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Assessment of genetic variability for yield and quality traits in snap melon (*Cucumis melo* var. *Momordica* Duth. and Full.)

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Abstract

The present investigation was carried out at Department of vegetable science, KRC College of horticulture, Arabhavi, Belagavi Dist. Karnataka, India during *kharif* 2019-2020. The experimental material comprised of 26 snap melon genotypes collected from various locations in and around Karnataka and also from other states of India. High genotypic and phenotypic coefficients of variation (GCV and PCV) were recorded for leaf area 60DAS (30.28 and 32.20%), number of branches 60 DAS (22.20 and 28.29%), number of fruits per vine (18.15 and 23.02%), fruit weight (19.24 and 23.57%), fruit length (28.20 and 29.16%), fruit diameter (25.03 and 27.07%) and titratable acidity (22.09 and 26.37%). High level of heritability with moderate genetic advance as percentage mean (GAM) was recorded by leaf area 60DAS, number of branches per vine 60DAS, node to first male flower appearance, fruit weight, fruit length, fruit diameter, number of fruits per vine, TSS, ascorbic acid.

Keywords: Snap melon, variability, heritability and genetic advance as per cent of mean

1. Introduction

Cucurbits belong to the family cucurbitaceous, also called as gourd family and consist of 118 genera and 825 species mainly grown in tropical and subtropical regions. The most important generas are *Cucurbita. Cucumis, Citrullus, Lagenaria* and *Luffa*. Cucurbits are the most important plant families that supply to human with edible products and useful fibres. Among cucurbits, melons are the important commercially grown crops all over India. Melons can be classified into many species and it has a divergent crop nature and cultivation (Muthuselvi *et al.*, 2019) [11]. Among the melons oriental pickling melon and snap melon are unique and have considerable variability in Western Ghats. Fergany *et al.* (2011) have collected melon germplasm of the humid tropics of southern India and they reported that the collected populations belong to two groups: *C. melo* var. *acidulus* and *C. melo* var. *momordica* (Roxb.) Duthie et Fuller. They also recommended that additional collections of melon genetic resources should be made from southern India as this could lead to the discovery of genetic diversity not present in the existing world collections of melon.

Snap melon (*Cucumis melo* var. *Momordica* Duth. and Full.) is an underutilized member of the family cucurbitaceae, with a diploid chromosome number 2n =24. Snap melon is commonly known as 'Phoot' which means to 'split'. Snap melon is a locally grown dessert melon in Goa and coastal Maharashtra known as 'Chibud', in areas of Karnataka as 'Hibadihannu' or 'Phoottikai' and in Kerala it is known as 'Pottuvellari'. Snap melon is resistance to various pest and diseases *viz.* powdery mildew, downy mildew and cucumber green mottle mosaic virus and resistance to abiotic stress (Maurya *et al.*, 2004) [10]. It is hardy crop which is cultivated as a solo in summer season and as mixed crop along with field crops like maize, sorghum and pearl millet in rainy season (Seshadri and More, 2009) [20].

For crop improvement, genetic variability is the most significant component, it is the basic prerequisite for any successful programme of breeding. It is important to have sound knowledge of the existing variability in the genotypes to choose a suitable type. According to Vavilov (1951) [22] there is a better scope to select the desired types from wide range of variability. Heritability of a character that indicates to what measure the trait can be transmitted from one generation to another generation (Balouch *et al.*, 2003) [1] and is a prominent tool to foresee the magnitude of genetic gain that follows choosing a trait.

2. Materials and Methods

The present investigation carried out at Department of Vegetable Science Research field, KRC College of Horticulture Arabhavi, University of Horticultural Science, Baglkote during *Kharif*, 2019-2020.Which falls under northern dry zone (zone No. 3, Region-2) of Karnataka at 16^0 12 N latitude and 74^0 54' E longitude, at an altitude of 640m above mean sea level. It is considered to have the benefit of both south-west and north-east monsoons. A total of 26 genotypes of snap melon were raised in a randomized block design (RBD) with two replications. Recording the observations for vine length 60 das (cm), number of leaves per vine 60das, number of branches per vine 60das, leaf area 60das (cm^2), days to first male flower, days to first female flower, node to first male flower, node to first female flower, sex ratio, fruit weight (kg), fruit length (cm), fruit diameter (cm), days to first harvest, number of fruits per vine, fruit yield per vine (kg), TSS (^{0} brix), titratable acidity (%),ascorbic acid (mg/100g) were analysed under present study. The mean over replications for each character was subjected to statistical analysis. The phenotypic and genotypic coefficients of variations (PCV, GCV) were estimated by using the formulae suggested by Burton and Devane (1953) [4]. Heritability in broad sense was estimated by using the formulae suggested by Lush (1940) and expected genetic advance was computed by using formulae suggested by Johnson *et al.*, 1955 [6].

3. Results and Discussion

3.1 Analysis of Variances

Analysis of variance had shown highly significant (P=0.01) difference among genotypes for all the traits related to growth and yield parameters was presented in Table (1). This indicates the existence of high degree of genetic variability among the genotypes and enough scope for bringing about improvement in the desirable direction. Analysis of variance by itself is not enough and conclusive to explain all the inherent genotypic divergence in the collections. This is revealed by determining the total genetic variability inherent in the genotypes obtained after due partitioning of the phenotypic variance.

The estimates of variability on the basis of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV), heritability and genetic advance as per cent of mean (GAM) are presented in Table (2). In general, the genotypic variance and genotypic coefficient of variation were lesser than the phenotypic variance and phenotypic coefficient of variation, respectively. The present study meets out, the extent of variability available in 26 genotypes collected from different sources and the scope of selection through heritability and genetic advance estimates was analysed and the results obtained are discussed here under. The analysis of variance revealed significant differences among the 26 genotypes for all the characters studied. The results support the selection programme for more fruit yield.

Table 1: Analysis of variance (mean sum of squares) for growth, yield and quality parameters in snap melon genotypes

Sl. No.	Character	Replication	Genotypes	Error	SEm±	CD @ 5%
	Degrees of freedom	**1**	**25**	**25**		
1	Vine length 60 DAS	2.23	7205.43**	799.92	3.92	11.65
2	Number of leaves per vine 60DAS	4.25	6297.74**	1455.84	5.39	15.71
3	Leaf area 60DAS	11652.96	34719011.36	2129340.25	206.36	601.07
4	Number of branches per vine 60DAS	4.80	30.85**	7.33	0.38	1.11
5	Days to first male flower	5.90	236.46**	90.45	1.34	3.91
6	Days to first female flower	3.25	182.34**	64.30	1.13	3.30
7	Node to first male flower	1.07	18.37**	6.34	0.35	1.03
8	Node to first female flower	0.30	10.96**	3.97	0.28	0.82
9	Sex ratio	0.01	7.68**	2.22	0.21	0.61
10	Fruit weight (kg)	0.04	1.68**	0.33	0.08	0.23
11	Fruit length (cm)	5.91	1143.24**	38.35	0.87	2.55
12	Fruit diameter (cm)	1.17	290.24**	22.72	0.67	1.96
13	Days to first harvest	4.79	992.20**	384.74	2.77	8.07
14	Number of fruits per vine	0.0002	95.32**	22.22	0.66	1.94
15	Fruit yield per vine (kg)	1.69	48.40**	16.29	0.57	1.66
16	TSS (^{0} Brix)	0.14	35.33**	6.21	0.35	1.02
17	Titrableacidity (%)	0.01	0.44**	0.07	0.04	0.11
18	Ascorbic acid (mg/100g)	0.001	28.89**	2.33	0.21	0.62

Note: * and ** indicate significant at 5 and 1 per cent probability level, respectively. DAS – Days after sowing.

Table 2: Mean, GCV, PCV, Heritability and Genetic advance as per cent of mean for growth, yield and quality parameters in snap melon genotypes

Sl. No.	Character	Range	Mean	GCV (%)	PCV (%)	h^2 (%)	GA	GAM%
1	Vine length 60DAS (cm)	83.50-133.25	108.07	10.47	11.70	80.02	20.85	19.29
2	Number of leaves per vine 60DAS	30.27-91.50	70.84	13.89	17.57	62.45	16.01	22.61
3	Leaf area 60DAS (cm)	1151.70-4101.63	2665.71	30.28	32.20	88.44	1564.05	58.67
4	Number of branches per vine 60DAS	1.70-4.50	3.08	22.20	28.29	61.57	1.10	35.89
5	Days to first male flower	31.70-39.90	36.51	4.68	7.00	44.66	2.35	6.44
6	Days to first female flower	39.3-46.9	42.49	3.61	5.22	47.86	2.18	5.15
7	Nodes to first male flower	2.60-5.05	3.35	14.62	20.96	70.50	0.70	21.01
8	Node to first female flower	4.20-6.30	5.04	7.41	10.83	46.83	0.52	10.45
9	Sex ratio	1.35-2.96	2.03	16.26	21.91	50.49	0.50	24.85
10	Fruit weight (kg)	0.35-1.02	0.85	19.24	23.57	66.66	0.27	32.34
11	Fruit length (cm)	8.41-25.81	16.66	28.20	29.16	93.51	9.36	56.18

12	Fruit diameter (cm)	5.03-14.60	9.24	25.03	27.07	85.48	4.40	47.67
13	Days to first harvest	67.47-85.90	76.74	4.54	6.83	44.12	4.76	6.21
14	No. of fruits per vine	4.95-12.20	6.65	18.15	23.02	62.19	1.96	29.49
15	Fruit yield per vine (kg)	4.36-7.63	5.66	14.13	20.06	49.63	1.16	20.51
16	TSS (^{0}Brix)	3.15-6.85	4.27	17.86	21.3	70.08	1.31	30.81
17	Titrableacidity (%)	0.19-0.54	0.39	22.09	26.37	70.18	0.14	38.13
18	Ascorbic acid (mg/100 g)	4.65-7.15	5.89	12.37	12.41	85.04	1.38	23.50

3.2 Genotypic and phenotypic coefficients of variation

High GCV and PCV (>20%) were recorded for parameters like leaf area 60 DAS, number of branches per vine 60 DAS, number of fruits per vine, fruit weight, fruit length, fruit diameter and titratable acidity. These results are in similar with the findings of earlier workers *viz*., Reddy *et al*. (2013) [19] in muskmelon, for number of branches per vine; Borthakur and Baruah (2006) [3] in bitter gourd and Rakhi and Rajamony (2005) [17] in culinary melon for leaf area; Muthaselvi *et al*. (2019) [11] in snap melon, Kamagoud *et al*. (2018) [7] in oriental pickling melon, Rakhi and Rajamony (2005) [17] in culinary melon for fruit weight; Karthick *et al*. (2019) [8] in cucumber, Kamagoud *et al*. (2018) [7] in oriental pickling melon for fruit length and fruit diameter; Reddy and Shanthi (2013) [19], Tomar *et al*. (2008) [21] in muskmelon and Karthick *et al*. (2019) [8] in cucumber for number of fruits per vine; Tomar *et al*. (2008) [21] in muskmelon for titrableacidity. This indicated that these traits are less effect or influence by environment and more variability present in these traits there is more scope for improvement of these parameter would be possible through direct selection.

Moderate GCV and PCV (10-20%) were observed for vine length, number of leaves per vine 60DAS, nodes to first male flower, sex ratio, fruit yield per vine, TSS (^{0}Brix) and ascorbic acid (mg/100 g). The similar result were earlier recorded by Reddy and Shanthi (2013) [19], Tomar *et al*. (2008) [21] in muskmelon and Pandey *et al*. (2003 and 2009) [13, 12] in snap melon; and Rakesh *et al*. (2013) [16] in bitter gourd for vine length; Vishwanatha (2003) [23] in muskmelon for number of leaves per vine; Pandey *et al*. (2003) [13] in snap melon and Balvir and Dhillon (2002) in culinary melon for node to first male flower; Reddy and Shanthi (2013) [19], Tomar *et al*. (2008) [21] in muskmelon, Kamagoud *et al*. (2018) [7] in oriental pickling melon and Karthick *et al*. (2019) [8] in cucumber for fruit yield per vine; Kamagoud *et al*. (2018) [7] for sex ratio; Reddy and Shanthi (2013) [19] and Tomar *et al*. (2008) [21] in muskmelon, Muthaselvi *et al*. (2019) [11] in snap melon and Kamagoud *et al*. (2018) [7] in oriental pickling melon for TSS; Rajawat and Collis (2017) [15] in cucumber, Tomar *et al*. (2008) [21] and Vishwanatha (2003) [23] in muskmelon for ascorbic acid.

Whereas low GCV and PCV (<10%) were observed for days to first male flower, days to first female flower, node to first female flower, days to first harvest. These results are in similar with the findings of earlier workers *viz*., Islam *et al*. (2009) [5] in bitter gourd, Samadia (2007) in round melon, Prasad *et al*. (2004) in muskmelon and Kumar *et al*. (2011) in cucumber for first female flower appearance. Reddy and Shanthi (2013) [19] and Vishwanatha (2003) [23] in muskmelon and Islam *et al*. (2009) [5] in bitter gourd for first female flower appearance; Reddy and Shanthi (2013) [19] in muskmelon for node to first female flower; Muthaselvi *et al*. (2019) [11] in snap melon, and Rad *et al*. (2010) [14] in melon for days to first harvest. This indicates presence of moderate amount of variability and environment also influencing expression for these characters. Other traits recorded low PCV and GCV indicating less variability and not useful for selection and further improvement of crop.

3.3 Heritability and genetic advance as per cent mean

High heritability (>60%) combined with high genetic (> 20%) advance as per cent mean were observed for number of leaves per vine 60DAS, number of branches per vine 60DAS, leaf area 60DAS (cm), nodes to first male flower, fruit weight (kg), fruit length (cm), fruit diameter (cm), number of fruits per vine, TSS (^{0}brix), titrableacidity (%), ascorbic acid (mg/100 g). Vishwanatha (2003) [23] in muskmelon, Borthakur and Baruah (2006) [3] in bitter gourd for number of leaves per vine and leaf area, Ramana (2000) [18] in oriental pickling melon and Rakesh *et al*. (2013) [16] in ridge guard for number of branches per vine; Muthaselvi *et al*. (2019) [11] in snap melon for fruit weight, fruit length, fruit diameter, number of fruits per vine, TSS; Rajawat and Collis (2017) [15] in cucumber for ascorbic acid and Tomar *et al*. (2008) [21] in muskmelon for titrableacidity and ascorbic acid.

High level of heritability (>60%) with moderate genetic advance as percentage mean (10-11%) was recorded by Vine length 60DAS (cm). Low heritability (<60%) and moderate genetic advance as percentage mean (10-11%) were observed for sex ratio, fruit yield per vine (kg). Low heritability (<60%) with low genetic advance as percentage mean (<10%) days to first male flower, days to first female flower, node to first female flower, days to first harvest. similar results were recorded by earlier worker *viz*., Vishwanatha (2003) [23] in muskmelon for vine length; Muthaselvi *et al*. (2019) [11] in snap melon for fruit yield per vine and days to first harvest; Karthick *el al*. (2019) [8] in cucumber for days to first male flower, days to first female flower; Kamagoud *et al*. (2018) [7] in oriental pickling melon for node to first male flower appearance and Rakhi and Rajamony (2005) [17] in culinary melon for days to first female flower and sex ratio.

4. Conclusion

In this present study, most of the characters revealed high heritability estimates and from this it was concluded that there was more number of additive genes were acting for these characters. Considering the diverse nature of the material, the genotypes under investigation in the present study had the greater quantity of heritable variation particularly for fruit weight, fruit length, fruit diameter, number of fruits per plant and yield per plant and there is possibility for improvement of these parameters by selection.

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