Analysis of variance components for quantitative traits in muskmelon (*Cucumis melo* L.)

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ABSTRACT

An experiment with different contributing charactersof 26 genotypes of muskmelon (Cucumis meloL.) was performed in a randomized block design with three replications during the Zaid season (Feb-May) of 2019, at Banaras Hindu University, Varanasi in order to understand the genetics of yield formation characteristics with yield enhancement potentials. Analysis of varian cerevealed the presence of significant differences among all genotypes for almost all the characters indicating that there is a plenty of room to improve the population for these traits. The range of variation was documented widest for the characters viz.; fruit weight (179.7 to 777.1 g), yield of fruit per plant (360.3 to 3109.5 g), pulp weight (107.0 to 557.2 g), and seeds per fruit (183.6 to 477.3). Genotypic coefficients of variation values were lower than phenotypic coefficients of variation for all characters.The fruit yield per plant revealed the highest phenotypic and genotypic coefficients of variation values followed by titratable acidity, pulp weight, total number of female flowers and seed weight. Also, fruit yield per plant, total number of female flowers, node to first female flower, total number of fruits, fruit weight, and total soluble solids had high estimates of heritability and high genetic advance as per cent of mean, suggesting that selection for these traits might be effective.

Key words: Genetic advance, genotype, genotypic coefficient of variation, heritability, phenotypic coefficient of variation.

INTRODUCTION

Muskmelon (*Cucumis melo* L.) is dicotyledonous annual veining fruit vegetable in the Cucurbitaceae family. Melons are classified as a polymorphic taxon because they have a wide range of biochemical, morphological, and physiological diversity. They are drought-tolerant Cucurbitaceae crop that grows in warm temperate, sub-tropical, and tropical climates. The melons grown in dry regions are sweeter and tastier than those of wet grown situations.The germplasm collections of muskmelon have not been extensively characterised in terms of their use for increasing production in general and improving fruit quality in particular. Because muskmelon is a cross-pollinated crop, plant architectural and fruit character variability among its population may be high. In India, a lack of improved varieties, as well as other production limitations, has contributed to low muskmelon yield and quality. That's why, better muskmelon varieties/hybrids that are adapted to certain agro-ecological environments and end uses are needed.

However, the germplasm of Indian muskmelon contains genes for distinctive characteristics like as fruit quality and tolerance to biotic and abiotic stimuli, which may be transmitted to current cultivars through hybridization.

The availability of desirable genetic diversity for the goal traits determines the effectiveness of conventional breeding (Ara *et al.*, 2009). So, plant breeders can use genetic resources to develop innovative plant gene combinations and crop varieties that are better adapted to the demands of various agricultural systems (Glaszmann *et al.*, 2010).Direct selection for yield, however, may not result in good crop improvement since yield is a complicated quantitative characteristic. As a result, genetic factors such as genotypic and phenotypic coefficients of variation, heritability, and genetic advancement must be calculated to partition observed variability into heritable and non-heritable components. Hence, a key pre-requisite for developing high-yielding variants for a systematic breeding effort in muskmelon is knowledge of genetic variability. Keeping in view all the above facts, the objective of this study

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was to estimate genetic variability, genetic advance and heritability for fruit yield and its component traits to predict the selection response.

MATERIALS AND METHODS

The investigation was carried out at Vegetables Research Farm of Banaras Hindu University, Varanasi, during Zaid season (Feb-May), of 2019. The farm is located at 25°15' North latitude and 83°03' East longitude, with an elevation of 129.23 metres above mean sea level. The experiment was performed in a randomized block designwith three replications. Seeds of 26 genotypes (GP-73, GP-150, RM-102, RM-43, Kazri, RM-101, GP-128(+), GP-105, Durgapur Kranti, MHY-3, MHY-5(+), GP-20, Pusa Madhuras, GP-176, Durgapur Madhu, GP-168, Golden Yellow, Durgapur Selection, RM-49, RM-50, VRMM-46, MMIIHR-653, Punjab Sunehri, MM-1, Kashi Madhu and VRM-4) were directly sown in the basins, with a row to row spacing of 1.5 m and plant to plant spacing of 0.5 m on 25th of February, 2019. In each replication, every germplasm was grown on 4 consecutive basins having at least ten plants in total. Standard packages of practices were followed to raise healthy and disease-pest free plant population. The observations on various characters were recorded on five randomly selected plants for days to first male flower, days to first female flower, node to first male flower, node to first female flower, petiole length (cm), leaf area (cm²), chlorophyll content (spad value), total number of male flowers, total number of female flowers, sex ratio (m/f), total no. of leaves, total no. of 1° branches, total no. of fruits, vine length (m), days to first fruit harvest, fruit weight (g), yield of fruit per plant (g), thickness of flesh (cm), fruit length (cm), fruit diameter (cm), pulp weight (g), seeds per fruit, seed weight (g), index seed weight (g), pulp to seed ratio , TSS (°B), ascorbic acid (mg/100g), titratable acidity (%), and phenol content (mg/g). TSS was measured by Abbe's Hand Refractometer (0-32 %), titratable acidity and ascorbic acid were determined by visual titration method given by Ranganna (1986).The analysis of variance was calculated individually according to standard statistical methods based on randomized block design for each character (Panse and Sukhatme, 1985). Analysis of variance

components, the genotypic (σ^2_g) and phenotypic (σ^2_p) variances were calculated according to the standard formula. The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) was calculated according to the formula suggested by Burton (1952) and Johnson *et al.* (1955) and it was classified as low (<10%), moderate (>10-20%) and high (>20%). Heritability values (broad sense) (h^2)was estimated by the formula suggested by Johnson *et al.* (1955) and were categorized as low (0-30%), medium (30-60%) and high (above 60%). The expected genetic advance (GA) expressed in percentage of mean was calculated by using the method suggested by Johnson *et al.* (1955) and was classified as percent of mean as low below 10%, moderate in range of 10-20% and high more than 20%.

RESULTS AND DISCUSSION

The analysis of variance (Table 1), performed to partition the total variation into variation due to genotypes and other sources for characters studied yielded a highly significant mean sum of square due to genotype except for characterpulp to seed ratio which showed significance at 1%, even it suggested the presence of considerable variability among all the genotypes for all characters studied and ultimately the scope for improving the population for these traits. The mean performance of the genotypes affirmed a wide range of variability for all the characters. The range of variation was documented highest for the characters *viz.;* leaf area (28.0 to 68.5 cm²),), total male flowers (48.4 to 112), sex ratio (14.2 to 46.8), fruit weight (179.7 to 777.1 g), yield of fruit per plant (360.3 to 3109.5 g), pulp weight (107.0 to 557.2 g), seeds per fruit (183.6 to 477.3), and pulp to seed ratio (22.8 to 91.7). Data revealed differences in fruit weight due to increased assimilate translocation into fruits during post-reproductive growth phases, leaf area due to increased assimilate translocation to leaves during vegetative growth phases, and a ratio of male to female flowers due to maternal changes influenced by various environmental factors. Overall, no single accession was shown to be a superior mean performance for all of the characteristics studied. Potekar *et al.* (2014), Reddy *et al.* (2013), and Janghel *et al.* (2013) have all reported similar findings.

Table 1: Analysis of variance (ANOVA) of twenty six genotypes/treatments for different characters in muskmelon

Characters	Range		General mean	Treatments	Replications	Error
	Min.	Max.				
Degree of freedom				25	2	50
Days to first male flower	38.9	44.9	41.7	5.14019**	2.0159	0.55243
Days to first female flower	42.3	48.9	46.6	9.17**	0.806	0.68
Node to first male flower	2.2	4.5	3.6	1.36**	0.2	0.1474
Node to first female flower	3.3	7.7	5.4	3.4**	0.137	0.2141
Petiole length (cm)	8.1	18.4	13.0	17.6925**	7.27982	.68447
Leaf area (cm²)	28.1	68.5	52.7	336.02**	0.7839	1.302
Chlorophyll content	41.3	60.4	51.3	48.951**	0.922	1.84
Total male flowers	48.4	112.0	80.6	708.7**	3.32	1.154
Total female flowers	1.9	7.5	3.3	6.96**	2	0.1957
Sex ratio (M/F)	14.2	46.8	28.2	187.31**	195.55	23.439
Total no. of leaves	16.9	34.5	26.6	63.17**	0.66	0.883
Total no. of 1° branches	2.7	5.4	3.8	1.86**	0.329	0.3569
Total no. of fruits	1.6	4.5	2.4	2.02191**	0.93808	0.11674
Vine length (m)	0.9	2.6	1.7	0.4674**	0.0347	0.0294
Days to first fruit harvest	73.9	91.5	83.3	55.687**	0.1451	0.4821
Fruit weight (g)	179.8	777.1	384.6	91838.72**	3220.896	1228.56
Yield of fruit/plant (g)	360.3	3109.5	931.9	1094731**	234555.1	26289.78
Thickness of flesh (cm)	1.2	3.0	1.9	0.5764**	0.012615	0.00375
Fruit length (cm)	5.7	12.3	8.3	6.92**	0.00484	0.0877
Fruit diameter (cm)	6.0	10.7	8.3	5.1288**	0.03294	0.04681
Pulp weight (g)	107.1	557.2	268.2	62702.88**	3586.53	1260.382
Seeds per fruit	183.7	477.3	296.7	13706.32**	3409.24	655.59
Seed weight (g)	2.1	12.4	5.5	18.919**	2.35	0.3691
Index seed weight (g)	0.8	3.0	1.7	.97659**	0.0349	0.03573
Pulp to seed ratio	22.8	91.8	46.1	1066.029*	4952.506	318.1079
TSS (°B)	6.3	13.9	9.5	10.9395**	0.99038	0.18398
Ascorbic acid (mg/100 g)	14.3	30.3	20.9	59.3375**	0.86605	0.772724
Titratable acidity (%)	0.4	2.7	1.2	1.2896**	0.01171	0.00283
Phenol content (mg/g)	0.1	0.3	0.2	0.00523**	0.003859	7.79E-05

*Significant at 1%　　**Significant at less than 1% i.e. highly Significant

Coefficient of variation calculated at phenotypic and genotypic levels revealed that magnitude of the phenotypic coefficient of variation (PCV) was greater than that of the genotypic coefficient of variation (GCV) for most of the characters with a narrow difference indicating minute environmental influence on the expression of characters (Table 2). High magnitude of maximum GCV was recorded for fruit yield per plant (64.0%) followed by titratable acidity (57.2%), pulp weight (53.4%), total number of female flowers (46.0%), fruit weight (45.2%), seed weight (45.2%), pulp to seed ratio (34.3%), total number of fruits (33.5%), index seed weight (33.1%), sex ratio (26.2%), phenol content (23.9%), thickness of flesh (23.5%), seeds per fruit (22.2%), vine length (22.1%), ascorbic acid content (21.2%) and leaf area (20.0%). Similarly, PCV was found to be high for

fruit yield per plant (66.4 %) followed by titratable acidity (57.4 %), pulp weight (55 %), pulp to seed ratio (51.7 %), total number of female flowers (48 %), seed weight (47 %), fruit weight (46.0 %), total number of fruits (36.4 %), index seed weight (35 %), sex ratio (31.4 %), phenol content (24.4 %), total number of 1° branches per plant (24.3 %), vine length (24.2 %), seeds per fruit (23.9 %), thickness of flesh (23.8 %), ascorbic acid content (21.6 %), node to first female flower (20.9 %), node to first male flower (20.9 %), total soluble solids (20.4 %) and leaf area (20.2 %). These high (>20 %) estimates of both GCV and PCV are showing a large range of variance and greater room for selective improvement. The moderate GCV was recorded for traits *viz.*, total soluble solids (19.9%), total number of male flowers (19.0%), node to first female flower (19.0%), total number of 1°

branches per plant (18.6%), petiole length (18.2%), fruit length (18.2%), node to first male flower (17.9%), total number of leaves (17.2%) and fruit diameter (15.6%). While, the moderate PCV was recorded for traits *viz.*, petiole length (19.3 %), total number of male flowers (19.1 %), fruit length (18.5 %), total number of leaves (17.5 %) and fruit diameter (15.8 %)suggested that there is a lot of variation in the population, and that these traits should be prioritised throughout the selection process. Whereas, the low GCV was recorded for chlorophyll content (7.7%) followed by days to first fruit harvesting (5.2%), first female flower (3.6%), and first male flower

(3%). The low PCV was recorded for chlorophyll content (8.2%) followed by days to first fruit harvesting (5.2%), days to first female flower (4.0%), and male flower (3.5%).However, using only the coeffcients of variation to determine the virtual amount of heritable and non-heritable components of variation present in the population is difficult. Estimating heritability and genetic advancement would be useful additions to this parameter. These findings are in consistent with Kumar *et al.* (2013) in sponge gourd and Chaudhari *et al.* (2011) in muskmelon.

Table 2: Estimate of variability, heritability and expected genetic advance for different characters in muskmelon

Characters	Variance		Coefficient of Variation		h^2 (%)	Genetic Advance 5%	Genetic Advance as % of mean 5%
	Phenotypic	Genotypic	PCV	GCV			
Days to first male flower	2.1	1.5	3.5	3.0	0.7	2.2	5.2
Days to first female flower	3.5	2.8	4.0	3.6	0.8	3.1	6.7
Node to first male flower	0.6	0.4	20.9	17.9	0.7	1.1	31.5
Node to first female flower	1.3	1.1	20.9	19.0	0.8	1.9	35.8
Petiole length (cm)	6.3	5.7	19.3	18.2	0.9	4.6	35.5
Leaf area (cm²)	112.9	111.6	20.2	20.0	1.0	21.6	41.0
Chlorophyll content	17.6	15.7	8.2	7.7	0.9	7.7	15.1
Total male flowers	237.0	235.9	19.1	19.1	1.0	31.6	39.1
Total female flowers	2.5	2.3	48.0	46.0	0.9	3.0	91.0
Sex ratio (M/F)	78.1	54.6	31.4	26.3	0.7	12.7	45.2
Total no. of leaves	21.7	20.8	17.5	17.2	1.0	9.2	34.6
Total no. of 1° branches	0.9	0.5	24.3	18.6	0.6	1.1	29.3
Total no. of fruits	0.8	0.6	36.4	33.5	0.9	1.5	63.4
Vine length (m)	0.2	0.2	24.2	22.1	0.8	0.7	41.5
Days to first fruit harvest	18.9	18.4	5.2	5.2	1.0	8.7	10.5
Fruit weight (g)	31432.0	30203.4	46.1	45.2	1.0	350.9	91.2
Yield of fruit/plant (g)	382436.8	356147.0	66.4	64.0	0.9	1186.4	127.3
Thickness of flesh (cm)	0.2	0.2	23.8	23.5	1.0	0.9	48.0
Fruit length (cm)	2.4	2.3	18.5	18.2	1.0	3.1	36.8
Fruit diameter (cm)	1.7	1.7	15.8	15.6	1.0	2.7	31.8
Pulp weight (g)	21741.2	20480.8	55.0	53.4	0.9	286.1	106.7
Seeds per fruit	5005.8	4350.3	23.9	22.2	0.9	126.7	42.7
Seed weight (g)	6.6	6.2	47.0	45.6	0.9	5.0	91.3
Index seed weight (g)	0.4	0.3	35.0	33.1	0.9	1.1	64.7
Pulp to seed ratio	567.4	249.3	51.7	34.3	0.4	21.6	46.8
TSS (°B)	3.8	3.6	20.4	19.9	1.0	3.8	40.1
Ascorbic acid (mg/100 g)	20.3	19.5	21.6	21.2	1.0	8.9	42.8
Titratable acidity (%)	0.4	0.4	57.4	57.2	1.0	1.4	117.4
Phenol content (mg/g)	0.0	0.0	24.4	23.9	1.0	0.1	48.2

GCV: genotypic coefficient of variation; PCV: phenotypic coefficient of variation; h^2 : heritability in broad sense

Heritability in broad sense varied from 35% to 100% for total number of male flowers. High value of heritability were observed in most of the traits, such as days to first female flower

(81%), leaf area (99%), chlorophyll content (90%), total number of female flowers (92%), total number of fruits (85%), vine length (83%), days to first fruit harvest (97%), TSS (95%), fruit

weight (96%), fruit diameter (97%), fruit yield per plant (93%) and phenol content (96%). This showed that these traits were under genetic control and were unaffected by the environment, implying that selection based on phenotypic performance would be trustworthy. However, because broad sense heritability is based on genetic variance, which encompasses both fxable (additive) and non fxable (dominance and epistatic) variances, these qualities may not be helpful for further development through selection. The moderate heritability was recorded for total number of branches (58%) and pulp to seed ratio (44%) pointing to the importance of non-additive gene activity, such as dominance and epistasis. The low heritability was not reported in any of the characters studied.

High GAM (above 20%) was observed for node to first female flower (35.8%), leaf area (41.0%), total number of female flowers (91%), total number of 1° branches (29.3%), total number of fruits (63.4%), vine length (41.5%)and TSS (40.0%). As a result of the function of additive gene action, straight-forward selection based on these characteristics phenotypic performance may be efficient. In muskmelon, Janghel *et al.* (2018) reported similar results. Whereas, the moderate GAM was noted for chlorophyll content (15.0%) and days to first fruit harvest (10.5%) while, low GAM was observed for days to first male (5.2%), and first female (6.7%) flower pointing to the role of non-additive gene activity.

In general, high heritability combined with a high genetic advance in a trait indicates that the inheritance of that trait is governed primarily by additive gene effects, and thus simple selection based on phenotypic performance may be effective. The traits leaf area, total number of female flowers, total number of fruits, vine length and total soluble solids all had high heritability accompanied with high genetic advance. The results are in close proximity with the findings of Potekar *et al.* (2014) and Janghel *et al.* (2018) in muskmelon.

It may be concluded from the results that the analysis of variance demonstrated the presence of significant differences among genotypes for almost all the characters studied. The characters, fruit yield per plant (g) revealed the highest PCV and GCV values, followed by titratable acidity, pulp weight, total number of female flowers and seed weight. Also, high estimates of heritability coupled with high genetic advance as per cent of mean were obtained for leaf area, total number of female flowers, total number of fruits, vine length and total soluble solids. As a result, these traits should be given higher weight in selection and hence additive genes are predicted to influence them.

ACKNOWLEDGEMENT

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