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Studies on genetic variability, heritability and genetic advance in muskmelon [*Cucumis melo* L.] genotypes

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Abstract

Genetic variability parameters were estimated for yield and yield attributing traits in One hundred and twenty-four diverse genotypes of muskmelon (*Cucumis melo* L.) during summer 2019 at Main Vegetable Research Station, Anand Agricultural University, Anand in Randomized Complete Block Design with two replications. Analysis of variance had shown highly significant difference among genotypes for all the fourteen characters related to growth and yield traits. The estimate of PCV is higher than GCV in all the characters studied indicating the influence of environment towards expression of characters. Higher PCV and GCV were recorded for fruit yield per plant, total soluble sugar, phenol, fruit weight, β -carotene, flavonoid and total soluble solids indicating the higher variability present for these characters. High heritability coupled with high GAM recorded for primary branches per plant, fruit length, fruit girth, fruit weight, fruits per plant, flesh thickness, total soluble solid, phenol, total soluble sugar, β -carotene, flavonoid and fruit yield per plant indicating predominance of additive components and hence, these traits can be improved by following simple selection.

Keywords: Muskmelon, variability, heritability, genotypic coefficient of variance, germplasm, genetic advance, phenotypic coefficient of variance

Introduction

Muskmelon (*Cucumis melo* L.), popularly known as Kharbuja in India, is one of the important species of fruit vegetables with a diploid chromosome number $2n = 2x = 24$ grown throughout the world, particularly in tropical and sub-tropical countries. It is believed to be originated in tropical Africa and India is regarded as its secondary centre of origin (Chadha and Lal 1993)^[5]. The fruits of muskmelon are sweet with musky flavour which is mainly grown as a dessert crop and has good export potential. In India muskmelon is cultivated in around 54000 ha area with 1.14 MT production (Anonymous 2019)^[1]. Despite its recognized potential as high-value dessert fruit vegetable, commercial muskmelon cultivation is less remunerative due to low yield potential and sub-optimal fruit quality of current open-pollinated cultivars. Hence, further genetic improvement in cultivars for yield and quality is needed. The wide genetic variability within the available genotypes and cultivars offers ample scope for further improvement.

In general, variability is the basic material and pre-requisite for any crop improvement programme. Therefore, knowledge about the existence of genetic variability is the useful adjunct to carry out effective selection for improving yield. Genetic variability study will help in estimating genetic parameters viz., phenotypic coefficient of variation, genotypic coefficient of variation, heritability and genetic advance as percent mean which are essential for effective selection of superior genotypes and partition the observed variability into heritable and non-heritable components.

An estimate of phenotypic and genotypic variation quantifies the amount of variability present within a set of breeding material with regard to its essential characteristics. Genetic advance denotes the improvement in the mean genotypic values of selected families over base population and thus helps the breeder to select the progenies in the earlier generation itself. Sufficient variability present in this crop for fruit colour, size, shape fruit weight etc. with this information, the present investigation was undertaken to assess the genetic variability for growth and yield characters in musk melon genotypes.

Melon and its related species and genera co-exist in India and have rich genetic resources, which are characterized by a considerable amount of variability for horticultural traits and insect-pests and disease resistance (Roy *et al.*, 2011)^[20]. Therefore, efforts should be made to collect, conserve and evaluate the genetic resources of melon in India.

To enhance the utilization of such genetic resources, systematic evaluation for different characters are prime important.

However, there is a need to develop superior muskmelon varieties/hybrids suited to different agro ecological conditions with specific end use. The success of conventional breeding is predominantly governed by the availability of desired genetic variability for the target traits (Ara *et al.*, 2009) [2]. Genetic resources permit the plant breeders to create novel plant gene combinations and select crop varieties more suited to the needs of diverse agricultural systems (Glaszmann *et al.*, 2010) [7]. To develop high yielding varieties for a systematic breeding programme in muskmelon, information on genetic variability is a basic pre-requisite. Wider the genetic variability more will be the chances of improvement through selection. However, the yield being a complex quantitative trait direct selection for yield may not result in successful crop improvement. Information on character association, direct and indirect effects of component traits on yield would greatly help in formulating the selection criteria and using them effectively in the crop improvement programme. Therefore, it is necessary to partition the observed variability into heritable and non-heritable components by calculating genetic parameters such as genotypic and phenotypic coefficient of variation, heritability and genetic advance.

Materials and Methods

The present study carried out at main vegetable research station, AAU, Anand, Gujarat during summer 2019. The 124

genotypes were assessed in a field experiment under a randomized complete block design with two replications. Ten plants maintained in each treatment with spacing of 2.0 × 1.0 m between rows and plants, respectively. The data were recorded on three randomly selected plants from each genotype for eighteen growth and yield characters. Observations recorded for days to 50% male flowering, days to 50% female flowering, primary branches per plant, fruit length, fruit girth, fruit weight, fruits per plant, fruit yield per plant, flesh thickness, total soluble solid, phenol, total soluble sugar, β-carotene, flavonoid, fruit colour, fruit shape, pulp colour and taste.

The total variability of the one hundred and twenty-four genotypes for each of the quantitative trait was partitioned into sources attributable to genotype, replication and error using ANOVA technique (Panse and Sukhatme, 1967) [17]. Genetic variability parameters like genotypic and phenotypic co-efficient of variation (GCV and PCV) were computed as per Burton (1953) [4]. The heritability in broad sense and genetic advance as percent mean (GAM) were determined by using the formula given by Johnson *et al.* (1955) [11].

Results and Discussion

Analysis of Variances Analysis of variance had shown highly significant difference among genotypes for all the fourteen quantitative characters related to growth and yield parameters were presented in table.1. The estimate of PCV is higher than GCV in all the characters studied (Table 2) and indicates the influence of environment on genotypes.

Table 1: Analysis of variance (mean sum of squares) for different characters in muskmelon

Sr. No.	Characters	df	Mean Sum of Square		
			Replications	Genotypes	Error
			1	123	123
1.	Days to 50% male flowering		382.516**	34.471**	9.126
2.	Days to 50% female flowering		72.403**	21.823**	7.265
3.	Primary branches per plant		0.581**	0.716**	0.033
4.	Fruit length		2.776	24.898**	1.975
5.	Fruit girth		30.240	66.265**	10.607
6.	Fruit weight		8,997.977	49,744.277**	5,460.548
7.	Fruits per plant		0.229	0.875**	0.093
8.	Flesh thickness		0.007	0.203**	0.028
9.	TSS		0.000542	3.914**	0.312
10.	Phenol		0.064**	0.098**	0.020
11.	Total soluble sugar		0.010	0.229**	0.005
12.	β – carotene		0.050	0.534**	0.03066
13.	Flavonoid		0.038	0.055**	0.020
14.	Fruit yield per plant		31,673.674	1,746,865.322**	30,009.192

Note: ** indicate significant at 1% level

Table 2: The estimates of variance components and other genetic parameters for different characters in muskmelon

Sr. No.	Characters	σ^2_g	σ^2_p	GCV (%)	PCV (%)	H ² _b (%)	GA% Mean
1.	Days to 50% male flowering	12.67	21.80	6.74	8.84	58.14	10.58
2.	Days to 50% female flowering	7.28	14.54	4.63	6.54	50.05	6.74
3.	Primary branches per plant	0.3412	0.3746	19.39	20.31	91.09	38.12
4.	Fruit length	11.46	13.44	19.01	20.59	85.30	36.18
5.	Fruit girth	27.83	38.44	15.16	17.82	72.40	26.58
6.	Fruit weight	22141.86	27602.41	31.05	34.67	80.22	57.29
7.	Fruits per plant	0.3911	0.4841	12.61	14.03	80.78	23.35
8.	Flesh thickness	0.0879	0.1156	14.52	16.55	76.03	26.07
9.	TSS	1.8006	2.1129	21.22	22.99	85.22	40.36
10.	Phenol	0.001401	0.001492	40.45	41.24	96.24	81.75
11.	Total soluble sugar	0.1120	0.1171	44.44	45.44	95.64	89.52
12.	β – carotene	0.2520	0.2828	31.36	33.22	89.13	60.99

13.	Flavonoid	0.0011	0.0126	31.53	36.00	76.74	56.90
14.	Fruit yield per plant	858428.06	888437.26	47.01	47.83	96.62	95.20

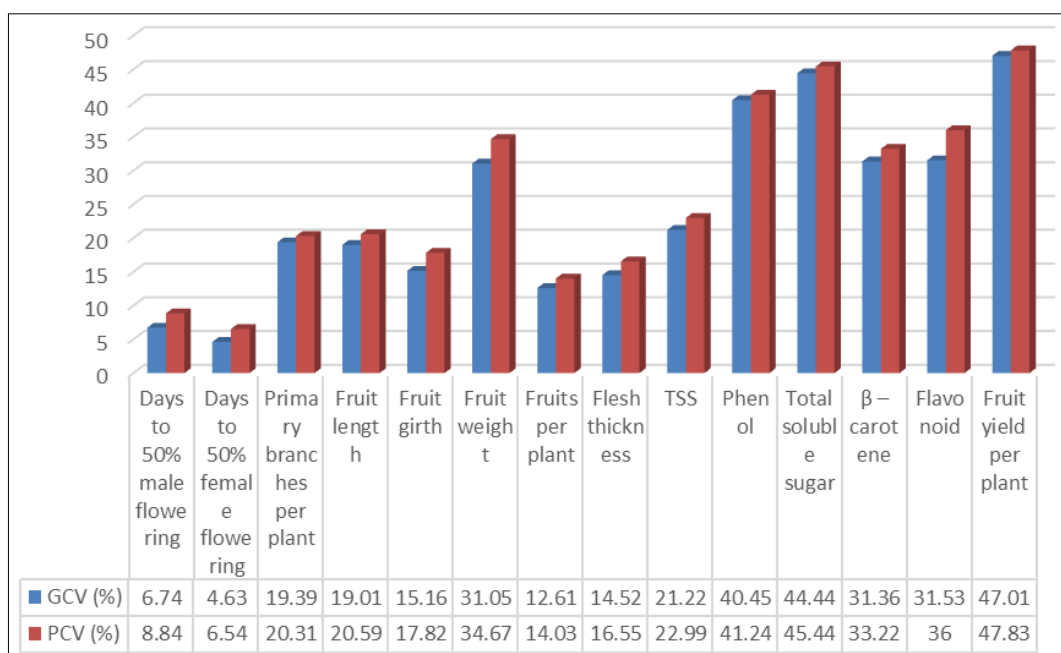


Fig 1: Graphical representation of GCV (%) and PCV (%) for different characters in muskmelon

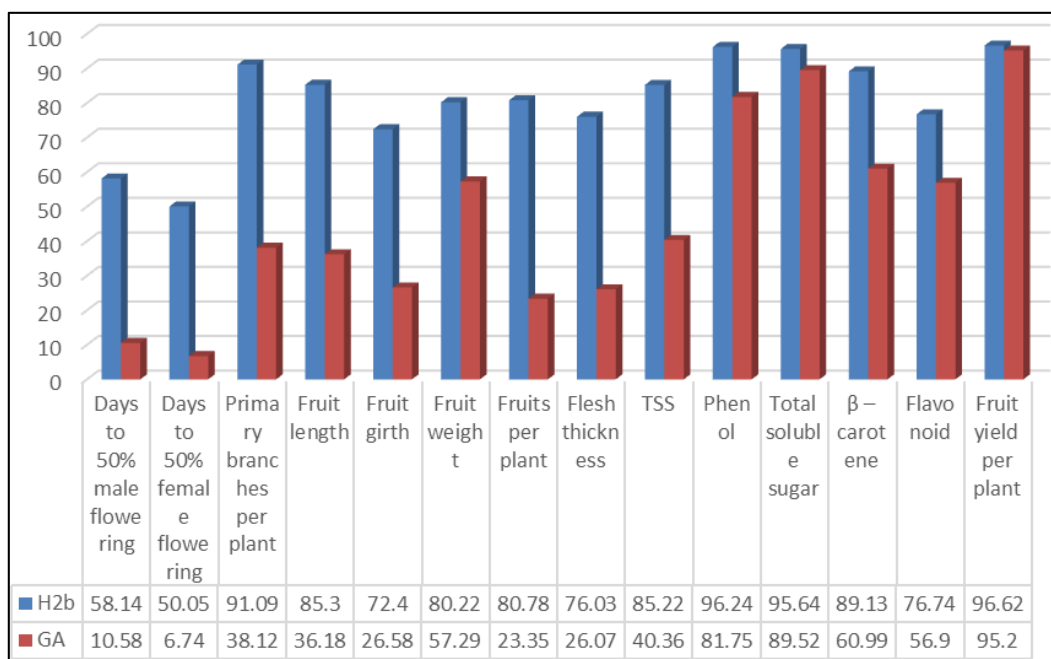


Fig 2: Graphical representation of H²_b (%) and GA percent of mean for different characters in muskmelon

The analysis of variance revealed significant differences among genotypes for all the characters under study, which indicated that experimental material had sufficient variability for different traits. The perusal of the data of *per se* performance revealed that the genotypes GP-MM 27, GMM 3, GP-MM 22, GP-MM 12 and GP-MM 3 were elite genotypes based on yield. Whereas, huge variation was recorded for quality characters among the genotypes. The genotype GMM 3 found to be the most promising genotype for quality traits. However, their potentiality should be confirmed by testing them over environments (multilocation trial) with keeping consumer preference in mind. The difference between phenotypic and genotypic variance

was less for the characters, *viz.*, primary branches per plant, fruit length, Fruits per plant, TSS, phenol, total soluble sugar, β-carotene and flavonoid. It indicated that the influence of environment was less for the expression of these characters and heritability found mainly due to the genotypic difference. This also suggests the good breeding value for all these characters and the selection based on phenotype may be rewarding.

On the other hand, days to 50% male flowering, days to 50% female flowering, fruit girth, fruit weight, flesh thickness and fruit yield per plant showed greater influence of environmental factors for their expression. The high genotypic and phenotypic coefficient of variations were

observed for fruit yield per plant, total soluble sugar, phenol, fruit weight, β -carotene, flavonoid and total soluble solids with marginal difference between them in these traits which indicated less influence of environment and high genetic variability.

Similar findings were reported by Kadi and Sambhaj (2003)^[12], Potekar *et al.* (2014)^[19], Mishra *et al.* (2017)^[15], Janghel *et al.* (2018)^[10], Kamagoudand Shet (2018)^[13], Muthuselvi *et al.* (2019)^[16] and Torkadi *et al.* (2019)^[24].

While, GCV and PCV were moderate for primary branches per plant, fruit length, fruit girth, flesh thickness and fruits per plant. The estimates of GCV and PCV were low for days to 50% male flowering and days to 50% female flowering which indicated less variability for these traits in the genotype studied.

The supporting results also reported by Samadia (2007)^[22], Tomar *et al.* (2008)^[23], Bhimappa *et al.* (2017)^[3], Ibrahim and Ramdan (2013)^[9].

The characters like primary branches per plant, fruit length, fruit girth, fruit weight, fruits per plant, flesh thickness, total soluble solid, phenol, total soluble sugar, β -carotene, flavonoid and fruit yield per plant exhibited high heritability coupled with high genetic advance indicated that heritability in genotypes were due to additive gene effects reflecting better scope for the improvement in the characters by effective selection. While, the characters like days to 50% male flowering, days to 50% female flowering exhibited moderate heritability with moderate genetic advance. The results indicated the involvement of non-additive gene effect for expression of these traits.

High heritability couple with high genetic advance as percent of mean for fruit length, fruit girth, fruit weight, fruits per plant and fruit yields per plant were observed by Kadi and Sambhaj (2003)^[12], Iathetand Piluek (2006)^[8], Samadia (2007)^[22], Tomar *et al.* (2008)^[23], Choudhary *et al.* (2011)^[6], Ibrahim and Ramdan (2013)^[9], Potekar *et al.* (2014)^[19], Bhimappa *et al.* (2017)^[3], Mishra *et al.* (2017)^[14], Kamagoud and Shet (2018)^[13], Saha *et al.* (2018)^[21], Pasha *et al.* (2019)^[18] and Torkadi *et al.* (2019)^[24]. For flesh thickness high heritability couple with high genetic advance as percent of mean were observed by Kadi and Sambhaj (2003)^[12], Janghel *et al.* (2018)^[10], while, for primary branches per plant was observed by Mali *et al.* (2015)^[14].

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