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Assessment of genetic variability for fruit yield and quality traits in F₂ generation of intraspecific hybrids derived from muskmelon and Mangalore melon

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Abstract

The evaluation of F₂ population of three intraspecific crosses (Cross-I Haramadhu X MS-78, cross- II Madhuras X MS-79 and cross- III Arka Siri X SS-17) was carried out at college of Horticulture Sirsi during *Kharif* 2020. The study indicated that considerable variability observed for all characters studied. More variability was observed for vine length, average fruit weight, no. of fruits per vine, fruit yield per vine, flesh thickness and shelf-life. The high phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), and heritability coupled with genetic advance over mean observed for fruit yield per vine, average fruit weight, no. of fruits per vine, fruit length, fruit shape index, peduncle length in all the crosses. It indicates much scope for improvement of these characters through direct and indirect selection.

Keywords: F₂ generation, genetic variability, intraspecific hybrid

Introduction

Cucumis melo L. (2n=2x=24) is an important horticultural crop across the world. Africa has been generally regarded as the centre of origin of *C. melo*, while India is designated as centre of diversification. Muskmelon is one of the most economically important cucurbits, cultivated in many tropical, subtropical and temperate regions and it prefers hot and dry climatic conditions and hence well suited for Indian sub-tropical conditions and across the range of soils. India is the fifth leading country in melon production, with 1346 million tons of melon grown (Anonymous, 2022) [3] in 0.69 mha. Area Uttar Pradesh stands first in production with an annual production of 584.33 metric tonnes contributing about 56.52 percent followed by Andhra Pradesh, Punjab, Madhya Pradesh and Haryana. While Karnataka stands 8th position in muskmelon production.

The uses of these Melons are extremely diverse, depending on the type of fruit (Akashi *et al.*, 2002) [2]. However, its poor yield and susceptibility to fruit fly and Downey mildew and also the muskmelon fruits are highly perishable and they don't find a ready market and deteriorate fast because of poor shelf life. Most of the muskmelon varieties are climacteric and have shelf life of 10-15 days and the fruit deteriorates with transient rise in respiration rate and autocatalytic ethylene production.

On the contrary, Culinary melons [*Cucumis melo* var. *conomon acidulous* Thunberg; (2n = 2x = 24)], popularly known as Mangalore melons which are grown in coastal regions of South Indian has possessed an average shelf life of 150 days (Shet *et al.*, 2022) [32]. It is a culinary melon, mostly used as vegetable is highly appreciated by consumers for its unique taste, nutritive and medicinal value and long shelf-life. It's a short duration crop with high production potential, well suited for sequential cropping after the harvest of rice in rainfed, irrigated rice fallows during the Late *Kharif* and summer seasons.

Encouragingly, both muskmelon and Mangalore melon have the same chromosome numbers and are readily crossable to each other (Subha *et al.*, 1986) [34], hence a great opportunity to utilise these cross combinations to enhance the shelf life of muskmelon. However, Mangalore melons are non-dessert types characterised by low sweetness, unacceptable flesh colour and flavour and other undesirable agronomic traits (Manohar and Murthy 2012) [20].

Genetic variability is an essential requirement for any melon crop improvement programme. To begin breeding activities breeder should have a large number of variable populations.

In the process of improvement desirable plants are continuously selected from a genetically variable population. Fruit yield is the most important economic character in any crop. Other supporting characters influencing the fruit yield and yield itself are governed by polygenes and are quantitatively inherited (Hayes *et al.*, 1955) [12]. Since the selection is based on phenotypic observations their reflection on genotypic value may not hold good unless observation on quantitative traits is subjected and interpreted according to statistical procedures as fruit yield in culinary melon is much influenced by environmental factors. Therefore, parameters like mean, range, and coefficient, phenotypic and genotypic variation for different characters in intraspecific hybrids F₂ segregating generation of melon have been computed to draw some valid inferences from the three F₂ generation in the present investigation.

Exploitation of variability is the prime step in any plant breeding programme. Therefore, knowledge about genetic variability is a valuable adjunct to effective selection for improving yield. Estimating phenotypic and genotypic variation quantifies the variability within a set of breeding materials about its essential characteristics. Heritability and genetic advance reveal the quantum of improvement possible through selection (Hayes *et al.*, 1955) [12].

Segregating generation is a perfect generation which have high segregation and recombination for imposing selection (Thirugnanakumar *et al.*, 2011) [35]. Genetic variability is a prerequisite for successful selection of superior progenies from segregating generations for further selection. The genetics of the traits can be better understood using third and fourth degree statistics *i.e.* skewness and kurtosis in segregating generations (Savitha and Ushakumari, 2015) [29]. Hence, the present study was conducted to assess the variability, frequency distribution for yield and yield component traits to identify a superior segregants in F₂ generation of intraspecific hybrids derived from Muskmelon and Mangalore melon.

Materials and Method

The study was conducted during the late *Kharif* 2020 at the Department of Biotechnology and Crop Improvement, College of Horticulture, Sirsi, Karnataka, India. The material for the present study comprised of the F₂ generation of three intraspecific crosses (Haramadhu X MS-78 (cross I), Madhuras X MS-79 (cross II) and Arka Siri X SS-17 (cross III) developed under UHSB-PNASF project utilising Muskmelon and Mangalore melon were grown separately along with respective parents by maintaining the spacing of 60 cm vine to vine and 2 m row to row. All the recommended agronomic practices of melon were followed to raise a good healthy crop. Drip irrigation and mulching system were adopted to conserve soil moisture and control weeds. Plant protection measures were taken to achieve healthy growth of vines. Observations were recorded on all individual vines in F₂ populations of three crosses along with parents for following quantitative traits *viz.* Vine length (cm), Days to first harvest, Fruit length (cm), Fruit width (cm), Fruit shape Index, Avg. fruit weight (g), No. of fruits per vine, Hundred seed weight (g), No. of seeds per fruit, Peduncle length (cm), Flesh thickness (cm), TSS (^obrix), Seed cavity length (cm), Seed cavity width (cm), Shelf life (days) and Fruit yield per vine (g). The genetic parameters were estimated by using the formula suggested by Burton (1952) [7] and skewness and

curtsies by STATISTICA software.

Results and Discussion

Genetic variability for growth, yield and quality traits in the F₂ population

The F₂ population of three intraspecific crosses (Cross-I Haramadhu X MS-78, cross- II Madhuras X MS-79 and cross- III Arka Siri X SS-17) exhibited considerable variability in respect of all characters studied (Table 1). More variability was observed for vine length, average fruit weight, number of fruits per vine, fruit yield per vine, flesh thickness and shelf-life. It indicates much scope for improvement of these characters through direct and indirect selection. These results are in accordance with Gichimu *et al.* (2008) [10], Ohashi *et al.* (2009) [24], Babu (2013) [5], Ganiger *et al.* (2014) [9], Kamagoud *et al.* (2018) [16], Shah *et al.* (2018) [30], Singh and Kandaswamy (2020) [31], Kalgudi *et al.* (2021) [15] and Kumbar *et al.* (2021) [18].

Coefficient of skewness and kurtosis in F₂ segregating population for three crosses

Studying distributional characteristics such coefficients of skewness (a third degree statistic) and kurtosis (a fourth-degree statistic) might reveal information about the kind of gene action and the number of genes that regulate a trait, respectively (Robson, 1956) [27]. A characteristic's skewed distribution, in general, indicates that the trait is under the control of non-additive gene activity, particularly epistasis, and is impacted by environmental factors (Pooni *et al.*, 1977; Kimberg and Bingham., 1998 and Roy., 2000) [25, 17, 28].

Skewed distribution of traits suggests dominant genes influencing the characteristic, regardless of whether those genes have an augmenting or inhibitory influence on the trait's expression. Overall, the F₂ generation distribution pattern pointed to dominance and dominance based epistasis as the main causes of the considerable variance and asymmetrical distribution of the preponderance of the characteristics examined in the current study.

Fewer and more genes regulated features with leptokurtic and platykurtic distributions, respectively. Kurtosis is negative or near to zero when there are no gene interactions and positive when there are present (Pooni *et al.*, 1977 [25] and Choo and Reinbergs 1982) [8]. These results focuses on the proportion of genes and the kind of genetic control of several features in the F₂ generation of the intraspecific of Muskmelon and Mangalore melon.

The frequency distribution was positively skewed with platykurtic for fruit shape index (1.04, 7.41, 0.05 and 0.09, 64.82, -0.81), shelf-life (0.14, 0.14, 0.31 and -2.0, -2.0, -1.93) in all the crosses and fruit width (0.34, 0.27 and -0.36, -0.98), TSS (0.26, 0.52 and 0.65, -0.24) in both crosses cross I and II, average fruit weight (0.51, 1.52 and -0.73, 2.97) and hundred seed weight (0.47, 0.41 and -0.72, -0.48) in cross I and III, seed cavity width (0.43, 0.43 and), vine length (0.76, 1.28 and 0.87, 2.46) in both cross II and III. Rest of the traits restricted to individual crosses. Traits observed with positive skewness indicate that more proportion of individuals are present in low end of distribution but transgressive segregants were also obtained for these traits. Hence, selection of single plants from the transgressive segregants will improve the positively skewed traits. The results indicate that studies traits are governed by multiple genes with equal frequency with either increasing or decreasing effects with complementary epistasis

on trait expression. The results agree with the similar findings in tomato (Yogendra, 2011) [38].

The frequency distribution was negatively skewed with platykurtic for node at first male flower (-0.31, -0.24 and -1.93,-1.65), node at first female flower (-0.14, -0.40 and -0.55,-1.86), number of branches (-1.04, -0.76 and -0.92,-0.20) and fruit yield per vine (-0.78,-0.94 and 0.23, 0.16) in both the crosses I and II. Number of fruits per vine (14.13,-0.39 and 199.82, -0.25) and number of seeds per fruit (1.45,-0.67 and 5.08, 1.00) in both crosses II and III. Peduncle length in cross I (-0.20 and -0.53) and days to harvest (-0.27 and -1.29) in cross II but days to first female flower (-10.32, 13.82 and 131.32, 194.24) negatively skewed with leptokurtic. This kind of distribution of character will help to protect the individual plant from deleterious alleles arising from existing variability (Roy., 2000) [28]. The results are in agreement with the findings of Yogendra (2011) [38].

The frequency distribution was positively skewed with leptokurtic for sex ratio (13.52, 9.56,1.84 and 188.43,107.43,5.47), fruit length (0.16,7.33,1.29 and -0.45,79.66,3.58) in all three crosses, seed cavity length (3.69,4.86 and 27.58,47.41) in both crosses I and III, peduncle length (10.25,10.05 and 110.53,105.24), flesh thickness (12.87,1.60 and 176.83, 3.62) in both crosses II and III. Vine length (1.11 and 5.58) and seed cavity width (2.16 and 8.52) in cross I, average fruit weight (0.71 and 0.28), number of fruits per vine (14.13 and 199.82) and hundred seed weight (3.16 and 20.34) in cross II, fruit width (0.27 and -0.98), days to harvest (10.49 and 117.6), TSS (9.45 and 95.23), fruit yield per vine (1.51 and 11.89) in cross III. It reflects an intense selection from the available variability to maximize the genetic gain (Roy., 2000) [28].

Estimates of genetic variability parameters in F₂ population of three crosses.

The results of present investigation revealed that PCV values are higher than GCV for most of the traits, which indicates the greater influence of the environment. The influence of genetic variability, heritability and genetic advance on for various characters are discussed here. (Table 2).

The high phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability coupled with

genetic advance over mean observed in all the crosses viz., fruit yield per vine, average fruit weight, no. of fruits per vine, fruit length, fruit shape index, peduncle length. TSS, shelf-life in cross I exhibited and also in cross II sex ratio. It shows existence of broad genetic base, which would be accessible for subsequent selection. The results are accordance with Ahmed *et al.* (2004) [1], Tomar *et al.* (2008) [36] for fruit weight, Mehta *et al.* (2010) [22] in muskmelon for fruit yield and no. of fruits per vine, Ohashi *et al.* (2009) [24] in muskmelon for average fruit weight, Ibrahim (2013) in sweet melon for fruit weight, fruit length and fruit yield per vine Babu (2013) [5], Tyagaraj *et al.* (2014) [37], Shah *et al.* (2018) [30], Janghel *et al.*(2018) [14], Silpa *et al.* (2020) [33] and Kalgudi *et al.* (2021) [15].

High PCV coupled with moderate value of GCV observed in the traits such as node at first male flowers appearance in the segregating population of all the crosses and also in cross III Seed cavity width and no. branches indicating more environmental influence on the characters. These results are same as the results of Gichimu *et al.* (2008) [10], Babu (2013) [5], Lakshmi *et al.* (2017), Silpa *et al.* (2020) [33] and Kalgudi *et al.* (2021) [15].

Moderate PCV and GCV was observed in the traits such as flesh thickness in all the three crosses and also along with that trait seed cavity width, vine length, fruit width in cross I and hundred seed weight, TSS (cross II). Fruit width, peduncle length (cross III). Which indicates that there is moderate amount of variability was found in these traits it representing that the trait is controlled by both additive and non-additive gene actions. Hence, recurrent selection can be practiced for improvement. These results are same as the results of Gichimu *et al.* (2008) [10], Mehta *et al.*, (2010) [22] in muskmelon for node at first female flower, Babu (2013) [5], Lakshmi *et al.* (2017) and Silpa *et al.* (2020) [33].

Moderate PCV and low GCV with was observed for the traits such as fruit width (cross II). No. of seeds per fruit showed in cross III. It depicts the high magnitude of environment of on these traits. These findings similar with the Gichimu *et al.* (2008) [10], Mehta *et al.*, (2010) [22] in muskmelon for fruit width Babu (2013) [5], Shah *et al.* (2018) [30], Janghel *et al.* (2018) [14] and Silpa *et al.* (2020) [33].

Table 1: Mean, range, skewness and kurtosis values for growth and quality and yield traits in F₂ generations of the three crosses

Sl. No	Traits	Mean ± SE			Range						Skewness			Kurtosis		
		I	II	III	I		II		III		I	II	III	I	II	III
					Min	Max	Min	Max	Min	Max						
1	Vine length (cm)	181.29±1.74	142.73±0.82	148.99±0.81	126.00	222.00	123.00	172.00	108.00	178.00	1.11	0.76	1.28	5.58	0.87	2.46
2	Days to first harvest	72.92±0.17	76.56±0.09	77.77±0.09	67.00	79.00	74.00	82.00	70.00	81.00	0.45	0.27	10.49	-0.17	-1.29	117.63
3	Fruit length(cm)	11.88±0.26	9.12±0.19	10.01±0.19	5.00	20.40	4.50	17.5	4.50	19.50	0.16	7.33	1.29	-0.45	79.66	3.58
4	Fruit width(cm)	8.38±0.10	9.23±0.10	8.88±0.10	5.25	11.62	6.21	11.88	2.71	13.05	0.34	0.27	13.37	-0.36	-0.98	185.35
5	Fruit shape Index	1.42±0.03	0.99±0.02	1.13±0.02	0.71	2.73	0.54	2.24	0.63	3.29	1.04	7.41	0.05	0.09	64.82	-0.81
6	Avg. fruit weight (g)	527.07±20.25	457.04±13.30	481.93±13.28	85.00	1428.00	182	1013	124.	1417	0.51	0.71	1.52	-0.73	0.28	2.97
7	No. of fruits per vine	2.38±0.04	2.63±0.08	2.69±0.03	1.00	4.00	1.00	4.00	1.00	3.00	-0.20	14.13	-0.39	-0.77	199.82	-0.25
8	Hundred seed weight (g)	1.45±0.01	1.47±0.02	1.38±0.02	1.22	1.61	1.23	4.53	1.09	1.87	0.47	3.16	0.41	-0.72	20.34	-0.48
9	No. of seeds per fruit	471.38±2.86	469.74±2.27	318.10±2.22	328	535.00	386	516	272	391	-0.21	1.45	-0.67	0.50	5.08	1.002
10	Peduncle length (cm)	2.27±0.04	2.42±0.04	2.20±0.04	1.10	3.50	1.10	6.50	1.10	3.50	-0.20	10.25	10.05	-0.53	110.53	105.24
11	Flesh thickness (cm)	1.99±0.02	2.062±0.02	1.99±0.02	1.15	2.55	0.40	3.80	1.15	3.60	12.57	12.87	1.60	170.90	176.30	3.62
12	TSS (°brix)	4.61±0.08	5.19±0.06	8.98±0.06	2.20	7.30	3.60	6.50	3.20	12.20	0.26	0.52	9.45	0.65	-0.24	95.23
13	Seed cavity length (cm)	10.70±0.16	6.75±0.12	6.38±0.12	6.10	14.20	4.60	9.80	4.10	14.00	3.69	0.73	4.86	27.58	0.25	47.41
14	Seed cavity width (cm)	4.65±0.06	5.79±0.04	4.35±0.04	2.80	7.60	4.80	7.50	2.60	9.50	2.16	0.43	0.43	8.52	-0.46	-0.31
15	Shelf life (days)	20.09±0.50	16.45±0.35	29.65±0.35	10.00	40.00	10.00	32.00	10.00	48.00	0.14	0.14	0.31	-2.00	-2.00	-1.93
16	Fruit yield per vine (g)	1238.85±33.98	1173.42±47.49	1280.76±12.17	112.00	4048.00	182	3472	180	1417	-0.78	-0.94	1.51	-0.23	0.16	11.89

I- Haramadhu X MS-78

II- Madhuras X MS-79

III - Arka Siri X SS-17

Table 2: Estimates of genetic parameters for growth and quality and yield traits in F₂ segregating generations of three crosses

Sl. No	Traits	Mean ± SE			PCV (%)			GCV (%)			h ² bs (%)			GAM (%)		
		I	II	III	I	II	III	I	II	III	I	II	III	I	II	III
1	Vine length(cm)	181.29±1.74	142.73±0.82	148.99±0.81	13.66	8.20	7.48	13.38	7.62	6.60	95.98	86.36	77.80	27.00	14.58	11.98
2	Days to harvest	72.92±0.17	76.56±0.09	77.77±0.09	3.31	1.62	2.84	2.83	1.22	2.64	73.27	56.70	86.32	4.99	1.89	5.05
3	Fruit length(cm)	11.88±0.26	9.12±0.19	10.01±0.19	31.12	28.86	29.28	28.20	25.14	26.50	82.14	75.91	81.89	52.65	45.12	49.40
4	Fruit width(cm)	8.38±0.10	9.23±0.10	8.88±0.10	16.97	15.07	16.83	14.67	3.27	14.63	74.66	4.71	75.61	26.11	1.46	26.21
5	Fruit shape Index	1.42±0.03	0.99±0.02	1.13±0.02	27.19	27.34	25.93	25.54	22.92	24.61	88.26	70.28	90.07	49.43	39.59	48.11
6	Avg. fruit weight (g)	527.07±20.25	457.04±13.30	453.76±13.28	54.75	41.46	50.44	54.03	37.28	47.20	97.39	80.86	87.57	109.80	69.06	90.99
7	No. of fruits per vine	2.38±0.04	2.63±0.08	1.40±0.03	44.38	41.49	39.27	39.70	37.40	35.14	79.99	81.26	80.09	73.14	69.45	64.79
8	Hundred seed weight (g)	1.45±0.01	1.47±0.02	1.38±0.02	7.02	16.99	6.56	6.81	16.29	5.42	94.01	91.82	68.18	13.60	32.15	9.22
9	No. of seeds per fruit	471.38±2.86	469.74±2.27	318.10±2.22	8.64	6.87	10.31	8.28	5.35	8.44	91.94	60.68	67.02	16.36	8.59	14.23
10	Peduncle length (cm)	2.268±0.04	2.42±0.04	2.20±0.04	25.54	25.34	19.97	22.77	21.37	17.65	79.47	71.12	78.09	41.81	37.13	32.12
11	Flesh thickness (cm)	1.99±0.02	2.062±0.02	1.99±0.02	15.09	14.99	16.03	15.04	12.73	14.38	99.38	72.10	80.48	30.89	22.27	26.57
12	TSS (°brix)	4.61±0.08	5.19±0.06	8.98±0.06	24.83	15.81	20.80	22.99	12.39	20.29	85.74	61.38	95.16	43.85	19.99	40.77
13	Seed cavity length (cm)	10.70±0.16	6.75±0.12	6.38±0.12	21.28	24.38	26.14	20.66	23.53	22.69	94.30	93.11	75.33	41.33	46.77	40.56
14	Seed cavity width (cm)	4.65±0.06	5.79±0.04	4.35±0.04	17.71	9.57	21.94	16.60	7.73	18.79	87.90	65.27	73.41	32.06	12.86	33.17
15	Shelf life (days)	20.09±0.50	16.45±0.35	29.65±0.35	36.23	30.07	29.29	35.30	22.59	23.97	94.97	56.43	67.00	70.87	34.95	40.42
16	Fruit yield per vine (g)	1238.85±33.00	1173.42±47.40	762.50±12.17	72.32	57.66	63.38	69.92	55.70	62.37	93.49	93.30	96.85	139.2	110.83	126.45

PCV- Phenotypic coefficient of variation, GCV-Genotypic coefficient of variation, h²- Heritability in broadsense, GAM- Genetic Advance over Mean I- Haramadhu X MS-78. II- Madhuras X MS-79 III- Arka Siri X SS-17

Low PCV and GCV was notice for the traits viz., days to first harvest in all three crosses and also hundred seed weight, no. of seeds per fruit in cross I, but in both cross II and III vine length showed low PCV and GCV. This suggested that these traits have a narrow genetic base and that variability must be developed for them by introduction, hybridization of divergent genotypes to recover transgressive segregants or mutation breeding. These, results are accordance with Gichimu *et al.* (2008) [10], Babu *et al.* (2013) [5], Singh and Kandaswamy (2020) [31] and Kalgudi *et al.* (2021) [15].

High estimates of heritability coupled with high values of GAM were observed for the characters viz., average fruit weight, seed cavity length, fruit yield per vine, fruit shape index, number of fruits per vine, fruit width, flesh thickness, peduncle length, fruit length in all the three crosses but seed cavity width and shelf-life, TSS in cross I and III. Vine length in cross I, hundred seed weight in the cross II. This indicates predominance of additive components for these traits and hence direct selection would be more effective in improving these traits. These, results are accordance with Gichimu *et al.* (2008) [10], Babu (2013) [5], Shah *et al.* (2018) [30], Janghel *et al.* (2018) [14] and Silpa *et al.* (2020) [33].

High heritability coupled with moderate GAM were observed for the traits viz., no. of seeds per fruit in cross I and III and vine length in both cross II and III. Hundred seed weight in cross I TSS and seed cavity width in cross II. Which, indicated that prevalence of non-additive components and there can be little response to selection and these traits can be exploited through heterosis breeding. The results are accordance with Ahmed *et al.* (2004) [1], Ohashi *et al.* (2009) [24], Babu (2013) [5], Tyagaraj *et al.* (2014) [37], Shah *et al.* (2018) [30], Janghel *et al.* (2018) [14], Silpa *et al.* (2020) [33] and Kalgudi *et al.* (2021) [15].

High heritability coupled with low GAM were observed for the days to harvest in both the crosses I and III and also no. of seeds per fruit in cross II and hundred seed weight in the cross III. These, findings elucidate prevalence of non-additive components and higher influence of environment on these traits and hence, selection will be quite difficult or ineffective. These, results are accordance with Aravindakumar *et al.* (2005), Bairagi *et al.* (2005), Gichimu *et al.* (2008) [10], Ningaraju *et al.* (2014) and Singh and Kandaswamy (2020) [31].

Moderate heritability with the high GAM was observed for

shelf-life in cross II. Moderate heritability coupled with low GAM were observed for the trait days to harvest in cross II. These findings reveal prevalence of non-additive components and more environment effect on these traits and hence, selection will be quite difficult or ineffective. Similar results were also observed by Aravindakumar *et al.* (2005), Bairagi *et al.* (2005), Gichimu *et al.* (2008) [10], Ningaraju *et al.* (2014) and Singh and Kandaswamy (2020) [31].

Similarly fruit width in cross III had low heritability coupled with low GAM. Which indicated limited scope for improving this character through direct selection. These results are in confirmation with the findings of Glala *et al.* (2002) [11], Ahmed *et al.* (2004) [1], Maqsood *et al.* (2004) [21], Gichimu *et al.* (2008) [10], Reddy *et al.* (2013), Janghel *et al.* (2018) [14] and Kamagoud *et al.* (2018) [16].

Conclusion

More variability was observed for vine length, average fruit weight, number of fruits per vine, fruit yield per vine, flesh thickness and shelf-life. It indicates much scope for improvement of these characters through direct and indirect selection. The high phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability coupled with genetic advance over mean observed for fruit yield per vine, average fruit weight, number of fruits per vine, fruit length, fruit shape index, peduncle length in all the crosses. It shows existence of broad genetic base, which would be accessible for subsequent selection.

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