	120.75 **	84.03 **
1L x 5T	56.37	0.25	1.98	3.00 *	-2.46 *	-0.02	0.04	-41.13	-30.29
2L x 1T	75.14	-0.12	-0.35	3.65 *	-7.5	-0.30	-0.25	-197.48	-150.24
3L x 12T	1171.33 **	1.46	6.13 **	-1.19	-0.98	-0.21	-0.21	-52.34	-7.36
5L x 1T	745.13 **	0.53	4.34 **	-0.49	2.57 *	-0.02	-0.07	38.08	43.91 *
SEm ±	256.12	0.90	1.59	1.47	1.01	0.08	0.09	24.69	18.95
CD (0.05)	512.50	1.80	3.19	2.94	2.03	0.17	0.190	49.38	37.90

*Significant at P=0.05; **Significant at P=0.01

combination of 3L x 1T had higher sca value for fruit cavity size trait, similar studies have been reported by Munshi and Verma (1997) and Gurav *et al.,* (2000). Total soluble solids trait was significant for crosses 1L x 4T, 1L x 5T and 2L x 1T, similar effects were reported by Liou *et al.,* (1995).

Heterosis is the manifestation of hybrid vigour. The heterotic effect of hybrids is due to cumulative effect of divergent alleles from two contrasting parents. The present investigation involving seventeen parents (five lines and twelve testers) and their sixty hybrids were evaluated to determine the magnitude of heterosis over parental mean, better parent and standard check hybrid (Akany). Inclusion of a commercial hybrid as a standard check is desirable over a variety, as increase in yield over a prevailing hybrid that would enable detecting hybrids for large scale cultivation aiming at increased productivity.

Fruit weight and fruit diameter are important traits having a positive association with fruit yield. The highest significant positive heterosis for fruit weight and fruit diameter was recorded by 4L X 4T (182.13%), 5L X 1T (93.38%) for mid-parent heterosis, respectively.

Highest significant positive heterosis for fruit weight and fruit diameter was recorded by 5L X 1T (148.58%) and 4L X 8T (86.96%) for better parent heterosis. A large number of crosses showed the significant

TABLE 5

Estimates heterosis for fruit and seed quality traits in muskmelon

Characters	Mid parent heterosis		Better parent heterosis		Standard heterosis	
Fruit weight (g)	4L X 4T	182.13 **	5L X 1T	148.58 **	3L X 11T	121.15 **
Fruit cavity size (cm)	1L X 1T	-151.58 *	1L X 1T	-149.00 *	1L X 1T	-157.51 *
Fruit diameter (cm)	5L X 1T	93.38 **	4L X 8T	86.96 **	4L X 8T	72.00 **
TSS (p Brix)	5L X 12T	42.86 *	5L X 12T	38.89	4L X 11T	27.75
Germination (%)	1L X 1T	13.33 **	1L X 12T	11.90 **	1L X 4T	3.24 *
Shoot Length (cm)	2L X 11T	29.78 **	3L X 11T	23.18 **	2L X 11T	2.99 *
Root Length (cm)	2L X 11T	29.03 **	2L X 12T	37.37 **	2L X 11T	2.94 *
Seedling vigour index-I	2L X 12T	36.40 **	2L X 2T	33.07 **	2L X 2T	-2.59
Seedling vigour index-II	1L X 4T	42.24 **	1L X 4T	34.61 **	1L X 4T	6.81 **

*Significant at P=0.05; **Significant at P=0.01

heterosis in desirable direction for the traits attributing to fruit yield. The highest standard heterosis was exhibited by 3L X 11T (121.55%) for fruit weight and 4L X 8T (72%) for fruit diameter.

The highest negative heterosis was exhibited by 1L X 1T for fruit cavity trait which contributes to smaller seed cavity in hybrid. It's important to note that line-1 was used in most of the crosses which exhibited significant heterosis, which is a good combiner for seed cavity size. Germination per cent, 1L X 1T (13.33%), 1L X 12T (11.90%) and 1L X 4T (3.24%) exhibited significant mid-parent, better-parent and standard heterosis, respectively. Shoot length an d root length hybrid 2L X 11T exhibited significantly higher mid-parent (29.78%, 29.03%), Standard heterosis (2.99%, 2.94%) and significantly higher better-parent heterosis was reported in 3L X 11T (23.18%) for shoot length and 2L X 12T reported higher better parent heterosis (37.37%).

Highest significant mid-parent (36.40%) heterosis for seedling vigour index-I was recorded by 2L X 12T and 2L X 2T recorded higher better parent and standard heterosis. 1L X 4T recorded significantly higher mid-parent (42.24 %), better-parent (34.61 %) and standard heterosis (6.81 %). Munshi and Verma (1997) and Mohanty and Mishra (1999) reported similar findings in muskmelon.

The present investigation revealed that three hybrids *viz*., 3L x 12T, 5L x 1T and 1L x 4T were found promising and they were significantly better with the commercial check for fruit weight and fruit diameter along with other important attributes. The results of the present investigation were based on single location evaluation. Thus, the above three F_1 hybrids could be tested over multi-locations to make the results more reliable and to identify stable hybrids.

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