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Assessment of variability in snap melon (*Cucumis melo* var. *Momordica* duth. & full) genotypes

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Abstract

The present investigation was carried out at Department of Vegetable Crops, TNAU, Coimbatore – 03 during 2016 – 2017. The experimental material comprised of 23 snap melon genotypes collected from various locations in and around Tamil Nadu and also from other states of India. The experiment was laid out in randomized block design with three replications. Analysis of variance revealed that there is a considerable variability exists among the genotypes for all the twenty one characters. High phenotypic and genotypic coefficients of variation were recorded for number of primary branches (28.16 and 28.22), node at which first male flower appearance (34.19 and 34.26), stem thickness (20.20 and 20.98), length of the fruit (27.50 and 27.67), weight of the fruit (29.54 and 29.69), number of fruits per plant (29.79 and 29.92), yield per plant (34.54 and 34.63), vine length (22.94 and 24.07) and Ascorbic acid (26.15 and 26.34). High level of heritability with moderate genetic advance as percentage mean was recorded by days to first male flower appearance (89.53 and 14.09 per cent) and days to first female flower appearance (90.11 and 18.94 per cent).

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

Introduction

India is one of the main centre of origin for many cucurbitaceous vegetables, where these plants are capable of thriving and performing well even under the hot summer. As the other crops like legumes and cereals, the cultivated cucurbits are not merely as significant in man's economy but they are crops cultivated ordinary in the tropics, subtropics and some portions of temperate zones. The vegetables of the family Cucurbitaceae constitute the largest group of cultivated vegetables. In cucurbitaceae family, melons are the important commercial crops grown throughout India. Melons can be classified into many species and it has a divergent crop nature and cultivation. Many scientists described about melon and its classification from the past years.

One of the most recent classification and widely used in literature, proposed to divide the species into six botanical groups: *cantaloupensis*, *inodorus*, *conomon*, *dudaim*, *flexuosus* and *momordica* (Robinson & Decker- Walters, 1997) [15]. Many of these groups are economically important in developed countries and they were based on their culinary attributes.

These varieties exhibit tremendous variation in fruit traits such as size, shape, colour, taste, texture, and biochemical composition. Such a variation provides breeders with a rich genetic resource, and thus there is increased interest to understand their genetic diversity. 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* L. ($2n = 2x = 24$), is an underutilized cucurbitaceous crop morphologically diverse, out-crossing horticultural crop of broad economic importance and it belongs to the family Cucurbitaceae. It is grown throughout the India and the fruit has an immense use for any human being. Indian snap melon accessions have been reported to be a good source for disease and insect pest resistance, and many of them are used as reference accessions worldwide (Pitrat *et al.*, 2000; Cohen *et al.*, 1996) [10, 4]. In India, snap melon is generally grown during rainy season as an intercrop with maize and sorghum by the resource poor farmers for their own consumption.

The presence of genetic variation in the breeding material determines the success or failure of any breeding programme. Therefore the measurement of genetic variation and understanding the mode of inheritance of qualitative and quantitative traits are the essentials in any crop improvement programme. This study was undertaken to assess genetic variability in snap

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melon and grouping of genotypes on the basis of morphological and physiological traits and to find the relationship among morphological and physiological traits.

Materials and Methods

The present study was carried out at the College Orchard, Department of Vegetable Crops, Horticultural College and Research Institute, Tamil Nadu Agricultural University, Coimbatore during 2016-2017 which is situated at 11° N latitude and 77° E longitude and at an elevation of 426.6 m above mean sea level. A total of 23 genotypes of snap melon were raised in a randomized block design (RBD) with three replications. All recommended package of practices were followed during the crop production. Five plants at random were taken from each plot for recording the observations on number of primary branches, node at which first male flower appearance, node at which first female flower appearance, days to first male flower, days to first female flower, internodal length (cm), stem thickness (cm), peduncle length (cm), number of male flowers per vine, number of female flowers per vine, length of the fruit (cm), girth of the fruit (cm), weight of the fruit (kg), days to first harvest, number of fruits per plant, yield per plant (kg), vine length (m), flesh thickness (cm), and quality characters like total soluble solids (°Brix), ascorbic acid (mg/100g) and carbohydrate content (mg/100g) were analyzed in this 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 (1952)^[2]. Heritability in broad sense was estimated by using the formulae suggested by Lush (1940)^[9] and expected genetic advance was computed by using formulae suggested by Johnson *et al.*, 1955.

Results and Discussion

The estimates of variability on the basis of genotypic variance, phenotypic variance, genotypic coefficient of variation and phenotypic coefficient of variation, heritability and genetic advance as per cent of mean are presented in Table (1).

Variability is the most important characteristic feature of any population. Estimation of genetic variability is an important pre-requisite for realizing response to selection as the progress in breeding depends upon its amount, nature and magnitude of genetic variability. The breeder should have the capability of distinguishing the genetic and non-genetic components of variation occurring in a population. In the present investigation, a similar analysis of variability was carried out. An insight into the magnitude of variability present in a crop species and heritability of characters is essential as it provides the basis of effective selection (Anandhi and Oommen, 2007)^[1]. 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 23 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 23 genotypes for all the traits studied. The results support the selection programme for high fruit yield.

Phenotypic and genotypic coefficients of variation

High phenotypic and genotypic coefficients of variation were recorded for number of primary branches (28.16 and 28.22), node at which first male flower appearance (34.19 and 34.26), stem thickness (20.20 and 20.98), length of the fruit (27.50 and 27.67), weight of the fruit (29.54 and 29.69), number of fruits per plant (29.79 and 29.92), yield per plant (34.54 and 34.63), vine length (22.94 and 24.07) and Ascorbic acid (26.15 and 26.34). This is in accordance with the findings of Ahirwar and Singh, 2018 for fruit length and yield in cucumber. Ibrahim *et al.* 2012 observed high PCV and GCV for fruit weight, yield per plant and fruit length. This is in accordance with the findings of Rahman *et al.* (2002)^[12] in snake gourd, Rakhi and Rajamony in 2005, Taha *et al.* (2007)^[13], Naroui Rad *et al.* (2010)^[11], Yadav *et al.* (2009)^[20] in cucumber. Similar high GCV and PCV were observed for leaf area, number of fruits per vine, average fruit weight, fruit length, fruit breadth, yield per vine, fruit cavity size, number of seed per fruit, fruit flesh thickness, TSS, vitamin C and seed to pulp ratio was evaluated by Karadi *et al.* (2017)^[17] in wild melon.

Moderate phenotypic and genotypic coefficients of variation were recorded for node at which first female flower appearance (18.51 and 18.65), internodal length (17.90 and 18.09), peduncle length (12.76 and 13.12), flesh thickness (19.84 and 19.99), number of male flowers per vine (12.53 and 12.85), number of female flowers per vine (15.86 and 16.08), TSS (16.97 and 17.18) and Carbohydrate content (18.41 and 18.63). This moderate GCV is in justification with the findings of Kandasamy, 2017 in cucumber for number of secondary branches, vine length, fruit girth. He also observed moderate PCV for the characters like node number of first female flower, vine length, fruit length, fruit girth and 1000 seed weight. Moderate estimates of GCV and PCV were obtained for the number of the node at which first female flower appeared and fruit weight was observed by Tomar *et al.* (2008)^[16]. Said and Fatiha, 2015 in water melon recorded moderate values of phenotypic correlation were observed between TSS and Fruit weight and Fruit length. In pointed gourd, Khan *et al.* (2009)^[8] observed that moderately high genotypic coefficient of variation was evident in fruit number, yield, fruit weight, Pulp weight per fruit and fruit weight per plant, respectively.

Low phenotypic and genotypic coefficients of variation were recorded for days to first male flower appearance (7.23 and 7.64), days to first female flower appearance (9.69 and 10.20), days to first harvest (3.87 and 4.63). Similar results were reported by Rakhi and Rajamony, 2005 for days to first harvest, days to first male flower appearance, days to first female flower appearance, internodal length, leaf petiole length, number of primary branches and pollen viability. The PCV and GCV estimates were low for traits *viz.*, days to first male flower, days to first female flower and days to first fruit harvest was suggested by Babu and Rao, 2018. Lower PCV and GCV estimates for these traits were also observed by Rad *et al.* (2010)^[11].

The result from this study indicated that phenotypic coefficient of variation was higher than the genotypic coefficient of variation for all the characters in twenty three genotypes under study. Even though PCV was more than GCV but the difference was very narrow suggesting that, there is less influence of environment on alteration of these characters. Hence, these characters can be relied upon and simple selection can be practiced for further improvement.

Heritability and genetic advance as percent mean

High heritability combined with high genetic advance as percent mean were observed for number of primary branches (99.57 and 57.88 per cent), node at which first male flower appearance (99.62 and 70.30 per cent), node at which first female flower appearance (98.52 and 37.86 per cent), internodal length (97.91 and 36.49 per cent), stem thickness (92.68 and 40.06 per cent), peduncle length (94.49 and 25.55 per cent), flesh thickness (98.53 and 40.58 per cent), number of male flowers per vine (95.17 and 25.19 per cent), number of female flowers per vine 97.32 and 32.44 per cent), length of the fruit (98.82 and 56.33 per cent), weight of the fruit (98.96 and 60.54 per cent), number of fruits per plant (99.12 and 61.10 per cent), yield per plant (99.94 and 70.95 per cent), vine length (90.88 and 45.06 per cent), TSS (97.47 and 34.51 per cent), Ascorbic acid (98.62 and 53.51 per cent) and Carbohydrate content (97.67 and 37.49 per cent).

High level of heritability with moderate genetic advance as percentage mean was recorded by days to first male flower appearance (89.53 and 14.09 per cent) and days to first female flower appearance (90.11 and 18.94 per cent). Similar result

of high heritability with high genetic advance and high heritability with moderate genetic advance for the above characters was also reported by Tomar *et al.* (2008) [16]. High level of heritability with low genetic advance as percentage mean was recorded by days to first harvest (69.89 and 6.67 per cent). This result was also discussed by Kandasamy, 2017 in cucumber.

In this study, all the characters exhibited 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, number of fruits per plant and yield per plant and there is possibility for improvement of these traits by selection.

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Table 1: Mean, GCV, PCV, Heritability and Genetic advance as per cent of mean for 21 characters in snap melon

Characters	Mean	GCV (%)	PCV (%)	ECV (%)	Heritability	Genetic advance as per cent of mean
Number of primary branches	4.58	28.16	28.22	1.84	99.57	57.88
Node at which 1 st male flower appearance	1.49	34.19	34.26	2.11	99.62	70.30
Node at which 1 st female flower appearance	3.61	18.51	18.65	2.27	98.52	37.86
Days to 1 st male flower appearance	22.62	7.23	7.64	2.47	89.53	14.09
Days to 1 st female flower appearance	32.47	9.69	10.20	3.20	90.11	18.94
Internodal length (cm)	8.45	17.90	18.09	2.61	97.91	36.49
Stem thickness (cm)	2.93	20.20	20.98	5.67	92.68	40.06
Peduncle length (cm)	3.71	12.76	13.12	3.08	94.49	25.55
Flesh thickness (cm)	1.37	19.84	19.99	2.42	98.53	40.58
Number of male flowers per vine	119.20	12.53	12.85	2.82	95.17	25.19
Number of female flowers per vine	18.38	15.86	16.08	2.63	97.32	32.24
Length of the fruit (cm)	26.18	27.50	27.67	3.00	98.82	56.33
Girth of the fruit (cm)	12.75	10.30	10.59	2.43	94.72	20.66
Weight of the fruit (kg)	1.11	29.54	29.69	3.02	98.96	60.54
Days to 1 st harvest	60.60	3.87	4.63	2.54	69.89	6.67
Number of fruits per plant	9.37	29.79	29.92	2.80	99.12	61.10
Yield per plant (Kg)	7.47	34.54	34.63	2.58	99.44	70.95
Vine length (m)	1.52	22.94	24.07	7.26	90.88	45.06
TSS (°Brix)	5.23	16.97	17.18	2.73	97.47	34.51
Ascorbic acid (mg/100g)	6.60	26.15	26.34	3.09	98.62	53.51
Carbohydrates (mg/100g)	15.10	18.41	18.63	2.84	97.67	37.49

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