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# Genetic variability, heritability and genetic advance of melons from different botanical groups (*Cucumis melo* L.)

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## Abstract

Genetic variability, broad sense heritability and genetic advance was determined in 41 melons accessions of different botanical groups including one wild relative anguria. The analysis of variance was done for 19 quantitative traits such as cotyledon length, cotyledon width, days to 1st pistillate flowering, ovary length, ovary width, days to first fruit harvest, fruit length, average fruit weight, flesh thickness, seed cavity, fruit diameter, blossom end scar, seed length, seed width, total soluble solids (TSS), pH and titratable acidity. All the traits showed highly significant difference at 5% level of significance. The phenotypic and genotypic co-efficient of variation were high for the quantitative traits such as cotyledon length, cotyledon width, ovary length, ovary width, number of fruits per vine, fruit length, average fruit weight, fruit yield per plant, flesh thickness, seed cavity, fruit diameter, blossom end scar, seed length, seed width, TSS and titratable acidity. Moderate GCV and PCV were observed for traits such as days to first female flowering, days to first fruit maturity and pH. The high broad sense heritability was coupled with high genetic advance as percent mean for cotyledon length, cotyledon width, days to first female flowering, ovary length, ovary width, number of fruits per vine,days to first fruit maturity, fruit length, average fruit weight, fruit yield per plant, flesh thickness, seed cavity, fruit diameter, blossom end scar, seed length, seed width, TSS, pH and titratable acidity.

**Keywords:** Heritability, melon, inter-botanical groups, GCV, PCV, genetic advance

## Introduction

Melon (*Cucumis melo* L., 2n=24) belongs to Cucurbitaceae family and cultivated worldwide for its diverse uses such as fruits, vegetables types are used for cooking, pickling and salad purpose, seeds and fragrant fruits. Knowledge about the presence of genetic variability for yield and yield component traits is essential for formulating efficient breeding programmes. Improvement of melons can be achieved only with prior knowledge of nature and magnitude of variability present among accessions, which aids in selection of trait. *Cucumis melo* L. is considered as diverse species of *Cucumis* genus (Whitaker and Davis 1962; Jeffrey, 1980; Kirkbride, 1993; Bates and Robinson, 1995) [11, 22, 8]. First attempt of subspecies classification was made by Jeffrey, 1980 [7] based on ovary pubescence. Later Kirkbride (1993) [11] classified melons into two subspecies *Cucumis melo* L. subsp. *melo*and *Cucumis melo* L. subsp. *agrestis*based on hypanthium hariness. Based on combination of characters 19 botanical groups classification was proposed by Pitrat (2016) [15] which is most accepted taxonomical classification till date. The present study provides insight into the genetic variability of yield and yield related traits in melon accessions of different botanical groups.

## Material and Methods

Forty one melon accessions from different botanical groups namely, *momordica*, *acidulous*, *chandalak*, *kachri*, *cantalopensis*, *flexosus*, *indicus* and *inodorous*, *callosus*, *agrestis* and unknown botanical group. A wild relative of melon *anguria* (*Cucumis anguria* commonly called as West Indian gherkin with chromosome number 2n = 24) was also included in the study. Seedlings were raised in portrays and transplanted to soil after 15 days after sowing. Details of the accessions used in the study are given in Table 1. The experiment was conducted in *rabi* 2018 under polyhouse condition at conducted at the Regional Horticultural Research and Extension Centre, Bengaluru. Paired row system of planting with raised beds with 45×60 cm spacing and Randomized Complete Block Design (RCBD) was employed. Observations were recorded for cotyledon length (cm), cotyledon width (cm), days to first pistillate flowering, ovary length (cm), ovary width (cm), days to first fruit maturity, number of fruits per vine, fruit length (cm), average fruit weight (kg), fruit yield per plant (kg), flesh thickness (cm), seed cavity (cm), fruit diameter (cm), blossom end scar (cm), seed length (cm) and seed width (cm) on five randomly selected plants for each treatment in each replication. Biochemical analysis was done for TSS, pH and titratable acidity under laboratory with two replications for each sample.

Analysis of variance for individual character was done on the basis of mean values as suggested by Panse and Sukhatme (1985) [14]. Genotypic and phenotypic coefficients of variation were computed according to Buston and Devane (1953) [2]. The genotypic and phenotypic coefficient of variation was categorized by Shivasubramanian and Menon (1973) [18] into three categories. Broad sense heritability was estimated as the ratio of genotypic variance to the phenotypic variance and was expressed in percentage (Falconer, 1981) [4]. Genetic advance and genetic advance as per cent mean of each character was worked out by adopting formula given by Johnson *et al*. (1955) [8].

**Table 1:** Description of melon (*Cucumis melo* L.) accessions of different botanical groups included in the study

| Sl. No. | Botonical group | Accessions | Source of germplasm | Cultivated/ Uncultivated | Use |
|---|---|---|---|---|---|
| 1 | *momordica* | Kekkarale | Shivamogga district, Karnataka | Cultivated | Ripen fruits consumed with jaggery |
| 2 | | Kekkarike | Hassan district, Karnataka | | |
| 3 | *acidulus* | Wild Melon | Arunachal Pradesh | | Ripen fruits for cooking and pickling |
| 4 | | Mekkekaayi | Bagalkot district, Karnataka | | |
| 5 | | Sambar savathe | Sirsi district, Karnataka | | Ripen fruits for cooking |
| 6 | | Yeresavathe | Darwad district, Karnataka | | Ripen fruits for cooking and immature for salad |
| 7 | | Magekaayi | Mangalore district, Karnataka | | |
| 8 | | Giriyaala | Gadag District, Karnataka | | |
| 9 | | Puttikaayi 41 | Bijapur district, Karnataka | Uncultivated /Weed | Ripen fruits consumed with jaggery |
| 10 | | PuttikaayiMavinahalli | | | |
| 11 | | PuttikaayiBijapur | | | |
| 12 | Intermidiate form of *acidulus* and *momordica* | Puttikaayi Indi | | | |
| 13 | *indicus* | Alpur Green | Kadapa, Andra Pradesh | Cultivated | Ripen fruits for table purpose |
| 14 | | Alpur Red | | | |
| 15 | | Ganjam | Davanagere district, Karnataka | | |
| 16 | | Banaspathre | | | |
| 17 | | IC321371 | NBPGR, New Delhi | | |
| 18 | *ameri* | Kadapa Local | Kadapa, Andra Pradesh | | |
| 19 | *cantalopensis* | Cantaloupe Canada | Canada | | |
| 20 | | F39 | USA | | |
| 21 | *flexosus* | Arka Sheetal | IIHR, Bengaluru Karnataka | | Immature fruits for salad |
| 22 | | Punjab Long | Punjab | | |
| 23 | *kachri* | Kachri | Rajasthan | Cultivated | Ripen fruits for cooking |
| 24 | | Budamekaayi | Tumkur district, Karnataka | Uncultivated /Weed | Not used |
| 25 | *inodorous* | Honeydew | Canada | Cultivated | Ripen fruits for table purpose |
| 26 | *callosus* | Small Melon | Rajasthan | Uncultivated /Weed | Not used |
| 27 | *agrestis* | Agrestis | | | |
| 28 | *chandalak* | Kashi Madhu | Uttar Pradesh | Cultivated | Ripen fruits for table purpose |
| 29 | | IC321334 | NBPGR, New Delhi | | |
| 30 | | IC321348 | | | |
| 31 | | Kotamballiminake | Chamarajanagar district, Karnataka | | |
| 32 | | IC321367 | NBPGR, New Delhi | | |
| 33 | | Pappusa | Kadapa, Andra Pradesh | | |
| 34 | | Sidoota | | | |
| 35 | | Sidoota | Davanagere district, Karnataka | | |
| 36 | | Karbooj | | | |
| 37 | | Minake | Maduvanahalli, Chamarajanagar district, Karnataka | | Ripen fruits for slicing and juice making |
| 38 | Intermidiate form of *chandalak* and *momordica* | Minake 1 | | | |
| 39 | | Minake 22 | | | |
| 40 | unknown | Sharabathanara | Kadapa, | | |

| | | | | | |
|---|---|---|---|---|---|
| | | | Andra Pradesh | | |
| 41* | *anguria* | Anguria | Bagalkot district, Karnataka | Uncultivated /Weed | |

* Anguria (*Cucumis anguria*, 2n = 24) is a wild relative taken as a reference genotype

## Results and Discussion

The analysis of variance for all the growth, fruit and yield traits indicated significant differences among the melon genotypes at one per cent level of significance (Table 4).

### Variability and other genetic parameters for growth, fruit and yield parameters

To understand the extent to which the observed variations are due to genetic factors, overall variability was partitioned into heritable and non-heritable components with the aid of genetic components such as mean, range, genotypic co-efficients of variation (GCV) and phenotypic co-efficients of variation (PCV), heritability and genetic advance over per cent mean. The results in respect of these characters for the 19 traits were estimated and presented in Table 5.

### Cotyledon length (cm)

Cotyledon length ranged from 0.75 cm (Wild melon) to 3.73 cm (Kadapa Local) with a mean of 2.32 cm. High PCV (28.72%) and GCV (28.44%) for cotyledon length were observed. High heritability (98%) coupled with high genetic advance as per cent mean (58.03%) was observed for this trait.

### Cotyledon width (cm)

Cotyledon width ranged from 0.42 cm in Wild melon to 2.26 cm in IC321334 with a mean value of 1.30 cm. PCV (26.85%) and GCV (26.63%) were found to be high for this trait. High heritability (99%) coupled with high genetic advance as per cent mean of 54.47 per cent was observed.

### Days to first pistillated / perfect/female flowering

Days to appearance of first pistillated flower was found to be highest in Anguria, a wild relative of *Cucumis melo* L. with 78.50 days followed by AlpurGeen (59.67 days) and lowest in Kachri of Rajasthan (36.25 days) with a mean of 49.68 days. Moderate PCV and GCV were observed with values of 15.42 per cent and 14.97 per cent, respectively. High heritability (94%) coupled with high genetic advance as per cent mean (29.91%) was observed for this trait.

### Ovary length (cm)

Mean ovary length of 1.77 cm was observed and it ranged from 0.55 cm to 3.11 cm in Anguria and Punjab long, respectively. Wild melon had an ovary length of 0.7 cm. PCV (35.82) and GCV (35.65) were found to be high. High heritability of 99 per cent coupled with high genetic advance as per cent mean (73.07%) was observed for this trait.

### Ovary width (cm)

Mean ovary width of 0.64 cm was observed and it ranged from 0.26 cm (Anguria) to 1.27 cm (Banaspathre). Both wild melon and small melon had an ovary width of 0.3 cm. High PCV (35.89%) and GCV (35.66%) with high heritability (99%) and genetic advance as per cent mean (72.99%) are noticed for this trait.

### Days to first fruit maturity

Days to first fruit maturity was found to be maximum in Anguria (108.50 days) followed by Honeydew melon (105.5 days) and minimum in Arka Sheetal (52.92 days) with a mean of 77.98 days. Moderate PCV (14.44%) and GCV (14.12%) were noticed with high heritability of 96 per cent and genetic advance as per cent mean of 28.43 per cent.

**Table 4:** Analysis of variance for growth, fruit traits, yield and selected biochemical components in melon genotypes

| Source of variation | Degrees of freedom | Mean sum of squares | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | | X1 | X2 | X3 | X4 | X5 | X6 | X7 | X8 | X9 | X10 |
| Genotype | 40 | 0.880*** | 0.242*** | 113.896*** | 0.796*** | 0.105*** | 248.080*** | 76.520*** | 119.728*** | 3.728*** | 5.221*** |
| Replication | 1 | 0.006 | 0.004 | 0.416 | 0.004 | 0.0004 | 0.625 | 0.149 | 3.782 | 0.003 | 0.001 |
| Error | 40 | 0.008 | 0.002 | 3.417 | 0.004 | 0.001 | 5.637 | 1.728 | 2.535 | 0.031 | 0.506 |
| CV (%) | | 3.956 | 3.193 | 3.721 | 3.528 | 4.043 | 3.045 | 22.738 | 11.423 | 15.843 | 28.716 |

| Source of variation | Degrees of freedom | Mean sum of squares | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| | | X11 | X12 | X13 | X14 | X15 | X16 | X17 | X18 | X19 |
| Genotype | 40 | 3.192*** | 6.063*** | 26.622*** | 6.397*** | 0.091*** | 0.016*** | 20.957*** | 1.588*** | 0.004*** |
| Replication | 1 | 0.069 | 0.171 | 0.059 | 0.016 | 0.008 | 0.0001 | 0.003 | 0.094 | 0.004 |
| Error | 40 | 0.066 | 0.207 | 0.437 | 0.116 | 0.006 | 0.0002 | 1.667 | 0.078 | 0.0001 |
| CV (%) | | 11.724 | 10.092 | 7.421 | 22.850 | 8.697 | 4.133 | 18.720 | 5.030 | 8.550 |

***= Significance at 1% level
X1= Cotyledon length (cm)
X2= Cotyledon width (cm)
X3= Days to 1st pistillate flowering
X4= Ovary length (cm)
X5= Ovary width (cm)
X6= Days to maturity
X7= Number of fruits per vine
X8= Fruit length (cm)
X9= Average fruit weight (kg)
X10= Fruit yield/plant (kg)
X11= Flesh thickness (cm)
X12= Seed cavity (cm)
X13= Fruit diameter (cm)
X14= Blossom end scar(cm)
X15= Seed length (cm)
X16= Seed width (cm)
X17=Total Soluble Solids (°B)
X18= pH
X19= Titratable acidity (%)

**Table 5:** Components of variance for melon genotypes for quantitative characters

| Character | Mean | Range | | PCV | GCV | h$^2$ (%) | GA | GAM |
|---|---|---|---|---|---|---|---|---|
| | | Minimum | Maximum | | | | | |
| Cotyledon length (cm) | 2.32 | 0.75 | 3.73 | 28.72 | 28.44 | 98 | 1.35 | 58.03 |
| Cotyledon width (cm) | 1.30 | 0.42 | 2.26 | 26.82 | 26.63 | 99 | 0.71 | 54.47 |
| Days to 1st pistillate flowering | 49.68 | 36.25 | 78.50 | 15.42 | 14.97 | 94 | 14.86 | 29.91 |
| Ovary length (cm) | 1.77 | 0.55 | 3.11 | 35.82 | 35.65 | 99 | 1.29 | 73.07 |
| Ovary width (cm) | 0.64 | 0.26 | 1.27 | 35.89 | 35.66 | 99 | 0.47 | 72.99 |
| Days to first fruit maturity | 77.98 | 52.92 | 108.50 | 14.44 | 14.12 | 96 | 22.17 | 28.43 |
| Number of fruits per vine | 5.78 | 1.00 | 22.50 | 108.21 | 105.79 | 96 | 12.32 | 213.06 |
| Fruit length (cm) | 13.94 | 3.55 | 31.38 | 56.10 | 54.92 | 96 | 15.44 | 110.77 |
| Average fruit weight (kg) | 1.12 | 0.02 | 5.86 | 122.77 | 121.74 | 98 | 2.78 | 248.69 |
| Fruit yield/plant (kg) | 2.48 | 0.41 | 6.79 | 68.31 | 61.98 | 82 | 2.87 | 115.85 |
| Flesh thickness (cm) | 2.20 | 0.18 | 6.00 | 58.07 | 56.88 | 96 | 2.52 | 114.75 |
| Seed cavity (cm) | 4.51 | 1.63 | 7.45 | 39.25 | 37.93 | 93 | 3.41 | 75.50 |
| Fruit diameter (cm) | 8.90 | 2.38 | 14.65 | 41.31 | 40.63 | 97 | 7.33 | 82.34 |
| Blossom end scar (cm) | 1.49 | 0.10 | 6.22 | 120.92 | 118.74 | 96 | 3.58 | 240.20 |
| Seed length (cm) | 0.89 | 0.38 | 1.17 | 24.83 | 23.26 | 88 | 0.40 | 44.88 |
| Seed width (cm) | 0.38 | 0.14 | 0.51 | 23.32 | 22.95 | 97 | 0.18 | 46.52 |
| Total Soluble solids (°B) | 6.90 | 3.15 | 13.00 | 48.77 | 45.03 | 85 | 5.91 | 85.65 |
| pH | 5.54 | 4.11 | 7.04 | 16.47 | 15.69 | 91 | 1.70 | 30.77 |
| Titratable acidity (%) | 0.20 | 0.16 | 0.36 | 23.95 | 22.38 | 87 | 0.09 | 43.06 |

PCV - Phenotypic co-efficient of variation GA - Genetic advance
GCV - Genotypic co-efficient of variation GAM - Genetic advance as per cent mean h$^2$ - Broad sense heritability

**Number of fruits per vine**

Maximum number of fruits per vine was noticed in Budamekaayi (22.50) and only one fruit per vine was observed in Kekkarle, Kekkarike, Sidoota and Karbooj genotypes with a mean of 5.78 fruits per vine. High PCV (108.21%) and GCV (105.79%) were recorded. High heritability (96%) was coupled with high genetic advance as per cent mean (213.06%) for this trait.

**Fruit length (cm)**

Fruit length was found to be maximum in Punjab long (31.38 cm) and minimum in Anguria (3.55 cm). Budamekayi had a fruit length of 4.34 cm. Mean fruit length was 13.94 cm. PCV (56.10%) and GCV (54.92%) were high with high heritability (96%) coupled with high genetic advance as per cent mean (110.77%).

**Average fruit weight (kg)**

Average fruit weight ranged from 0.02 kg (Budamekaayi) to 5.86 kg (Karbooj) with a mean value of 1.12 kg. High PCV (122.77%) and GCV (121.74%) were observed for this trait. High heritability of 98 per cent was coupled with high genetic advance as per cent mean (248.69%) for average fruit weight.

**Fruit yield per plant (kg)**

The fruit yield per plant ranged from 0.41 kg (Budamekaayi) to 6.79 kg (Ganjam) with a mean of 2.48 kg. PCV (68.31%) and GCV (61.98%) were high for this trait. High heritability of 82 per cent and high genetic advance as per cent mean of 115.85 per cent were observed for fruit yield.

**Flesh thickness (cm)**

Flesh thickness of melon genotypes ranged from 0.18 cm (Budamekaayi) to 6.00 cm (Magekaayi) with a mean value of 2.20 cm. PCV and GCV for flesh thickness were found to be high with values of 58.07 per cent and 56.88 per cent, respectively. High heritability (96%) with high genetic advance as per cent mean (114.75%) was noticed.

**Seed cavity (cm)**

The observed mean value for seed cavity was 4.51 cm and it ranged from 1.63 cm (Anguria) to 7.45 cm (Kadapa local). Yeresavathe had a seed cavity of 1.83cm. PCV of 39.25 per cent and GCV of 37.93 per cent were observed. High heritability (93%) with high genetic advance as per cent mean of 75.50 per cent was recorded.

**Fruit diameter (cm)**

Mean fruit diameter of 8.90 cm was noticed with maximum and minimum fruit diameter of 14.65 cm (Banaspathre) and 2.38 cm (Anguria), respectively. Budamekayi had a fruit diameter of 2.93 cm. High PCV (41.31%) and GCV (40.63%) were observed. High heritability (97%) was coupled with high genetic advance as per cent mean (82.34%) for fruit diameter.

**Blossom end scar (cm)**

Blossom end scar diameter ranged from 0.10 cm (Anguria, Agrestis, Budamekaayi, Giriyaala and Kekkarle) to 6.22 cm (IC321367). The PCV and GCV values were high for this trait with 120.92 per cent and 118.74 per cent, respectively. Heritability (96%) was high and it was coupled with high genetic advance as per cent mean (240.20%).

**Seed length (cm)**

The mean value for seed length observed was 0.89 cm and it ranged from 0.38 cm to 1.17 cm in Wild melon and IC321367, respectively. High PCV of 24.83 per cent and GCV of 23.26 per cent were noticed for seed length. High heritability of 88 per cent was coupled with high genetic advance as per cent mean (44.88%).

**Seed width (cm)**

The values for seed width ranged from 0.14 cm (Wild melon) to 0.51 cm (Sidoota) with a mean of 0.38 cm. PCV and GCV were found to be high with values of 23.32 per cent and 22.95 per cent, respectively. High heritability of 97 per cent was coupled with high genetic advance as per cent mean (46.52%).

### Total soluble solids (TSS) (°Brix)

Mean value for TSS observed was 6.90° B and it ranged from 3.15° B (Mekkekaayi) to 13° B (IC321367). PCV and GCV were found to be high with values of 48.77 per cent and 45.03per cent, respectively. High heritability (85%) was coupled with high genetic advance as per cent mean (85.65%).

### pH

pH values for melon genotypes ranged from 4.11 (Giriyaala) to 7.04 (Cantaloupe F39) with a mean pH of 5.54. Moderate PCV (16.47%) and GCV (15.68%) were observed. Heritability (91%) for this trait was found to be high and it was coupled with high genetic advance as per cent mean (30.77%).

### Titratable acidity (%)

Titratable acidity ranged from 0.16 per cent (Arka Sheetal, Punjab long, IC321371 and Agrestis) to 0.36 per cent (Smallmelon) with a mean value of 0.20%. High PCV and GCV values of 23.95 per cent and 22.38 per cent were obtained, respectively. High heritability of 87 per cent was coupled with high genetic advance as per cent mean (43.06%).

Melons exhibit large variation for flower and fruit traits. Traits namely high yield, early maturity, uniform fruit shape and size, quality of fruits are of high breeding value (Zalapa *et al*., 2006) [23]. In melon, economic traits such as fruit length, fruit weight, fruit yield, early maturity, flesh thickness and TSS are quantitatively inherited and affected by genotype, environment and genotype × environment interaction. Improvement of melons is possible by selection of cultivars with high genetic gain (Mohammadi *et al*., 2014) [13].

Knowledge about the presence of genetic variability for yield and yield component traits is essential for formulating efficient breeding programmes. Estimating the range of variation is the simplest way to determine variability present among genotypes. Determining the genetics of economic traits and components of variance is important for selection of traits to increase the economic value of the crop. Components of variance for melon genotypes for quantitative characters are presented in Table 6. Significant difference was observed for various traits.

The components of variance namely GCV, PCV, genetic advance, genetic advance mean as per cent and broad sense heritability among 41 genotypes were estimated. High GCV and PCV were observed for cotyledon length, cotyledon width, ovary length, ovary width, number of fruits per vine, fruit length, average fruit weight, fruit yield per plant, flesh thickness, seed cavity, fruit diameter, blossom end scar, seed length, seed width, TSS and titratable acidity. Estimated PCV was higher than GCV for all the traits, indicating that variance observed was not only by genotypes but also influenced by environment. If the difference observed is less it indicates the less influence of environment. Moderate GCV and PCV were observed for traits such as days to first female flowering, days to first fruit maturity and pH. Singh and Lal (2005) [19] recorded highest phenotypic coefficient of variation (PCV) for flesh thickness and the lowest for days to first fruit harvest. The maximum GCV was observed again for flesh thickness and the minimum for days to first fruit harvest in muskmelon. High PCV and GCV were also observed for number of fruits per vine and yield per vine by Torkadi *et al.* (2007) [21]; Tomar *et al.* (2008) [20]; Mehta *et al.* (2009) [12]; Ibrahim (2012) [5]; Choudhary *et al.* (2011) [3] and Sachin (2018) reported similar results in melon. High PCV and GCV were also observed for flesh thickness, ovary length, ovary width, fruit length, size of pistil scar, number of fruits per vine, yield per vine by Kavya (2017) [10]. Moderate PCV and GCV were observed for days to appearance of first female flower and days to first fruit harvest by Kavya (2017) [10] in $F_2$ individuals, Rakhi and Rajmony (2005) [16] in culinary melons, Choudary *et al*. (2011) [3] in melons.

Selection will be practiced based on the superior phenotypic performance of genotypes which in turn influenced by genetic makeup of the plant as well as environment. Estimating the heritability aids in selection of genotypes based on variation present among them. The large number of fixable additive genes will be present if the estimated heritability is high and selection for this trait is effective (Javanmard *et al*., 2018) [6]. In present study estimated broad sense heritability was high among all the traits and it was coupled with high genetic advance as per cent mean. It indicates that the genetic gain is more and selection for these traits is effective. The results are in accordance with those of studies by Kalloo *et al*. (1983) [9] who observed high heritability coupled with high genetic advance for fruit and yield traits among muskmelon genotypes. Singh and Lal (2005) [19] reported high heritability, genetic advance and high genetic advance at per cent mean for average fruit weight and moderate heritability coupled with high genetic advance as per cent mean for fruit yield per plant in muskmelon. Rakhi and Rajmony (2005) [16] reported high heritability for fruit length, fruit girth, 1000 seed weight, average fruit weight, keeping quality of fruit, flesh-cavity ratio and yield per plant. Tomar *et al.* (2008) [20] reported high heritability coupled with high genetic advance for average weight for fruit and fruit cavity, flesh thickness and number of fruits per vine. Low heritability and genetic advance was noticed for days to fruiting.

## Conclusion

Estimated PCV was higher than GCV for all the traits, indicating that variance observed was not only by genotypes but also influenced by environment. The difference observed was less it indicates the less influence of environment. Broad sense heritability was high for all the traits and it was coupled with high genetic advance as per cent mean which indicates that the selection for these traits will be effective and can be utilized in further crop improvement.

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